

48% of the HLA-B*5701-positive patients develop a severe and potentially life-threatening hypersensitivity reaction to abacavir.

Abacavir is contra-indicated for HLA-B*5701-positive patients.

- avoid abacavir

Literature:

1. Sousa-Pinto B et al. Pharmacogenetics of abacavir hypersensitivity: a systematic review and meta-analysis of the association with HLA-B*57:01. *J Allergy Clin Immunol* 2015;136:1092-4.e3.
2. Tangamornsuksan W et al. Association of HLA-B*5701 genotypes and abacavir-induced hypersensitivity reaction: a systematic review and meta-analysis. *J Pharm Pharm Sci* 2015;18:68-76.
3. Cargnin S et al. Diagnostic accuracy of HLA-B*57:01 screening for the prediction of abacavir hypersensitivity and clinical utility of the test: a meta-analytic review. *Pharmacogenomics* 2014;15:963-76.
4. Saag M et al. High sensitivity of human leukocyte antigen-b*5701 as a marker for immunologically confirmed abacavir hypersensitivity in white and black patients. *Clin Infect Dis* 2008;46:1111-8.
5. Mallal S et al. HLA-B*5701 screening for hypersensitivity to abacavir. *N Engl J Med* 2008;358:568-79.
6. Waters LJ et al. Prospective HLA-B*5701 screening and abacavir hypersensitivity: a single centre experience. *AIDS* 2007;21:2533-4.
7. Rodríguez-Nóvoa S et al. Value of the HLA-B*5701 allele to predict abacavir hypersensitivity in Spaniards. *AIDS Res Hum Retroviruses* 2007;23:1374-6.
8. Zucman D et al. Prospective screening for human leukocyte antigen-B*5701 avoids abacavir hypersensitivity reaction in the ethnically mixed French HIV population. *J Acquir Immune Defic Syndr* 2007;45:1-3.
9. Rauch A et al. Prospective genetic screening decreases the incidence of abacavir hypersensitivity reactions in the Western Australian HIV cohort study. *Clin Infect Dis* 2006;43:99-102.
10. Stekler J et al. Abacavir hypersensitivity reaction in primary HIV infection. *AIDS* 2006;20:1269-74.
11. Phillips EJ et al. Clinical and immunogenetic correlates of abacavir hypersensitivity. *AIDS* 2005;19:979-81.
12. Hughes DA et al. Cost-effectiveness analysis of HLA B*5701 genotyping in preventing abacavir hypersensitivity. *Pharmacogenetics* 2004;14:335-42.
13. Martin AM et al. Predisposition to abacavir hypersensitivity conferred by HLA-B*5701 and a haplotypic Hsp70-Hom variant. *Proc Natl Acad Sci U S A* 2004;101:4180-5.
14. Hughes AR et al. Association of genetic variations in HLA-B region with hypersensitivity to abacavir in some, but not all, populations. *Pharmacogenomics* 2004;5:203-11.
15. Hetherington S et al. Genetic variations in HLA-B region and hypersensitivity reactions to abacavir. *Lancet* 2002;359:1121-2.
16. Mallal S et al. Association between presence of HLA-B*5701, HLA-DR7, and HLA-DQ3 and hypersensitivity to HIV-1 reverse-transcriptase inhibitor abacavir. *Lancet* 2002;359:727-32.
17. SmPC Ziagen (NL en VS).

Date 13-05-2019

CYP2C9 IM ANDERS: acenocoumarol

2521

NO action is needed for this gene-drug interaction.

Genetic variation may lead to a decrease in the required maintenance dose. However, there is insufficient evidence that this causes problems when therapy is initiated as usual (i.e. with frequent INR monitoring).

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CYP2C9 PM ANDERS: acenocoumarol

[2522](#)

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 31. Verstuyft C et al. Early acenocoumarol overanticoagulation among cytochrome P450 2C9 poor metabolizers. *Pharmacogenetics* 2001;11:735-7.
 32. Thijssen HH et al. Altered pharmacokinetics of R- and S-acenocoumarol in a subject heterozygous for CYP2C9*3. *Clin Pharmacol Ther* 2001;70:292-8.
 33. Rettie AE et al. A case study of acenocoumarol sensitivity and genotype-phenotype discordancy explained by combinations of polymorphisms in VKORC1 and CYP2C9. *Br J Clin Pharmacol* 2006;62:617-20.
 34. Thijssen HH et al. The possession of the CYP2C9*3 allele is associated with low dose requirement of acenocoumarol. *Pharmacogenetics* 2000;10:757-60.

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CYP2C9*1/*3: acenocoumarol

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CYP2C9*2/*2: acenocoumarol

[2518](#)

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Literature:

1. Varnai R et al. CYP2C9 and VKORC1 in therapeutic dosing and safety of acenocoumarol treatment: implication for clinical practice in Hungary. *Environ Toxicol Pharmacol* 2017;56:282-289.
2. Kalpana SR et al. Influence of VKORC1 and CYP2C9 polymorphisms on daily acenocoumarol dose requirement in South Indian patients with mechanical heart valves. *Clin Appl Thromb Hemost* 2017;23:876-882.
3. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
4. Cerezo-Manchado JJ et al. Genotype-guided therapy improves initial acenocoumarol dosing. Results from a prospective randomised study. *Thromb Haemost* 2016;115:117-25.
5. Jiménez-Varo E et al. Pharmacogenetics role in the safety of acenocoumarol therapy. *Thromb Haemost* 2014;112:522-36.
6. Cerezo-Manchado JJ et al. Effect of VKORC1, CYP2C9 and CYP4F2 genetic variants in early outcomes during acenocoumarol treatment. *Pharmacogenomics* 2014;15:987- 96.
7. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
8. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
9. Gschwind L et al. Impact of CYP2C9 polymorphisms on the vulnerability to pharmacokinetic drug-drug interactions during acenocoumarol treatment. *Pharmacogenomics* 2013;14:745-53.
10. Verhoef TI et al. Long-term anticoagulant effects of the CYP2C9 and VKORC1 genotypes in acenocoumarol users. *J Thromb Haemost* 2012;10:606-14.
11. Esmerian MO et al. Influence of CYP2C9 and VKORC1 polymorphisms on warfarin and acenocoumarol in a sample of Lebanese people. *J Clin Pharmacol* 2011;51:1418-28.
12. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
13. Wijnen PA et al. Variant VKORC1 and CYP2C9 alleles in patients with diffuse alveolar hemorrhage caused by oral anticoagulants. *Mol Diagn Ther* 2010;14:23-30.
14. Teichert M et al. Genotypes associated with reduced activity of VKORC1 and CYP2C9 and their modification of acenocoumarol anticoagulation during the initial treatment period. *Clin Pharmacol Ther* 2009;85:379-86.
15. Montes R et al. The influence of polymorphisms of VKORC1 and CYP2C9 on major gastrointestinal bleeding risk in anticoagulated patients. *Br J Haematol* 2008;143:727- 33.
16. Markatos CN et al. VKORC1 and CYP2C9 allelic variants influence acenocoumarol dose requirements in Greek patients. *Pharmacogenomics* 2008;9:1631-8.
17. Spreafico M et al. Effects of CYP2C9 and VKORC1 on INR variations and dose requirements during initial phase of anticoagulant therapy. *Pharmacogenomics* 2008;9:1237-50.
18. González-Conejero R et al. The genetic interaction between VKORC1 c1173t and calumenin a29809g modulates the anticoagulant response of acenocoumarol. *J Thromb Haemost* 2007;5:1701-6.
19. Beinema MJ et al. The influence of NSAIDs on coumarin sensitivity in patients with CYP2C9 polymorphism after total hip replacement surgery. *Mol Diagn Ther* 2007;11:123-8.
20. Mark L et al. Cytochrome P450 2C9 polymorphism and acenocoumarol therapy. *Kardiol Pol* 2006;64:397-402.
21. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and acenocoumarol anticoagulation status: interaction between both genotypes affects overanticoagulation. *Clin Pharmacol Ther* 2006;80:13-22.
22. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
23. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
24. Morin S et al. Pharmacogenetics of acenocoumarol pharmacodynamics. *Clin Pharmacol Ther* 2004;75:403-14.
25. Schalekamp T et al. Acenocoumarol stabilization is delayed in CYP2C9*3 carriers. *Clin Pharmacol Ther*

2004;75:394-402.

26. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
27. Thijssen HH et al. Acenocoumarol pharmacokinetics in relation to cytochrome P450 2C9 genotype. *Clin Pharmacol Ther* 2003;74:61-8.
28. Verstuyft C et al. Genetic and environmental risk factors for oral anticoagulant overdose. *Eur J Clin Pharmacol* 2003;58:739-45.
29. Tassies D et al. Pharmacogenetics of acenocoumarol: cytochrome P450 CYP2C9 polymorphisms influence dose requirements and stability of anticoagulation. *Haematologica* 2002;87:1185-91.
30. Hermida J et al. Differential effects of 2C9*3 and 2C9*2 variants of cytochrome P-450 CYP2C9 on sensitivity to acenocoumarol. *Blood* 2002;99:4237-9.

Date 14-05-2018

CYP2C9*2/*3: acenocoumarol

[2519](#)

NO action is needed for this gene-drug interaction.

Genetic variation may lead to a decrease in the required maintenance dose. However, there is insufficient evidence that this causes problems when therapy is initiated as usual (i.e. with frequent INR monitoring).

Literature:

1. Varnai R et al. CYP2C9 and VKORC1 in therapeutic dosing and safety of acenocoumarol treatment: implication for clinical practice in Hungary. *Environ Toxicol Pharmacol* 2017;56:282-289.
2. Kalpana SR et al. Influence of VKORC1 and CYP2C9 polymorphisms on daily acenocoumarol dose requirement in South Indian patients with mechanical heart valves. *Clin Appl Thromb Hemost* 2017;23:876-882.
3. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
4. Cerezo-Manchado JJ et al. Genotype-guided therapy improves initial acenocoumarol dosing. Results from a prospective randomised study. *Thromb Haemost* 2016;115:117-25.
5. Krishna Kumar D et al. An acenocoumarol dosing algorithm exploiting clinical and genetic factors in South Indian (Dravidian) population. *Eur J Clin Pharmacol* 2015;71:173-81.
6. Jiménez-Varo E et al. Pharmacogenetics role in the safety of acenocoumarol therapy. *Thromb Haemost* 2014;112:522-36.
7. Cerezo-Manchado JJ et al. Effect of VKORC1, CYP2C9 and CYP4F2 genetic variants in early outcomes during acenocoumarol treatment. *Pharmacogenomics* 2014;15:987-96.
8. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
9. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
10. Gschwind L et al. Impact of CYP2C9 polymorphisms on the vulnerability to pharmacokinetic drug-drug interactions during acenocoumarol treatment. *Pharmacogenomics* 2013;14:745-53.
11. Verhoef TI et al. Long-term anticoagulant effects of the CYP2C9 and VKORC1 genotypes in acenocoumarol users. *J Thromb Haemost* 2012;10:606-14.
12. Esmerian MO et al. Influence of CYP2C9 and VKORC1 polymorphisms on warfarin and acenocoumarol in a sample of Lebanese people. *J Clin Pharmacol* 2011;51:1418-28.
13. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
14. Wijnen PA et al. Variant VKORC1 and CYP2C9 alleles in patients with diffuse alveolar hemorrhage caused by oral anticoagulants. *Mol Diagn Ther* 2010;14:23-30.
15. Teichert M et al. Genotypes associated with reduced activity of VKORC1 and CYP2C9 and their modification of acenocoumarol anticoagulation during the initial treatment period. *Clin Pharmacol Ther* 2009;85:379-86.
16. Montes R et al. The influence of polymorphisms of VKORC1 and CYP2C9 on major gastrointestinal bleeding risk in anticoagulated patients. *Br J Haematol* 2008;143:727-33.
17. Markatos CN et al. VKORC1 and CYP2C9 allelic variants influence acenocoumarol dose requirements in Greek patients. *Pharmacogenomics* 2008;9:1631-8.
18. Spreafico M et al. Effects of CYP2C9 and VKORC1 on INR variations and dose requirements during initial phase of anticoagulant therapy. *Pharmacogenomics* 2008;9:1237-50.
19. González-Conejero R et al. The genetic interaction between VKORC1 c1173t and calumenin a29809g modulates the anticoagulant response of acenocoumarol. *J Thromb Haemost* 2007;5:1701-6.
20. Beinema MJ et al. The influence of NSAIDs on coumarin sensitivity in patients with CYP2C9 polymorphism after total hip replacement surgery. *Mol Diagn Ther* 2007;11:123-8.
21. Mark L et al. Cytochrome P450 2C9 polymorphism and acenocoumarol therapy. *Kardiol Pol* 2006;64:397-402.
22. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and acenocoumarol anticoagulation status: interaction between both genotypes affects overanticoagulation. *Clin Pharmacol Ther* 2006;80:13-22.
23. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.

24. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
25. Morin S et al. Pharmacogenetics of acenocoumarol pharmacodynamics. *Clin Pharmacol Ther* 2004;75:403-14.
26. Schalekamp T et al. Acenocoumarol stabilization is delayed in CYP2C9*3 carriers. *Clin Pharmacol Ther* 2004;75:394-402.
27. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
28. Thijssen HH et al. Acenocoumarol pharmacokinetics in relation to cytochrome P450 2C9 genotype. *Clin Pharmacol Ther* 2003;74:61-8.
29. Verstuyft C et al. Genetic and environmental risk factors for oral anticoagulant overdose. *Eur J Clin Pharmacol* 2003;58:739-45.
30. Tassies D et al. Pharmacogenetics of acenocoumarol: cytochrome P450 CYP2C9 polymorphisms influence dose requirements and stability of anticoagulation. *Haematologica* 2002;87:1185-91.
31. Thijssen HH et al. The possession of the CYP2C9*3 allele is associated with low dose requirement of acenocoumarol. *Pharmacogenetics* 2000;10:757-60.

Date 14-05-2018

CYP2C9*3/*3: acenocoumarol

[2520](#)

NO action is needed for this gene-drug interaction.

Genetic variation may lead to a decrease in the required maintenance dose and possibly an increase in the time needed to reach a stable INR. However, there is insufficient evidence that this causes problems when therapy is initiated as usual (i.e. with frequent INR monitoring).

Literature:

1. Varnai R et al. CYP2C9 and VKORC1 in therapeutic dosing and safety of acenocoumarol treatment: implication for clinical practice in Hungary. *Environ Toxicol Pharmacol* 2017;56:282-289.
2. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
3. Cerezo-Manchado JJ et al. Genotype-guided therapy improves initial acenocoumarol dosing. Results from a prospective randomised study. *Thromb Haemost* 2016;115:117-25.
4. Jiménez-Varo E et al. Pharmacogenetics role in the safety of acenocoumarol therapy. *Thromb Haemost* 2014;112:522-36.
5. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
6. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
7. Gschwind L et al. Impact of CYP2C9 polymorphisms on the vulnerability to pharmacokinetic drug-drug interactions during acenocoumarol treatment. *Pharmacogenomics* 2013;14:745-53.
8. Verhoef TI et al. Long-term anticoagulant effects of the CYP2C9 and VKORC1 genotypes in acenocoumarol users. *J Thromb Haemost* 2012;10:606-14.
9. Esmerian MO et al. Influence of CYP2C9 and VKORC1 polymorphisms on warfarin and acenocoumarol in a sample of Lebanese people. *J Clin Pharmacol* 2011;51:1418-28.
10. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
11. Wijnen PA et al. Variant VKORC1 and CYP2C9 alleles in patients with diffuse alveolar hemorrhage caused by oral anticoagulants. *Mol Diagn Ther* 2010;14:23-30.
12. Teichert M et al. Genotypes associated with reduced activity of VKORC1 and CYP2C9 and their modification of acenocoumarol anticoagulation during the initial treatment period. *Clin Pharmacol Ther* 2009;85:379-86.
13. Montes R et al. The influence of polymorphisms of VKORC1 and CYP2C9 on major gastrointestinal bleeding risk in anticoagulated patients. *Br J Haematol* 2008;143:727-33.
14. Spreafico M et al. Effects of CYP2C9 and VKORC1 on INR variations and dose requirements during initial phase of anticoagulant therapy. *Pharmacogenomics* 2008;9:1237-50.
15. González-Conejero R et al. The genetic interaction between VKORC1 c1173t and calumenin a29809g modulates the anticoagulant response of acenocoumarol. *J Thromb Haemost* 2007;5:1701-6.
16. Beinema MJ et al. The influence of NSAIDs on coumarin sensitivity in patients with CYP2C9 polymorphism after total hip replacement surgery. *Mol Diagn Ther* 2007;11:123-8.
17. Mark L et al. Cytochrome P450 2C9 polymorphism and acenocoumarol therapy. *Kardiol Pol* 2006;64:397-402.
18. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and acenocoumarol anticoagulation status: interaction between both genotypes affects overanticoagulation. *Clin Pharmacol Ther* 2006;80:13-22.
19. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
20. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
21. Morin S et al. Pharmacogenetics of acenocoumarol pharmacodynamics. *Clin Pharmacol Ther*

- 2004;75:403-14.
22. Schalekamp T et al. Acenocoumarol stabilization is delayed in CYP2C9*3 carriers. Clin Pharmacol Ther 2004;75:394-402.
23. Verstuyft C et al. Genetic and environmental risk factors for oral anticoagulant overdose. Eur J Clin Pharmacol 2003;58:739-45.
24. Hermida J et al. Differential effects of 2C9*3 and 2C9*2 variants of cytochrome P-450 CYP2C9 on sensitivity to acenocoumarol. Blood 2002;99:4237-9.
25. Verstuyft C et al. Early acenocoumarol overanticoagulation among cytochrome P450 2C9 poor metabolizers. Pharmacogenetics 2001;11:735-7.

Date 14-05-2018

VKORC1 -1639 AA: acenocoumarol

[2563](#)

An INR ≥ 6 , resulting in an increased risk of bleeding, occurs in 8-12% of these patients during the first weeks of treatment with standard regulation by the Anticoagulation Clinic. The genetic variation increases the sensitivity to acenocoumarol.

- Monitoring by the ANTICOAGULATION CLINIC (National INR Monitoring Service):
 - recommend to use 50% of the standard initial dose
- OTHERWISE:
 - recommend to use 50% of the standard initial dose
 - recommend more frequent monitoring of the INR

The initial dose and the maintenance dose can be calculated using an algorithm.

However, for patients with two or more VKORC1 and/or CYP2C9 variations, the algorithm used in EU-PACT (see <https://www.knmp.nl/patientenzorg/medicatiebewaking/farmacogenetica> for a calculation tool in the form of an Excel file) did not result in a significant reduction in the incidence of INRs above the target range when compared to an algorithm without genetic information. We are therefore unable to recommend the use of this algorithm at this time.

A (non-validated) algorithm has been prescribed for children that should result in a better prediction of the maintenance dose for AA than the current guideline used by the Anticoagulation Clinic (Maagdenberg H et al. The pediatric acenocoumarol dosing algorithm: The Children Anticoagulation and Pharmacogenetics Study. J Thromb Haemost 2018 Jun 23 [Epub ahead of print]. PubMed PMID: 29935043).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. J Thromb Haemost 2017;15:454-464.
2. Cerezo-Manchado JJ et al. Effect of VKORC1, CYP2C9 and CYP4F2 genetic variants in early outcomes during acenocoumarol treatment. Pharmacogenomics 2014;15:987-96.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. NEJM 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. J Thromb Haemost 2017;15:465-472.
5. Verhoef TI et al. Long-term anticoagulant effects of the CYP2C9 and VKORC1 genotypes in acenocoumarol users. J Thromb Haemost 2012;10:606-14.
6. Esmerian MO et al. Influence of CYP2C9 and VKORC1 polymorphisms on warfarin and acenocoumarol in a sample of Lebanese people. J Clin Pharmacol 2011;51:1418-28.
7. Kovac MK et al. The c.-1639G>A polymorphism of the VKORC1 gene in Serbian population: retrospective study of the variability in response to oral anticoagulant therapy. Blood Coagul Fibrinolysis 2010;21:558-63.
8. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. Eur J Clin Pharmacol 2010;66:253-60.
9. Wijnen PA et al. Variant VKORC1 and CYP2C9 alleles in patients with diffuse alveolar hemorrhage caused by oral anticoagulants. Mol Diagn Ther 2010;14:23-30.
10. Stepien E et al. A vitamin K epoxide reductase-oxidase complex gene polymorphism (-1639G>A) and interindividual variability in the dose-effect of vitamin K antagonists. J Appl Genet 2009;50:399-403.
11. Teichert M et al. Genotypes associated with reduced activity of VKORC1 and CYP2C9 and their modification of acenocoumarol anticoagulation during the initial treatment period. Clin Pharmacol Ther 2009;85:379-86.
12. Montes R et al. The influence of polymorphisms of VKORC1 and CYP2C9 on major gastrointestinal bleeding risk in anticoagulated patients. Br J Haematol 2008;143:727-33.
13. Markatos CN et al. VKORC1 and CYP2C9 allelic variants influence acenocoumarol dose requirements in Greek patients. Pharmacogenomics 2008;9:1631-8.
14. Spreafico M et al. Effects of CYP2C9 and VKORC1 on INR variations and dose requirements during initial phase of anticoagulant therapy. Pharmacogenomics 2008;9:1237-50.
15. Gonzalez-Conejero R et al. The genetic interaction of VKORC1 c1173t/calumenin a29809g modulates the anticoagulant response of acenocoumarol. J Thromb Haemost 2007;5:1701-6.

16. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and acenocoumarol anticoagulation status: interaction between both genotypes affects overanticoagulation. Clin Pharmacol Ther 2006;80:13-22.
17. Montes R et al. The c.-1639G > A polymorphism of the VKORC1 gene is a major determinant of the response to acenocoumarol in anticoagulated patients. Br J Haematol 2006;133:183-7.
18. Reitsma PH et al. A C1173T dimorphism in the VKORC1 gene determines coumarin sensitivity and bleeding risk. PLoS Med 2005;2:e312.
19. Bodin L et al. Cytochrome P450 2C9 (CYP2C9) and vitamin K epoxide reductase (VKORC1) genotypes as determinants of acenocoumarol sensitivity. Blood 2005;106:135-140.

Date 10-09-2018

VKORC1 -1639 GA: acenocoumarol

[2562](#)

NO action is needed for this gene-drug interaction.

The genetic variation results in a reduction of the required dose, but with the current practice of initiating or reviewing treatment this results in little or no increased risk of bleeding or excessive anticoagulation.

Literature:

1. Cerezo-Manchado JJ et al. Effect of VKORC1, CYP2C9 and CYP4F2 genetic variants in early outcomes during acenocoumarol treatment. Pharmacogenomics 2014; 15: 987-96.
2. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. NEJM 2013;369: 2304-12.
3. Verhoef TI et al. Long-term anticoagulant effects of the CYP2C9 and VKORC1 genotypes in acenocoumarol users. J Thromb Haemost 2012;10:606-14.
4. Esmerian MO et al. Influence of CYP2C9 and VKORC1 polymorphisms on warfarin and acenocoumarol in a sample of Lebanese people. J Clin Pharmacol 2011;51:1418-28.
5. Kovac MK et al. The c.-1639G>A polymorphism of the VKORC1 gene in Serbian population: retrospective study of the variability in response to oral anticoagulant therapy. Blood Coagul Fibrinolysis 2010;21:558-63.
6. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. Eur J Clin Pharmacol 2010;66:253-60.
7. Wijnen PA et al. Variant VKORC1 and CYP2C9 alleles in patients with diffuse alveolar hemorrhage caused by oral anticoagulants. Mol Diagn Ther 2010;14:23-30.
8. Stepien E et al. A vitamin K epoxide reductase-oxidase complex gene polymorphism (-1639G>A) and interindividual variability in the dose-effect of vitamin K antagonists. J Appl Genet 2009;50:399-403.
9. Teichert M et al. Genotypes associated with reduced activity of VKORC1 and CYP2C9 and their modification of acenocoumarol anticoagulation during the initial treatment period. Clin Pharmacol Ther 2009;85:379-86.
10. Montes R et al. The influence of polymorphisms of VKORC1 and CYP2C9 on major gastrointestinal bleeding risk in anticoagulated patients. Br J Haematol 2008;143:727- 33.
11. Markatos CN et al. VKORC1 and CYP2C9 allelic variants influence acenocoumarol dose requirements in Greek patients. Pharmacogenomics 2008;9:1631-8.
12. Spreafico M et al. Effects of CYP2C9 and VKORC1 on INR variations and dose requirements during initial phase of anticoagulant therapy. Pharmacogenomics 2008;9:1237-50.
13. Gonzalez-Conejero R et al. The genetic interaction of VKORC1 c1173t/calumenin a29809g modulates the anticoagulant response of acenocoumarol. J Thromb Haemost 2007;5:1701-6.
14. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and acenocoumarol anticoagulation status: interaction between both genotypes affects overanticoagulation. Clin Pharmacol Ther 2006;80:13-22.
15. Montes R et al. The c.-1639G > A polymorphism of the VKORC1 gene is a major determinant of the response to acenocoumarol in anticoagulated patients. Br J Haematol 2006;133:183-7.
16. Reitsma PH et al. A C1173T dimorphism in the VKORC1 gene determines coumarin sensitivity and bleeding risk. PLoS Med 2005;2:e312.
17. Bodin L et al. Cytochrome P450 2C9 (CYP2C9) and vitamin K epoxide reductase (VKORC1) genotypes as determinants of acenocoumarol sensitivity. Blood 2005;106:135-140.

Date 10-09-2018

ABCG2 141KK: allopurinol

[7250](#)

The effectiveness of allopurinol is reduced, meaning that a higher dose is required. The gene variation reduces the excretion of uric acid by kidneys and intestines, meaning that a stronger inhibition of the uric acid production by allopurinol is required to achieve the desired uric acid concentration.

- use 1.4 times the standard dose

This equates to a dose titration schedule of 100, 300, 400, 600 and 700 mg/day instead of the usual schedule of 100, 200, 300, 400 and 500 mg/day.

Literature:

1. Stamp LK et al. Relationships between allopurinol dose, oxypurinol concentration and urate-lowering response -in search of a minimum effective oxypurinol concentration. Clin Transl Sci 2020;13:110-5.
2. Brackman DJ et al. Genome-wide association and functional studies reveal novel pharmacological mechanisms for allopurinol. Clin Pharmacol Ther 2019;106:623-31.
3. Zhang K et al. ABCG2 gene polymorphism rs2231142 is associated with gout comorbidities but not allopurinol response in primary gout patients of a Chinese Han male population. Hereditas 2019;156:26.
4. Wright DFB et al. The impact of diuretic use and ABCG2 genotype on the predictive performance of a published allopurinol dosing tool. Br J Clin Pharmacol 2018;84:937- 43.
5. Wallace MC et al. Association between ABCG2 rs2231142 and poor response to allopurinol: replication and meta-analysis. Rheumatology (Oxford) 2018;57:656-60.
6. Roberts RL et al. ABCG2 loss-of-function polymorphism predicts poor response to allopurinol in patients with gout. Pharmacogenomics J 2017;17:201-3.
7. Wen CC et al. Genome-wide association study identifies ABCG2 (BCRP) as an allopurinol transporter and a determinant of drug response. Clin Pharmacol Ther 2015;97:518-25.

Date 07-06-2021

ABCG2 141QK: allopurinol

[7251](#)

The effectiveness of allopurinol is reduced, meaning that a higher dose is required. The gene variation reduces the excretion of uric acid by kidneys and intestines, meaning that a stronger inhibition of the uric acid production by allopurinol is required to achieve the desired uric acid concentration.

- use 1.25 times the standard dose

This equates to a dose titration schedule of 100, 200, 400 and 500 mg/day instead of the usual schedule of 100, 200, 300 and 400 mg/day.

Literature:

1. Stamp LK et al. Relationships between allopurinol dose, oxypurinol concentration and urate-lowering response -in search of a minimum effective oxypurinol concentration. Clin Transl Sci 2020;13:110-5.
2. Brackman DJ et al. Genome-wide association and functional studies reveal novel pharmacological mechanisms for allopurinol. Clin Pharmacol Ther 2019;106:623-31.
3. Zhang K et al. ABCG2 gene polymorphism rs2231142 is associated with gout comorbidities but not allopurinol response in primary gout patients of a Chinese Han male population. Hereditas 2019;156:26.
4. Torres RJ et al. GLUT9 influences uric acid concentration in patients with Lesch-Nyhan disease. Int J Rheum Dis 2018;21:1270-6.
5. Wright DFB et al. The impact of diuretic use and ABCG2 genotype on the predictive performance of a published allopurinol dosing tool. Br J Clin Pharmacol 2018;84:937- 43.
6. Wallace MC et al. Association between ABCG2 rs2231142 and poor response to allopurinol: replication and meta-analysis. Rheumatology (Oxford) 2018;57:656-60.
7. Roberts RL et al. ABCG2 loss-of-function polymorphism predicts poor response to allopurinol in patients with gout. Pharmacogenomics J 2017;17:201-3.
8. Petru L et al. Genetic background of uric acid metabolism in a patient with severe chronic tophaceous gout. Clin Chim Acta 2016;460:46-9.
9. Wen CC et al. Genome-wide association study identifies ABCG2 (BCRP) as an allopurinol transporter and a determinant of drug response. Clin Pharmacol Ther 2015;97:518-25.

Date 07-06-2021

HLA-B*5801: allopurinol

[5901](#)

A strongly increased risk of developing the life-threatening cutaneous side effects Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) and DRESS is present in patients with this genetic variation. The risk of an allopurinol-induced life-threatening cutaneous side effect (mortality 11%) in these patients is 1.6-2.0% for the entire group and 8-18% for the group with chronic renal insufficiency.

- Choose an alternative, such as febuxostat

Another option is to induce allopurinol tolerance first:

To induce allopurinol tolerance, the allopurinol dose is increased every 3 days until a dose of 100 mg/day has been achieved on Day 28. The consecutive daily doses in the induction protocol are 50 µg, 100 µg, 200 µg, 500 µg, 1 mg, 5 mg, 10 mg, 25 mg, 50 mg and 100 mg.

Literature:

1. Park HW et al. Efficacy of the HLA-B*58:01 screening test in preventing allopurinol-induced severe cutaneous adverse reactions in patients with chronic renal insufficiency-a prospective study. *J Allergy Clin Immunol Pract* 2019;7:1271-6.
2. Yu KH et al. Diagnostic utility of HLA-B*5801 screening in severe allopurinol hypersensitivity syndrome: an updated systematic review and meta-analysis. *Int J Rheum Dis* 2017;20:1057-71.
3. Saksit N et al. Risk factors of allopurinol-induced severe cutaneous adverse reactions in a Thai population. *Pharmacogenet Genomics* 2017;27:255-63.
4. Wu R et al. Impact of HLA-B*58:01 allele and allopurinol-induced cutaneous adverse drug reactions: evidence from 21 pharmacogenetic studies. *Oncotarget* 2016;7:81870-9.
5. Ng CY et al. Impact of the HLA-B(*)58:01 allele and renal impairment on allopurinol-induced cutaneous adverse reactions. *J Invest Dermatol* 2016;136:1373-81.
6. Jung JW et al. An effective strategy to prevent allopurinol-induced hypersensitivity by HLA typing. *Genet Med* 2015;17:807-14.
7. Ko TM et al. Use of HLA-B*58:01 genotyping to prevent allopurinol induced severe cutaneous adverse reactions in Taiwan: national prospective cohort study. *BMJ* 2015;351:h4848.
8. Cheng L et al. HLA-B*58:01 is strongly associated with allopurinol-induced severe cutaneous adverse reactions in Han Chinese patients: a multicentre retrospective case- control clinical study. *Br J Dermatol* 2015;173:555-8.
9. Jung JW et al. HLA-DR9 and DR14 are associated with the allopurinol-induced hypersensitivity in hematologic malignancy. *Tohoku J Exp Med* 2014;233:95-102.
10. Zineh I et al. Allopurinol pharmacogenetics: assessment of potential clinical usefulness. *Pharmacogenomics* 2011;12:1741-9.
11. Somkruea R et al. Association of HLA-B*5801 allele and allopurinol-induced Stevens Johnson syndrome and toxic epidermal necrolysis: a systematic review and meta- analysis. *BMC Med Genet* 2011;12:118.
12. Lonjou C et al. A European study of HLA-B in Stevens-Johnson syndrome and toxic epidermal necrolysis related to five high-risk drugs. *Pharmacogenet Genomics* 2008;18:99-107.
13. SPC Zyloric.

Date 07-06-2021

CYP2D6 IM: amiodaron

[2932](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2D6 PM: amiodaron

[2931](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2D6 UM: amiodaron

[2933](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2C19 IM: amitriptyline

[6944](#)

NO action is required for this gene-drug interaction.

The gene variation has an effect on the exposure to amitriptyline, but not on the exposure to amitriptyline + the active metabolite nortriptyline, which determines the effect and side effects.

Literature:

1. Richards-Belle A et al. Associations of antidepressants and antipsychotics with lipid parameters: Do

- CYP2C19/CYP2D6 genes play a role? A UK population-based study. *J Psychopharmacol* 2023;37:396-407.
2. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022;55:246-54.
 3. Mifsud Buhagiar L et al. The interplay between pharmacogenetics, concomitant drugs and blood levels of amitriptyline and its main metabolites. *Per Med* 2022;19:113-23.
 4. Zhou WC et al. Role of serum amitriptyline concentration and CYP2C19 polymorphism in predicting the response to low-dose amitriptyline in irritable bowel syndrome. *Dig Liver Dis* 2021;53:1422-7.
 5. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. *Front Pharmacol* 2021;12:688950.
 6. Ryu S et al. A study on CYP2C19 and CYP2D6 polymorphic effects on pharmacokinetics and pharmacodynamics of amitriptyline in healthy Koreans. *Clin Transl Sci* 2017;10:93-101.
 7. Atasayar G et al. Association of MDR1, CYP2D6, and CYP2C19 gene polymorphisms with prophylactic migraine treatment response. *J Neurol Sci* 2016;366:149-154.
 8. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.
 9. van der Weide J et al. Metabolic ratios of psychotropics as indication of cytochrome P450 2D6/2C19 genotype. *Ther Drug Monit* 2005;27:478-83.
 10. Steimer W et al. Amitriptyline or not, that is the question: pharmacogenetic testing of CYP2D6 and CYP2C19 identifies patients with low or high risk for side effects in amitriptyline therapy. *Clin Chem* 2005;51:376-85.
 11. Steimer W et al. Allele-specific change of concentration and functional gene dose for the prediction of steady-state serum concentrations of amitriptyline and nortriptyline in CYP2C19 and CYP2D6 extensive and intermediate metabolizers. *Clin Chem* 2004;50:1623-33.
 12. Shimoda K et al. The impact of CYP2C19 and CYP2D6 genotypes on metabolism of amitriptyline in Japanese psychiatric patients. *J Clin Psychopharmacol* 2002;22:371-8.
 13. Jiang ZP et al. The role of CYP2C19 in amitriptyline N-demethylation in Chinese subjects. *Eur J Clin Pharmacol* 2002;58:109-13.

Date 08-02-2024

CYP2C19 PM: amitriptyline

[6945](#)

NO action is required for this gene-drug interaction.

The gene variation has an effect on the exposure to amitriptyline, but not on the exposure to amitriptyline + the active metabolite nortriptyline, which determines the effect and side effects.

Literature:

1. Richards-Belle A et al. Associations of antidepressants and antipsychotics with lipid parameters: Do CYP2C19/CYP2D6 genes play a role? A UK population-based study. *J Psychopharmacol* 2023;37:396-407.
2. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022;55:246-54.
3. Zhou WC et al. Role of serum amitriptyline concentration and CYP2C19 polymorphism in predicting the response to low-dose amitriptyline in irritable bowel syndrome. *Dig Liver Dis* 2021;53:1422-7.
4. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. *Front Pharmacol* 2021;12:688950.
5. Ryu S et al. A study on CYP2C19 and CYP2D6 polymorphic effects on pharmacokinetics and pharmacodynamics of amitriptyline in healthy Koreans. *Clin Transl Sci* 2017;10:93-101.
6. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.
7. van der Weide J et al. Metabolic ratios of psychotropics as indication of cytochrome P450 2D6/2C19 genotype. *Ther Drug Monit* 2005;27:478-83.
8. Steimer W et al. Amitriptyline or not, that is the question: pharmacogenetic testing of CYP2D6 and CYP2C19 identifies patients with low or high risk for side effects in amitriptyline therapy. *Clin Chem* 2005;51:376-85.
9. Steimer W et al. Allele-specific change of concentration and functional gene dose for the prediction of steady-state serum concentrations of amitriptyline and nortriptyline in CYP2C19 and CYP2D6 extensive and intermediate metabolizers. *Clin Chem* 2004;50:1623-33.
10. Shimoda K et al. The impact of CYP2C19 and CYP2D6 genotypes on metabolism of amitriptyline in Japanese psychiatric patients. *J Clin Psychopharmacol* 2002;22:371-8.
11. Jiang ZP et al. The role of CYP2C19 in amitriptyline N-demethylation in Chinese subjects. *Eur J Clin Pharmacol* 2002;58:109-13.
12. SmPC Amitriptyline HCl Auro.

CYP2C19 UM: amitriptyline[6946](#)

NO action is required for this gene-drug interaction.

The gene variation decreases the exposure to amitriptyline and increases the exposure to the active metabolite nortriptyline, but there is no evidence to indicate that this results in an increase in side effects or a decrease in efficacy. A higher dose is required to achieve the therapeutic range of amitriptyline+nortriptyline, but the therapeutic range of nortriptyline is achieved at the lower dose.

Literature:

1. Richards-Belle A et al. Associations of antidepressants and antipsychotics with lipid parameters: Do CYP2C19/CYP2D6 genes play a role? A UK population-based study. *J Psychopharmacol* 2023;37:396-407.
2. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022;55:246-54.
3. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. *Front Pharmacol* 2021;12:688950.
4. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.

Date 08-02-2024

CYP2D6 IM: amitriptyline[2569](#)

The risk of side effects is increased, because the gene variation leads to higher plasma concentrations of the active metabolite nortriptyline and to a lesser extent of amitriptyline.

Recommendation:

- use 75% of the standard dose and monitor the efficacy and side effects or the plasma concentrations of amitriptyline and nortriptyline in order to set the maintenance dose

Literature:

1. Scherf-Clavel M et al. Effect of CYP2D6 pharmacogenetic phenotype and phenoconversion on serum concentrations of antidepressants and antipsychotics: a retrospective cohort study. *Int J Clin Pharm* 2023;45:1107-17.
2. Richards-Belle A et al. Associations of antidepressants and antipsychotics with lipid parameters: Do CYP2C19/CYP2D6 genes play a role? A UK population-based study. *J Psychopharmacol* 2023;37:396-407.
3. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022;55:246-54.
4. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. *Front Pharmacol* 2021;12:688950.
5. Chaudhry M et al. Impact of CYP2D6 genotype on amitriptyline efficacy for the treatment of diabetic peripheral neuropathy: a pilot study. *Pharmacogenomics* 2017;18:433-443.
6. Ryu S et al. A study on CYP2C19 and CYP2D6 polymorphic effects on pharmacokinetics and pharmacodynamics of amitriptyline in healthy Koreans. *Clin Transl Sci* 2017;10:93-101.
7. Atasayar G et al. Association of MDR1, CYP2D6, and CYP2C19 gene polymorphisms with prophylactic migraine treatment response. *J Neurol Sci* 2016;366:149-154.
8. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.
9. Koski A et al. CYP2D6 and CYP2C19 genotypes and amitriptyline metabolite ratios in a series of medicolegal autopsies. *Forensic Sci Int* 2006;158:177-83.
10. Steimer W et al. Amitriptyline or not, that is the question: pharmacogenetic testing of CYP2D6 and CYP2C19 identifies patients with low or high risk for side effects in amitriptyline therapy. *Clin Chem* 2005;51:376-85.
11. Steimer W et al. Allele-specific change of concentration and functional gene dose for the prediction of steady-state serum concentrations of amitriptyline and nortriptyline in CYP2C19 and CYP2D6 extensive and intermediate metabolizers. *Clin Chem* 2004;50:1623-33.
12. Shimoda K et al. The impact of CYP2C19 and CYP2D6 genotypes on metabolism of amitriptyline in Japanese psychiatric patients. *J Clin Psychopharmacol* 2002;22:371-8.
13. Breyer-Pfaff U et al. Enantioselective amitriptyline metabolism in patients phenotyped for two cytochrome P450 isozymes. *Clin Pharmacol Ther* 1992;52:350-8.
14. Mellstrom B et al. Amitriptyline metabolism: association with debrisoquin hydroxylation in nonsmokers.

15. Baumann P et al. Amitriptyline pharmacokinetics and clinical response: II. Metabolic polymorphism assessed by hydroxylation of debrisoquine and mephenytoin. Int Clin Psychopharmacol 1986;1:102-12.

Date 08-02-2024

CYP2D6 PM: amitriptyline

[2570](#)

In theory, risk of side effects is increased, because the genetic variation results in higher plasma concentrations of the active metabolite nortriptyline and to a lesser extent of amitriptyline.

- use 60% of the standard dose and monitor the effect and side effects or the plasma concentrations of amitriptyline and nortriptyline in order to set the maintenance dose

Literature:

1. Scherf-Clavel M et al. Effect of CYP2D6 pharmacogenetic phenotype and phenoconversion on serum concentrations of antidepressants and antipsychotics: a retrospective cohort study. Int J Clin Pharm 2023;45:1107-17.
2. Richards-Belle A et al. Associations of antidepressants and antipsychotics with lipid parameters: Do CYP2C19/CYP2D6 genes play a role? A UK population-based study. J Psychopharmacol 2023;37:396-407.
3. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022;55:246-54.
4. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. Front Pharmacol 2021;12:688950.
5. Atasayar G et al. Association of MDR1, CYP2D6, and CYP2C19 gene polymorphisms with prophylactic migraine treatment response. J Neurol Sci 2016;366:149-154.
6. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
7. Halling J et al. The CYP2D6 polymorphism in relation to the metabolism of amitriptyline and nortriptyline in the Faroese population. Br J Clin Pharmacol 2008;65:134-8.
8. Koski A et al. CYP2D6 and CYP2C19 genotypes and amitriptyline metabolite ratios in a series of medicolegal autopsies. Forensic Sci Int 2006;158:177-83.
9. Steimer W et al. Amitriptyline or not, that is the question: pharmacogenetic testing of CYP2D6 and CYP2C19 identifies patients with low or high risk for side effects in amitriptyline therapy. Clin Chem 2005;51:376-85.
10. Breyer-Pfaff U et al. Enantioselective amitriptyline metabolism in patients phenotyped for two cytochrome P450 isozymes. Clin Pharmacol Ther 1992;52:350-8.
11. Mellstrom B et al. Amitriptyline metabolism: association with debrisoquin hydroxylation in nonsmokers. Clin Pharmacol Ther 1986;39:369-71.
12. Baumann P et al. Amitriptyline pharmacokinetics and clinical response: II. Metabolic polymorphism assessed by hydroxylation of debrisoquine and mephenytoin. Int Clin Psychopharmacol 1986;1:102-12.
13. SmPCs Amitriptyline HCl Auro (NL) and Amitriptyline Hydrochloride Sandoz (USA).

Date 08-02-2024

CYP2D6 UM: amitriptyline

[2571](#)

The risk of ineffectiveness is increased and the risk of cardiotoxic side effects may be increased. The gene variation leads to increased conversion of amitriptyline and the active metabolite nortriptyline to less active and inactive metabolites

- increase the dose to 1.6 times the normal dose, monitor the effect and side effects or the plasma concentrations and be alert to increased plasma concentrations of the cardiotoxic Z-10-hydroxy metabolites.
Plasma concentrations of Z-hydroxy nortriptyline or Z-hydroxy amitriptyline higher than 40 ng/mL are considered toxic.
- if a dose increase is not desirable due to the cardiotoxic hydroxy metabolite: avoid amitriptyline Antidepressants that are not metabolised by CYP2D6, or to a lesser extent, include citalopram and sertraline.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022;55:246-54.
2. Matthaei J et al. Effects of genetic polymorphism in CYP2D6, CYP2C19, and the organic cation transporter OCT1 on amitriptyline pharmacokinetics in healthy volunteers and depressive disorder patients. Front Pharmacol 2021;12:688950.
3. Mifsud Buhagiar L et al. Practical liquid chromatography-tandem mass spectrometry method for the

simultaneous quantification of amitriptyline, nortriptyline and their hydroxy metabolites in human serum. *Biomed Chromatogr* 2019;33:e4679.

4. Chaudhry M et al. Impact of CYP2D6 genotype on amitriptyline efficacy for the treatment of diabetic peripheral neuropathy: a pilot study. *Pharmacogenomics* 2017;18:433-443.
5. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.
6. Steimer W et al. Allele-specific change of concentration and functional gene dose for the prediction of steady-state serum concentrations of amitriptyline and nortriptyline in CYP2C19 and CYP2D6 extensive and intermediate metabolizers. *Clin Chem* 2004;50:1623-33.
7. Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. *Eur J Clin Pharmacol* 2004;60:329-36.
8. Bertilsson L et al. Extremely rapid hydroxylation of debrisoquine: a case report with implication for treatment with nortriptyline and other tricyclic antidepressants. *Ther Drug Monit* 1985;7:478-80.
9. Baumann P et al. Amitriptyline pharmacokinetics and clinical response: II. Metabolic polymorphism assessed by hydroxylation of debrisoquine and mephenytoin. *Int Clin Psychopharmacol* 1986;1:102-12.

Date 08-02-2024

CYP2D6 IM: aripiprazol

[2388](#)

NO action is needed for this gene-drug interaction.

The genetic variation increases the plasma concentration of the sum of aripiprazole and the active metabolite dehydroaripiprazole to a limited degree. There is insufficient evidence that this increases the risk of side effects.

Literature:

1. Jallaq SA et al. CYP2D6 phenotype influences aripiprazole tolerability in pediatric patients with mood disorders. *J Child Adolesc Psychopharmacol* 2021;31:56-62.
2. Koller D et al. The effects of aripiprazole and olanzapine on pupillary light reflex and its relationship with pharmacogenetics in a randomized multiple-dose trial. *Br J Clin Pharmacol* 2020;86:2051-62. en persoonlijke communicatie (supplementaire files)
3. Tveito M et al. Impact of age and CYP2D6 genetics on exposure of aripiprazole and dehydroaripiprazole in patients using long-acting injectable versus oral formulation: relevance of poor and intermediate metabolizer status. *Eur J Clin Pharmacol* 2020;76:41-9.
4. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6(5):418-26. en persoonlijke communicatie (correcte aantal patiënten per fenotype en per genotypegroep in de kinetisasubgroep)
5. Belmonte C et al. Influence of CYP2D6, CYP3A4, CYP3A5 and ABCB1 polymorphisms on pharmacokinetics and safety of aripiprazole in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:596-605.
6. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. *Eur J Clin Pharmacol* 2016;72:175-84.
7. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.
8. Suzuki T et al. Effects of genetic polymorphisms of CYP2D6, CYP3A5, and ABCB1 on the steady-state plasma concentrations of aripiprazole and its active metabolite, dehydroaripiprazole, in Japanese patients with schizophrenia. *Ther Drug Monit* 2014;36:651-5.
9. Suzuki T et al. Effects of the CYP-2D6*10 allele on the steady-state plasma concentrations of aripiprazole and its active metabolite, dehydroaripiprazole, in Japanese patients with schizophrenia. *Ther Drug Monit* 2011;33:21-4.
10. Hendset M et al. Impact of the CYP2D6 genotype on steady-state serum concentrations of aripiprazole and dehydroaripiprazole. *Eur J Clin Pharmacol* 2007;63:1147-51.
11. Kubo M et al. Pharmacokinetics of aripiprazole, a new antipsychotic, following oral dosing in healthy adult Japanese volunteers: influence of CYP2D6 polymorphism. *Drug Metab Pharmacokinet* 2007;22:358-66.
12. Kim E et al. Effects of DRD2 and CYP2D6 genotypes on delta EEG power response to aripiprazole in healthy male volunteers: a preliminary study. *Hum Psychopharmacol* 2006;21:519-28.
13. Kubo M et al. Influence of itraconazole co-administration and CYP2D6 genotype on the pharmacokinetics of the new antipsychotic aripiprazole. *Drug Metab Pharmacokinet* 2005;20:55-64.

Date 13-09-2021

CYP2D6 PM: aripiprazol

[2389](#)

The risk of side effects is increased. The genetic variation leads to an increase in the sum of the plasma

concentrations of aripiprazole and the active metabolite.

- administer no more than 10 mg/day or 300 mg/month (68-75% of the standard maximum dose of aripiprazole).

Literature:

1. Jallaq SA et al. CYP2D6 phenotype influences aripiprazole tolerability in pediatric patients with mood disorders. *J Child Adolesc Psychopharmacol* 2021;31:56-62.
2. Tveito M et al. Impact of age and CYP2D6 genetics on exposure of aripiprazole and dehydroaripiprazole in patients using long-acting injectable versus oral formulation: relevance of poor and intermediate metabolizer status. *Eur J Clin Pharmacol* 2020;76:41-9.
3. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6(5):418-26. en persoonlijke communicatie (correcte aantal patiënten per fenotype en per genotypegroep in de kinetisasubgroep)
4. Belmonte C et al. Influence of CYP2D6, CYP3A4, CYP3A5 and ABCB1 polymorphisms on pharmacokinetics and safety of aripiprazole in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:596-605.
5. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. *Eur J Clin Pharmacol* 2016;72:175-84.
6. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.
7. Hendset M et al. Impact of the CYP2D6 genotype on steady-state serum concentrations of aripiprazole and dehydroaripiprazole. *Eur J Clin Pharmacol* 2007;63:1147-51.
8. Oosterhuis M et al. Safety of aripiprazole: high serum levels in a CYP2D6 mutated patient. *Am J Psychiatry* 2007;164:175.
9. SmPC's Abilify (NL), Abilify Maintena (NL), Abilify (USA) en Aristad (USA).

Date 13-09-2021

CYP2D6 UM: aripiprazol

[2390](#)

NO action is needed for this gene-drug interaction.

The genetic variation decreases the plasma concentration of the sum of aripiprazole and the active metabolite dehydroaripiprazole to a limited degree. There is no evidence that this increases the risk of reduced effectiveness.

Literature:

1. Jallaq SA et al. CYP2D6 phenotype influences aripiprazole tolerability in pediatric patients with mood disorders. *J Child Adolesc Psychopharmacol* 2021;31:56-62.
2. Koller D et al. The effects of aripiprazole and olanzapine on pupillary light reflex and its relationship with pharmacogenetics in a randomized multiple-dose trial. *Br J Clin Pharmacol* 2020;86:2051-62. en persoonlijke communicatie (supplementaire files)
3. Tveito M et al. Impact of age and CYP2D6 genetics on exposure of aripiprazole and dehydroaripiprazole in patients using long-acting injectable versus oral formulation: relevance of poor and intermediate metabolizer status. *Eur J Clin Pharmacol* 2020;76:41-9.
4. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6(5):418-26. en persoonlijke communicatie (correcte aantal patiënten per fenotype en per genotypegroep in de kinetisasubgroep)
5. Belmonte C et al. Influence of CYP2D6, CYP3A4, CYP3A5 and ABCB1 polymorphisms on pharmacokinetics and safety of aripiprazole in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:596-605.
6. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. *Eur J Clin Pharmacol* 2016;72:175-84.
7. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.

Date 13-09-2021

UGT1A1*1/*28: atazanavir

[8201](#)

NO action is needed for this gene-drug interaction.

This gene variation (*1/*28) is more common in Western populations than the so-called wild type (*1/*1). This means that treatment choice is largely tailored to patients with this gene variation. Adjusting treatment choice is therefore not useful.

Literature

1. Du P et al. Association between the UGT1A1/*28 allele and hyperbilirubinemia in HIV-positive patients receiving atazanavir: a meta-analysis. *Biosci Rep* 2019;39:BSR20182105.
2. Leger P et al. Race/ethnicity difference in the pharmacogenetics of bilirubin-related atazanavir discontinuation. *Pharmacogenet Genomics* 2018;28:1-6.
3. Falvella FS et al. Pharmacogenetics-based optimisation of atazanavir treatment: potential role of new genetic predictors. *Drug Metab Pers Ther* 2017;32:115-7.
4. Lin KY et al. Cholelithiasis and nephrolithiasis in HIV-positive patients in the era of combination antiretroviral therapy. *PLoS One* 2015;10:e0137660.
5. Vardhanabhuti S et al. Screening for UGT1A1 genotype in study A5257 would have markedly reduced premature discontinuation of atazanavir for hyperbilirubinemia. *Open Forum Infect Dis* 2015;2:ofv085.
6. Johnson DH et al. Genome-wide association study of atazanavir pharmacokinetics and hyperbilirubinemia in AIDS Clinical Trials Group protocol A5202. *Pharmacogenet Genomics* 2014;24:195-203.
7. Ribaudo HJ et al. Impact of UGT1A1 Gilbert variant on discontinuation of ritonavir-boosted atazanavir in AIDS Clinical Trials Group Study A5202. *J Infect Dis* 2013;207:420-5.
8. Ferraris L et al. Switching to unboosted atazanavir reduces bilirubin and triglycerides without compromising treatment efficacy in UGT1A1*28 polymorphism carriers. *J Antimicrob Chemother* 2012;67:2236-42.
9. Lubomirov R et al. Association of pharmacogenetic markers with premature discontinuation of first-line anti-HIV therapy: an observational cohort study. *J Infect Dis* 2011;203:246-57.
10. Park WB et al. Genetic factors influencing severe atazanavir-associated hyperbilirubinemia in a population with low UDP-glucuronosyltransferase 1A1/*28 allele frequency. *Clin Infect Dis* 2010;51:101-6.

Date 16-5-2023

UGT1A1*28/*28: atazanavir

[8202](#)

The risk of atazanavir discontinuation is increased in patients with this gene variation. In two studies, discontinuation rates of 60% and 63% were observed (compared with discontinuation rates of 5% and 19% for patients without this gene variation). The gene variation potentiates the atazanavir-induced reduction in bilirubin conversion, leading to a higher risk of the benign side effects jaundice and hyperbilirubinemia.

- avoid atazanavir if there is a suitable alternative
- if there is no suitable alternative:
 - tell the patient that jaundice and hyperbilirubinemia are benign, i.e. not indicative of liver damage, and that they are reversible even after long-term use of atazanavir
 - tell the patient what the disadvantages of the possible alternatives are

Literature

1. Du P et al. Association between the UGT1A1/*28 allele and hyperbilirubinemia in HIV-positive patients receiving atazanavir: a meta-analysis. *Biosci Rep* 2019;39:BSR20182105.
2. Leger P et al. Race/ethnicity difference in the pharmacogenetics of bilirubin-related atazanavir discontinuation. *Pharmacogenet Genomics* 2018;28:1-6.
3. Falvella FS et al. Pharmacogenetics-based optimisation of atazanavir treatment: potential role of new genetic predictors. *Drug Metab Pers Ther* 2017;32:115-7.
4. Vardhanabhuti S et al. Screening for UGT1A1 genotype in study A5257 would have markedly reduced premature discontinuation of atazanavir for hyperbilirubinemia. *Open Forum Infect Dis* 2015;2:ofv085.
5. Johnson DH et al. Genome-wide association study of atazanavir pharmacokinetics and hyperbilirubinemia in AIDS Clinical Trials Group protocol A5202. *Pharmacogenet Genomics* 2014;24:195-203.
6. Ribaudo HJ et al. Impact of UGT1A1 Gilbert variant on discontinuation of ritonavir-boosted atazanavir in AIDS Clinical Trials Group Study A5202. *J Infect Dis* 2013;207:420-5.
7. Ferraris L et al. Switching to unboosted atazanavir reduces bilirubin and triglycerides without compromising treatment efficacy in UGT1A1*28 polymorphism carriers. *J Antimicrob Chemother* 2012;67:2236-42.
8. Lubomirov R et al. Association of pharmacogenetic markers with premature discontinuation of first-line anti-HIV therapy: an observational cohort study. *J Infect Dis* 2011;203:246-57.
9. Park WB et al. Genetic factors influencing severe atazanavir-associated hyperbilirubinemia in a population with low UDP-glucuronosyltransferase 1A1/*28 allele frequency. *Clin Infect Dis* 2010;51:101-6.

Date 16-05-2023

UGT1A1 IM OTHER: atazanavir

[8203](#)

NO action is needed for this gene-drug interaction.

This gene variation (IM) is more common in Western populations than the so-called wild type (*1/*1). This means that treatment choice is largely tailored to patients with this gene variation. Adjusting treatment choice is therefore not useful

Literature

1. Park WB et al. Genetic factors influencing severe atazanavir-associated hyperbilirubinemia in a population with low UDP-glucuronosyltransferase 1A1*28 allele frequency. Clin Infect Dis 2010;51:101-6.

Date 16-05-2023

UGT1A1 PM OTHER: atazanavir

[8204](#)

NO action is needed for this gene-drug interaction.

In contrast to for *28/*28, that results in a higher risk of hyperbilirubinemia than PM OTHER, no increase of atazanavir-induced severe hyperbilirubinemia has been observed for PM OTHER.

Literature

1. Park WB et al. Genetic factors influencing severe atazanavir-associated hyperbilirubinemia in a population with low UDP-glucuronosyltransferase 1A1*28 allele frequency. Clin Infect Dis 2010;51:101-6.

Date 16-05-2023

CYP2D6 IM: atenolol

[2847](#)

This is NOT a gene-drug interaction.

Literature:

1. Bijl MJ et al. Genetic variation in the CYP2D6 gene is associated with a lower heart rate and blood pressure in beta-blocker users. Clin Pharmacol Ther 2009;85:45-50.
2. Lewis RV et al. Timolol and atenolol: relationships between oxidation phenotype, pharmacokinetics and pharmacodynamics. Br J Clin Pharmacol 1985;19:329-33.
3. Dayer P et al. Interindividual variation of beta-adrenoceptor blocking drugs, plasma concentration and effect: influence of genetic status on behaviour of atenolol, bopindolol and metoprolol. Eur J Clin Pharmacol 1985;28:149-53.

Date 12-09-2022

CYP2D6 PM: atenolol

[2846](#)

This is NOT a gene-drug interaction.

Literature:

1. Bijl MJ et al. Genetic variation in the CYP2D6 gene is associated with a lower heart rate and blood pressure in beta-blocker users. Clin Pharmacol Ther 2009;85:45-50.
2. Lewis RV et al. Timolol and atenolol: relationships between oxidation phenotype, pharmacokinetics and pharmacodynamics. Br J Clin Pharmacol 1985;19:329-33.
3. Dayer P et al. Interindividual variation of beta-adrenoceptor blocking drugs, plasma concentration and effect: influence of genetic status on behaviour of atenolol, bopindolol and metoprolol. Eur J Clin Pharmacol 1985;28:149-53.
4. Freestone S et al. Comparison of two long-acting preparations of metoprolol with conventional metoprolol and atenolol in healthy men during chronic dosing. Br J Clin Pharmacol 1982;14:713-8.

CYP2D6 UM: atenolol

[2848](#)

This is NOT a gene-drug interaction.

Literature:

1. Lewis RV et al. Timolol and atenolol: relationships between oxidation phenotype, pharmacokinetics and pharmacodynamics. *Br J Clin Pharmacol* 1985;19:329-33.
2. Dayer P et al. Interindividual variation of beta-adrenoceptor blocking drugs, plasma concentration and effect: influence of genetic status on behaviour of atenolol, bopindolol and metoprolol. *Eur J Clin Pharmacol* 1985;28:149-53.

Date 12-09-2022

CYP2D6 IM: atomoxetine

[2430](#)

The dose requirement can be reduced, because the genetic variation results in a higher atomoxetine plasma concentration.

- in the event of side effects occurring and/or a response later than 9 weeks: reduce the dose and check whether the effect is conserved
- The plasma concentration of atomoxetine is a factor of 2-3 times higher for IM than for NM at the same dose

Literature:

1. Jung EH et al. Effects of paroxetine on the pharmacokinetics of atomoxetine and its metabolites in different CYP2D6 genotypes. *Arch Pharm Res* 2020;43:1356-63.
2. Kim SH et al. Physiologically based pharmacokinetic modelling of atomoxetine with regard to CYP2D6 genotypes. *Sci Rep* 2018;8:12405.
3. Brown JT et al. Single dose, CYP2D6 genotype-stratified pharmacokinetic study of atomoxetine in children with ADHD. *Clin Pharmacol Ther* 2016;99:642-50.
4. Byeon JY et al. Effects of the CYP2D6*10 allele on the pharmacokinetics of atomoxetine and its metabolites. *Arch Pharm Res* 2015;38:2083-91.
5. Fijal BA et al. CYP2D6 predicted metabolizer status and safety in adult patients with attention-deficit hyperactivity disorder participating in a large placebo-controlled atomoxetine maintenance of response clinical trial. *J Clin Pharmacol* 2015;55:1167-74.
6. Matsui A et al. Pharmacokinetics, safety, and tolerability of atomoxetine and effect of CYP2D6*10/*10 genotype in healthy Japanese men. *J Clin Pharmacol* 2012;52:388- 403.
7. ter Laak MA et al. Recognition of impaired atomoxetine metabolism because of low CYP2D6 activity. *Pediatr Neurol* 2010;43:159-62.
8. Cui YM et al. Atomoxetine pharmacokinetics in healthy Chinese subjects and effect of the CYP2D6*10 allele. *Br J Clin Pharmacol* 2007;64:445-9.

Date 31-01-2022

CYP2D6 PM: atomoxetine

[2429](#)

The risk of side effects is increased, because the genetic variation results in a higher atomoxetine plasma concentration.

- start with the normal initial dose, bearing in mind that an increase in this dose probably will not be required
 - advise the patient to report side effects (such as decreased appetite, vomiting, abdominal pain, constipation, insomnia, early waking, drowsiness, irritability, pupil dilation and itching)
 - if the medicine is effective, but side effects occur: reduce the dose and check whether the effect is conserved
- The plasma concentration of atomoxetine is a factor of 8-11 times higher for PM than for NM at the same dose.

Literature:

1. Brown JT et al. Single dose, CYP2D6 genotype-stratified pharmacokinetic study of atomoxetine in children with ADHD. *Clin Pharmacol Ther* 2016;99:642-50.
2. Fijal BA et al. CYP2D6 predicted metabolizer status and safety in adult patients with attention-deficit hyperactivity disorder participating in a large placebo-controlled atomoxetine maintenance of response clinical trial. *J Clin Pharmacol* 2015;55:1167-74.
3. Loghin C et al. Effects of atomoxetine on the QT interval in healthy CYP2D6 poor metabolizers. *Br J Clin Pharmacol* 2013;75:538-49.

- Matsui A et al. Pharmacokinetics, safety, and tolerability of atomoxetine and effect of CYP2D6*10/*10 genotype in healthy Japanese men. *J Clin Pharmacol* 2012;52:388- 403.
- Ramos N et al. A Haplotype of the Norepinephrine Transporter (Net) Gene Slc6a2 is Associated with Clinical Response to Atomoxetine in Attention-Deficit Hyperactivity Disorder (ADHD). *Neuropsychopharmacology* 2009;34:2135-42.
- Trzepacz PT et al. CYP2D6 metabolizer status and atomoxetine dosing in children and adolescents with ADHD. *Eur Neuropsychopharmacol* 2008;18:79-86.
- Cui YM et al. Atomoxetine pharmacokinetics in healthy Chinese subjects and effect of the CYP2D6*10 Michelson D et al. CYP2D6 and clinical response to atomoxetine in children and adolescents with ADHD. *J Am Acad Child Adolesc Psychiatry* 2007;46:242-51.
- Sauer JM et al. Disposition and metabolic fate of atomoxetine hydrochloride: the role of CYP2D6 in human disposition and metabolism. *Drug Metab Dispos* 2003;31:98- 107.
- SmPC's Strattera (NL en VS).
- Data on file, Lilly Research Laboratories, 2006. Atomoxetine - comparison of data of extensive metaboliser and poor metaboliser patients.

Date 31-01-2022

CYP2D6 UM: atomoxetine

[2431](#)

Efficacy can be reduced due to the gene variation. The gene variation results in an increased conversion of atomoxetine to the active metabolite 4-hydroxyatomoxetine, which has a much lower plasma concentration. As a result, the plasma concentration of the active ingredients decreases.

- be extra alert to reduced efficacy of the treatment
 - advise the patient to report an inadequate effect
 - an alternative can be selected as a precaution
- Clonidine is not metabolised by CYP2D6.

Literature:

- Brown JT et al. Single dose, CYP2D6 genotype-stratified pharmacokinetic study of atomoxetine in children with ADHD. *Clin Pharmacol Ther* 2016;99:642-50.

Date 31-01-2022

SLCO1B1 521CC: atorvastatine

[3983](#)

The risk of myopathy may be increased. The gene variation may lead to reduced atorvastatin transport to the liver, which may increase the atorvastatin plasma concentration.

Patient has ADDITIONAL SIGNIFICANT RISK FACTORS for statin-induced myopathy:

- Choose an alternative
 - Rosuvastatin and pravastatin are influenced to a lesser extent by the SLCO1B1 gene variation, but are not influenced by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem.
 - Fluvastatin is not influenced significantly by the SLCO1B1 gene variation or CYP3A4 inhibitors.
- If an alternative is not an option:
 - keep atorvastatin dosage as low as possible (e.g. by adding ezetimib)
 - advise the patient to report muscle symptoms.

Patient has NO additional significant risk factors for statin-induced myopathy:

- Advise the patient to report muscle symptoms.

Risk factors for statin-induced myopathy are included in the table "Risk group" in the last part of the risk analysis for atorvastatin.

Literature:

- Voora D et al. SLCO1B1*5 allele is associated with atorvastatin discontinuation and adverse muscle symptoms in the context of routine care. *Clin Pharmacol Ther* 2022;111:1075-83.
- Lu B et al. Effect of SLCO1B1 T521C on statin-related myotoxicity with use of lovastatin and atorvastatin. *Clin Pharmacol Ther* 2021;110:733-40.
- Turongkaravee S et al. A systematic review and meta-analysis of genotype-based and individualized data analysis of SLCO1B1 gene and statin-induced myopathy. *Pharmacogenomics J* 2021;21:296-307.
- Xiang Q et al. Correlation between single-nucleotide polymorphisms and statin-induced myopathy: a mixed-effects model meta-analysis. *Eur J Clin Pharmacol* 2021;77:569-81.
- Linskey DW et al. Association of SLCO1B1 c.521T>C (rs4149056) with discontinuation of atorvastatin due to statin-associated muscle symptoms. *Pharmacogenet Genomics* 2020;30:208-11.
- Turner RM et al. A genome-wide association study of circulating levels of atorvastatin and its major

- metabolites. Clin Pharmacol Ther 2020;108:287-97.
7. Liu JE et al. SLCO1B1 521T > C polymorphism associated with rosuvastatin-induced myotoxicity in Chinese coronary artery disease patients: a nested case-control study. Eur J Clin Pharmacol 2017;73:1409-16.
 8. Jiang J et al. Association between SLCO1B1 -521T>C and -388A>G polymorphisms and risk of statin-induced adverse drug reactions: a meta-analysis. Springerplus 2016;5:1368.
 9. Fukunaga K et al. ABCB1 polymorphism is associated with atorvastatin-induced liver injury in Japanese population. BMC Genet 2016;17:79.
 10. Hou Q et al. Association between SLCO1B1 gene T521C polymorphism and statin-related myopathy risk: a meta-analysis of case-control studies. Medicine (Baltimore) 2015;94:e1268.
 11. Giannakopoulou E et al. No impact of SLCO1B1 521 T>C, 388A>G and 411G>A polymorphisms on response to statin therapy in the Greek population. Mol Biol Rep 2014;41:4631-8.
 12. de Keyser CE et al. The SLCO1B1 c.521T>C polymorphism is associated with dose decrease or switching during statin therapy in the Rotterdam Study. Pharmacogenet Genomics 2014;24:43-51.
 13. Fu Q et al. Lack of association between SLCO1B1 polymorphism and the lipid-lowering effects of atorvastatin and simvastatin in Chinese individuals. Eur J Clin Pharmacol 2013;69:1269-74.
 14. Carr DF et al. SLCO1B1 genetic variant associated with statin-induced myopathy: a proof-of-concept study using the Clinical Practice Research Datalink. Clin Pharmacol Ther 2013;94:695-701.
 15. Francesca Notarangelo M et al. Genetic predisposition to atorvastatin-induced myopathy: a case report. J Clin Pharm Ther 2012;37:604-6.
 16. Brunham LR et al. Differential effect of the rs4149056 variant in SLCO1B1 on myopathy associated with simvastatin and atorvastatin. Pharmacogenomics J 2012;12:233-7.
 17. Santos PC et al. SLCO1B1 haplotypes are not associated with atorvastatin-induced myalgia in Brazilian patients with familial hypercholesterolemia. Eur J Clin Pharmacol 2012;68:273-9.
 18. Rodrigues AC et al. Pharmacogenetics of OATP transporters reveals that SLCO1B1 c.388A>G variant is determinant of increased atorvastatin response. Int J Mol Sci 2011;12:5815-27.
 19. Puccetti L et al. Genetic involvement in statins induced myopathy. Preliminary data from an observational case-control study. Atherosclerosis 2010;211:28-9.
 20. Lee YJ et al. Effects of SLCO1B1 and ABCB1 genotypes on the pharmacokinetics of atorvastatin and 2-hydroxyatorvastatin in healthy Korean subjects. Int J Clin Pharmacol Ther 2010;48:36-45.
 21. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. J Am Coll Cardiol 2009;54:1609-16.
 22. Mega JL et al. Identification of genetic variants associated with response to statin therapy. Arterioscler Thromb Vasc Biol 2009;29:1310-5.
 23. He YJ et al. Rifampicin alters atorvastatin plasma concentration on the basis of SLCO1B1 521T>C polymorphism. Clin Chim Acta 2009;405:49-52.
 24. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. Pharmacogenet Genomics 2008;18:921-6.
 25. Pasanen MK et al. Different effects of SLCO1B1 polymorphism on the pharmacokinetics of atorvastatin and rosuvastatin. Clin Pharmacol Ther 2007;82:726-33.
 26. Hermann M et al. Exposure of atorvastatin is unchanged but lactone and acid metabolites are increased several-fold in patients with atorvastatin-induced myopathy. Clin Pharmacol Ther 2006;79:532-9.
 27. Thompson JF et al. An association study of 43 SNPs in 16 candidate genes with atorvastatin response. Pharmacogenomics J 2005;5:352-8.
 28. SmPC Lipitor.

Date 16-05-2023

SLCO1B1 521TC: atorvastatine

[3982](#)

The risk of myopathy can be elevated. The gene variation may lead to reduced atorvastatin transport to the liver, which may increase atorvastatin plasma concentrations.

Patient has ADDITIONAL SIGNIFICANT RISK FACTORS for statin-induced myopathy:

- Choose an alternative

Rosuvastatin and pravastatin are influenced to a similar extent by the SLCO1B1 gene variation, but are not influenced by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem.

Fluvastatin is not influenced significantly by the SLCO1B1 gene variation or CYP3A4 inhibitors.

- If an alternative is not an option:

- keep atorvastatin dosage as low as possible (e.g. by adding ezetimib)
- advise the patient to report muscle symptoms.

Patient has NO additional significant risk factors for statin-induced myopathy:

- Advise the patient to report muscle symptoms.

Risk factors for statin-induced myopathy are included in the table "Risk group" in the last part of the risk analysis for atorvastatin.

Literature:

1. Voora D et al. SLCO1B1*5 allele is associated with atorvastatin discontinuation and adverse muscle symptoms in the context of routine care. Clin Pharmacol Ther 2022;111:1075-83.
2. Lu B et al. Effect of SLCO1B1 T521C on statin-related myotoxicity with use of lovastatin and atorvastatin. Clin Pharmacol Ther 2021;110:733-40.

3. Turongkaravee S et al. A systematic review and meta-analysis of genotype-based and individualized data analysis of SLCO1B1 gene and statin-induced myopathy. *Pharmacogenomics J* 2021;21:296-307.
4. Xiang Q et al. Correlation between single-nucleotide polymorphisms and statin-induced myopathy: a mixed-effects model meta-analysis. *Eur J Clin Pharmacol* 2021;77:569-81.
5. Linskey DW et al. Association of SLCO1B1 c.521T>C (rs4149056) with discontinuation of atorvastatin due to statin-associated muscle symptoms. *Pharmacogenet Genomics* 2020;30:208-11.
6. Turner RM et al. A genome-wide association study of circulating levels of atorvastatin and its major metabolites. *Clin Pharmacol Ther* 2020;108:287-97.
7. Liu JE et al. SLCO1B1 521T > C polymorphism associated with rosuvastatin-induced myotoxicity in Chinese coronary artery disease patients: a nested case-control study. *Eur J Clin Pharmacol* 2017;73:1409-16.
8. Jiang J et al. Association between SLCO1B1 -521T>C and -388A>G polymorphisms and risk of statin-induced adverse drug reactions: a meta-analysis. *Springerplus* 2016;5:1368.
9. Fukunaga K et al. ABCB1 polymorphism is associated with atorvastatin-induced liver injury in Japanese population. *BMC Genet* 2016;17:79.
10. Hou Q et al. Association between SLCO1B1 gene T521C polymorphism and statin-related myopathy risk: a meta-analysis of case-control studies. *Medicine (Baltimore)* 2015;94:e1268.
11. Giannakopoulou E et al. No impact of SLCO1B1 521 T>C, 388A>G and 411G>A polymorphisms on response to statin therapy in the Greek population. *Mol Biol Rep* 2014;41:4631-8.
12. de Keyser CE et al. The SLCO1B1 c.521T>C polymorphism is associated with dose decrease or switching during statin therapy in the Rotterdam Study. *Pharmacogenet Genomics* 2014;24:43-51.
13. Fu Q et al. Lack of association between SLCO1B1 polymorphism and the lipid-lowering effects of atorvastatin and simvastatin in Chinese individuals. *Eur J Clin Pharmacol* 2013;69:1269-74.
14. Carr DF et al. SLCO1B1 genetic variant associated with statin-induced myopathy: a proof-of-concept study using the Clinical Practice Research Datalink. *Clin Pharmacol Ther* 2013;94:695-701.
15. Francesca Notarangelo M et al. Genetic predisposition to atorvastatin-induced myopathy: a case report. *J Clin Pharm Ther* 2012;37:604-6.
16. Brunham LR et al. Differential effect of the rs4149056 variant in SLCO1B1 on myopathy associated with simvastatin and atorvastatin. *Pharmacogenomics J* 2012;12:233-7.
17. Santos PC et al. SLCO1B1 haplotypes are not associated with atorvastatin-induced myalgia in Brazilian patients with familial hypercholesterolemia. *Eur J Clin Pharmacol* 2012;68:273-9.
18. Rodrigues AC et al. Pharmacogenetics of OATP transporters reveals that SLCO1B1 c.388A>G variant is determinant of increased atorvastatin response. *Int J Mol Sci* 2011;12:5815-27.
19. Puccetti L et al. Genetic involvement in statins induced myopathy. Preliminary data from an observational case-control study. *Atherosclerosis* 2010;211:28-9.
20. Lee YJ et al. Effects of SLCO1B1 and ABCB1 genotypes on the pharmacokinetics of atorvastatin and 2-hydroxyatorvastatin in healthy Korean subjects. *Int J Clin Pharmacol Ther* 2010;48:36-45.
21. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. *J Am Coll Cardiol* 2009;54:1609-16.
22. Mega JL et al. Identification of genetic variants associated with response to statin therapy. *Arterioscler Thromb Vasc Biol* 2009;29:1310-5.
23. He YJ et al. Rifampicin alters atorvastatin plasma concentration on the basis of SLCO1B1 521T>C polymorphism. *Clin Chim Acta* 2009;405:49-52.
24. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. *Pharmacogenet Genomics* 2008;18:921-6.
25. Pasanen MK et al. Different effects of SLCO1B1 polymorphism on the pharmacokinetics of atorvastatin and rosuvastatin. *Clin Pharmacol Ther* 2007;82:726-33.
26. Hermann M et al. Exposure of atorvastatin is unchanged but lactone and acid metabolites are increased several-fold in patients with atorvastatin-induced myopathy. *Clin Pharmacol Ther* 2006;79:532-9.
27. Thompson JF et al. An association study of 43 SNPs in 16 candidate genes with atorvastatin response. *Pharmacogenomics J* 2005;5:352-8.

Date 16-05-2023

NUDT15 IM: azathioprine/6-mercaptopurine

[6954](#)

Grade ≥ 2 leukopaenia occurs in 42% of these patients with standard immunosuppression therapy. The gene variation increases the concentration of the fully activated metabolite of azathioprine and 6-mercaptopurine.

- IMMUNOSUPPRESSION:

- start with 50% of the standard dose

Adjustment of the initial dose should be performed based on toxicity (monitoring of the blood counts) and efficacy.

Note: The percentage of 50% is based on the analogy with TPMT, for which the gene variants have a comparable effect on toxicity to those of NUDT15. A percentage of <70% was calculated for NUDT15, but there were insufficient data available to calculate the exact percentage.

Note: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

- LEUKAEMIA:

- start at 50% of the standard mercaptopurine dose, or start with the standard dose and reduce to 50% if side effects necessitate a dose reduction

It is not known whether dose reduction in advance results in the same efficacy as dose reduction based on toxicity.

Adjustment of the initial dose should be performed based on toxicity (monitoring of the blood counts) and efficacy.

Note: The percentage of 50% is based on the analogy with TPMT, for which the gene variants have a comparable effect on toxicity to those of NUDT15. A percentage of <70% was calculated for NUDT15, but there were insufficient data available to calculate the exact percentage.

Note: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

Note: more stringent dose reductions are necessary if the patient is also TPMT IM or TPMT PM.

Literature:

1. Zhu Y et al. Combination of common and novel rare NUDT15 variants improves predictive sensitivity of thiopurine-induced leukopenia in children with acute lymphoblastic leukemia. *Haematologica* 2018 Mar 8 [Epub ahead of print].
2. Zhang AL et al. Association of NUDT15 c.415C>T allele and thiopurine-induced leukocytopenia in Asians: a systematic review and meta-analysis. *Ir J Med Sci* 2018;187:145-153.
3. Yi ES et al. NUDT15 variants cause hematopoietic toxicity with low 6-TGN levels in children with acute lymphoblastic leukemia. *Cancer Res Treat* 2017 Sep 13 [Epub ahead of print].
4. Kim H et al. APEX1 polymorphism and mercaptopurine-related early onset neutropenia in pediatric acute lymphoblastic leukemia. *Cancer Res Treat* 2017 Sep 4 [Epub ahead of print].
5. Chao K et al. Combined detection of NUDT15 variants could highly predict thiopurine-induced leukopenia in Chinese patients with inflammatory bowel disease: a multicenter analysis. *Inflamm Bowel Dis* 2017;23:1592-9.
6. Yin D et al. Impact of NUDT15 polymorphisms on thiopurines-induced myelotoxicity and thiopurines tolerance dose. *Oncotarget* 2017;8:13575-85.
7. Liang DC et al. NUDT15 gene polymorphism related to mercaptopurine intolerance in Taiwan Chinese children with acute lymphoblastic leukemia. *Pharmacogenomics J* 2016;16:536-9.
8. Zhu X et al. NUDT15 polymorphisms are better than thiopurine S-methyltransferase as predictor of risk for thiopurine-induced leukopenia in Chinese patients with Crohn's disease. *Aliment Pharmacol Ther* 2016;44:967-75.
9. Moriyama T et al. NUDT15 polymorphisms alter thiopurine metabolism and hematopoietic toxicity. *Nat Genet* 2016;48:367-73.
10. Yang JJ et al. Inherited NUDT15 variant is a genetic determinant of mercaptopurine intolerance in children with acute lymphoblastic leukemia. *J Clin Oncol* 2015;33:1235- 42.
11. Yang SK et al. A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. *Nat Genet* 2014;46:1017-20.
12. SmPC's Puri-Nethol en Imuran.

Date 17-09-2019

NUDT15 PM: azathioprine/6-mercaptopurine

[6955](#)

Grade ≥ 2 leukopaenia occurs in 96% of these patients with standard therapy. The gene variation increases the concentration of the fully activated metabolite of azathioprine and 6-mercaptopurine.

- avoid azathioprine and 6-mercaptopurine

- if it is not possible to avoid azathioprine and mercaptopurine: use 10% of the standard dose and advise patients to seek medical attention when symptoms of myelosuppression (such as severe sore throat in combination with fever, regular nosebleeds and tendency to bruising) occur

Any adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and efficacy.

Note: The percentage of 10% is based on the analogy with TPMT, for which the gene variants have a comparable effect on toxicity to those of NUDT15. A percentage of <20% was calculated for NUDT15 PM, but there were insufficient data available to calculate the exact percentage

Note: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

Literature:

1. Zhu Y et al. Combination of common and novel rare NUDT15 variants improves predictive sensitivity of thiopurine-induced leukopenia in children with acute lymphoblastic leukemia. *Haematologica* 2018 Mar 8 [Epub ahead of print].
2. Zhang AL et al. Association of NUDT15 c.415C>T allele and thiopurine-induced leukocytopenia in Asians: a systematic review and meta-analysis. *Ir J Med Sci* 2018;187:145-153.
3. Yi ES et al. NUDT15 variants cause hematopoietic toxicity with low 6-TGN levels in children with acute lymphoblastic leukemia. *Cancer Res Treat* 2017 Sep 13 [Epub ahead of print].
4. Kim H et al. APEX1 polymorphism and mercaptopurine-related early onset neutropenia in pediatric acute lymphoblastic leukemia. *Cancer Res Treat* 2017 Sep 4 [Epub ahead of print].
5. Chao K et al. Combined detection of NUDT15 variants could highly predict thiopurine-induced

- leukopenia in Chinese patients with inflammatory bowel disease: a multicenter analysis. *Inflamm Bowel Dis* 2017;23:1592-9.
6. Yin D et al. Impact of NUDT15 polymorphisms on thiopurines-induced myelotoxicity and thiopurines tolerance dose. *Oncotarget* 2017;8:13575-85.
 7. Liang DC et al. NUDT15 gene polymorphism related to mercaptopurine intolerance in Taiwan Chinese children with acute lymphoblastic leukemia. *Pharmacogenomics J* 2016;16:536-9.
 8. Zhu X et al. NUDT15 polymorphisms are better than thiopurine S-methyltransferase as predictor of risk for thiopurine-induced leukopenia in Chinese patients with Crohn's disease. *Aliment Pharmacol Ther* 2016;44:967-75.
 9. Moriyama T et al. NUDT15 polymorphisms alter thiopurine metabolism and hematopoietic toxicity. *Nat Genet* 2016;48:367-73.
 10. Yang JJ et al. Inherited NUDT15 variant is a genetic determinant of mercaptopurine intolerance in children with acute lymphoblastic leukemia. *J Clin Oncol* 2015;33:1235- 42.
 11. Yang SK et al. A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. *Nat Genet* 2014;46:1017-20.
 12. SmPC's Puri-Nethol en Imuran.

Date 17-09-2019

TPMT IM: azathioprine/6-mercaptopurine

[2558](#)

Grade ≥ 2 leukopaenia occurs in 23% of these patients with normal therapy for immunosuppression. The gene variation increases the amount of the active metabolites of azathioprine and 6-mercaptopurine.

- IMMUNOSUPPRESSION

- Start with 50% of the normal dose

Adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and effectiveness.

Dose adjustment is not required for doses lower than 1.5 mg/kg per day for azathioprine or 0.75 mg/kg per day for 6-mercaptopurine.

- LEUKAEMIA:

- start with 50% of the normal 6-mercaptopurine dose, or start with the normal dose and reduce to 50% if side effects necessitate a dose reduction. It is not known whether dose reduction in advance results in the same efficacy as dose reduction based on toxicity.

Adjustment of the initial dose should be guided by toxicity (monitoring of the blood counts) and effectiveness.

Note: more stringent dose reductions are necessary if the patient is also NUDT15 IM or NUDT15 PM.

Literature:

1. Sheu HS et al. Thiopurine S-methyltransferase polymorphisms predict hepatotoxicity in azathioprine-treated patients with autoimmune diseases. *J Pers Med* 2022;12:1399.
2. Casajús A et al. Genotype-guided prescription of azathioprine reduces the incidence of adverse drug reactions in TPMT intermediate metabolizers to a similar incidence as normal metabolizers. *Adv Ther* 2022;39:1743-53.
3. Dickson AL et al. TPMT and NUDT15 variants predict discontinuation of azathioprine for myelotoxicity in patients with inflammatory disease: real-world clinical results. *Clin Pharmacol Ther* 2022;111:263-71.
4. Nielsen SN et al. No association between relapse hazard and thiopurine methyltransferase geno- or phenotypes in non-high risk acute lymphoblastic leukemia: a NOPHO ALL2008 sub-study. *Cancer Chemother Pharmacol* 2021;88:271-9.
5. Miao Q et al. Association of genetic variants in TPMT, ITPA, and NUDT15 with azathioprine-induced myelosuppression in Southwest China patients with autoimmune hepatitis. *Sci Rep* 2021;11:7984.
6. Jena A et al. Prevalence of polymorphisms in thiopurine metabolism and association with adverse outcomes: a South Asian region-specific systematic review and meta-analysis. *Expert Rev Clin Pharmacol* 2021;14:491-501.
7. Dreisig K et al. TPMT polymorphisms and minimal residual disease after 6-mercaptopurine post-remission consolidation therapy of childhood acute lymphoblastic leukaemia. *Pediatr Hematol Oncol* 2021;38:227-38.
8. van Gennep S et al. Systematic review with meta-analysis: risk factors for thiopurine-induced leukopenia in IBD. *Aliment Pharmacol Ther* 2019;50:484-506.
9. Fan X et al. NUDT15 polymorphism confer increased susceptibility to thiopurine-induced leukopenia in patients with autoimmune hepatitis and related cirrhosis. *Front Pharmacol* 2019;10:346.
10. Choi R et al. Pathway genes and metabolites in thiopurine therapy in Korean children with acute lymphoblastic leukaemia. *Br J Clin Pharmacol* 2019;85:1585.
11. Eriksen PL et al. Enrichment of genetic variants in the glucocorticoid receptor signalling pathway in autoimmune hepatitis with failure of standard treatment. *Basic Clin Pharmacol Toxicol* 2017;121:189-94.
12. Liu C et al. A genome-wide approach validates that thiopurine methyltransferase activity is a monogenic pharmacogenomic trait. *Clin Pharmacol Ther* 2017;101:373-381.

13. Coenen MJ et al. Identification of patients with variants in TPMT and dose reduction reduces hematologic events during thiopurine treatment of inflammatory bowel disease. *Gastroenterology* 2015;149:907-17.
14. Lennard L et al. Thiopurine methyltransferase and treatment outcome in the UK acute lymphoblastic leukaemia trial ALL2003. *Br J Haematol* 2015;170:550-8.
15. Lennard L et al. Thiopurine dose intensity and treatment outcome in childhood lymphoblastic leukaemia: the influence of thiopurine methyltransferase pharmacogenetics. *Br J Haematol* 2015;169:228-40.
16. Kim MJ et al. Monitoring thiopurine metabolites in Korean pediatric patients with inflammatory bowel disease. *Yonsei Med J* 2014;55:1289-96.
17. Levinsen M et al. Pharmacogenetically based dosing of thiopurines in childhood acute lymphoblastic leukemia: influence on cure rates and risk of second cancer. *Pediatr Blood Cancer* 2014;61:797-802.
18. Booth RA et al. Assessment of thiopurine S-methyltransferase activity in patients prescribed thiopurines: a systematic review. *Ann Intern Med* 2011;154:814-23, W-295-8.
19. Newnham WG et al. A pragmatic randomized controlled trial of thiopurine methyltransferase genotyping prior to azathioprine treatment: the TARGET study. *Pharmacogenomics* 2011;12:815-26.
20. Dong XW et al. Thiopurine S-methyltransferase polymorphisms and thiopurine toxicity in treatment of inflammatory bowel disease. *World J Gastroenterol* 2010;16:3187-95.
21. Hindorf U et al. Characterisation and utility of thiopurine methyltransferase and thiopurine metabolite measurements in autoimmune hepatitis. *J Hepatol* 2010;52:106-11.
22. Sheffield LJ et al. Thiopurine methyltransferase and thiopurine metabolite testing in patients with inflammatory bowel disease who are taking thiopurine drugs. *Pharmacogenomics* 2009;10:1091-9.
23. Ansari A et al. Influence of xanthine oxidase on thiopurine metabolism in Crohn's disease. *Aliment Pharmacol Ther* 2008;28:749-57.
24. Gardiner SJ et al. Thiopurine dose in intermediate and normal metabolizers of thiopurine methyltransferase may differ three-fold. *Clin Gastroenterol Hepatol* 2008;6:654-60.
25. Moloney FJ et al. The frequency and significance of thiopurine S-methyltransferase gene polymorphisms in azathioprine-treated renal transplant recipients. *Br J Dermatol* 2006;154:1199-200.
26. Zelinkova Z et al. Inosine triphosphate pyrophosphatase and thiopurine s-methyltransferase genotypes relationship to azathioprine-induced myelosuppression. *Clin Gastroenterol Hepatol* 2006;4:44-9.
27. Jun JB et al. Thiopurine S-methyltransferase polymorphisms and the relationship between the mutant alleles and the adverse effects in systemic lupus erythematosus patients taking azathioprine. *Clin Exp Rheumatol* 2005;23:873-6.
28. Stocco G et al. TPMT genotype and the use of thiopurines in paediatric inflammatory bowel disease. *Dig Liver Dis* 2005;37:940-5.
29. Kurzawski M et al. The impact of thiopurine s-methyltransferase polymorphism on azathioprine-induced myelotoxicity in renal transplant recipients. *Ther Drug Monit* 2005;27:435-41.
30. Fabre MA et al. The impact of thiopurine S-methyltransferase polymorphisms on azathioprine dose 1 year after renal transplantation. *Transpl Int* 2004;17:531-9.
31. Geary RB et al. Thiopurine S-methyltransferase (TPMT) genotype does not predict adverse drug reactions to thiopurine drugs in patients with inflammatory bowel disease. *Aliment Pharmacol Ther* 2003;18:395-400.
32. Gilissen LP et al. Some cases demonstrating the clinical usefulness of therapeutic drug monitoring in thiopurine-treated inflammatory bowel disease patients. *Eur J Gastroenterol Hepatol* 2004;16:705-10.
33. Ansari A et al. Thiopurine methyltransferase activity and the use of azathioprine in inflammatory bowel disease. *Aliment Pharmacol Ther* 2002;16:1743-50.
34. Langley PG et al. Thiopurine methyltransferase phenotype and genotype in relation to azathioprine therapy in autoimmune hepatitis. *J Hepatol* 2002;37:441-7.
35. Regueiro M et al. Determination of thiopurine methyltransferase genotype or phenotype optimizes initial dosing of azathioprine for the treatment of Crohn's disease. *J Clin Gastroenterol* 2002;35:240-4.
36. Pandya B et al. Azathioprine toxicity and thiopurine methyltransferase genotype in renal transplant patients. *Transplant Proc* 2002;34:1642-5.
37. Campbell S et al. Relevance of thiopurine methyltransferase activity in inflammatory bowel disease patients maintained on low-dose azathioprine. *Aliment Pharmacol Ther* 2002;16:389-98.
38. Colombel JF et al. Genotypic analysis of thiopurine S-methyltransferase in patients with Crohn's disease and severe myelosuppression during azathioprine therapy. *Gastroenterology* 2000;118:1025-30.
39. Black AJ et al. Thiopurine methyltransferase genotype predicts therapy-limiting severe toxicity from azathioprine. *Ann Intern Med* 1998;129:716-8.
40. Higgs JE et al. Are patients with intermediate TPMT activity at increased risk of myelosuppression when taking thiopurine medications? *Pharmacogenomics* 2010;11:177-88.
41. Stanulla M et al. Thiopurine methyltransferase (TPMT) genotype and early treatment response to mercaptopurine in childhood acute lymphoblastic leukemia. *JAMA* 2005;293:1485-9.
42. Evans WE et al. Preponderance of thiopurine S-methyltransferase deficiency and heterozygosity among patients intolerant to mercaptopurine or azathioprine. *J Clin Oncol* 2001;19:2293-301.
43. Relling MV et al. Mercaptopurine therapy intolerance and heterozygosity at the thiopurine S-methyltransferase gene locus. *J Natl Cancer Inst* 1999;91:2001-8.
44. McLeod HL et al. Analysis of thiopurine methyltransferase variant alleles in childhood acute lymphoblastic leukaemia. *Br J Haematol* 1999;105:696-700.
45. SmPCs Imuran (NL and USA) and Purinethol (USA).

Grade ≥ 2 leukopaenia and intolerance occur in 98% of these patients with normal therapy. The gene variation increases the amount of active metabolites of azathioprine and 6-mercaptopurine.

- Choose an alternative or use 10% of the normal dose.
Adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and effectiveness.
- If the dose is decreased: advise the patient to report symptoms of myelosuppression (such as severe sore throat in combination with fever, regular nosebleeds and tendency to bruising).
Note: more stringent dose reductions are necessary if the patient is also NUDT15 IM or NUDT15 PM.

Literature:

1. Sheu HS et al. Thiopurine S-methyltransferase polymorphisms predict hepatotoxicity in azathioprine-treated patients with autoimmune diseases. *J Pers Med* 2022;12:1399.
2. Dickson AL et al. TPMT and NUDT15 variants predict discontinuation of azathioprine for myelotoxicity in patients with inflammatory disease: real-world clinical results. *Clin Pharmacol Ther* 2022;111:263-71.
3. Jena A et al. Prevalence of polymorphisms in thiopurine metabolism and association with adverse outcomes: a South Asian region-specific systematic review and meta-analysis. *Expert Rev Clin Pharmacol* 2021;14:491-501.
4. van Gennep S et al. Systematic review with meta-analysis: risk factors for thiopurine-induced leukopenia in IBD. *Aliment Pharmacol Ther* 2019;50:484-506.
5. Fan X et al. NUDT15 polymorphism confer increased susceptibility to thiopurine-induced leukopenia in patients with autoimmune hepatitis and related cirrhosis. *Front Pharmacol* 2019;10:346.
6. Liu C et al. A genome-wide approach validates that thiopurine methyltransferase activity is a monogenic pharmacogenomic trait. *Clin Pharmacol Ther* 2017;101:373-381.
7. van Moorsel SA et al. Azathioprine therapy in a pediatric TPMT-deficient patient - still an option. *Ther Drug Monit* 2017;39:1-4.
8. Coenen MJ et al. Identification of patients with variants in TPMT and dose reduction reduces hematologic events during thiopurine treatment of inflammatory bowel disease. *Gastroenterology* 2015;149:907-17.
9. Lennard L et al. Thiopurine methyltransferase and treatment outcome in the UK acute lymphoblastic leukaemia trial ALL2003. *Br J Haematol* 2015;170:550-8.
10. Lennard L et al. Thiopurine dose intensity and treatment outcome in childhood lymphoblastic leukaemia: the influence of thiopurine methyltransferase pharmacogenetics. *Br J Haematol* 2015;169:228-40.
11. Belen BF et al. Severe myelotoxicity associated with thiopurine S-methyltransferase*3A/ *3C polymorphisms in a patient with pediatric leukemia and the effect of steroid therapy. *Turk J Haematol* 2014;31:399-402.
12. Kim MJ et al. Monitoring thiopurine metabolites in korean pediatric patients with inflammatory bowel disease. *Yonsei Med J* 2014;55:1289-96.
13. Levinsen M et al. Pharmacogenetically based dosing of thiopurines in childhood acute lymphoblastic leukemia: influence on cure rates and risk of second cancer. *Pediatr Blood Cancer* 2014;61:797-802.
14. Demlova R et al. Augmenting clinical interpretability of thiopurine methyltransferase laboratory evaluation. *Oncology* 2014;86:152-8.
15. Lee MN et al. Successful azathioprine treatment with metabolite monitoring in a pediatric inflammatory bowel disease patient homozygous for TPMT*3C. *Yonsei Med J* 2013;54:1545-9.
16. Kim H et al. Pharmacogenetic analysis of pediatric patients with acute lymphoblastic leukemia: a possible association between survival rate and ITPA polymorphism. *PLoS One* 2012;7:e45558.
17. Booth RA et al. Assessment of thiopurine S-methyltransferase activity in patients prescribed thiopurines: a systematic review. *Ann Intern Med* 2011;154:814-23, W-295-8.
18. Newman WG et al. A pragmatic randomized controlled trial of thiopurine methyltransferase genotyping prior to azathioprine treatment: the TARGET study. *Pharmacogenomics* 2011;12:815-26.
19. Dong XW et al. Thiopurine S-methyltransferase polymorphisms and thiopurine toxicity in treatment of inflammatory bowel disease. *World J Gastroenterol* 2010;16:3187-95.
20. Ansari A et al. Influence of xanthine oxidase on thiopurine metabolism in Crohn's disease. *Aliment Pharmacol Ther* 2008;28:749-57.
21. Zelinkova Z et al. Inosine triphosphate pyrophosphatase and thiopurine s-methyltransferase genotypes relationship to azathioprine-induced myelosuppression. *Clin Gastroenterol Hepatol* 2006;4:44-9.
22. Kurzawski M et al. The impact of thiopurine s-methyltransferase polymorphism on azathioprine-induced myelotoxicity in renal transplant recipients. *Ther Drug Monit* 2005;27:435-41.
23. Gardiner SJ et al. Two cases of thiopurine methyltransferase (TPMT) deficiency--a lucky save and a near miss with azathioprine. *Br J Clin Pharmacol* 2006;62:473-6.

24. Kurzwski et al. Severe azathioprine-induced myelotoxicity in a kidney transplant patient with thiopurine S-methyltransferase-deficient genotype (TPMT*3A/*3C). *Transpl Int* 2005;18:623-5.
25. Gearry RB et al. Thiopurine S-methyltransferase (TPMT) genotype does not predict adverse drug reactions to thiopurine drugs in patients with inflammatory bowel disease. *Aliment Pharmacol Ther* 2003;18:395-400.
26. Gilissen LP et al. Some cases demonstrating the clinical usefulness of therapeutic drug monitoring in thiopurine-treated inflammatory bowel disease patients. *Eur J Gastroenterol Hepatol* 2004;16:705-10.
27. Kaskas BA et al. Safe treatment of thiopurine S-methyltransferase deficient Crohn's disease patients with azathioprine. *Gut* 2003;52:140-2.
28. Colombel JF et al. Genotypic analysis of thiopurine S-methyltransferase in patients with Crohn's disease and severe myelosuppression during azathioprine therapy. *Gastroenterology* 2000;118:1025-30.
29. Higgs JE et al. Are patients with intermediate TPMT activity at increased risk of myelosuppression when taking thiopurine medications? *Pharmacogenomics* 2010;11:177-88.
30. Stanulla M et al. Thiopurine methyltransferase (TPMT) genotype and early treatment response to mercaptopurine in childhood acute lymphoblastic leukemia. *JAMA* 2005;293:1485-9.
31. Schaeffeler et al. A novel TPMT missense mutation associated with TPMT deficiency in a 5-year-old boy with ALL. *Leukemia* 2003;17:1422-4.
32. Evans WE et al. Preponderance of thiopurine S-methyltransferase deficiency and heterozygosity among patients intolerant to mercaptopurine or azathioprine. *J Clin Oncol* 2001;19:2293-301.
33. Relling MV et al. Mercaptopurine therapy intolerance and heterozygosity at the thiopurine S-methyltransferase gene locus. *J Natl Cancer Inst* 1999;91:2001-8.
34. McLeod HL et al. Analysis of thiopurine methyltransferase variant alleles in childhood acute lymphoblastic leukaemia. *Br J Haematol* 1999;105:696-700.
35. Andersen JB et al. Pharmacokinetics, dose adjustments, and 6-mercaptopurine/methotrexate drug interactions in two patients with thiopurine methyltransferase deficiency. *Acta Paediatr* 1998;87:108-11.
36. SmPC's Imuran (NL en VS) en Puri-Nethol (NL en VS).

Date 25-9-2023

CYP2D6 IM: bisoprolol

[2850](#)

This is NOT a gene-drug interaction.

Literature:

1. Fontana V et al. Chromosomal region 11p14.1 is associated with pharmacokinetics and pharmacodynamics of bisoprolol. *Pharmacogenomics Pers Med* 2022;15:249-60.
2. Chan SW et al. Influence of CYP2D6 and CYP3A5 polymorphisms on the pharmacokinetics and pharmacodynamics of bisoprolol in hypertensive Chinese patients. *Front Med (Lausanne)* 2021;8:683498.
3. Nozawa T et al. Influence of CYP2D6 genotype on metoprolol plasma concentration and beta-adrenergic inhibition during long-term treatment: a comparison with bisoprolol. *J Cardiovasc Pharmacol* 2005;46:713-20.
4. Taguchi M et al. Pharmacokinetic variability of routinely administered bisoprolol in middle-aged and elderly Japanese patients. *Biol Pharm Bull* 2005;28:876-81.

Date 12-09-2022

CYP2D6 PM: bisoprolol

[2849](#)

This is NOT a gene-drug interaction.

Literature:

1. Fontana V et al. Chromosomal region 11p14.1 is associated with pharmacokinetics and pharmacodynamics of bisoprolol. *Pharmacogenomics Pers Med* 2022;15:249-60.
2. Chan SW et al. Influence of CYP2D6 and CYP3A5 polymorphisms on the pharmacokinetics and pharmacodynamics of bisoprolol in hypertensive Chinese patients. *Front Med (Lausanne)* 2021;8:683498.
3. Deroubaix X et al. Comparative bioavailability of a metoprolol controlled release formulation and a bisoprolol normal release tablet after single oral dose administration in healthy volunteers.

Date 12-09-2022

CYP2D6 UM: bisoprolol[2851](#)

This is NOT a gene-drug interaction.

Literature:

1. Fontana V et al. Chromosomal region 11p14.1 is associated with pharmacokinetics and pharmacodynamics of bisoprolol. *Pharmgenomics Pers Med* 2022;15:249

Date 12-09-2022

CYP2D6 IM: brexpiprazol[6980](#)

NO action is required for this gene-drug interaction.

There are indications supporting an increase in the exposure to brexpiprazole, but no indications supporting an increase in side effects in patients with this gene variation.

Literature:

1. Ishigooka J et al. Pharmacokinetics and safety of brexpiprazole following multiple-dose administration to Japanese patients with schizophrenia. *J Clin Pharmacol* 2018;58:74-80.
2. EPAR Rxulti.

Date 13-09-2021

CYP2D6 PM: brexpiprazol[6979](#)

The risk of side effects is theoretically increased, because the gene variation reduces the metabolism of brexpiprazole.

- use half of the standard dose

Literature:

1. SmPC en EPAR Rxulti (NL) en SmPC Rexulti (VS).

Date 13-09-2021

CYP2D6 UM: brexpiprazol[6988](#)

NO action is required for this gene-drug interaction.

The gene variation results in a reduction of the exposure to brexpiprazole, but there are no indications supporting a decrease in efficacy.

Literature:

1. EPAR Rxulti.

Date 13-09-2021

HLA-A*3101: carbamazepine[5781](#)

An increased risk of the life-threatening cutaneous side effects DRESS and Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) within the first three months is present in patients with this genetic variation. The risk of carbamazepine-induced DRESS in these patients is 0.89%.

- Carefully weigh the risk of DRESS and SJS/TEN against the benefits.
- Avoid carbamazepine if an alternative is possible.
- If it is not possible to avoid carbamazepine, advise the patient to report any skin rash immediately.

Literature:

1. Nicoletti P et al. Shared genetic risk factors across carbamazepine-induced hypersensitivity reactions. *Clin Pharmacol Ther* 2019;106:1028-36.
2. Mushiroda T et al. Association of HLA-A*31:01 screening with the incidence of carbamazepine-induced

- cutaneous adverse reactions in a Japanese population. *JAMA Neurol* 2018;75:842-9.
3. Genin E et al. HLA-A*31:01 and different types of carbamazepine-induced severe cutaneous adverse reactions: an international study and meta-analysis. *Pharmacogenomics J* 2014;14:281-8.
 4. Bloch KM et al. Pharmacogenetics of antiepileptic drug-induced hypersensitivity. *Pharmacogenomics* 2014;15:857-68.
 5. Grover S et al. HLA alleles and hypersensitivity to carbamazepine: an updated systematic review with meta-analysis. *Pharmacogenet Genomics* 2014;24:94-112.
 6. Yip VL et al. HLA genotype and carbamazepine-induced cutaneous adverse drug reactions: a systematic review. *Clin Pharmacol Ther* 2012;92:757-65.
 7. SmPC's Tegretol (NL en VS).

Date 23-5-2022

HLA-B*1502: carbamazepine

[5780](#)

The risk of carbamazepine-induced SJS/TEN is strongly increased the first three months in patients with the HLA-B*15:02 allele. The risk of carbamazepine-induced SJS/TEN in these patients is 1.8-7.7%.

- Avoid carbamazepine.

Phenytoin, lamotrigine and oxcarbazepine also pose an increased risk of SJS/TEN in these patients, but the final risk is 5-10-fold lower for these medicines than for carbamazepine. Furthermore, in the case of oxcarbazepine, the most severe forms (SJS/TEN overlap and TEN) have not been observed.

Literature:

1. Sukasem C et al. Spectrum of cutaneous adverse reactions to aromatic antiepileptic drugs and human leukocyte antigen genotypes in Thai patients and meta-analysis. *Pharmacogenomics J* 2021;21:682-90.
2. Chouchi M et al. The HLA-B*15:02 polymorphism and Tegretol®-induced serious cutaneous reactions in epilepsy: an updated systematic review and meta-analysis. *Rev Neurol (Paris)* 2018;174:278-91.
3. Bloch KM et al. Pharmacogenetics of antiepileptic drug-induced hypersensitivity. *Pharmacogenomics* 2014;15:857-68.
4. Grover S et al. HLA alleles and hypersensitivity to carbamazepine: an updated systematic review with meta-analysis. *Pharmacogenet Genomics* 2014;24:94-112.
5. Tangamornsuksan W et al. Relationship between the HLA-B*1502 allele and carbamazepine-induced Stevens-Johnson syndrome and toxic epidermal necrolysis: a systematic review and meta-analysis. *JAMA Dermatol* 2013;149:1025-32.
6. Yip VL et al. HLA genotype and carbamazepine-induced cutaneous adverse drug reactions: a systematic review. *Clin Pharmacol Ther* 2012;92:757-65.
7. Chen P et al. Carbamazepine-induced toxic effects and HLA-B*1502 screening in Taiwan. *N Engl J Med* 2011;364:1126-33.
8. SmPC's Tegretol (NL en VS).
9. Hung SI et al. HLA-B genotyping to detect carbamazepine-induced Stevens-Johnson syndrome: implications for personalizing medicine. *Personalized Med* 2005;2:225-37.

Date 23-5-2022

HLA-B*1511: carbamazepine

[5782](#)

The risk of the life-threatening cutaneous side effect Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) in the first three months is increased in patients with this genetic variation. The risk of carbamazepine-induced SJS/TEN in patients with the HLA-B*1502 allele, which carries a 1.6-9.9 times higher risk than the HLA-B*1511 allele, is 1.8-7.7%. This would equate to a risk of carbamazepine-induced SJS/TEN in this patient of 0.18-4.8%.

- Carefully weigh the risk of SJS/TEN against the benefits.

- Avoid carbamazepine, if an alternative is possible.

- If it is not possible to avoid carbamazepine, advise the patient to report any skin rash immediately.

Literature:

1. Wang Q et al. Association between the HLA-B alleles and carbamazepine-induced SJS/TEN: a meta-analysis. *Epilepsy Res* 2017;135:19-28.
2. Grover S et al. HLA alleles and hypersensitivity to carbamazepine: an updated systematic review with meta-analysis. *Pharmacogenet Genomics* 2014;24:94-112.

Date 23-5-2022

CYP2D6 IM: carvedilol

[2757](#)

NO action is required for this gene-drug interaction.

The plasma concentration of carvedilol can be elevated. This does not, however, result in an increase in side effects.

Literature:

1. Jung E et al. Influence of CYP2D6 polymorphism on the pharmacokinetic/pharmacodynamic characteristics of carvedilol in healthy Korean volunteers. *J Korean Med Sci* 2018;33:e182.
2. Luzum JA et al. CYP2D6 genetic variation and beta-blocker maintenance dose in patients with heart failure. *Pharm Res* 2017;34:1615-25.
3. Shihmanter R et al. Variation in the CYP2D6 genotype is not associated with carvedilol dose changes in patients with heart failure. *J Clin Pharm Ther* 2014;39:432-8.
4. Nikolic VN et al. Population pharmacokinetics of carvedilol in patients with congestive heart failure. *J Pharm Sci* 2013;102:2851-8.
5. Sehr D et al. Carvedilol pharmacokinetics and pharmacodynamics in relation to CYP2D6 and ADRB pharmacogenetics. *Pharmacogenomics* 2011;12:783-95.
6. Saito M et al. Population pharmacokinetics of R- and S-carvedilol in Japanese patients with chronic heart failure. *Biol Pharm Bull* 2010;33:1378-84.
7. Baudhuin LM et al. Relation of ADRB1, CYP2D6, and UGT1A1 polymorphisms with dose of, and response to, carvedilol or metoprolol therapy in patients with chronic heart failure. *Am J Cardiol* 2010;106:402-8.
8. Horiuchi I et al. Pharmacokinetics of R- and S-carvedilol in routinely treated Japanese patients with heart failure. *Biol Pharm Bull* 2008;31:976-80.
9. Takekuma Y et al. Evaluation of effects of polymorphism for metabolic enzymes on pharmacokinetics of carvedilol by population pharmacokinetic analysis. *Biol Pharm Bull* 2007;30:537-42.
10. Honda M et al. Multiple regression analysis of pharmacogenetic variability of carvedilol disposition in 54 healthy Japanese volunteers. *Biol Pharm Bull* 2006;29:772-8.
11. Takekuma Y et al. Contribution of polymorphisms in UDP-glucuronosyltransferase and CYP2D6 to the individual variation in disposition of carvedilol. *J Pharm Pharm Sci* 2006;9:101-12.
12. Honda M et al. Effect of CYP2D6*10 on the pharmacokinetics of R- and S-carvedilol in healthy Japanese volunteers. *Biol Pharm Bull* 2005;28:1476-9.

Date 12-09-2022

CYP2D6 PM: carvedilol

[2756](#)

NO action is required for this gene-drug interaction.

The plasma concentration of carvedilol can be elevated. This does not, however, result in an increase in side effects.

Literature:

1. Luzum JA et al. CYP2D6 genetic variation and beta-blocker maintenance dose in patients with heart failure. *Pharm Res* 2017;34:1615-25.
2. Shihmanter R et al. Variation in the CYP2D6 genotype is not associated with carvedilol dose changes in patients with heart failure. *J Clin Pharm Ther* 2014;39:432-8.
3. Sehr D et al. Carvedilol pharmacokinetics and pharmacodynamics in relation to CYP2D6 and ADRB pharmacogenetics. *Pharmacogenomics* 2011;12:783-95.
4. Baudhuin LM et al. Relation of ADRB1, CYP2D6, and UGT1A1 polymorphisms with dose of, and response to, carvedilol or metoprolol therapy in patients with chronic heart failure. *Am J Cardiol* 2010;106:402-8.
5. Giessmann T et al. CYP2D6 genotype and induction of intestinal drug transporters by rifampin predict presystemic clearance of carvedilol in healthy subjects. *Clin Pharmacol Ther* 2004;75:213-22.
6. Zhou HH et al. Stereoselective disposition of carvedilol is determined by CYP2D6. *Clin Pharmacol Ther* 1995;57:518-24.
7. SmPC's Carvedilol Sandoz (Nederland) en Coreg (VS).

Date 12-09-2022

CYP2D6 UM: carvedilol

[2758](#)

NO action is required for this gene-drug interaction.

The plasma concentration of carvedilol can be reduced. This does not, however, result in a decrease in the effectiveness.

Literature:

1. Cabrera M et al. A use case to support precision medicine for frequently hospitalized older adults with

- polypharmacy. AMIA Jt Summits Transl Sci Proc 2016;2016:16-21.
2. Shihmanter R et al. Variation in the CYP2D6 genotype is not associated with carvedilol dose changes in patients with heart failure. J Clin Pharm Ther 2014;39:432-8.
 3. Sehrt D et al. Carvedilol pharmacokinetics and pharmacodynamics in relation to CYP2D6 and ADRB pharmacogenetics. Pharmacogenomics 2011;12:783-95.
 4. Baudhuin LM et al. Relation of ADRB1, CYP2D6, and UGT1A1 polymorphisms with dose of, and response to, carvedilol or metoprolol therapy in patients with chronic heart failure. Am J Cardiol 2010;106:402-8.

Date 12-09-2022

CYP2C19 IM: citalopram

[4081](#)

The risk of QT prolongation and torsades de pointes is theoretically increased because the gene variation leads to an increased citalopram plasma concentration. If you follow the dose recommendation below, the increased plasma concentration and the theoretically increased risk of QT prolongation will be offset.

Do not exceed the following daily doses:

- adults up to 65 years: 30 mg as tablets or 22 mg as drops
- adults 65 years or older: 15 mg as tablets or 10 mg as drops

Literature:

1. Kumar Y et al. CYP2C19 variation, not citalopram dose nor serum level, is associated with QTc prolongation. J Psychopharmacol 2014;28:1143-8.
2. Chen B et al. Estimation of CYP2D6*10 genotypes on citalopram disposition in Chinese subjects by population pharmacokinetic assay. J Clin Pharm Ther 2013;38:504-11.
3. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
4. Mrazek DA et al. CYP2C19 variation and citalopram response. Pharmacogenet Genomics 2011;2:1-9.
5. Fudio S et al. Evaluation of the influence of sex and CYP2C19 and CYP2D6 polymorphisms in the disposition of citalopram. Eur J Pharmacol 2010;25:200-4.
6. Hilli J et al. MAO-A and COMT genotypes as possible regulators of perinatal serotonergic symptoms after in utero exposure to SSRIs. Eur Neuropsychopharmacol 2009;19:363-70.
7. Peters EJ et al. Pharmacokinetic genes do not influence response or tolerance to citalopram in the STAR*D sample. PLoS ONE 2008;3:e1872.
8. Yin OQ et al. Phenotype-genotype relationship and clinical effects of citalopram in Chinese patients. J Clin Psychopharmacol 2006;26:367-72.
9. Rudberg I et al. Heterozygous mutation in CYP2C19 significantly increases the concentrations/dose ratio of racemic citalopram and escitalopram (S-citalopram). Ther Drug Monitor 2006;28:102-5.
10. Yu BN et al. Pharmacokinetics of citalopram in relation to genetic polymorphism of CYP2C19. Drug Metab Dispos 2003;31:1255-9.
11. Jimmink A et al. Clinical toxicology of citalopram after acute intoxication with the sole drug or in combination with other drugs: overview of 26 cases. Ther Drug Monit 2008;30:365-71.

Date 14-05-2018

CYP2C19 PM: citalopram

[4082](#)

The risk of QT prolongation and therefore also the theoretical risk of torsades de pointes is increased as the gene variation leads to an increased citalopram plasma concentration. If you follow the dose recommendation below, the increased plasma concentration and the increased risk of QT prolongation will be offset.

do not exceed the following daily doses (50% of the standard maximum dose):

- adults up to 65 years: 20 mg as tablets or 16 mg as drops
- adults 65 years or older: 10 mg as tablets or 8 mg as drops

Literature:

1. Kumar Y et al. CYP2C19 variation, not citalopram dose nor serum level, is associated with QTc prolongation. J Psychopharmacol 2014;28:1143-8.
2. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
3. Mrazek DA et al. CYP2C19 variation and citalopram response. Pharmacogenet Genomics 2011;2:1-9.
4. Fudio S et al. Evaluation of the influence of sex and CYP2C19 and CYP2D6 polymorphisms in the disposition of citalopram. Eur J Pharmacol 2010;25:200-4.

5. Hilli J et al. MAO-A and COMT genotypes as possible regulators of perinatal serotonergic symptoms after in utero exposure to SSRIs. *Eur Neuropsychopharmacol* 2009;19:363-70.
6. Peters EJ et al. Pharmacokinetic genes do not influence response or tolerance to citalopram in the STAR*D sample. *PLoS ONE* 2008;3:e1872.
7. Yin OQ et al. Phenotype-genotype relationship and clinical effects of citalopram in Chinese patients. *J Clin Psychopharmacol* 2006;26:367-72.
8. Herrlin K et al. Metabolism of citalopram enantiomers in CYP2C19/CYP2D6 phenotyped panels of healthy Swedes. *Br J Clin Pharmacol* 2003;56:415-21.
9. Yu BN et al. Pharmacokinetics of citalopram in relation to genetic polymorphism of CYP2C19. *Drug Metab Dispos* 2003;31:1255-9.
10. Baumann P et al. A double-blind, placebo-controlled study of citalopram with and without lithium in the treatment of therapy-resistant depressive patients: a clinical, pharmacokinetic, and pharmacogenetic investigation. *J Clin Psychopharmacol* 1996;16:307-14.
11. Sindrup SH et al. Pharmacokinetics of citalopram in relation to the sparteine and the mephenytoin oxidation polymorphisms. *Ther Drug Monit* 1993;15:11-7.
12. Jimmink A et al. Clinical toxicology of citalopram after acute intoxication with the sole drug or in combination with other drugs: overview of 26 cases. *Ther Drug Monit* 2008;30:365-71.
13. SPC's Cipramil en Celexa (VS).

Date 14-05-2018

CYP2C19 UM: citalopram

[4083](#)

NO action is needed for this gene-drug interaction.

The gene variation increases conversion of citalopram to a weakly active metabolite. However, there is no significant effect on the plasma concentration of citalopram, the tolerance or the response.

Literature:

1. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67.
2. Mrazek DA et al. CYP2C19 variation and citalopram response. *Pharmacogenet Genomics* 2011;2:1-9.
3. Hilli J et al. MAO-A and COMT genotypes as possible regulators of perinatal serotonergic symptoms after in utero exposure to SSRIs. *Eur Neuropsychopharmacol* 2009;19:363-70.
4. Peters EJ et al. Pharmacokinetic genes do not influence response or tolerance to citalopram in the STAR*D sample. *PLoS ONE* 2008;3:e1872.
5. Jimmink A et al. Clinical toxicology of citalopram after acute intoxication with the sole drug or in combination with other drugs: overview of 26 cases. *Ther Drug Monit* 2008;30:365-71.

Date 14-05-2018

CYP2D6 IM: citalopram/escitalopram

[2585](#)

This is NOT a gene-drug interaction.

Literature:

1. Chen B et al. Estimation of CYP2D6*10 genotypes on citalopram disposition in Chinese subjects by population pharmacokinetic assay. *J Clin Pharm Ther* 2013;38:504-11. PubMed PMID: 23981149.
2. Han KM et al. CYP2D6 P34S polymorphism and outcomes of escitalopram treatment in Koreans with major depression. *Psychiatry Investig* 2013;10:286-93. PubMed PMID: 24302953.
3. Huez-Diaz P et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. *J Psychopharmacol* 2012;26:398-407. PubMed PMID: 21926427.
4. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. *Pharmacogenomics J* 2011;11:359-67. PubMed PMID: 20531370.
5. Mrazek DA et al. CYP2C19 variation and citalopram response. *Pharmacogenet Genomics* 2011;21:1-9. PubMed PMID: 21192344.
6. Tsai MH et al. Genetic polymorphisms of cytochrome P450 enzymes influence metabolism of the antidepressant escitalopram and treatment response. *Pharmacogenomics* 2010;11:537-46. PubMed PMID: 20350136.
7. Fudio S et al. Evaluation of the influence of sex and CYP2C19 and CYP2D6 polymorphisms in the disposition of citalopram. *Eur J Pharmacol* 2010;626:200-4. PubMed PMID: 19840783.
8. Peters EJ et al. Pharmacokinetic genes do not influence response or tolerance to citalopram in the STAR*D sample. *PLoS One* 2008;3:e1872. PubMed PMID: 18382661.
9. Carlsson B et al. Enantioselective analysis of citalopram and metabolites in adolescents. *Ther Drug*

Monit 2001;23:658-64.
10. SPC Cipramil.

Date 14-05-2018

CYP2D6 PM: citalopram/escitalopram

[2584](#)

This is NOT a gene-drug interaction.

Literature:

1. Huezo-Diaz P et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. J Psychopharmacol 2012;26:398-407. PubMed PMID: 21926427.
2. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67. PubMed PMID: 20531370.
3. Mrazek DA et al. CYP2C19 variation and citalopram response. Pharmacogenet Genomics 2011;21:1-9. PubMed PMID: 21192344.
4. Peters EJ et al. Pharmacokinetic genes do not influence response or tolerance to citalopram in the STAR*D sample. PLoS One 2008;3:e1872. PubMed PMID: 18382661.
5. Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. Eur J Clin Pharmacol 2004;60:329-36.
6. Herrlin K et al. Metabolism of citalopram enantiomers in CYP2C19/CYP2D6 phenotyped panels of healthy Swedes. Br J Clin Pharmacol 2003;56:415-21.
7. Bondolfi G et al. Non-response to citalopram in depressive patients: pharmacokinetic and clinical consequences of a fluvoxamine augmentation. Psychopharmacology 1996;128:421-5.
8. Sindrup SH et al. Pharmacokinetics of citalopram in relation to the sparteine and the mephenytoin oxidation polymorphisms. Ther Drug Monit 1993;15:11-7.
9. SPC's Cipramil, Lexapro (NL en VS) en Celexa (VS).

Date 14-05-2018

CYP2D6 UM: citalopram/escitalopram

[2586](#)

This is NOT a gene-drug interaction.

Literature:

1. Huezo-Diaz P et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. J Psychopharmacol 2012;26:398-407. PubMed PMID: 21926427.
2. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67. PubMed PMID: 20531370.
3. Mrazek DA et al. CYP2C19 variation and citalopram response. Pharmacogenet Genomics 2011;21:1-9. PubMed PMID: 21192344.
4. Carlsson B et al. Enantioselective analysis of citalopram and metabolites in adolescents. Ther Drug Monit 2001;23:658-64.
5. SPC Cipramil.

Date 14-05-2018

CYP2C19 IM: clomipramine

[6958](#)

NO action is required for this gene-drug interaction.

The gene variation does increase clomipramine plasma concentrations, but not clomipramine+desmethylclomipramine plasma concentrations, which determines side effects and efficacy in depression. The increase in the plasma concentration of clomipramine is favourable for the efficacy in anxiety and obsessive compulsive disorder.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.

3. Yokono A et al. The effect of CYP2C19 and CYP2D6 genotypes on the metabolism of clomipramine in Japanese psychiatric patients. J Clin Psychopharmacol 2001; 21:549-55.

Date 08-02-2024

CYP2C19 PM: clomipramine

[6959](#)

NO action is required for this gene-drug interaction.

The gene variation increases the plasma concentration of clomipramine. However, there is insufficient evidence to substantiate an increase of the plasma concentration of clomipramine+desmethyldomipramine to such an extent that it increases the risk of side effects. The increase in the plasma concentration of clomipramine is favourable for the efficacy in anxiety and obsessive compulsive disorder.

Literature:

1. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
2. Yokono A et al. The effect of CYP2C19 and CYP2D6 genotypes on the metabolism of clomipramine in Japanese psychiatric patients. J Clin Psychopharmacol 2001; 21:549- 55.
3. Nielsen KK et al. Single-dose kinetics of clomipramine: relationship to the sparteine and S-mephenytoin oxidation polymorphisms. Clin Pharmacol Ther 1994;55:518-27.

Date 08-02-2024

CYP2C19 UM: clomipramine

[6960](#)

The gene variation increases the risk of ineffectiveness for obsessive compulsive disorder and anxiety disorders by reducing the plasma concentration of clomipramine. The gene variation has little to no effect on the plasma concentration of clomipramine+desmethyldomipramine, which determines the efficacy for depression and side effects.

- Indication OBSESSIVE COMPULSIVE DISORDER or ANXIETY DISORDERS:

- avoid clomipramine

Antidepressants that are not metabolised by CYP2C19 - or to a lesser extent - include, for example, fluoxetine, fluvoxamine and paroxetine.

- if it is not possible to avoid clomipramine:

- monitor the effect and side effects or the plasma concentrations of clomipramine and desmethyldomipramine

- add a low dose of fluvoxamine if necessary, to inhibit CYP2C19 and CYP1A2 and thereby inhibit the conversion of clomipramine to desmethyldomipramine.

- Indication DEPRESSION:

- no action required

Literature:

1. De Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.

Date 08-02-2024

CYP2D6 IM: clomipramine

[2374](#)

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of clomipramine and the active metabolite desmethyldomipramine.

- use 70% of the standard dose and monitor the effect and side effects or the plasma concentrations of clomipramine and desmethyldomipramine.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
3. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and

clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67, persoonlijke communicatie.

4. Vandel P et al. Clomipramine, fluoxetine and CYP2D6 metabolic capacity in depressed patients. Hum Psychopharmacol 2004;19:293-8.
5. Yokono A et al. The effect of CYP2C19 and CYP2D6 genotypes on the metabolism of clomipramine in Japanese psychiatric patients. Clin Psychopharmacol 2001;21:549-55.
6. Balant-Gorgia et al. High blood concentrations of imipramine or clomipramine and therapeutic failure: a case report study using drug monitoring data. Ther Drug Monit 1989;11:415-20.

Date 08-02-2024

CYP2D6 PM: clomipramine

[2373](#)

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of clomipramine and the active metabolite desmethylclomipramine.

- Indication DEPRESSION:

- use 50% of the standard dose and monitor the effect and side effects or the plasma concentrations of clomipramine and desmethylclomipramine in order to set the maintenance dose.

- Indication ANXIETY DISORDERS or OBSESSIVE COMPULSIVE DISORDER:

- if side effects occur: use 50% of the standard dose and monitor the effect and side effects or the plasma concentrations of clomipramine and desmethylclomipramine in order to set the maintenance dose. It is not known whether it is possible to reduce the dose to such an extent that the side effects disappear while the effectiveness is retained. Clomipramine and desmethylclomipramine both contribute to the side effects. Only clomipramine contributes to the effectiveness.
- if dose reduction does not have the desired effect: avoid clomipramine. Antidepressants that are not metabolised by CYP2D6, or to a lesser extent, include citalopram and sertraline.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. de Jong C et al. Clomipramine toxicity in a CYP 2D6 poor metabolizer patient who suddenly stopped smoking. J Clin Psychopharmacol 2018;38:389-391.
3. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
4. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67, personal communication.
5. Stephan PL et al. Adverse drug reactions following nonresponse in a depressed patient with CYP2D6 deficiency and low CYP 3A4/5 activity. Pharmacopsychiatry 2006;39:150-2.
6. Danish University Antidepressant Group. Clomipramine dose-effect study in patients with depression: clinical end points and pharmacokinetics. Clin Pharmacol Ther 1999;66:152-65.
7. Nielsen KK et al. Single-dose kinetics of clomipramine: relationship to the sparteine and S-mephenytoin oxidation polymorphisms. Clin Pharmacol Ther 1994;55:518-27.
8. Tacke U et al. Debrisoquine hydroxylation phenotypes of patients with high versus low to normal serum antidepressant concentrations. J Clin Psychopharmacol 1992;12:262-7.
9. Nielsen KK et al. Steady-state plasma levels of clomipramine and its metabolites: impact of the sparteine/debrisoquine oxidation polymorphism. Eur J Clin Pharmacol 1992;43:405-11.
10. Balant-Gorgia AE et al. High plasma concentrations of desmethylclomipramine after chronic administration of clomipramine to a poor metabolizer. Eur J Clin Pharmacol 1987;32:101-2.
11. Balant-Gorgia AE et al. High blood concentrations of imipramine or clomipramine and therapeutic failure: a case report study using drug monitoring data. Ther Drug Monit 1989;11:415-20.
12. SmPC Anafranil (USA).

Date 08-02-2024

CYP2D6 UM: clomipramine

[2375](#)

The risk of ineffectiveness and cardiotoxic side effects may be increased. The gene variation leads to reduced plasma concentrations of clomipramine and the active metabolite desmethylclomipramine and to increased concentrations of the potentially cardiotoxic hydroxy metabolites.

- use 1.5 times the normal dose and monitor the effect and side effects of the plasma concentrations of clomipramine and desmethylclomipramine to set the maintenance dose.
- if a dose increase is not wanted due to potential cardiotoxic hydroxy metabolites: avoid clomipramine. Antidepressants that are not metabolised by CYP2D6, or to a lesser extent, include citalopram and

sertraline.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67.
3. de Vos A et al. Association between CYP2C19*17 and metabolism of amitriptyline, citalopram and clomipramine in Dutch hospitalized patients. Pharmacogenomics J 2011;11:359-67, personal communication.
4. Baumann P et al. Ultrarapid metabolism of clomipramine in a therapy-resistant depressive patient, as confirmed by CYP2 D6 genotyping. Pharmacopsychiatry 1998;31:72.
5. Bertilsson L et al. Molecular basis for rational megaprescribing in ultrarapid hydroxylators of debrisoquine. Lancet 1993;341:63.

Date 08-02-2024

CYP2D6 IM: clonidine

[2919](#)

This is NOT a gene-drug interaction.

Literature:

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Date 31-01-2022

CYP2D6 PM: clonidine

[2919](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 31-01-2022

CYP2D6 UM: clonidine

[2921](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 31-01-2022

CYP2C19 IM: clopidogrel

[2938](#)

The risk of serious cardiovascular and cerebrovascular events is increased in patients undergoing balloon angioplasty or stent placement (percutaneous coronary intervention) and in patients with a stroke or TIA, as the genetic variation reduces the activation of clopidogrel. No negative clinical consequences have been observed in other patients.

- PERCUTANEOUS CORONARY INTERVENTION, STROKE or TIA:
 - choose an alternative or double the dose to 150 mg/day (600 mg loading dose)
Prasugrel and ticagrelor (percutaneous coronary intervention)
and acetylsalicylic acid/dipyridamole (stroke or TIA)
are not metabolised by CYP2C19 (or to a lesser extent).
- OTHER INDICATIONS:
 - no action required

Literature:

1. Lee J et al. CYP2C19 polymorphism is associated with amputation rates in patients taking clopidogrel after endovascular intervention for critical limb ischaemia. Eur J Vasc Endovasc Surg 2019;58:373-82.
2. Lan H et al. Anti-platelet therapy in mild cerebral infarction patients on the basis of CYP2C19 metabolizer status. Cell Transplant 2019;28:1039-44.

3. Kheiri B et al. CYP2C19 pharmacogenetics versus standard of care dosing for selecting antiplatelet therapy in patients with coronary artery disease: a meta-analysis of randomized clinical trials. *Catheter Cardiovasc Interv* 2019;93:1246-52.
4. Williams AK et al. CYP2C19 genotype-guided antiplatelet therapy and 30-day outcomes after percutaneous coronary intervention. *Circ Genom Precis Med* 2019;12:e002441.
5. Lee CR et al. Clinical outcomes and sustainability of using CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *Circ Genom Precis Med* 2018;11:e002069.
6. Zhong Z et al. Effect of cytochrome P450 2C19 polymorphism on adverse cardiovascular events after drug-eluting stent implantation in a large Hakka population with acute coronary syndrome receiving clopidogrel in southern China. *Eur J Clin Pharmacol* 2018;74:423-31.
7. Wu Y et al. Impact of CYP2C19 polymorphism in prognosis of minor stroke or TIA patients with declined eGFR on dual antiplatelet therapy: CHANCE substudy. *Pharmacogenomics J* 2018;18:713-20.
8. Cavallari LH et al. Multisite investigation of outcomes with implementation of CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *JACC Cardiovasc Interv* 2018;11:181-91.
9. Lin Y et al. Impact of glycemic control on efficacy of clopidogrel in transient ischemic attack or minor stroke patients with CYP2C19 genetic variants. *Stroke* 2017;48:998- 1004.
10. Pan Y et al. Genetic polymorphisms and clopidogrel efficacy for acute ischemic stroke or transient ischemic attack: a systematic review and meta-analysis. *Circulation* 2017;135:21-33.
11. Wang Y et al. Association between CYP2C19 loss-of-function allele status and efficacy of clopidogrel for risk reduction among patients with minor stroke or transient ischemic attack. *JAMA* 2016;316:70-8.
12. Ogawa H et al. Effects of CYP2C19 allelic variants on inhibition of platelet aggregation and major adverse cardiovascular events in Japanese patients with acute coronary syndrome: The PRASFIT-ACS study.
13. Shen DL et al. Clinical value of CYP2C19 genetic testing for guiding the antiplatelet therapy in a Chinese population. *J Cardiovasc Pharmacol* 2016;67:232-6.
14. Niu X et al. CYP2C19 polymorphism and clinical outcomes among patients of different races treated with clopidogrel: a systematic review and meta-analysis. *J Huazhong Univ Sci Technolog Med Sci* 2015;35:147-56.
15. Sorich MJ et al. CYP2C19 genotype has a greater effect on adverse cardiovascular outcomes following percutaneous coronary intervention and in Asian populations treated with clopidogrel: a meta-analysis. *Circ Cardiovasc Genet* 2014;7:895-902.
16. Mao L et al. Cytochrome CYP2C19 polymorphism and risk of adverse clinical events in clopidogrel-treated patients: a meta-analysis based on 23,035 subjects. *Arch Cardiovasc Dis* 2013;106:517-27.
17. Xie X et al. Personalized antiplatelet therapy according to CYP2C19 genotype after percutaneous coronary intervention: a randomized control trial. *Int J Cardiol* 2013;168:3736-40.
18. Jang JS et al. Meta-analysis of cytochrome P450 2C19 polymorphism and risk of adverse clinical outcomes among coronary artery disease patients of different ethnic groups treated with clopidogrel. *Am J Cardiol* 2012;110:502-8.
19. Holmes MV et al. CYP2C19 genotype, clopidogrel metabolism, platelet function, and cardiovascular events: a systematic review and meta-analysis. *JAMA* 2011;306:2704- 14.
20. Liu YP et al. Association of genetic variants in CYP2C19 and adverse clinical outcomes after treatment with clopidogrel: an updated meta-analysis. *Thromb Res* 2011;128:593-4.
21. Mega JL et al. Dosing clopidogrel based on CYP2C19 genotype and the effect on platelet reactivity in patients with stable cardiovascular disease. *JAMA* 2011;306:2221-8.
22. Simon T et al. Genetic polymorphisms and the impact of a higher clopidogrel dose regimen on active metabolite exposure and antiplatelet response in healthy subjects. *Clin Pharmacol Ther* 2011;90:287-95.
23. Collet JP et al. High doses of clopidogrel to overcome genetic resistance: the randomized cross-over CLOVIS-2 (Clopidogrel and Response Variability Investigation Study 2). *JACC Cardiovasc Interv* 2011;4:392-402.
24. Bonello-Palot N et al. Relation of body mass index to high on-treatment platelet reactivity and of failed clopidogrel dose adjustment according to platelet reactivity monitoring in patients undergoing percutaneous coronary intervention. *Am J Cardiol* 2009;104:1511-5.
25. Shuldiner AR et al. Association of cytochrome P450 2C19 genotype with the antiplatelet effect and clinical efficacy of clopidogrel therapy. *JAMA* 2009;302:849-57.
26. Aleil B et al. CYP2C19*2 polymorphism is not the sole determinant of the response to clopidogrel: implications for its monitoring. *J Thromb Haemost* 2009;7:1747-9.
27. Pena A et al. Can we override clopidogrel resistance? *Circulation* 2009;119:2854-7.
28. Sibbing D et al. Cytochrome P450 2C19 loss-of-function polymorphism and stent thrombosis following percutaneous coronary intervention. *Eur Heart J* 2009;30:916-22.
29. Brackbill ML et al. Frequency of CYP3A4, CYP3A5, CYP2C9, and CYP2C19 variant alleles in patients receiving clopidogrel that experience repeat acute coronary syndrome. *Heart Vessels* 2009;24:73-8.
30. Giusti B et al. Relation of cytochrome P450 2C19 loss-of-function polymorphism to occurrence of drug-eluting coronary stent thrombosis. *Am J Cardiol* 2009;103:806-11.
31. Collet JP et al. Cytochrome P450 2C19 polymorphism in young patients treated with clopidogrel after myocardial infarction: a cohort study. *Lancet* 2009;373:309-17.
32. Mega JL et al. Cytochrome p-450 polymorphisms and response to clopidogrel. *N Engl J Med* 2009;360:354-62.
33. Simon T et al. Genetic determinants of response to clopidogrel and cardiovascular events. *N Engl J*

Med 2009;360:363-75.

34. Geisler T et al. CYP2C19 and nongenetic factors predict poor responsiveness to clopidogrel loading dose after coronary stent implantation. *Pharmacogenomics* 2008;9:1251-9.
35. Umemura K et al. The common gene variants of CYP2C19 affect pharmacokinetics and pharmacodynamics in an active metabolite of clopidogrel in healthy subjects. *J Thromb Haemost* 2008;6:1439-41.
36. Chen BL et al. Inhibition of ADP-induced platelet aggregation by clopidogrel is related to CYP2C19 genetic polymorphisms. *Clin Exp Pharmacol Physiol* 2008;35:904-8.
37. Kim KA et al. The effect of CYP2C19 polymorphism on the pharmacokinetics and pharmacodynamics of clopidogrel: a possible mechanism for clopidogrel resistance. *Clin Pharmacol Ther* 2008;84:236-42.
38. Malek LA et al. Coexisting polymorphisms of P2Y12 and CYP2C19 genes as a risk factor for persistent platelet activation with clopidogrel. *Circ J* 2008;72:1165-9.
39. Trenk D et al. Cytochrome P450 2C19 681G>A polymorphism and high on-clopidogrel platelet reactivity associated with adverse 1-year clinical outcome of elective percutaneous coronary intervention with drug-eluting or bare-metal stents. *J Am Coll Cardiol* 2008;51:1925-34.
40. Frere C et al. Effect of cytochrome p450 polymorphisms on platelet reactivity after treatment with clopidogrel in acute coronary syndrome. *Am J Cardiol* 2008;101:1088- 93.
41. Fontana P et al. Biological effect of increased maintenance dose of clopidogrel in cardiovascular outpatients and influence of the cytochrome P450 2C19*2 allele on clopidogrel responsiveness. *Thromb Res* 2008;121:463-8.
42. Giusti B et al. Cytochrome P450 2C19 loss-of-function polymorphism, but not CYP3A4 IVS10 + 12G/A and P2Y12 T744C polymorphisms, is associated with response variability to dual antiplatelet treatment in high-risk vascular patients. *Pharmacogenet Genomics* 2007;17:1057-64.
43. Brandt JT et al. Common polymorphisms of CYP2C19 and CYP2C9 affect the pharmacokinetic and pharmacodynamic response to clopidogrel but not prasugrel. *J Thromb Haemost* 2007;5:2429-36.
44. Fontana P et al. Influence of CYP2C19 and CYP3A4 gene polymorphisms on clopidogrel responsiveness in healthy subjects. *J Thromb Haemost* 2007;5:2153-5.
45. Hulot JS et al. Cytochrome P450 2C19 loss-of-function polymorphism is a major determinant of clopidogrel responsiveness in healthy subjects. *Blood* 2006;108:2244-7.
46. CBO Conceptrichtlijn Diagnostiek, Preventie en Behandeling van Veneuze Trombo-embolie en Secundaire Preventie Arteriële Trombose, 2008. www.cbo.nl.

Date 23-12-2019

CYP2C19 PM: clopidogrel

2937

The risk of serious cardiovascular and cerebrovascular events is increased in patients undergoing balloon angioplasty or stent placement (percutaneous coronary intervention) and in patients with a stroke or TIA, because the genetic variation reduces the activation of clopidogrel. No negative clinical consequences have been proved in other patients.

- PERCUTANEOUS CORONARY INTERVENTION, STROKE or TIA:

- avoid clopidogrel

Prasugrel and, ticagrelor (percutaneous coronary intervention) and acetylsalicylic acid/dipyridamole (stroke or TIA) are not metabolised by CYP2C19 (or to a lesser extent).

- OTHER INDICATIONS:

- determine the level of inhibition of platelet aggregation by clopidogrel
- consider an alternative in poor responders

Prasugrel and ticagrelor are not metabolised by CYP2C19 (or to a lesser extent).

Literature:

1. Lee J et al. CYP2C19 polymorphism is associated with amputation rates in patients taking clopidogrel after endovascular intervention for critical limb ischaemia. *Eur J Vasc Endovasc Surg* 2019;58:373-82.
2. Lan H et al. Anti-platelet therapy in mild cerebral infarction patients on the basis of CYP2C19 metabolizer status. *Cell Transplant* 2019;28:1039-44.
3. Kheiri B et al. CYP2C19 pharmacogenetics versus standard of care dosing for selecting antiplatelet therapy in patients with coronary artery disease: a meta-analysis of randomized clinical trials. *Catheter Cardiovasc Interv* 2019;93:1246-52.
4. Williams AK et al. CYP2C19 genotype-guided antiplatelet therapy and 30-day outcomes after percutaneous coronary intervention. *Circ Genom Precis Med* 2019;12:e002441.
5. Lee CR et al. Clinical outcomes and sustainability of using CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *Circ Genom Precis Med* 2018;11:e002069.
6. Zhong Z et al. Effect of cytochrome P450 2C19 polymorphism on adverse cardiovascular events after

- drug-eluting stent implantation in a large Hakka population with acute coronary syndrome receiving clopidogrel in southern China. *Eur J Clin Pharmacol* 2018;74:423-31.
7. Wu Y et al. Impact of CYP2C19 polymorphism in prognosis of minor stroke or TIA patients with declined eGFR on dual antiplatelet therapy: CHANCE substudy. *Pharmacogenomics J* 2018;18:713-20.
 8. Cavallari LH et al. Multisite investigation of outcomes with implementation of CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *JACC Cardiovasc Interv* 2018;11:181-91.
 9. Lin Y et al. Impact of glycemic control on efficacy of clopidogrel in transient ischemic attack or minor stroke patients with CYP2C19 genetic variants. *Stroke* 2017;48:998- 1004.
 10. Pan Y et al. Genetic polymorphisms and clopidogrel efficacy for acute ischemic stroke or transient ischemic attack: a systematic review and meta-analysis. *Circulation* 2017;135:21-33.
 11. Deiman BA et al. Reduced number of cardiovascular events and increased cost-effectiveness by genotype-guided antiplatelet therapy in patients undergoing percutaneous coronary interventions in the Netherlands. *Neth Heart J* 2016;24:589-99.
 12. Wang Y et al. Association between CYP2C19 loss-of-function allele status and efficacy of clopidogrel for risk reduction among patients with minor stroke or transient ischemic attack. *JAMA* 2016;316:70-8.
 13. Ogawa H et al. Effects of CYP2C19 allelic variants on inhibition of platelet aggregation and major adverse cardiovascular events in Japanese patients with acute coronary syndrome: The PRASFIT-ACS study.
 14. Shen DL et al. Clinical value of CYP2C19 genetic testing for guiding the antiplatelet therapy in a Chinese population. *J Cardiovasc Pharmacol* 2016;67:232-6.
 15. Xiong R et al. A randomized controlled trial to assess the efficacy and safety of doubling dose clopidogrel versus ticagrelor for the treatment of acute coronary syndrome in patients with CYP2C19*2 homozygotes. *Int J Clin Exp Med* 2015;8:13310-6.
 16. Niu X et al. CYP2C19 polymorphism and clinical outcomes among patients of different races treated with clopidogrel: a systematic review and meta-analysis. *J Huazhong Univ Sci Technolog Med Sci* 2015;35:147-56.
 17. Sorich MJ et al. CYP2C19 genotype has a greater effect on adverse cardiovascular outcomes following percutaneous coronary intervention and in Asian populations treated with clopidogrel: a meta-analysis. *Circ Cardiovasc Genet* 2014;7:895-902.
 18. Mao L et al. Cytochrome CYP2C19 polymorphism and risk of adverse clinical events in clopidogrel-treated patients: a meta-analysis based on 23,035 subjects. *Arch Cardiovasc Dis* 2013;106:517-27.
 19. Xie X et al. Personalized antiplatelet therapy according to CYP2C19 genotype after percutaneous coronary intervention: a randomized control trial. *Int J Cardiol* 2013;168:3736-40.
 20. Jang JS et al. Meta-analysis of cytochrome P450 2C19 polymorphism and risk of adverse clinical outcomes among coronary artery disease patients of different ethnic groups treated with clopidogrel. *Am J Cardiol* 2012;110:502-8.
 21. Holmes MV et al. CYP2C19 genotype, clopidogrel metabolism, platelet function, and cardiovascular events: a systematic review and meta-analysis. *JAMA* 2011;306:2704- 14.
 22. Liu YP et al. Association of genetic variants in CYP2C19 and adverse clinical outcomes after treatment with clopidogrel: an updated meta-analysis. *Thromb Res* 2011;128:593-4.
 23. Mega JL et al. Dosing clopidogrel based on CYP2C19 genotype and the effect on platelet reactivity in patients with stable cardiovascular disease. *JAMA* 2011;306:2221-8.
 24. Simon T et al. Genetic polymorphisms and the impact of a higher clopidogrel dose regimen on active metabolite exposure and antiplatelet response in healthy subjects. *Clin Pharmacol Ther* 2011;90:287-95.
 25. Collet JP et al. High doses of clopidogrel to overcome genetic resistance: the randomized cross-over CLOVIS-2 (Clopidogrel and Response Variability Investigation Study 2). *JACC Cardiovasc Interv* 2011;4:392-402.
 26. Bonello-Palot N et al. Relation of body mass index to high on-treatment platelet reactivity and of failed clopidogrel dose adjustment according to platelet reactivity monitoring in patients undergoing percutaneous coronary intervention. *Am J Cardiol* 2009;104:1511-5.
 27. Shuldiner AR et al. Association of cytochrome P450 2C19 genotype with the antiplatelet effect and clinical efficacy of clopidogrel therapy. *JAMA* 2009;302:849-57.
 28. Aleil B et al. CYP2C19*2 polymorphism is not the sole determinant of the response to clopidogrel: implications for its monitoring. *J Thromb Haemost* 2009;7:1747-9.
 29. Pena A et al. Can we override clopidogrel resistance? *Circulation* 2009;119:2854-7.
 30. Sibbing D et al. Cytochrome P450 2C19 loss-of-function polymorphism and stent thrombosis following percutaneous coronary intervention. *Eur Heart J* 2009;30:916-22.
 31. Brackbill ML et al. Frequency of CYP3A4, CYP3A5, CYP2C9, and CYP2C19 variant alleles in patients receiving clopidogrel that experience repeat acute coronary syndrome. *Heart Vessels* 2009;24:73-8.
 32. Giusti B et al. Relation of cytochrome P450 2C19 loss-of-function polymorphism to occurrence of drug-eluting coronary stent thrombosis. *Am J Cardiol* 2009;103:806-11.
 33. Collet JP et al. Cytochrome P450 2C19 polymorphism in young patients treated with clopidogrel after myocardial infarction: a cohort study. *Lancet* 2009;373:309-17.
 34. Mega JL et al. Cytochrome p-450 polymorphisms and response to clopidogrel. *N Engl J Med* 2009;360:354-62.
 35. Simon T et al. Genetic determinants of response to clopidogrel and cardiovascular events. *N Engl J Med* 2009;360:363-75.
 36. Geisler T et al. CYP2C19 and nongenetic factors predict poor responsiveness to clopidogrel loading

- dose after coronary stent implantation. *Pharmacogenomics* 2008;9:1251-9.
37. Umemura K et al. The common gene variants of CYP2C19 affect pharmacokinetics and pharmacodynamics in an active metabolite of clopidogrel in healthy subjects. *J Thromb Haemost* 2008;6:1439-41.
 38. Chen BL et al. Inhibition of ADP-induced platelet aggregation by clopidogrel is related to CYP2C19 genetic polymorphisms. *Clin Exp Pharmacol Physiol* 2008;35:904-8.
 39. Kim KA et al. The effect of CYP2C19 polymorphism on the pharmacokinetics and pharmacodynamics of clopidogrel: a possible mechanism for clopidogrel resistance. *Clin Pharmacol Ther* 2008;84:236-42.
 40. Malek LA et al. Coexisting polymorphisms of P2Y12 and CYP2C19 genes as a risk factor for persistent platelet activation with clopidogrel. *Circ J* 2008;72:1165-9.
 41. Trenk D et al. Cytochrome P450 2C19 681G>A polymorphism and high on-clopidogrel platelet reactivity associated with adverse 1-year clinical outcome of elective percutaneous coronary intervention with drug-eluting or bare-metal stents. *J Am Coll Cardiol* 2008;51:1925-34.
 42. Frere C et al. Effect of cytochrome p450 polymorphisms on platelet reactivity after treatment with clopidogrel in acute coronary syndrome. *Am J Cardiol* 2008;101:1088- 93.
 43. Fontana P et al. Biological effect of increased maintenance dose of clopidogrel in cardiovascular outpatients and influence of the cytochrome P450 2C19*2 allele on clopidogrel responsiveness. *Thromb Res* 2008;121:463-8.
 44. Giusti B et al. Cytochrome P450 2C19 loss-of-function polymorphism, but not CYP3A4 IVS10 + 12G/A and P2Y12 T744C polymorphisms, is associated with response variability to dual antiplatelet treatment in high-risk vascular patients. *Pharmacogenet Genomics* 2007;17:1057-64.
 45. Brandt JT et al. Common polymorphisms of CYP2C19 and CYP2C9 affect the pharmacokinetic and pharmacodynamic response to clopidogrel but not prasugrel. *J Thromb Haemost* 2007;5:2429-36.
 46. FDA Drug Safety Communication: Reduced effectiveness of Plavix (clopidogrel) in patients who are poor metabolizers of the drug. 03-12-10.
 47. SPC's Clopidogrel Sandoz en Plavix (VS).
 48. CBO Conceptrichtlijn Diagnostiek, Preventie en Behandeling van Veneuze Trombo-embolie en Secundaire Preventie Arteriële Trombose, 2008. www.cbo.nl.

Date 23-12-2019

CYP2C19 UM: clopidogrel

[2939](#)

NO action is required for this gene-drug interaction.

The genetic variation results in increased conversion of clopidogrel to the active metabolite. However, this can result in both positive effects (reduction in the risk of serious cardiovascular and cerebrovascular events) and negative effects (increase in the risk of bleeding).

Literature:

1. Liu YP et al. Association of genetic variants in CYP2C19 and adverse clinical outcomes after treatment with clopidogrel: an updated meta-analysis. *Thromb Res* 2011;128:593-4.
2. Li Y et al. The gain-of-function variant allele CYP2C19*17: a double-edged sword between thrombosis and bleeding in clopidogrel-treated patients. *J Thromb Haemost* 2012;10:199-206.
3. Simon T et al. Genetic polymorphisms and the impact of a higher clopidogrel dose regimen on active metabolite exposure and antiplatelet response in healthy subjects. *Clin Pharmacol Ther* 2011;90:287-95.
4. Shuldiner AR et al. Association of cytochrome P450 2C19 genotype with the antiplatelet effect and clinical efficacy of clopidogrel therapy. *JAMA* 2009;302:849-57.
5. Frère C et al. The CYP2C19*17 allele is associated with better platelet response to clopidogrel in patients admitted for non-ST acute coronary syndrome. *J Thromb Haemost* 2009;7:1409-11.
6. Mega JL et al. Cytochrome p-450 polymorphisms and response to clopidogrel. *N Engl J Med* 2009;360:354-62.
7. Simon T et al. Genetic determinants of response to clopidogrel and cardiovascular events. *N Engl J Med* 2009;360:363-75.
8. Geisler T et al. CYP2C19 and nongenetic factors predict poor responsiveness to clopidogrel loading dose after coronary stent implantation. *Pharmacogenomics* 2008;9:1251-9.

Date 23-12-2019

CYP1A2 IM: clozapine

[4431](#)

This is NOT a gene-drug interaction.

Literature:

1. Allorge D et al. Identification of a novel splice-site mutation in the CYP1A2 gene. *Br J Clin Pharmacol* 2003;56:341-4.

Date 13-09-2021

CYP1A2 NM: clozapine

[4428](#)

This is NOT a gene-drug interaction.

Literature:

1. Ammar H et al. Clinical and genetic influencing factors on clozapine pharmacokinetics in Tunisian schizophrenic patients. *Pharmacogenomics J* 2021 Mar 17 (online ahead of print).
2. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
3. Lesche D et al. Impact of CYP1A2, CYP2C19, and CYP2D6 genotype- and phenoconversion-predicted enzyme activity on clozapine exposure and symptom severity. *Pharmacogenomics J* 2020;20:192-201.
4. Na Takuathung M et al. Impact of CYP1A2 genetic polymorphisms on pharmacokinetics of antipsychotic drugs: a systematic review and meta-analysis. *Acta Psychiatr Scand* 2019;139:15-25.
5. Vasudev K et al. Genetic determinants of clozapine-induced metabolic side effects. *Can J Psychiatry* 2017;62:138-49.
6. Huang HC et al. Cigarette smoking has a differential effect on the plasma level of clozapine in Taiwanese schizophrenic patients associated with the CYP1A2 gene -163A/C single nucleotide polymorphism. *Psychiatr Genet* 2016;26:172-7.
7. de Brito RB et al. The CYP1A2 -163C>A polymorphism is associated with super-refractory schizophrenia. *Schizophr Res* 2015;169:502-3.
8. Olsson E et al. Genetic and clinical factors affecting plasma clozapine concentration. *Prim Care Companion CNS Disord* 2015;17;10.4088/ PCC.14m01704.
9. Viikki M et al. CYP1A2 polymorphism -1545C > T (rs2470890) is associated with increased side effects to clozapine. *BMC Psychiatry* 2014;14:50.
10. Looman NMG et al. Associatie van genetische variatie in CYP1A2 en UGT1A4 met metabole stoornissen bij gebruikers van clozapine en olanzapine. *PW Wetenschappelijk Platform* 2013;7:a1310.
11. Kohlrausch FB et al. The CYP1A2 -163C>A polymorphism is associated with clozapine-induced generalized tonic-clonic seizures in Brazilian schizophrenia patients. *Psychiatry Res* 2013;209:242-5.
12. Rajkumar AP et al. Association between CYP1A2 gene single nucleotide polymorphisms and clinical responses to clozapine in patients with treatment-resistant schizophrenia. *Acta Neuropsychiatr* 2013;25:2-11.
13. Ferrari M et al. Association between CYP1A2 polymorphisms and clozapine-induced adverse reactions in patients with schizophrenia. *Psychiatry Res* 2012;200:1014-7.
14. Lee ST et al. Association study of 27 annotated genes for clozapine pharmacogenetics: validation of preexisting studies and identification of a new candidate gene, ABCB1, for treatment response. *J Clin Psychopharmacol* 2012;32:441-8.
15. Jaquenoud Sirot E et al. ABCB1 and cytochrome P450 polymorphisms: clinical pharmacogenetics of clozapine. *J Clin Psychopharmacol* 2009;29:319-26.
16. Melkersson KI et al. Impact of CYP1A2 and CYP2D6 polymorphisms on drug metabolism and on insulin and lipid elevations and insulin resistance in clozapine-treated patients. *J Clin Psychiatry* 2007;68:697-704.
17. Kootstra-Ros JE et al. The cytochrome P450 CYP1A2 genetic polymorphisms 1F and 1D do not affect clozapine clearance in a group of schizophrenic patients. *Ann Clin Biochem* 2005;42:216-9.
18. van der Weide J et al. The effect of smoking and cytochrome P450 CYP1A2 genetic polymorphism on clozapine clearance and dose requirement. *Pharmacogenetics* 2003;13:169-72.
19. Basile VS et al. Genetic dissection of atypical antipsychotic-induced weight gain: novel preliminary data on the pharmacogenetic puzzle. *J Clin Psychiatry* 2001;62:45-66.

Date 13-09-2021

CYP1A2 PM: clozapine

[4432](#)

This is NOT a gene-drug interaction.

Literature:

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Date 13-09-2021

CYP1A2*1A/*1F: clozapine

[4427](#)

This is NOT a gene-drug interaction.

Literature:

1. Ammar H et al. Clinical and genetic influencing factors on clozapine pharmacokinetics in Tunisian

- schizophrenic patients. *Pharmacogenomics J* 2021 Mar 17 (online ahead of print).
2. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
 3. Lesche D et al. Impact of CYP1A2, CYP2C19, and CYP2D6 genotype- and phenoconversion-predicted enzyme activity on clozapine exposure and symptom severity. *Pharmacogenomics J* 2020;20:192-201.
 4. Na Takuathung M et al. Impact of CYP1A2 genetic polymorphisms on pharmacokinetics of antipsychotic drugs: a systematic review and meta-analysis. *Acta Psychiatr Scand* 2019;139:15-25.
 5. Vasudev K et al. Genetic determinants of clozapine-induced metabolic side effects. *Can J Psychiatry* 2017;62:138-49.
 6. Huang HC et al. Cigarette smoking has a differential effect on the plasma level of clozapine in Taiwanese schizophrenic patients associated with the CYP1A2 gene -163A/C single nucleotide polymorphism. *Psychiatr Genet* 2016;26:172-7.
 7. de Brito RB et al. The CYP1A2 -163C>A polymorphism is associated with super-refractory schizophrenia. *Schizophr Res* 2015;169:502-3.
 8. Olsson E et al. Genetic and clinical factors affecting plasma clozapine concentration. *Prim Care Companion CNS Disord* 2015;17;10.4088/ PCC.14m01704.
 9. Viikki M et al. CYP1A2 polymorphism -1545C > T (rs2470890) is associated with increased side effects to clozapine. *BMC Psychiatry* 2014;14:50.
 10. Looman NMG et al. Associatie van genetische variatie in CYP1A2 en UGT1A4 met metabole stoornissen bij gebruikers van clozapine en olanzapine. *PW Wetenschappelijk Platform* 2013;7:a1310.
 11. Kohlrausch FB et al. The CYP1A2 -163C>A polymorphism is associated with clozapine-induced generalized tonic-clonic seizures in Brazilian schizophrenia patients. *Psychiatry Res* 2013;209:242-5.
 12. Rajkumar AP et al. Association between CYP1A2 gene single nucleotide polymorphisms and clinical responses to clozapine in patients with treatment-resistant schizophrenia. *Acta Neuropsychiatr* 2013;25:2-11.
 13. Ferrari M et al. Association between CYP1A2 polymorphisms and clozapine-induced adverse reactions in patients with schizophrenia. *Psychiatry Res* 2012;200:1014-7.
 14. Lee ST et al. Association study of 27 annotated genes for clozapine pharmacogenetics: validation of preexisting studies and identification of a new candidate gene, ABCB1, for treatment response. *J Clin Psychopharmacol* 2012;32:441-8.
 15. Jaquenoud Sirot E et al. ABCB1 and cytochrome P450 polymorphisms: clinical pharmacogenetics of clozapine. *J Clin Psychopharmacol* 2009;29:319-26.
 16. Melkersson KI et al. Impact of CYP1A2 and CYP2D6 polymorphisms on drug metabolism and on insulin and lipid elevations and insulin resistance in clozapine-treated patients. *J Clin Psychiatry* 2007;68:697-704.
 17. Kootstra-Ros JE et al. The cytochrome P450 CYP1A2 genetic polymorphisms *1F and *1D do not affect clozapine clearance in a group of schizophrenic patients. *Ann Clin Biochem* 2005;42:216-9.
 18. van der Weide J et al. The effect of smoking and cytochrome P450 CYP1A2 genetic polymorphism on clozapine clearance and dose requirement. *Pharmacogenetics* 2003;13:169-72.
 19. Basile VS et al. Genetic dissection of atypical antipsychotic-induced weight gain: novel preliminary data on the pharmacogenetic puzzle. *J Clin Psychiatry* 2001;62:45-66.

Date 13-09-2021

CYP1A2*1C-heterozygoot: clozapine

[4429](#)

This is NOT a gene-drug interaction.

Literature:

1. Ammar H et al. Clinical and genetic influencing factors on clozapine pharmacokinetics in Tunisian schizophrenic patients. *Pharmacogenomics J* 2021 Mar 17 (online ahead of print).
2. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
3. Vasudev K et al. Genetic determinants of clozapine-induced metabolic side effects. *Can J Psychiatry* 2017;62:138-49.
4. Huang HC et al. Cigarette smoking has a differential effect on the plasma level of clozapine in Taiwanese schizophrenic patients associated with the CYP1A2 gene -163A/C single nucleotide polymorphism. *Psychiatr Genet* 2016;26:172-7.
5. Kohlrausch FB et al. The CYP1A2 -163C>A polymorphism is associated with clozapine-induced generalized tonic-clonic seizures in Brazilian schizophrenia patients. *Psychiatry Res* 2013;209:242-5.
6. Rajkumar AP et al. Association between CYP1A2 gene single nucleotide polymorphisms and clinical responses to clozapine in patients with treatment-resistant schizophrenia. *Acta Neuropsychiatr* 2013;25:2-11.
7. Ferrari M et al. Association between CYP1A2 polymorphisms and clozapine-induced adverse reactions in patients with schizophrenia. *Psychiatry Res* 2012;200:1014-7.
8. Bolla E et al. Are CYP1A2*1F and *1C associated with clozapine tolerability?: a preliminary investigation. *Psychiatry Res* 2011;189:483.
9. Melkersson KI et al. Impact of CYP1A2 and CYP2D6 polymorphisms on drug metabolism and on insulin and lipid elevations and insulin resistance in clozapine-treated patients. *J Clin Psychiatry* 2007;68:697-704.

10. Kootstra-Ros JE et al. The cytochrome P450 CYP1A2 genetic polymorphisms *1F and *1D do not affect clozapine clearance in a group of schizophrenic patients. *Ann Clin Biochem* 2005;42:216-9.

Date 13-09-2021

CYP1A2*1C/*1C: clozapine

[4430](#)

This is NOT a gene-drug interaction.

Literature:

1. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
2. Kohlrausch FB et al. The CYP1A2 -163C>A polymorphism is associated with clozapine-induced generalized tonic-clonic seizures in Brazilian schizophrenia patients. *Psychiatry Res* 2013;209:242-5.
3. Rajkumar AP et al. Association between CYP1A2 gene single nucleotide polymorphisms and clinical responses to clozapine in patients with treatment-resistant schizophrenia. *Acta Neuropsychiatr* 2013;25:2-11.
4. Ferrari M et al. Association between CYP1A2 polymorphisms and clozapine-induced adverse reactions in patients with schizophrenia. *Psychiatry Res* 2012;200:1014-7.
5. Bolla E et al. Are CYP1A2*1F and *1C associated with clozapine tolerability?: a preliminary investigation. *Psychiatry Res* 2011;189:483.

Date 13-09-2021

CYP2D6 IM: clozapine

[2377](#)

NO action is required for this gene-drug interaction.

The genetic variation results in a slightly elevated plasma concentration of clozapine, but there are no clinical consequences.

Literature:

1. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
2. Lesche D et al. Impact of CYP1A2, CYP2C19, and CYP2D6 genotype- and phenoconversion-predicted enzyme activity on clozapine exposure and symptom severity. *Pharmacogenomics J* 2020;20:192-201.
3. Tóth K et al. Potential role of patients' CYP3A-status in clozapine pharmacokinetics. *Int J Neuropsychopharmacol* 2017;20:529-37.
4. Akamine Y et al. Quantification of the steady-state plasma concentrations of clozapine and N-desmethylozapine in Japanese patients with schizophrenia using a novel HPLC method and the effects of CYPs and ABC transporters polymorphisms. *Ann Clin Biochem* 2017;54:677-85.
5. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. *Pharmacogenomics J* 2016;16:357-65.
6. Lee ST et al. Association study of 27 annotated genes for clozapine pharmacogenetic: validation of preexisting studies and identification of a new candidate gene, ABCB1, for treatment response. *J Clin Psychopharmacol* 2012; 32:441-8.
7. Jaquenoud Sirot E et al. ABCB1 and cytochrome P450 polymorphisms: clinical pharmacogenetics of clozapine. *J Clin Psychopharmacol* 2009;29:318-26.
8. Melkersson KI et al. Impact of CYP1A2 and CYP2D6 polymorphisms on drug metabolism and on insulin and lipid elevations and insulin resistance in clozapine-treated patients. *J Clin Psychiatry* 2007;68:697-704.
9. Dettling M et al. Long-term therapeutic drug monitoring of clozapine and metabolites in psychiatric in- and outpatients. *Psychopharmacology* 2000;152:80-86.

Date 13-09-2021

CYP2D6 PM: clozapine

[2376](#)

NO action is required for this gene-drug interaction.

The genetic variation results in a slightly elevated plasma concentration of clozapine, but there are no clinical consequences.

Literature:

1. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
2. Lesche D et al. Impact of CYP1A2, CYP2C19, and CYP2D6 genotype- and phenoconversion-predicted enzyme activity on clozapine exposure and symptom severity. *Pharmacogenomics J* 2020;20:192-201.
3. Tóth K et al. Potential role of patients' CYP3A-status in clozapine pharmacokinetics. *Int J Neuropsychopharmacol* 2017;20:529-37.
4. Akamine Y et al. Quantification of the steady-state plasma concentrations of clozapine and N-desmethylclozapine in Japanese patients with schizophrenia using a novel HPLC method and the effects of CYPs and ABC transporters polymorphisms. *Ann Clin Biochem* 2017;54:677-85.
5. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. *Pharmacogenomics J* 2016;16:357-65.
6. Lee ST et al. Association study of 27 annotated genes for clozapine pharmacogenetic: validation of preexisting studies and identification of a new candidate gene, ABCB1, for treatment response. *J Clin Psychopharmacol* 2012; 32:441-8.
7. Jaquenoud Sirot E et al. ABCB1 and cytochrome P450 polymorphisms: clinical pharmacogenetics of clozapine. *J Clin Psychopharmacol* 2009;29:318-26.
8. Melkersson KI et al. Impact of CYP1A2 and CYP2D6 polymorphisms on drug metabolism and on insulin and lipid elevations and insulin resistance in clozapine-treated patients. *J Clin Psychiatry* 2007;68:697-704.
9. Dettling M et al. Long-term therapeutic drug monitoring of clozapine and metabolites in psychiatric in- and outpatients. *Psychopharmacology* 2000;152:80-86.
10. Dettling M et al. Clozapine-induced agranulocytosis and hereditary polymorphisms of clozapine metabolizing enzymes: no association with myeloperoxidase and cytochrome P4502D6. *Pharmacopsychiatry* 2000;33:218-20.
11. Arranz MJ et al. Cytochrome P4502D6 genotype does not determine response to clozapine. *Br J Clin Pharmacol* 1995;39:417-20.
12. Dahl ML et al. Disposition of clozapine in man: lack of association with debrisoquine and S-mephenytoin hydroxylation polymorphisms. *Br J Clin Pharmacol* 1994;37:71-4.
13. SmPC Clozaril (VS).

Date 13-09-2021

CYP2D6 UM: clozapine

[2378](#)

NO action is required for this gene-drug interaction.

The genetic variation has a small effect on the plasma concentration of clozapine, but there are no clinical consequences.

Literature:

1. Ortega-Vázquez A et al. Alcohol intake potentiates clozapine adverse effects associated to CYP1A2*1C in patients with refractory psychosis. *Drug Dev Res* 2020 Dec 17 (online ahead of print).
2. Lesche D et al. Impact of CYP1A2, CYP2C19, and CYP2D6 genotype- and phenoconversion-predicted enzyme activity on clozapine exposure and symptom severity. *Pharmacogenomics J* 2020;20:192-201.
3. Tóth K et al. Potential role of patients' CYP3A-status in clozapine pharmacokinetics. *Int J Neuropsychopharmacol* 2017;20:529-37.
4. Jaquenoud Sirot E et al. ABCB1 and cytochrome P450 polymorphisms: clinical pharmacogenetics of clozapine. *J Clin Psychopharmacol* 2009;29:318-26.
5. Dettling M et al. Long-term therapeutic drug monitoring of clozapine and metabolites in psychiatric in- and outpatients. *Psychopharmacology* 2000;152:80-86.
6. Dettling M et al. Clozapine-induced agranulocytosis and hereditary polymorphisms of clozapine metabolizing enzymes: no association with myeloperoxidase and cytochrome P4502D6. *Pharmacopsychiatry* 2000;33:218-20.

Date 13-09-2021

CYP2D6 IM: codeine

[2415](#)

The genetic variation reduces the conversion of codeine to morphine. This can result in reduced analgesia.

Recommendation:

- For COUGH:
 - no action required
- For PAIN:

It is not possible to offer adequately substantiated advice for dose adjustment based on the limited available literature for this phenotype.

- be alert to a reduced effectiveness
- in the case of inadequate effectiveness:
 - try a dose increase
 - if this does not work: choose an alternative
- Do not select tramadol, as this is also metabolised by CYP2D6
- Morphine is not metabolised by CYP2D6.
- Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in analgesia in patients.
- if no alternative is selected: advise the patient to report inadequate analgesia

Literature:

1. Baber M et al. The pharmacogenetics of codeine pain relief in the postpartum period. *Pharmacogenomics J* 2015;15:430-5.
2. Prows CA et al. Codeine-related adverse drug reactions in children following tonsillectomy: a prospective study. *Laryngoscope* 2014;124:1242-50.
3. Kelly LE et al. A clinical tool for reducing central nervous system depression among neonates exposed to codeine through breast milk. *PLoS One* 2013;8:e70073.
4. VanderVaart S et al. CYP2D6 polymorphisms and codeine analgesia in postpartum pain management: a pilot study. *Ther Drug Monit* 2011;33:425-32.
5. Williams DG et al. Pharmacogenetics of codeine metabolism in an urban population of children and its implications for analgesic reliability. *Br J Anaesth* 2002;89:839-45.
6. Tseng CY et al. Formation of morphine from codeine in Chinese subjects of different CYP2D6 genotypes. *Clin Pharmacol Ther* 1996;60:177-82.
7. SPC Codeïnefosfaat Ratiopharm.

Date 20-11-2017

CYP2D6 PM: codeine

[2414](#)

The genetic variation reduces the conversion of codeine to morphine. This can result in reduced analgesia.

Recommendation:

- For COUGH:
 - no action required
- For PAIN:

It is not possible to offer adequately substantiated advice for dose adjustment based on the limited available literature for this phenotype.

 - choose an alternative
- Do not select tramadol, as this is also metabolised by CYP2D6
- Morphine is not metabolised by CYP2D6.
- Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in analgesia in patients.
- if an alternative is not an option: advise the patient to report inadequate analgesia.

Literature:

1. Baber M et al. The pharmacogenetics of codeine pain relief in the postpartum period. *Pharmacogenomics J* 2015;15:430-5.
2. Prows CA et al. Codeine-related adverse drug reactions in children following tonsillectomy: a prospective study. *Laryngoscope* 2014;124:1242-50.
3. Kelly LE et al. A clinical tool for reducing central nervous system depression among neonates exposed to codeine through breast milk. *PLoS One* 2013;8:e70073.
4. Sistonen J et al. Prediction of codeine toxicity in infants and their mothers using a novel combination of maternal genetic markers. *Clin Pharmacol Ther* 2012;91:692-9.
5. VanderVaart S et al. CYP2D6 polymorphisms and codeine analgesia in postpartum pain management: a pilot study. *Ther Drug Monit* 2011;33:425-32.
6. Kirchheiner J et al. Pharmacokinetics of codeine and its metabolite morphine in ultra-rapid metabolizers due to CYP2D6 duplication. *Pharmacogenomics J* 2007;7:257-65.
7. Williams DG et al. Pharmacogenetics of codeine metabolism in an urban population of children and its implications for analgesic reliability. *Br J Anaesth* 2002;89:839-45.
8. Poulsen L et al. Codeine in post-operative pain. Study of the influence of sparteine phenotype and serum concentrations of morphine and morphine-6-glucuronide. *Eur J Clin Pharmacol* 1998;54:451-4.
9. Eckhardt K et al. Same incidence of adverse drug events after codeine administration irrespective of the genetically determined differences in morphine formation. *Pain* 1998;76:27-33.
10. Mikus G et al. Effect of codeine on gastrointestinal motility in relation to CYP2D6 phenotype. *Clin Pharmacol Ther* 1997;61:459-66.
11. Hasselstrom J et al. The effect of codeine on gastrointestinal transit in extensive and poor metabolisers of debrisoquine. *Eur J Clin Pharmacol* 1997;53:145-8.

12. Poulsen L et al. Codeine and morphine in extensive and poor metabolizers of sparteine: pharmacokinetics, analgesic effect and side effects. *Eur J Clin Pharmacol* 1996;51:289-95.
13. Persson K et al. Patient-controlled analgesia (PCA) with codeine for postoperative pain relief in ten extensive metabolisers and one poor metaboliser of dextromethorphan. *Br J Clin Pharmacol* 1995;39:182-6.
14. Yue QY et al. Pharmacokinetics of codeine and its metabolites in Caucasian healthy volunteers: comparisons between extensive and poor hydroxylators of debrisoquine. *Br J Clin Pharmacol* 1991;31:635-42.
15. Desmeules J et al. Impact of environmental and genetic factors on codeine analgesia. *Eur J Clin Pharmacol* 1991;41:23-6.
16. Sindrup SH et al. Codeine increases pain thresholds to copper vapor laser stimuli in extensive but not poor metabolizers of sparteine. *Clin Pharmacol Ther* 1990;48:686- 93.
17. SPC Codeïnefosfaat Ratiopharm.

Date 20-11-2017

CYP2D6 UM: codeine

[2416](#)

The genetic variation increases the conversion of codeine to morphine. This can result in an increase in side effects. Death has occurred in children who received analgesic doses. One adult with reduced kidney function and co-medication with two CYP3A4 inhibitors became comatose after use of codeine for a cough.

Recommendation:

- DOSES HIGHER THAN 20 mg every 6 hours for adults and 10 mg every 6 hours for children aged 12 years or older AND/OR ADDITIONAL RISK FACTORS, such as co-medication with CYP3A4 inhibitors and/or reduced kidney function:
Codeine is contra-indicated
 - if possible, select an alternative
 - For PAIN: do not select tramadol, as this is also metabolised by CYP2D6.
Morphine is not metabolised by CYP2D6.
Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in side effects in patients.
 - For COUGH: noscapine is not metabolised by CYP2D6.
- DOSES LOWER THAN OR EQUAL TO 20 mg every 6 hours for adults and 10 mg every 6 hours for children aged 12 years or older AND NO ADDITIONAL RISK FACTORS, such as co-medication with CYP3A4 inhibitors and/or reduced kidney function:
 - no action required

Literature:

1. Baber M et al. The pharmacogenetics of codeine pain relief in the postpartum period. *Pharmacogenomics J* 2015;15:430-5.
2. Ray JG et al. Risk of overdose and death following codeine prescription among immigrants. *J Epidemiol Community Health* 2014;68:1057-63.
3. Prows CA et al. Codeine-related adverse drug reactions in children following tonsillectomy: a prospective study. *Laryngoscope* 2014;124:1242-50.
4. Kelly LE et al. A clinical tool for reducing central nervous system depression among neonates exposed to codeine through breast milk. *PLoS One* 2013;8:e70073.
5. Kelly LE et al. More codeine fatalities after tonsillectomy in North American children. *Pediatrics* 2012;129:e1343-7.
6. Sistonen J et al. Prediction of codeine toxicity in infants and their mothers using a novel combination of maternal genetic markers. *Clin Pharmacol Ther* 2012;91:692-9.
7. VanderVaart S et al. CYP2D6 polymorphisms and codeine analgesia in postpartum pain management: a pilot study. *Ther Drug Monit* 2011;33:425-32.
8. Ciszkowski C et al. Codeine, ultrarapid-metabolism genotype, and postoperative death. *N Engl J Med* 2009;361:827-8.
9. Madadi P et al. Pharmacogenetics of neonatal opioid toxicity following maternal use of codeine during breastfeeding: a case-control study. *Clin Pharmacol Ther* 2009;85:31-5.
10. Koren G et al. Pharmacogenetics of morphine poisoning in a breastfed neonate of a codeine-prescribed mother. *Lancet* 2006;368:704.
11. Kirchheiner J et al. Pharmacokinetics of codeine and its metabolite morphine in ultra-rapid metabolizers due to CYP2D6 duplication. *Pharmacogenomics J* 2007;7:257-65.
12. Gasche Y et al. Codeine intoxication associated with ultrarapid CYP2D6 metabolism. *N Engl J Med* 2004;351:2827-31.
13. Dalen P et al. Quick onset of severe abdominal pain after codeine in an ultrarapid metabolizer of debrisoquine. *Ther Drug Monit* 1997;19:543-4.
14. European Medicines Agency. Restrictions on use of codeine for pain relief in children – CMDh endorses PRAC recommendation. 28-06-13.
15. SPC Codeïnefosfaat Ratiopharm.

16. SPC Codeine Sulfate Tablets (VS).

Date 20-11-2017

CYP2D6 IM: disopyramide

[2926](#)

This is NOT a gene-drug interaction.

Literature:

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Date 12-09-2022

CYP2D6 PM: disopyramide

[2925](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2D6 UM: disopyramide

[2927](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2C19 IM: doxepine

[6941](#)

NO action is required for this gene-drug interaction.

The gene variation has an effect on the exposure to doxepin, but not on the exposure to doxepin + the active metabolite nordoxepin, which determines the effect and side effects.

Literature:

1. Kirchheiner J et al. Contributions of CYP2D6, CYP2C9 and CYP2C19 to the biotransformation of E-and Z-doxepin in healthy volunteers. Pharmacogenetics 2002;12:571- 80.

Date 08-02-2024

CYP2C19 PM: doxepine

[6942](#)

NO action is required for this gene-drug interaction.

The gene variation has an effect on the exposure to doxepin, but not on the exposure to doxepin + the active metabolite nordoxepin, which determines the effect and side effects.

Literature:

1. Kirchheiner J et al. Contributions of CYP2D6, CYP2C9 and CYP2C19 to the biotransformation of E-and Z-doxepin in healthy volunteers. Pharmacogenetics 2002;12:571- 80.
2. SmPC Silenor (VS).

Date 08-02-2024

CYP2C19 UM: doxepine

[6943](#)

NO action is required for this gene-drug interaction.

The gene variations have an effect on the exposure to doxepin, but not on the exposure to doxepin + the active metabolite nordoxepin, which determines the effect and side effects.

Literature:

1. Kirchheiner J et al. Contributions of CYP2D6, CYP2C9 and CYP2C19 to the biotransformation of E- and Z-doxepin in healthy volunteers. Pharmacogenetics 2002;12:571-

Date 08-02-2024

CYP2D6 IM: doxepine

[2596](#)

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of doxepin and the active metabolite nordoxepin.

- use 80% of the standard dose and monitor the effect and side effects or the plasma concentrations of doxepin and nordoxepin in order to set the maintenance dose.

Literature:

1. Kirchheiner J et al. Contributions of CYP2D6, CYP2C9 and CYP2C19 to the biotransformation of E- and Z-doxepin in healthy volunteers. Pharmacogenetics 2002;12:571- 80.

Date 08-02-2024

CYP2D6 PM: doxepine

[2597](#)

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of doxepin and the active metabolite nordoxepin.

- use 40% of the standard dose and monitor the effect and side effects or the plasma concentrations of doxepin and nordoxepin in order to set the maintenance dose.

Literature:

1. Koski A et al. A fatal doxepin poisoning associated with a defective CYP2D6 genotype. Am J Forensic Med Pathol 2007;28:259-61.
2. Kirchheiner J et al. Impact of the CYP2D6 ultra-rapid metabolizer genotype on doxepin pharmacokinetics and serotonin in platelets. Pharmacogenet Genomics 2005;15:579-87.
3. Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. Eur J Clin Pharmacol 2004;60:329-36.
4. Kirchheiner J et al. Contributions of CYP2D6, CYP2C9 and CYP2C19 to the biotransformation of E- and Z-doxepin in healthy volunteers. Pharmacogenetics 2002;12:571- 80.
5. Tacke U et al. Debrisoquine hydroxylation phenotypes of patients with high versus low to normal serum antidepressant concentrations. J Clin Psychopharmacol 1992;12:262-7.
6. SmPC Silenor (VS).

Date 08-02-2024

CYP2D6 UM: doxepine

[2598](#)

The risk of ineffectiveness and cardiotoxic side effects may be increased. The gene variation leads to reduced plasma concentrations of doxepin and the active metabolite nordoxepin and an increase in the plasma concentrations of the potentially cardiotoxic hydroxy metabolites.

- double the standard dose and monitor the effect and side effects or the plasma concentrations of doxepin and nordoxepin in order to set the maintenance dose

- if a dose increase is not wanted due to the potentially cardiotoxic hydroxy metabolites: avoid doxepin. Antidepressants that are not metabolised by CYP2D6, or to a lesser extent, include citalopram and sertraline.

Literature:

1. Kirchheiner J et al. Impact of the CYP2D6 ultra-rapid metabolizer genotype on doxepin pharmacokinetics and serotonin in platelets. Pharmacogenet Genomics 2005;15:579-87.

Date 08-02-2024

CYP2D6 IM: duloxetine

[2435](#)

This is NOT a gene-drug interaction.

Literature:

1. Zastrozhin et al. Impact of polymorphism of CYP2D6 on equilibrium concentration of duloxetine in patients suffering from major depressive disorder. *Psychopharmacol Bull* 2020;50:47-57.
2. Kamei S et al. Rapid onset of syndrome of inappropriate antidiuretic hormone secretion induced by duloxetine in an elderly type 2 diabetic patient with painful diabetic neuropathy. *J Diabetes Investig* 2015;6:343-5.
3. Lobo ED et al. Pharmacokinetics of orally administered duloxetine in children and adolescents with major depressive disorder. *Clin Pharmacokinet* 2014;53:731-40.
4. Beatty NC et al. Pharmacogenetic workup of perioperative serotonin syndrome. *J Clin Anesth* 2013;25:662-5.
5. Tianmei S et al. Pharmacokinetics and tolerability of duloxetine following oral administration to healthy Chinese subjects. *Clin Pharmacokinet* 2007;46:767-75.

Date 14-11-2022

CYP2D6 PM: duloxetine

[2436](#)

This is NOT a gene-drug interaction.

Literature:

1. Kuzin M et al. The role of the poor metabolizer genotype CYP2D6 and CYP1A2 phenotype in the pharmacokinetics of duloxetine and venlafaxine-a case report. *Basic Clin Pharmacol Toxicol* 2020;127:354-7.
2. Ahmed AT et al. Pharmacokinetic-pharmacodynamic interaction associated with venlafaxine-XR remission in patients with major depressive disorder with history of citalopram / escitalopram treatment failure. *J Affect Disord* 2019;246:62-8.
3. Lobo ED et al. Pharmacokinetics of orally administered duloxetine in children and adolescents with major depressive disorder. *Clin Pharmacokinet* 2014;53:731-40.
4. Chan C et al. Duloxetine pharmacokinetics are similar in Japanese and Caucasian subjects. *Br J Clin Pharmacol* 2007;63:310-4.
5. SmPC Cymbalta.

Date 14-11-2022

CYP2D6 UM: duloxetine

[2437](#)

This is NOT a gene-drug interaction.

Literature:

1. Ahmed AT et al. Pharmacokinetic-pharmacodynamic interaction associated with venlafaxine-XR remission in patients with major depressive disorder with history of citalopram / escitalopram treatment failure. *J Affect Disord* 2019;246:62-8.
2. Lobo ED et al. Pharmacokinetics of orally administered duloxetine in children and adolescents with major depressive disorder. *Clin Pharmacokinet* 2014;53:731-40.

Date 14-11-2022

CYP2B6 IM: efavirenz

[4523](#)

Genetic variations increase the efavirenz plasma concentration and therefore the risk of side effects. However, the efavirenz plasma concentration remains within the therapeutic range for the majority of patients.

Recommendation:

- Determine the efavirenz plasma concentration if side effects occur and reduce the dose if needed. In 14 IM adults, a dose reduction to 400 mg/day (2/3rd of the standard dose) was sufficient to achieve therapeutic plasma concentrations and to reduce or resolve side effects.

The therapeutic range established for efavirenz is 1000-4000 ng/ml.

Literature:

1. Vujkovic M et al. CYP2B6 516G>T minor allele protective of late virologic failure in efavirenz-treated HIV-infected patients in Botswana. *J Acquir Immune Defic Syndr* 2017 May 5 [Epub ahead of print].
2. Leger P et al. Pharmacogenetics of efavirenz discontinuation for reported central nervous system symptoms appears to differ by race. *Pharmacogenet Genomics* 2016;26:473-80.
3. Cusato J et al. Efavirenz pharmacogenetics in a cohort of Italian patients. *Int J Antimicrob Agents* 2016;47:117-23.
4. Dickinson L et al. Comprehensive pharmacokinetic, pharmacodynamic and pharmacogenetic evaluation of once-daily efavirenz 400 and 600 mg in treatment-naïve HIV- infected patients at 96 weeks: results of the ENCORE1 study. *Clin Pharmacokinet* 2016;55:861-73.
5. Swart M et al. An expanded analysis of pharmacogenetics determinants of efavirenz response that includes 3'-UTR single nucleotide polymorphisms among black South African HIV/AIDS patients. *Front Genet* 2016;6:356.
6. Meng X et al. Effect of CYP2B6 gene polymorphisms on efavirenz plasma concentrations in Chinese patients with HIV infection. *PLoS One* 2015;10:e0130583.
7. Haas DW et al. Functional CYP2B6 variants and virologic response to an efavirenz-containing regimen in Port-au-Prince, Haiti. *J Antimicrob Chemother* 2014;69:2187-90.
8. Martín AS et al. Dose reduction of efavirenz: an observational study describing cost-effectiveness, pharmacokinetics and pharmacogenetics. *Pharmacogenomics* 2014;15:997-1006.
9. Bertrand J et al. Dependence of efavirenz- and rifampicin-isoniazid-based antituberculosis treatment drug-drug interaction on CYP2B6 and NAT2 genetic polymorphisms: ANRS 12154 study in Cambodia. *J Infect Dis* 2014;209:399-408.
10. Sarfo FS et al. Pharmacogenetic associations with plasma efavirenz concentrations and clinical correlates in a retrospective cohort of Ghanaian HIV-infected patients. *J Antimicrob Chemother* 2014;69:491-9. PubMed PMID: 24080498.
11. Ngaimisi E et al. Importance of ethnicity, CYP2B6 and ABCB1 genotype for efavirenz pharmacokinetics and treatment outcomes: a parallel-group prospective cohort study in two sub-Saharan Africa populations. *PLoS One* 2013;8:e67946. PubMed PMID: 23861838.
12. Yimer G et al. High plasma efavirenz level and CYP2B6*6 are associated with efavirenz-based HAART-induced liver injury in the treatment of naïve HIV patients from Ethiopia: a prospective cohort study. *Pharmacogenomics J* 2012;12:499-506. PubMed PMID: 21862974.
13. Mugusi S et al. Liver enzyme abnormalities and associated risk factors in HIV patients on efavirenz-based HAART with or without tuberculosis co-infection in Tanzania. *PLoS One* 2012;7:e40180. PubMed PMID: 22808112.
14. Wyen C et al. Cytochrome P450 2B6 (CYP2B6) and constitutive androstane receptor (CAR) polymorphisms are associated with early discontinuation of efavirenz- containing regimens. *J Antimicrob Chemother* 2011;66:2092-8. PubMed PMID: 21715435.
15. Carr DF et al. Haplotype structure of CYP2B6 and association with plasma efavirenz concentrations in a Chilean HIV cohort. *J Antimicrob Chemother* 2010;65:1889-93. PubMed PMID: 20639527.
16. Gatanaga H et al. Successful efavirenz dose reduction in HIV type 1-infected individuals with cytochrome P450 2B6 6 and 26. *Clin Infect Dis* 2007;45:1230-7. PubMed PMID: 17918089.
17. Haas DW et al. Pharmacogenetics of long-term responses to antiretroviral regimens containing efavirenz and/or nelfinavir: an Adult Aids Clinical Trials Group study. *J Infect Dis* 2005;192:1931-42. PubMed PMID: 16267764.

Date 05-03-2018

CYP2B6 PM: efavirenz

[4524](#)

Genetic variations increase the risk of side effects. The standard dose leads to an efavirenz concentration in the toxic range in the majority of patients with this genotype.

Recommendation:

- Efavirenz in MONOpreparation, adults and children FROM 40 KG:
 - Body mass index LESS THAN or EQUAL to 25:
 - The recommended initial dose is 400 mg/day and this dose should be titrated to plasma concentration if needed (further reduction to 200 mg/day or in rare cases an increase to 600 mg/day).
 - The therapeutic range established for efavirenz is 1000-4000 ng/ml.
 - Body mass index GREATER than 25:
 - The recommended initial dose is 600 mg/day and this dose should be titrated to plasma concentration if needed (reduction to 400 or 200 mg/day).
 - The therapeutic range established for efavirenz is 1000-4000 ng/ml.
- Efavirenz in MONOpreparation, children LIGHTER THAN 40 KG:
 - Start with the standard dose and titrate this dose to plasma concentration if needed.
 - In adults, therapeutic plasma concentrations were achieved at either 2/3rd of the standard dose (1/3rd of

the patients) or 1/3rd of the standard dose (2/3rd of the patients). In children younger than 3 years, therapeutic plasma concentrations were achieved at doses of approximately 10 mg/kg per day (as capsules) (100 mg/day for 7-14 kg and 150 mg/day for 14-17 kg; 50-75% of the standard dose). The therapeutic range established for efavirenz is 1000-4000 ng/ml.

- Efavirenz in COMBINATION preparation:

- Initiate the combination preparation and titrate the efavirenz dose to plasma concentration if needed (reduction to 400 or 200 mg/day)

The therapeutic range established for efavirenz is 1000-4000 ng/ml.

Note: the dosing recommendations above are based on PM patients with the *6/*6 genotype. There is evidence that the *18/*18 genotype in PM patients (only present in negroid patients) may require greater dose reductions.

Considerations:

Detailed justification for the recommendation is contained in the risk analysis. The considerations used for adults are also given below.

The median or mean plasma concentrations or AUC in PM patients are above the therapeutic range, except in 3 studies with low efavirenz plasma concentrations in EM patients (2 of the 3 studies performed in Africa and 1 study in the United States and Italy). A recent study showed a similar virological response for efavirenz 400 and 600 mg/day in patients not selected on genotype. The risk of underdose is therefore very small if the initial dose is reduced to 400 mg/day. Two small studies showed that dose reductions did not reduce the efficacy (HIV remained undetectable), but side effects did reduce in 24 PM patients.

Compliance improves with administration of a combination preparation and the absence of unnecessary side effects due to excessive plasma concentrations.

Consideration to CYP2B6 inducers such as rifampicin is not needed in PM patients. The significantly low or absent metabolic capacity of CYP2B6 makes induction of little to no relevance. Moreover, the effects of enzyme induction by rifampicin and enzyme inhibition by isoniazid on efavirenz plasma concentrations seem to largely cancel each other out, independent of the CYP2B6 phenotype of the patient.

Literature:

1. Vujkovic M et al. CYP2B6 516G>T minor allele protective of late virologic failure in efavirenz-treated HIV-infected patients in Botswana. *J Acquir Immune Defic Syndr* 2017 May 5 [Epub ahead of print].
2. Bolton Moore C et al. CYP2B6 genotype-directed dosing is required for optimal efavirenz exposure in children 3-36 months with HIV infection. *AIDS* 2017;31:1129-1136.
3. Leger P et al. Pharmacogenetics of efavirenz discontinuation for reported central nervous system symptoms appears to differ by race. *Pharmacogenet Genomics* 2016;26:473-80.
4. Cusato J et al. Efavirenz pharmacogenetics in a cohort of Italian patients. *Int J Antimicrob Agents* 2016;47:117-23.
5. Dickinson L et al. Comprehensive pharmacokinetic, pharmacodynamic and pharmacogenetic evaluation of once-daily efavirenz 400 and 600 mg in treatment-naïve HIV- infected patients at 96 weeks: results of the ENCORE1 study. *Clin Pharmacokinet* 2016;55:861-73.
6. Swart M et al. An expanded analysis of pharmacogenetics determinants of efavirenz response that includes 3'-UTR single nucleotide polymorphisms among black South African HIV/AIDS patients. *Front Genet* 2016;6:356.
7. Meng X et al. Effect of CYP2B6 gene polymorphisms on efavirenz plasma concentrations in Chinese patients with HIV infection. *PLoS One* 2015;10:e0130583.
8. Haas DW et al. Functional CYP2B6 variants and virologic response to an efavirenz-containing regimen in Port-au-Prince, Haiti. *J Antimicrob Chemother* 2014;69:2187-90.
9. Martín AS et al. Dose reduction of efavirenz: an observational study describing cost-effectiveness, pharmacokinetics and pharmacogenetics. *Pharmacogenomics* 2014;15:997-1006.
10. Bertrand J et al. Dependence of efavirenz- and rifampicin-isoniazid-based antituberculosis treatment drug-drug interaction on CYP2B6 and NAT2 genetic polymorphisms: ANRS 12154 study in Cambodia. *J Infect Dis* 2014;209:399-408.
11. Sarfo FS et al. Pharmacogenetic associations with plasma efavirenz concentrations and clinical correlates in a retrospective cohort of Ghanaian HIV-infected patients. *J Antimicrob Chemother* 2014;69:491-9. PubMed PMID: 24080498.
12. Ngaimisi E et al. Importance of ethnicity, CYP2B6 and ABCB1 genotype for efavirenz pharmacokinetics and treatment outcomes: a parallel-group prospective cohort study in two sub-Saharan Africa populations. *PLoS One* 2013;8:e67946. PubMed PMID: 23861838.
13. Yimer G et al. High plasma efavirenz level and CYP2B6*6 are associated with efavirenz-based HAART-induced liver injury in the treatment of naïve HIV patients from Ethiopia: a prospective cohort study. *Pharmacogenomics J* 2012;12:499-506. PubMed PMID: 21862974.
14. Mugusi S et al. Liver enzyme abnormalities and associated risk factors in HIV patients on efavirenz-based HAART with or without tuberculosis co-infection in Tanzania. *PLoS One* 2012;7:e40180. PubMed PMID: 22808112.
15. Wyen C et al. Cytochrome P450 2B6 (CYP2B6) and constitutive androstane receptor (CAR) polymorphisms are associated with early discontinuation of efavirenz- containing regimens. *J Antimicrob Chemother* 2011;66:2092-8. PubMed PMID: 21715435.
16. Ribaud HJ et al. Effect of CYP2B6, ABCB1, and CYP3A5 polymorphisms on efavirenz pharmacokinetics and treatment response: an AIDS Clinical Trials Group study. *J Infect Dis*

- 2010;202:717-22. PubMed PMID: 20662624.
17. Carr DF et al. Haplotype structure of CYP2B6 and association with plasma efavirenz concentrations in a Chilean HIV cohort. J Antimicrob Chemother 2010;65:1889-93. PubMed PMID: 20639527.
 18. Gatanaga H et al. Successful efavirenz dose reduction in HIV type 1-infected individuals with cytochrome P450 2B6 *6 and *26. Clin Infect Dis 2007;45:1230-7. PubMed PMID: 17918089.
 19. Haas DW et al. Pharmacogenetics of long-term responses to antiretroviral regimens containing efavirenz and/or nelfinavir: an Adult Aids Clinical Trials Group study. J Infect Dis 2005;192:1931-42. PubMed PMID: 16267764.
 20. SPC's Efavirenz Mylan en Sustiva (VS).
 21. ENCORE1 Study Group. Efficacy of 400 mg efavirenz versus standard 600 mg dose in HIV-infected, antiretroviral-naïve adults (ENCORE1): a randomised, double-blind, placebo-controlled, non-inferiority trial. Lancet 2014;383:1474-82.

Date 05-03-2018

CYP2D6 IM: eliglustat

[5705](#)

The gene variation reduces the conversion of eliglustat into inactive metabolites. However, in the absence of renal and hepatic impairment, this does not lead to a clinically significant increased risk of adverse reactions.

- MILD, MODERATE OR SEVERE RENAL IMPAIRMENT and/or MILD HEPATIC IMPAIRMENT:
Eliglustat is not recommended.
 - avoid eliglustat if possible

- OTHER:
 - no action required (i.e. same treatment as for normal metabolisers)

Literature:

1. Ruskin JN et al. How a concentration-effect analysis of data from the eliglustat thorough electrocardiographic study was used to support dosing recommendations. Mol Genet Metab 2020;131:211-8.
2. SmPCs Cerdelga (NL and USA).

Date 6-11-2023

CYP2D6 PM: eliglustat

[5704](#)

The gene variation reduces the conversion of eliglustat into inactive metabolites. This increases the risk of adverse reactions, such as a (small, dose-dependent) prolongation of the QT interval. CYP3A inhibitors and kidney and liver impairment further increase this risk.

- Co-medication with a STRONG CYP3A INHIBITOR (e.g. ketoconazole, clarithromycin, itraconazole, cobicistat, indinavir, lopinavir, ritonavir, saquinavir, telaprevir, tipranavir, posaconazole, voriconazole, telithromycin, conivaptan, boceprevir):
Eliglustat is contraindicated.
 - avoid eliglustat
- Co-medication with a MODERATE CYP3A INHIBITOR (e.g. erythromycin, ciprofloxacin, fluconazole, diltiazem, verapamil, aprepitant, atazanavir, darunavir, fosamprenavir, imatinib, cimetidine):
Eliglustat is not recommended.
 - avoid eliglustat if possible
- Co-medication with a WEAK CYP3A INHIBITOR (e.g. amlodipine, cilostazol, fluvoxamine, goldenseal, isoniazid, ranitidine, ranolazine):
 - avoid the weak CYP3A inhibitor if possible
 - if avoidance is not possible:
 - use a dose of 84 mg eliglustat once daily
 - be alert for adverse reactions
- Co-medication with a STRONG CYP3A INDUCTOR (e.g. rifampicin, carbamazepine, phenobarbital, phenytoin, rifabutin, hypericum):
Eliglustat is not recommended. Plasma concentrations may decrease to such an extent that a therapeutic effect is not achieved.
 - avoid eliglustat if possible

Note: This advice does not differ from that for normal metabolisers.

- KIDNEY and/or LIVER IMPAIRMENT:
Eliglustat is not recommended.
 - avoid eliglustat if possible

Note: This advice differs from that for normal metabolisers only in case of mild, moderate or severe kidney impairment and mild liver impairment.

- NO co-medication with a CYP3A inhibitor or strong CYP3A inducer and NO kidney and liver impairment:
- use a dose of 84 mg once daily

Literature:

1. Ruskin JN et al. How a concentration-effect analysis of data from the eliglustat thorough electrocardiographic study was used to support dosing recommendations. *Mol Genet Metab* 2020;131:211-8.
2. SmPCs Cerdelga (NL and USA).

Date 6-11-2023

CYP2D6 UM: eliglustat

[5706](#)

The normal dose is not effective. The gene variation increases the conversion of eliglustat into inactive metabolites. There are insufficient data to determine an effective dose for all UM.

Eliglustat is contraindicated.

- avoid eliglustat

Literature:

1. SPC's Cerdelga (Nederland en VS).

Date 6-11-2023

CYP2C19 IM: escitalopram

[2496](#)

The risk of QT prolongation and torsades de pointes is theoretically increased because the gene variation leads to an increased escitalopram plasma concentration. If you follow the dose recommendation below, the increased plasma concentration and the theoretically increased risk of QT prolongation will be offset.

- Do not exceed the following doses (75% of the standard maximum dose): adults < 65 years 15 mg/day, ≥65 years 7.5 mg/day

Literature:

1. Tsuchimine S et al. Effects of cytochrome P450 (CYP) 2C19 genotypes on steady-state plasma concentrations of escitalopram and its desmethyl metabolite in Japanese patients with depression. *Ther Drug Monit* 2018 Mar 22 [Epub ahead of print].
2. Jukić MM et al. Impact of CYP2C19 genotype on escitalopram exposure and therapeutic failure: a retrospective study based on 2,087 patients. *Am J Psychiatry* 2018 Jan 12 [Epub ahead of print].
3. He Q et al. Correlation between cytochrome P450 2C19 genetic polymorphism and treatment response to escitalopram in panic disorder. *Pharmacogenet Genomics* 2017;27:279-284.
4. Bishop JR et al. Escitalopram pharmacogenetics: CYP2C19 relationships with dosing and clinical outcomes in autism spectrum disorder. *Pharmacogenet Genomics* 2015:548-54.
5. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. *Psychopharmacology (Berl)* 2015;232: 2609-17.
6. Kumar Y et al. CYP2C19 variation, not citalopram dose nor serum level, is associated with QTc prolongation. *J Psychopharmacol* 2014;28:1143-8.
7. Waade RB et al. Impact of age on serum concentrations of venlafaxine and escitalopram in different CYP2D6 and CYP2C19 genotype subgroups. *Eur J Clin Pharmacol* 2014;70:933-40.
8. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. *J Psychopharmacol* 2014;28:133-41.
9. Ng C et al. Pharmacogenetic polymorphisms and response to escitalopram and venlafaxine over 8 weeks in major depression. *Hum Psychopharmacol* 2013;28:516-22.
10. Huezio-Díaz et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. *J Psychopharmacol* 2012;26:398-407.
11. Brasch-Andersen C et al. A candidate gene study of serotonergic pathway genes and pain relief during treatment with escitalopram in patients with neuropathic pain shows significant association to serotonin receptor2C (HTR2C). *Eur J Clin Pharmacol* 2011; 67:1131-7.
12. Tsai et al. Genetic polymorphisms of cytochrome P450 enzymes influence metabolism of the antidepressant escitalopram and treatment response. *Pharmacogenomics* 2010;11:537-46.
13. Jin Y et al. Effect of age, weight, and CYP2C19 genotype on escitalopram exposure. *J Clin Pharmacol* 2010;50:62-72.
14. Rudberg I et al. Impact of the ultrarapid CYP2C19*17 allele on serum concentration of escitalopram in psychiatric patients. *Clin Pharmacol Ther* 2008;83:322-7.
15. Rudberg I et al. Heterozygous mutation in CYP2C19 significantly increases the concentrations/dose

Date 14-05-2018

CYP2C19 PM: escitalopram

[2497](#)

The risk of switching to another antidepressant is increased. In addition, the risk of QT prolongation and torsades de pointes is theoretically increased because the gene variation leads to an increased escitalopram plasma concentration. If you follow the dose recommendation below, the increased plasma concentration, the theoretically increased risk of QT prolongation and the increased risk of switching to another antidepressant will be offset.

- Do not exceed the following doses (50% of the standard maximum dose): adults < 65 years 10 mg/day, ≥65 years 5 mg/day

Literature:

1. Tsuchimine S et al. Effects of cytochrome P450 (CYP) 2C19 genotypes on steady-state plasma concentrations of escitalopram and its desmethyl metabolite in Japanese patients with depression. Ther Drug Monit 2018 Mar 22 [Epub ahead of print].
2. Jukić MM et al. Impact of CYP2C19 genotype on escitalopram exposure and therapeutic failure: a retrospective study based on 2,087 patients. Am J Psychiatry 2018 Jan 12 [Epub ahead of print].
3. He Q et al. Correlation between cytochrome P450 2C19 genetic polymorphism and treatment response to escitalopram in panic disorder. Pharmacogenet Genomics 2017;27:279-284.
4. Asakura S et al. Long-term administration of escitalopram in patients with social anxiety disorder in Japan. Neuropsychiatr Dis Treat 2016;12:1817-25.
5. Bishop JR et al. Escitalopram pharmacogenetics: CYP2C19 relationships with dosing and clinical outcomes in autism spectrum disorder. Pharmacogenet Genomics 2015:548-54.
6. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. Psychopharmacology (Berl) 2015;232: 2609-17.
7. Kumar Y et al. CYP2C19 variation, not citalopram dose nor serum level, is associated with QTc prolongation. J Psychopharmacol 2014;28:1143-8.
8. Waade RB et al. Impact of age on serum concentrations of venlafaxine and escitalopram in different CYP2D6 and CYP2C19 genotype subgroups. Eur J Clin Pharmacol 2014;70:933-40.
9. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. J Psychopharmacol 2014;28:133-41.
10. Ng C et al. Pharmacogenetic polymorphisms and response to escitalopram and venlafaxine over 8 weeks in major depression. Hum Psychopharmacol 2013;28:516-22.
11. Huez-Diaz et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. J Psychopharmacol 2012;26:398-407.
12. Brasch-Andersen C et al. A candidate gene study of serotonergic pathway genes and pain relief during treatment with escitalopram in patients with neuropathic pain shows significant association to serotonin receptor2C (HTR2C). Eur J Clin Pharmacol 2011; 67:1131-7.
13. Tsai et al. Genetic polymorphisms of cytochrome P450 enzymes influence metabolism of the antidepressant escitalopram and treatment response. Pharmacogenomics 2010;11:537-46.
14. Noehr-Jensen et al. Impact of CYP2C19 phenotypes on escitalopram metabolism and an evaluation of pupillometry as a serotonergic biomarker. Eur J Clin Pharmacol 2009;65:887-94.
15. Jin Y et al. Effect of age, weight, and CYP2C19 genotype on escitalopram exposure. J Clin Pharmacol. 2010;50:62-72.
16. Rudberg I et al. Impact of the ultrarapid CYP2C19*17 allele on serum concentration of escitalopram in psychiatric patients. Clin Pharmacol Ther 2008;83:322-7.
17. SPC's Lexapro (NL en VS).

Date 14-05-2018

CYP2C19 UM: escitalopram

[2495](#)

The risk of switching to another antidepressant is increased as the gene variation leads to a reduction in the escitalopram plasma concentration.

- avoid escitalopram

Antidepressants that are not metabolised or that are metabolised to a lesser extent by CYP2C19 are, for example, paroxetine or fluvoxamine.

Literature:

1. Jukić MM et al. Impact of CYP2C19 genotype on escitalopram exposure and therapeutic failure: a retrospective study based on 2,087 patients. Am J Psychiatry 2018 Jan 12 [Epub ahead of print].
2. Bishop JR et al. Escitalopram pharmacogenetics: CYP2C19 relationships with dosing and clinical

- outcomes in autism spectrum disorder. *Pharmacogenet Genomics* 2015;548-54.
3. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. *Psychopharmacology (Berl)* 2015;232: 2609-17.
 4. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. *J Psychopharmacol* 2014;28:133-41.
 5. Huezo-Diaz et al. CYP2C19 genotype predicts steady state escitalopram concentration in GENDEP. *J Psychopharmacol* 2012;26:398-407.
 6. Brasch-Andersen C et al. A candidate gene study of serotonergic pathway genes and pain relief during treatment with escitalopram in patients with neuropathic pain shows significant association to serotonin receptor2C (HTR2C). *Eur J Clin Pharmacol* 2011; 67:1131-7.
 7. Jin Y et al. Effect of age, weight, and CYP2C19 genotype on escitalopram exposure. *J Clin Pharmacol* 2010;50:62-72.
 8. Ohlsson Rosenborg S et al. Kinetics of omeprazole and escitalopram in relation to the CYP2C19*17 allele in healthy subjects. *Eur J Clin Pharmacol* 2008 Jul 25. 4;1175-79.
 9. Rudberg I et al. Impact of the ultrarapid CYP2C19*17 allele on serum concentration of escitalopram in psychiatric patients. *Clin Pharmacol Ther* 2008;83:322-7.

Date 14-05-2018

CYP2C19 IM: esomeprazol

[2499](#)

NO action is needed for this gene-drug interaction.

Although the genetic variation leads to a higher plasma concentration of esomeprazole, there is insufficient evidence to support an effect on the therapeutic effectiveness and side effects.

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Hsu WH et al. Genetic polymorphisms of CYP2C19 and IL1B have no influence on esomeprazole treatment for mild erosive esophagitis. *Kaohsiung J Med Sci* 2015;31:255- 9.
3. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of H. pylori infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
4. Lee VW et al. Pharmacogenetics of esomeprazole or rabeprazole-based triple therapy in Helicobacter pylori eradication in Hong Kong non-ulcer dyspepsia Chinese subjects. *J Clin Pharm Ther* 2010;35:343-50.
5. Hunfeld NG et al. A comparison of the acid-inhibitory effects of esomeprazole and pantoprazole in relation to pharmacokinetics and CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2010;31:150-9.
6. Lou HY et al. Optimal dose regimens of esomeprazole for gastric acid suppression with minimal influence of the CYP2C19 polymorphism. *Eur J Clin Pharmacol* 2009;65:55-64.
7. Sheu BS et al. Body mass index can determine the healing of reflux esophagitis with Los Angeles Grades C and D by esomeprazole. *Am J Gastroenterol* 2008;103:2209-14.
8. Li ZS et al. Effect of esomeprazole and rabeprazole on intragastric pH in healthy Chinese: an open, randomized crossover trial. *J Gastroenterol Hepatol* 2007;22:815-20.
9. Schwab M et al. Esomeprazole-induced healing of gastroesophageal reflux disease is unrelated to the genotype of CYP2C19: evidence from clinical and pharmacokinetic data. *Clin Pharmacol Ther* 2005;78:627-34.
10. Kuo CH et al. Efficacy of levofloxacin-based rescue therapy for Helicobacter pylori infection after standard triple therapy: a randomized controlled trial. *J Antimicrob Chemother* 2009;63:1017-24.
11. Kang JM et al. Effect of the CYP2C19 polymorphism on the eradication rate of Helicobacter pylori infection by 7-day triple therapy with regular proton pump inhibitor dosage. *J Gastroenterol Hepatol* 2008;23:1287-91.
12. Miehlik S et al. One-week once-daily triple therapy with esomeprazole, moxifloxacin, and rifabutin for eradication of persistent Helicobacter pylori resistant to both metronidazole and clarithromycin. *Helicobacter* 2008;13:69-74.
13. Miehlik S et al. Randomized trial of rifabutin-based triple therapy and high-dose dual therapy for rescue treatment of Helicobacter pylori resistant to both metronidazole and clarithromycin. *Aliment Pharmacol Ther* 2006;24:395-403.
14. Sheu BS et al. Esomeprazole 40 mg twice daily in triple therapy and the efficacy of Helicobacter pylori eradication related to CYP2C19 metabolism. *Aliment Pharmacol Ther* 2005;21:283-8.

Date 05-03-2018

CYP2C19 PM: esomeprazol

[2500](#)

NO action is needed for this gene-drug interaction.

Although the genetic variation leads to a higher plasma concentration of esomeprazole, there is insufficient evidence to support an effect on the therapeutic effectiveness and side effects

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Hsu WH et al. Genetic polymorphisms of CYP2C19 and IL1B have no influence on esomeprazole treatment for mild erosive esophagitis. *Kaohsiung J Med Sci* 2015;31:255- 9.
3. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
4. Lee VW et al. Pharmacogenetics of esomeprazole or rabeprazole-based triple therapy in *Helicobacter pylori* eradication in Hong Kong non-ulcer dyspepsia Chinese subjects. *J Clin Pharm Ther* 2010;35:343-50.
5. Lou HY et al. Optimal dose regimens of esomeprazole for gastric acid suppression with minimal influence of the CYP2C19 polymorphism. *Eur J Clin Pharmacol* 2009;65:55-64.
6. Sheu BS et al. Body mass index can determine the healing of reflux esophagitis with Los Angeles Grades C and D by esomeprazole. *Am J Gastroenterol* 2008;103:2209-14.
7. Li ZS et al. Effect of esomeprazole and rabeprazole on intragastric pH in healthy Chinese: an open, randomized crossover trial. *J Gastroenterol Hepatol* 2007;22:815-20.
8. Schwab M et al. Esomeprazole-induced healing of gastroesophageal reflux disease is unrelated to the genotype of CYP2C19: evidence from clinical and pharmacokinetic data. *Clin Pharmacol Ther* 2005;78:627-34.
9. Kuo CH et al. Efficacy of levofloxacin-based rescue therapy for *Helicobacter pylori* infection after standard triple therapy: a randomized controlled trial. *J Antimicrob Chemother* 2009;63:1017-24.
10. Kang JM et al. Effect of the CYP2C19 polymorphism on the eradication rate of *Helicobacter pylori* infection by 7-day triple therapy with regular proton pump inhibitor dosage. *J Gastroenterol Hepatol* 2008;23:1287-91.
11. Miehlke S et al. One-week once-daily triple therapy with esomeprazole, moxifloxacin, and rifabutin for eradication of persistent *Helicobacter pylori* resistant to both metronidazole and clarithromycin. *Helicobacter* 2008;13:69-74.
12. Miehlke S et al. Randomized trial of rifabutin-based triple therapy and high-dose dual therapy for rescue treatment of *Helicobacter pylori* resistant to both metronidazole and clarithromycin. *Aliment Pharmacol Ther* 2006;24:395-403.
13. Sheu BS et al. Esomeprazole 40 mg twice daily in triple therapy and the efficacy of *Helicobacter pylori* eradication related to CYP2C19 metabolism. *Aliment Pharmacol Ther* 2005;21:283-8.
14. SPC Nexium (Nederlands en Amerikaans).

Date 05-03-2018

CYP2C19 UM: esomeprazol

[2501](#)

NO action is required for this gene-drug interaction.

Although the genetic variation may lead to faster inactivation of esomeprazole, there is insufficient evidence to support an effect on the therapeutic effectiveness and side effects.

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Dury S et al. Agranulocytosis induced by proton pump inhibitors. *J Clin Gastroenterol* 2012;46:859.
3. Hunfeld NG et al. A comparison of the acid-inhibitory effects of esomeprazole and pantoprazole in relation to pharmacokinetics and CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2010;31:150-9.

Date 05-03-2018

CYP2C9 IM ANDERS: fenprocoumon

[2528](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
8. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
9. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
10. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
11. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
12. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
13. Bohrer T et al. Left ventricular non-compaction associated with a genetic variant of the CYP2C9 gene. *Heart Lung Circ* 2006;15:269-71.
14. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.
15. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
16. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
17. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
18. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
19. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
20. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
21. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

Date 14-05-2018

CYP2C9 PM ANDERS: fenprocoumon

[2529](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma

- concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
8. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
 9. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
 10. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
 11. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
 12. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
 13. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.
 14. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
 15. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
 16. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
 17. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
 18. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
 19. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
 20. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

Date 14-05-2018

CYP2C9*1/*2: fenprocoumon

[2523](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
8. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
9. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
10. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
11. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
12. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
13. Bohrer T et al. Left ventricular non-compaction associated with a genetic variant of the CYP2C9 gene. *Heart Lung Circ* 2006;15:269-71.
14. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.

15. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
16. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
17. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
18. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
19. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
20. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
21. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

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CYP2C9*1/*3: fenprocoumon

[2524](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
8. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
9. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
10. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
11. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
12. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
13. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.
14. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
15. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
16. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
17. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
18. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
19. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
20. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

CYP2C9*2/*2: fenprocoumon[2525](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose and possibly in an extension of the time required to achieve a stable INR. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
8. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
9. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
10. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
11. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.
12. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
13. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
14. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
15. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
16. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
17. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.

Date 14-05-2018

CYP2C9*2/*3: fenprocoumon[2526](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
4. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
5. Abduljalil K. et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/pharmacodynamic model. *Clin Pharmacokinet*

2013;52:359-71.

6. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
7. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
8. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
9. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
10. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
11. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
12. zu Schwabedissen CM et al. Obesity is associated with a slower response to initial phenprocoumon therapy whereas CYP2C9 genotypes are not. *Eur J Clin Pharmacol* 2006;62:713-20.
13. Visser LE et al. Allelic variants of cytochrome P450 2C9 modify the interaction between nonsteroidal anti-inflammatory drugs and coumarin anticoagulants. *Clin Pharmacol Ther* 2005;77:479-85.
14. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
15. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
16. Visser LE et al. The risk of bleeding complications in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Thromb Haemost* 2004;92:61-6.
17. Visser LE et al. The risk of overanticoagulation in patients with cytochrome P450 CYP2C9*2 or CYP2C9*3 alleles on acenocoumarol or phenprocoumon. *Pharmacogenetics* 2004;14:27-33.
18. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
19. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

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CYP2C9*3/*3: fenprocoumon

[2527](#)

NO action is required for this gene-drug interaction.

The genetic variation can result in a reduction in the required maintenance dose. However, there is not enough evidence to confirm that this causes problems with normal initiation of the therapy (i.e. frequent INR monitoring).

Literature:

1. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
2. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
3. Werner D et al. Pharmacogenetic characteristics of patients with complicated phenprocoumon dosing. *Eur J Clin Pharmacol* 2009;65:783-8.
4. Schalekamp T et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
5. Schalekamp T et al. Effects of cytochrome P450 2C9 polymorphisms on phenprocoumon anticoagulation status. *Clin Pharmacol Ther* 2004;76:409-17.
6. Ufer M et al. Genetic polymorphisms of cytochrome P450 2C9 causing reduced phenprocoumon (S)-7-hydroxylation in vitro and in vivo. *Xenobiotica* 2004;34:847-59.
7. Kirchheiner J et al. Effects of CYP2C9 polymorphisms on the pharmacokinetics of R- and S-phenprocoumon in healthy volunteers. *Pharmacogenetics* 2004;14:19-26.
8. Hummers-Pradier E et al. Determination of bleeding risk using genetic markers in patients taking phenprocoumon. *Eur J Clin Pharmacol* 2003;59:213-9.

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VKORC1 -1639 AA: fenprocoumon

[2565](#)

An INR ≥ 6 , resulting in an increased risk of bleeding, occurs in 17% of these patients with standard regulation by the Anticoagulation Clinic.

The genetic variation increases the sensitivity to phenprocoumon.

- Monitoring by a ANTICOAGULATION CLINIC:
 - recommend to use 50% of the standard initial dose
- NO monitoring by a anticoagulation clinic:
 - recommend to use 50% of the standard initial dose
 - recommend more frequent monitoring of the INR

For patients younger than 75 years, the initial dose and the maintenance dose can be calculated using an algorithm as found in EU-PACT:

see <https://www.knmp.nl/patientenzorg/medicatiebewaking/farmacogenetica> for a calculation tool in the form of an Excel file.

However, for patients aged 75 years and older, this algorithm increases the risk of an INR above the therapeutic range compared to an algorithm without gene variations. Therefore, use of this algorithm is not recommended for these patients.

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.
3. Botton et al. A new algorithm for weekly phenprocoumon dose variation in a southern Brazilian population: role for CYP2C9, CYP3A4/5 and VKORC1 genes polymorphisms. *Basic Clin Pharmacol Toxicol* 2014;114:323-9.
4. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
5. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
6. Abduljalil K et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/ pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
7. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
8. Verhoef TI et al. Long-term anticoagulant effects of CYP2C9 and VKORC1 genotypes in phenprocoumon users. *J Thromb Haemost*. 2012;10:2610-2.
9. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
10. Teichert M et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1, CYP2C9, and CYP4F2 genes. *Pharmacogenet Genomics* 2011;21:26-34.
11. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
12. Nowak-Göttl U et al. In pediatric patients, age has more impact on dosing of vitamin K antagonists than VKORC1 or CYP2C9 genotypes. *Blood* 2010;116:6101-5.
13. Puehringer H et al. VKORC1 -1639G>A and CYP2C9*3 are the major genetic predictors of phenprocoumon dose requirement. *Eur J Clin Pharmacol* 2010;66:591-8.
14. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
15. Arnold ML et al. Pharmacogenetic testing for guiding de novo phenprocoumon therapy in stroke patients. *Cerebrovasc Dis* 2009;28:468-71.
16. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
17. Schalekamp et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
18. Reitsma PH et al. A C1173T dimorphism in the VKORC1 gene determines coumarin sensitivity and bleeding risk. *PLoS Med* 2005;2:e312.

Date 10-09-2018

VKORC1 -1639 GA: fenprocoumon

[2564](#)

NO action is needed for this gene-drug interaction.

The gene variation leads to a lower dose requirement, but regular monitoring of patients ensures that this does not lead to a distinct increase in the risk of bleeding.

Literature:

1. Zhang Y et al. Age-stratified outcome of a genotype-guided dosing algorithm for acenocoumarol and phenprocoumon. *J Thromb Haemost* 2017;15:454-464.
2. Brehm K et al. Genetic variations of phenprocoumon metabolism in patients with ventricular assist devices. *Eur J Cardiothorac Surg* 2016;50:275-80.

3. Botton et al. A new algorithm for weekly phenprocoumon dose variation in a southern Brazilian population: role for CYP2C9, CYP3A4/5 and VKORC1 genes polymorphisms. *Basic Clin Pharmacol Toxicol* 2014;114:323-9.
4. Verhoef TI et al. A randomized trial of genotype-guided dosing of acenocoumarol and phenprocoumon. *N Engl J Med* 2013;369:2304-12.
5. Baranova EV et al. Dosing algorithms for vitamin K antagonists across VKORC1 and CYP2C9 genotypes. *J Thromb Haemost* 2017;15:465-472.
6. Abduljalil K et al. Quantifying the effect of covariates on concentrations and effects of steady-state phenprocoumon using a population pharmacokinetic/ pharmacodynamic model. *Clin Pharmacokinet* 2013;52:359-71.
7. Brehm K et al. Mechanical heart valve recipients: anticoagulation in patients with genetic variations of phenprocoumon metabolism. *Eur J Cardiothorac Surg* 2013;44:309-14.
8. Verhoef TI et al. Long-term anticoagulant effects of CYP2C9 and VKORC1 genotypes in phenprocoumon users. *J Thromb Haemost*. 2012;10:2610-2.
9. Geisen C et al. Prediction of phenprocoumon maintenance dose and phenprocoumon plasma concentration by genetic and non-genetic parameters. *Eur J Clin Pharmacol* 2011;67:371-81.
10. Teichert M et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1, CYP2C9, and CYP4F2 genes. *Pharmacogenet Genomics* 2011;21:26-34.
11. Luxembourg B et al. Impact of pharmacokinetic (CYP2C9) and pharmacodynamic (VKORC1, F7, GGCX, CALU, EPHX1) gene variants on the initiation and maintenance phases of phenprocoumon therapy. *Thromb Haemost* 2011;105:169-80.
12. Nowak-Göttl U et al. In pediatric patients, age has more impact on dosing of vitamin K antagonists than VKORC1 or CYP2C9 genotypes. *Blood* 2010;116:6101-5.
13. Puehringer H et al. VKORC1 -1639G>A and CYP2C9*3 are the major genetic predictors of phenprocoumon dose requirement. *Eur J Clin Pharmacol* 2010;66:591-8.
14. Cadamuro J et al. Genetic determinants of acenocoumarol and phenprocoumon maintenance dose requirements. *Eur J Clin Pharmacol* 2010;66:253-60.
15. Arnold ML et al. Pharmacogenetic testing for guiding de novo phenprocoumon therapy in stroke patients. *Cerebrovasc Dis* 2009;28:468-71.
16. Qazim B et al. Dependency of phenprocoumon dosage on polymorphisms in the VKORC1 and CYP2C9 genes. *J Thromb Thrombolysis* 2009;28:211-4.
17. Schmeits PC et al. Investigating unexpected INRs: in search of the culprit--adherence, interactions, genetics, and superwarfarin. *Neth J Med* 2009;67:76-8.
18. Schalekamp et al. VKORC1 and CYP2C9 genotypes and phenprocoumon anticoagulation status: interaction between both genotypes affects dose requirement. *Clin Pharmacol Ther* 2007;81:185-93.
19. Reitsma PH et al. A C1173T dimorphism in the VKORC1 gene determines coumarin sensitivity and bleeding risk. *PLoS Med* 2005;2:e312.

Date 10-09-2018

CYP2C9 IM ANDERS: fenytoïne

2438

The risk of side effects is increased. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 70-75% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or rash).

Literature:

1. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
2. Su SC et al. HLA alleles and CYP2C9*3 as predictors of phenytoin hypersensitivity in East Asians. *Clin Pharmacol Ther* 2019;105:476-85.
3. Wu X et al. Association of CYP2C9*3 with phenytoin-induced Stevens-Johnson syndrome and toxic epidermal necrolysis: a systematic review and meta-analysis. *J Clin Pharm Ther* 2018;43:408-13.
4. Yampayon K et al. Influence of genetic and non-genetic factors on phenytoin-induced severe cutaneous adverse drug reactions. *Eur J Clin Pharmacol* 2017;73:855-65.
5. Tassaneeyakul W et al. Associations between HLA class I and cytochrome P450 2C9 genetic polymorphisms and phenytoin-related severe cutaneous adverse reactions in a Thai population. *Pharmacogenet Genomics* 2016;26:225-34.
6. Ortega-Vázquez A et al. CYP2C9, CYP2C19, ABCB1 genetic polymorphisms and phenytoin plasma concentrations in Mexican-Mestizo patients with epilepsy. *Pharmacogenomics J* 2016;16:286-92.
7. Yamamoto Y et al. Individualized phenytoin therapy for Japanese pediatric patients with epilepsy based on CYP2C9 and CYP2C19 genotypes. *Ther Drug Monit* 2015;37:229-35.
8. Chung WH et al. Genetic variants associated with phenytoin-related severe cutaneous adverse reactions. *JAMA* 2014;312:525-34.
9. Depondt C et al. A candidate gene study of antiepileptic drug tolerability and -efficacy identifies an association of CYP2C9 variants with phenytoin toxicity. *Eur J Neurol* 2011;18:1159-64.

10. Kesavan R et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on phenytoin-induced neurological toxicity in Indian epileptic patients. *Eur J Clin Pharmacol* 2010;66:689-96.
11. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
12. Hennessy S et al. CYP2C9, CYP2C19, and ABCB1 genotype and hospitalization for phenytoin toxicity. *J Clin Pharmacol* 2009;49:1483-7.
13. McCluggage LK et al. Phenytoin toxicity due to genetic polymorphism. *Neurocrit Care* 2009;10:222-4.
14. Lee SY et al. Contributions of CYP2C9/CYP2C19 genotypes and drug interaction to the phenytoin treatment in the Korean epileptic patients in the clinical setting. *J Biochem Mol Biol* 2007;40:448-52.
15. Tate SK et al. Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. *Proc Natl Acad Sci U S A* 2005;102:5507-12.
16. Hung CC et al. Dosage recommendation of phenytoin for patients with epilepsy with different CYP2C9/CYP2C19 polymorphisms. *Ther Drug Monit* 2004;26:534-40.
17. Van der Weide J et al. The effect of genetic polymorphism of cytochrome P450 CYP2C9 on phenytoin dose requirement. *Pharmacogenetics* 2001;11:287-91.
18. Ninomiya H et al. Genetic polymorphism of the CYP2C subfamily and excessive serum phenytoin concentration with central nervous system intoxication. *Ther Drug Monit* 2000;22:230-2.
19. Mamiya K et al. The effects of genetic polymorphisms of CYP2C9 and CYP2C19 on phenytoin metabolism in Japanese adult patients with epilepsy: studies in stereoselective hydroxylation and population pharmacokinetics. *Epilepsia* 1998;39:1317-23.
20. www.nvza.nl, TDM monografie voor fenytoïne.

Date 23-05-2022

CYP2C9 PM ANDERS: fenytoïne

[2439](#)

The risk of side effects is increased. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 40-50% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or rash).

Literature:

1. Ortega-Vázquez A et al. CYP2C9, CYP2C19, ABCB1 genetic polymorphisms and phenytoin plasma concentrations in Mexican-Mestizo patients with epilepsy. *Pharmacogenomics J* 2016;16:286-92.
2. Kidd RS et al. Identification of a null allele of CYP2C9 in an African-American exhibiting toxicity to phenytoin. *Pharmacogenetics* 2001;11:803-8.

Date 23-5-2022

CYP2C9*1/*2: fenytoïne

[2440](#)

There are indications of an increased risk of side effects. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 75% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or rash).

Literature:

1. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
2. Guevara N et al. Role of CYP2C9, CYP2C19 and EPHX polymorphism in the pharmacokinetic of phenytoin: a study on Uruguayan Caucasian subjects. *Pharmaceuticals (Basel)* 2017;10:73.
3. Ortega-Vázquez A et al. CYP2C9, CYP2C19, ABCB1 genetic polymorphisms and phenytoin plasma concentrations in Mexican-Mestizo patients with epilepsy. *Pharmacogenomics J* 2016;16:286-92.
4. Depondt C et al. A candidate gene study of antiepileptic drug tolerability and -efficacy identifies an association of CYP2C9 variants with phenytoin toxicity. *Eur J Neurol* 2011;18:1159-64.
5. Kesavan R et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on phenytoin-induced neurological toxicity in Indian epileptic patients. *Eur J Clin Pharmacol* 2010;66:689-96.
6. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
7. Hennessy S et al. CYP2C9, CYP2C19, and ABCB1 genotype and hospitalization for phenytoin toxicity. *J Clin Pharmacol* 2009;49:1483-7.
8. Rosemary J et al. Influence of the CYP2C9 AND CYP2C19 polymorphisms on phenytoin hydroxylation

- in healthy individuals from south India. *Indian J Med Res* 2006;123:665-70.
9. Tate SK et al. Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. *Proc Natl Acad Sci U S A* 2005;102:5507-12.
 10. Caraco Y et al. Phenytoin metabolic ratio: a putative marker of CYP2C9 activity in vivo. *Pharmacogenetics* 2001;11:587-96.
 11. Van der Weide J et al. The effect of genetic polymorphism of cytochrome P450 CYP2C9 on phenytoin dose requirement. *Pharmacogenetics* 2001;11:287-91.
 12. Kerb R et al. The predictive value of MDR1, CYP2C9, and CYP2C19 polymorphisms for phenytoin plasma levels. *Pharmacogenomics J* 2001;1:204-10.
 13. Aynacioglu AS et al. Frequency of cytochrome P450 CYP2C9 variants in a Turkish population and functional relevance for phenytoin. *Br J Clin Pharmacol* 1999;48:409-15.
 14. www.nvza.nl, TDM monografie voor fenytoïne.

Date 23-5-2022

CYP2C9*1/*3: fenytoïne

2441

The risk of side effects is increased. The life-threatening cutaneous side effects Stevens-Johnson syndrome/toxic epidermal necrolysis and DRESS may occur, especially in Asian patients. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 70% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- For patients with gene variant HLA-B*1502, take the extra increase in the risk of life threatening cutaneous adverse events into account while weighing the risks of phenytoin against the benefits. Dose reduction probably does not lower this risk.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or, especially in Asian patients, rash).

Literature:

1. Sukasem C et al. Genetic and clinical risk factors associated with phenytoin-induced cutaneous adverse drug reactions in Thai population. *Pharmacoepidemiol Drug Saf* 2020;29:565-74.
2. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
3. Su SC et al. HLA alleles and CYP2C9*3 as predictors of phenytoin hypersensitivity in East Asians. *Clin Pharmacol Ther* 2019;105:476-85.
4. Wu X et al. Association of CYP2C9*3 with phenytoin-induced Stevens-Johnson syndrome and toxic epidermal necrolysis: a systematic review and meta-analysis. *J Clin Pharm Ther* 2018;43:408-13.
5. Guevara N et al. Role of CYP2C9, CYP2C19 and EPHX polymorphism in the pharmacokinetic of phenytoin: a study on Uruguayan Caucasian subjects. *Pharmaceuticals (Basel)* 2017;10:73.
6. Yampayon K et al. Influence of genetic and non-genetic factors on phenytoin-induced severe cutaneous adverse drug reactions. *Eur J Clin Pharmacol* 2017;73:855-65.
7. Tassaneeyakul W et al. Associations between HLA class I and cytochrome P450 2C9 genetic polymorphisms and phenytoin-related severe cutaneous adverse reactions in a Thai population. *Pharmacogenet Genomics* 2016;26:225-34.
8. Yamamoto Y et al. Individualized phenytoin therapy for Japanese pediatric patients with epilepsy based on CYP2C9 and CYP2C19 genotypes. *Ther Drug Monit* 2015;37:229-35.
9. Chung WH et al. Genetic variants associated with phenytoin-related severe cutaneous adverse reactions. *JAMA* 2014;312:525-34.
10. Hung CC et al. Effects of polymorphisms in six candidate genes on phenytoin maintenance therapy in Han Chinese patients. *Pharmacogenomics* 2012;13:1339-49.
11. Depondt C et al. A candidate gene study of antiepileptic drug tolerability and -efficacy identifies an association of CYP2C9 variants with phenytoin toxicity. *Eur J Neurol* 2011;18:1159-64.
12. Kesavan R et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on phenytoin-induced neurological toxicity in Indian epileptic patients. *Eur J Clin Pharmacol* 2010;66:689-96.
13. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
14. Hennessy S et al. CYP2C9, CYP2C19, and ABCB1 genotype and hospitalization for phenytoin toxicity. *J Clin Pharmacol* 2009;49:1483-7.
15. McCluggage LK et al. Phenytoin toxicity due to genetic polymorphism. *Neurocrit Care* 2009;10:222-4.
16. Lee SY et al. Contributions of CYP2C9/CYP2C19 genotypes and drug interaction to the phenytoin treatment in the Korean epileptic patients in the clinical setting. *J Biochem Mol Biol* 2007;40:448-52.
17. Rosemary J et al. Influence of the CYP2C9 AND CYP2C19 polymorphisms on phenytoin hydroxylation in healthy individuals from south India. *Indian J Med Res* 2006;123:665-70.
18. Hung CC et al. Dosage recommendation of phenytoin for patients with epilepsy with different CYP2C9/CYP2C19 polymorphisms. *Ther Drug Monit* 2004;26:534-40.
19. Soga Y et al. CYP2C polymorphisms, phenytoin metabolism and gingival overgrowth in epileptic

- subjects. *Life Sci* 2004;74:827-34.
20. Caraco Y et al. Phenytoin metabolic ratio: a putative marker of CYP2C9 activity in vivo. *Pharmacogenetics* 2001;11:587-96.
 21. Kerb R et al. The predictive value of MDR1, CYP2C9, and CYP2C19 polymorphisms for phenytoin plasma levels. *Pharmacogenomics J* 2001;1:204-10.
 22. Ninomiya H et al. Genetic polymorphism of the CYP2C subfamily and excessive serum phenytoin concentration with central nervous system intoxication. *Ther Drug Monit* 2000;22:230-2.
 23. Aynacioglu AS et al. Frequency of cytochrome P450 CYP2C9 variants in a Turkish population and functional relevance for phenytoin. *Br J Clin Pharmacol* 1999;48:409-15.
 24. Mamiya K et al. The effects of genetic polymorphisms of CYP2C9 and CYP2C19 on phenytoin metabolism in Japanese adult patients with epilepsy: studies in stereoselective hydroxylation and population pharmacokinetics. *Epilepsia* 1998;39:1317-23.
 25. Odani A et al. Genetic polymorphism of the CYP2C subfamily and its effect on the pharmacokinetics of phenytoin in Japanese patients with epilepsy. *Clin Pharmacol Ther* 1997;62:287-92.
 26. Hashimoto Y et al. Effect of CYP2C polymorphisms on the pharmacokinetics of phenytoin in Japanese patients with epilepsy. *Biol Pharm Bull* 1996;19:1103-5.
 27. SmPC's Diphantoïne-Z (NL) en Dilantin (VS).

Date 23-5-2022

CYP2C9*2/*2: fenytoïne

[2442](#)

The risk of side effects is increased. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 50% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or rash).

Literature:

1. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
2. Guevara N et al. Role of CYP2C9, CYP2C19 and EPHX polymorphism in the pharmacokinetic of phenytoin: a study on Uruguayan Caucasian subjects. *Pharmaceuticals (Basel)* 2017;10:73.
3. Depondt C et al. A candidate gene study of antiepileptic drug tolerability and -efficacy identifies an association of CYP2C9 variants with phenytoin toxicity. *Eur J Neurol* 2011;18:1159-64.
4. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
5. Hennessy S et al. CYP2C9, CYP2C19, and ABCB1 genotype and hospitalization for phenytoin toxicity. *J Clin Pharmacol* 2009;49:1483-7.
6. Tate SK et al. Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. *Proc Natl Acad Sci U S A* 2005;102:5507-12.
7. Caraco Y et al. Phenytoin metabolic ratio: a putative marker of CYP2C9 activity in vivo. *Pharmacogenetics* 2001;11:587-96.
8. Van der Weide J et al. The effect of genetic polymorphism of cytochrome P450 CYP2C9 on phenytoin dose requirement. *Pharmacogenetics* 2001;11:287-91.
9. Kerb R et al. The predictive value of MDR1, CYP2C9, and CYP2C19 polymorphisms for phenytoin plasma levels. *Pharmacogenomics J* 2001;1:204-10.
10. Aynacioglu AS et al. Frequency of cytochrome P450 CYP2C9 variants in a Turkish population and functional relevance for phenytoin. *Br J Clin Pharmacol* 1999;48:409-15.
11. www.nvza.nl, TDM monografie voor fenytoïne.

Date 23-5-2022

CYP2C9*2/*3: fenytoïne

[2443](#)

The risk of side effects is increased. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 50% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or rash).

Literature:

1. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
2. Kesavan R et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on phenytoin-induced

- neurological toxicity in Indian epileptic patients. *Eur J Clin Pharmacol* 2010;66:689-96.
3. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
 4. Caraco Y et al. Phenytoin metabolic ratio: a putative marker of CYP2C9 activity in vivo. *Pharmacogenetics* 2001;11:587-96.
 5. Van der Weide J et al. The effect of genetic polymorphism of cytochrome P450 CYP2C9 on phenytoin dose requirement. *Pharmacogenetics* 2001;11:287-91.
 6. www.nvza.nl, TDM monografie voor fenytoïne.

Date 23-5-2022

CYP2C9*3/*3: fenytoïne

[2444](#)

The risk of side effects is increased. The life-threatening cutaneous side effects Stevens-Johnson syndrome/toxic epidermal necrolysis and DRESS may occur, especially in Asian patients. The gene variation increases the plasma concentration of phenytoin.

- The loading dose does not need to be adjusted.
- For the other doses, use 40% of the standard dose and assess the dose based on effect and serum concentration after 7-10 days.
- For patients with gene variant HLA-B*1502, take the extra increase in the risk of life threatening cutaneous adverse events into account while weighing the risks of phenytoin against the benefits. Dose reduction probably does not lower this risk.
- Advise the patient to report side effects (such as ataxia, nystagmus, slurred speech, sedation or, especially in Asian patients, rash).

Literature:

1. Sukasem C et al. Genetic and clinical risk factors associated with phenytoin-induced cutaneous adverse drug reactions in Thai population. *Pharmacoepidemiol Drug Saf* 2020;29:565-74.
2. Fohner AE et al. Assessing the clinical impact of CYP2C9 pharmacogenetic variation on phenytoin prescribing practice and patient response in an integrated health system. *Pharmacogenet Genomics* 2019;29:192-9.
3. Su SC et al. HLA alleles and CYP2C9*3 as predictors of phenytoin hypersensitivity in East Asians. *Clin Pharmacol Ther* 2019;105:476-85.
4. Wu X et al. Association of CYP2C9*3 with phenytoin-induced Stevens-Johnson syndrome and toxic epidermal necrolysis: a systematic review and meta-analysis. *J Clin Pharm Ther* 2018;43:408-13.
5. Yampayon K et al. Influence of genetic and non-genetic factors on phenytoin-induced severe cutaneous adverse drug reactions. *Eur J Clin Pharmacol* 2017;73:855-65.
6. Tassaneeyakul W et al. Associations between HLA class I and cytochrome P450 2C9 genetic polymorphisms and phenytoin-related severe cutaneous adverse reactions in a Thai population. *Pharmacogenet Genomics* 2016;26:225-34.
7. Chung WH et al. Genetic variants associated with phenytoin-related severe cutaneous adverse reactions. *JAMA* 2014;312:525-34.
8. Hung CC et al. Effects of polymorphisms in six candidate genes on phenytoin maintenance therapy in Han Chinese patients. *Pharmacogenomics* 2012;13:1339-49.
9. Kesavan R et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on phenytoin-induced neurological toxicity in Indian epileptic patients. *Eur J Clin Pharmacol* 2010;66:689-96.
10. Azzato EM et al. Maternal EPHX1 polymorphisms and risk of phenytoin-induced congenital malformations. *Pharmacogenet Genomics* 2010;20:58-63.
11. Jose L et al. Acenocoumarol and phenytoin toxicity in the presence of CYP2C9 mutation. *J Assoc Physicians India* 2008;56:250-2.
12. Ramasamy K et al. Severe phenytoin toxicity in a CYP2C9*3*3 homozygous mutant from India. *Neurol India* 2007;55:408-9.
13. Lee SY et al. Contributions of CYP2C9/CYP2C19 genotypes and drug interaction to the phenytoin treatment in the Korean epileptic patients in the clinical setting. *J Biochem Mol Biol* 2007;40:448-52.
14. Rosemary J et al. Influence of the CYP2C9 AND CYP2C19 polymorphisms on phenytoin hydroxylation in healthy individuals from south India. *Indian J Med Res* 2006;123:665-70.
15. Tate SK et al. Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. *Proc Natl Acad Sci U S A* 2005;102:5507-12.
16. Brandolese R et al. Severe phenytoin intoxication in a subject homozygous for CYP2C9*3. *Clin Pharmacol Ther* 2001;70:391-4.
17. Kerb R et al. The predictive value of MDR1, CYP2C9, and CYP2C19 polymorphisms for phenytoin plasma levels. *Pharmacogenomics J* 2001;1:204-10.
18. Aynacioglu AS et al. Frequency of cytochrome P450 CYP2C9 variants in a Turkish population and functional relevance for phenytoin. *Br J Clin Pharmacol* 1999;48:409-15.
19. Kidd RS et al. Pharmacokinetics of chlorpheniramine, phenytoin, glipizide and nifedipine in an individual homozygous for the CYP2C9*3 allele. *Pharmacogenetics* 1999;9:71-80.
20. SmPC's Diphantoïne-Z (NL) en Dilantin (VS).
21. www.nvza.nl, TDM monografie voor fenytoïne.

HLA-B*1502: fenytoine[6366](#)

The life-threatening cutaneous side effect Stevens-Johnson syndrome/toxic epidermal necrolysis (SJS/TEN) occurs more frequently in patients with this genetic variation. The calculated risk of phenytoin-induced SJS/TEN in patients with HLA-B*1502 is 0.65%.

- carefully weigh the risk of SJS/TEN against the benefits
- avoid phenytoin if an alternative is possible
Carbamazepine carries a 10-fold higher risk of SJS/TEN for these patients and is therefore not an alternative.
A comparable risk has been reported for lamotrigine as for phenytoin. The same applies for oxcarbazepine, but the most severe forms (SJS/TEN overlap and TEN) are not observed with oxcarbazepine.
- if it is not possible to avoid this medication, then advise the patient to report any skin rash immediately

Literature:

1. Phung TH et al. The association between HLA-B*15:02 and phenytoin-induced severe cutaneous adverse reactions: a meta-analysis. *Pharmacogenomics* 2022;23:49-59.
2. Sukasem C et al. Spectrum of cutaneous adverse reactions to aromatic antiepileptic drugs and human leukocyte antigen genotypes in Thai patients and meta-analysis. *Pharmacogenomics J* 2021;21:682-90.
3. Manuyakorn W et al. Association of HLA genotypes with phenytoin induced severe cutaneous adverse drug reactions in Thai children. *Epilepsy Res* 2020;162:106321.
4. Sukasem C et al. Genetic and clinical risk factors associated with phenytoin-induced cutaneous adverse drug reactions in Thai population. *Pharmacoepidemiol Drug Saf* 2020;29:565-74.
5. Su SC et al. HLA alleles and CYP2C9*3 as predictors of phenytoin hypersensitivity in East Asians. *Clin Pharmacol Ther* 2019;105:476-85.
6. Yampayon K et al. Influence of genetic and non-genetic factors on phenytoin-induced severe cutaneous adverse drug reactions. *Eur J Clin Pharmacol* 2017;73:855-865.
7. Shi YW et al. HLA-A*24:02 as a common risk factor for antiepileptic drug-induced cutaneous adverse reactions. *Neurology* 2017;88:2183-2191.
8. Chang CC et al. Association of HLA-B*15:13 and HLA-B*15:02 with phenytoin-induced severe cutaneous adverse reactions in a Malay population. *Pharmacogenomics J* 2017;17:170-173.
9. Tassaneeyakul W et al. Associations between HLA class I and cytochrome P450 2C9 genetic polymorphisms and phenytoin-related severe cutaneous adverse reactions in a Thai population. *Pharmacogenet Genomics* 2016;26:225-34.
10. Bloch KM et al. Pharmacogenetics of antiepileptic drug-induced hypersensitivity. *Pharmacogenomics* 2014;15:857-68.
11. Cheung YK et al. HLA-B alleles associated with severe cutaneous reactions to antiepileptic drugs in Han Chinese. *Epilepsia* 2013;54:1307-14.
12. Manuyakorn W et al. Phenobarbital-induced severe cutaneous adverse drug reactions are associated with CYP2C19*2 in Thai children. *Pediatr Allergy Immunol* 2013;24:299-303.
13. Hung SI et al. Common risk allele in aromatic antiepileptic-drug induced Stevens-Johnson syndrome and toxic epidermal necrolysis in Han Chinese. *Pharmacogenomics* 2010;11:349-56.
14. Locharernkul C et al. Carbamazepine and phenytoin induced Stevens-Johnson syndrome is associated with HLA-B*1502 allele in Thai population. *Epilepsia* 2008;49:2087- 91.
15. SmPC Diphantoïne-Z.
16. SmPC Dilantin (VS).

Date 23-05-2022

CYP2D6 IM: flecainide[2424](#)

The genetic variation reduces conversion of flecainide to inactive metabolites. This may increase the risk of side effects.

Recommendation:

- Indications other than diagnosis of Brugada syndrome:
 - reduce the dose to 75% of the standard dose and record an ECG and monitor the plasma concentration
- Provocation test for diagnosis of Brugada syndrome:
No action required.
At a dose of 2.0 mg/kg body weight to a maximum of 150 mg, the response is better for patients with alleles that result in reduced activity.
All 5 patients with these alleles and 20% of the patients with two fully active alleles exhibited a response

within 30 minutes.

Literature:

1. Poh BH et al. Complete heart block secondary to flecainide toxicity: is it time for CYP2D6 genotype testing? *Pediatrics* 2020;146:e20192608.
2. Calvo D et al. Time-dependent responses to provocative testing with flecainide in the diagnosis of Brugada syndrome. *Heart Rhythm* 2015;12:350-7.
3. Hu M et al. Effects of CYP2D6 10, CYP3A53, CYP1A2*1F, and ABCB1 C3435T polymorphisms on the pharmacokinetics of flecainide in healthy Chinese subjects. *Drug Metabol Drug Interact* 2012;27:33-9.
4. Lim KS et al. Changes in the QTc interval after administration of flecainide acetate, with and without coadministered paroxetine, in relation to cytochrome P450 2D6 genotype: data from an open-label, two-period, single-sequence crossover study in healthy Korean male subjects. *Clin Ther* 2010;32:659-66.
5. Lim KS et al. Pharmacokinetic interaction of flecainide and paroxetine in relation to the CYP2D6*10 allele in healthy Korean subjects. *Br J Clin Pharmacol* 2008;66:660-6.
6. Doki K et al. Effect of CYP2D6 genotype on flecainide pharmacokinetics in Japanese patients with supraventricular tachyarrhythmia. *Eur J Clin Pharmacol* 2006;62:919-26.

Date 12-09-2022

CYP2D6 PM: flecainide

[2423](#)

The genetic variation reduces conversion of flecainide to inactive metabolites. This increases the risk of side effects.

Recommendation:

- reduce the dose to 50% of the standard dose and record an ECG and monitor the plasma concentration

Literature:

1. Palmiere C et al. Usefulness of post-mortem biochemistry in forensic pathology: illustrative case reports. *Leg Med (Tokyo)* 2012;14:27-35.
2. Tenneze L et al. Pharmacokinetics and electrocardiographic effects of a new controlled-release form of flecainide acetate: comparison with the standard form and influence of the CYP2D6 polymorphism. *Clin Pharmacol Ther* 2002;72:112-22.
3. Funck-Brentano C et al. Variable disposition kinetics and electrocardiographic effects of flecainide during repeated dosing in humans: contribution of genetic factors, dose-dependent clearance, and interaction with amiodarone. *Clin Pharmacol Ther* 1994;55:256-69.
4. Gross AS et al. Polymorphic flecainide disposition under conditions of uncontrolled urine flow and pH. *Eur J Clin Pharmacol* 1991;40:155-62.
5. Gross AS et al. Stereoselective disposition of flecainide in relation to the sparteine/ debrisoquine metaboliser phenotype. *Br J Clin Pharmacol* 1989;28:555-66.
6. Mikus G et al. The influence of the sparteine/debrisoquin phenotype on the disposition of flecainide. *Clin Pharmacol Ther* 1989;45:562-7.

Date 12-09-2022

CYP2D6 UM: flecainide

[2425](#)

The genetic variation increases conversion of flecainide to inactive metabolites. A higher dose is possibly required as a result.

Recommendation:

There are no data about the pharmacokinetics and/or the effects of flecainide in UM.

- monitor the plasma concentration as a precaution and record an ECG or select an alternative
Examples of anti-arrhythmic drugs that are not metabolised via CYP2D6 (or to a lesser extent) include sotalol, disopyramide, quinidine and amiodarone.

Literature:

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Date 12-09-2022

HLA-B*5701-positive patients have a 37-80-fold elevated risk of flucloxacillin-induced liver injury. However, the incidence is low (on average 1-2 per 1000 individuals; 7-14 per 1000 individuals older than 70 years).

- regularly monitor the patient's liver function
- choose an alternative if liver enzymes and/or bilirubin levels are elevated

Literature:

1. Teixeira M et al. Flucloxacillin-induced hepatotoxicity - association with HLA-B*5701. Rev Assoc Med Bras 2020;66:12-7.
2. Nicoletti P et al. Drug-induced liver injury due to flucloxacillin: relevance of multiple human leukocyte antigen alleles. Clin Pharmacol Ther 2019;106:245-53.
3. Vera JH et al. The safety of flucloxacillin in HIV-infected patients with positive HLA-B*5701 genotype. Aids 2013;27:484-5.
4. Philips EJ and Mallal SA. HLA-B*5701 and flucloxacillin associated drug-induced liver disease. Aids 2013;27:491-2.
5. Daly AK et al. HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. Nature Genetics 2009;41:816-9.
6. SmPC Floxapen.

Date 15-11-2021

DPD AS 0: flucytosine[7170](#)

A risk of life-threatening toxicity is increased by gene variation. A small proportion of flucytosine is converted to fluorouracil and patients with this gene variation are intolerant even to small quantities of fluorouracil.

- avoid flucytosine

Literature:

1. Mylan Healthcare LLC. Important risk information: Adapted recommendations for the use of flucytosine (Ancotil, solution for infusion 10 mg/ml, RVG 08533) in patients with dihydropyrimidine dehydrogenase (DPD) deficiency. Direct Healthcare Professional Communication (Orange Hand Letter) 05-06-20.
2. SmPC Ancotil.

Date 15-11-2021

DPD AS 1,5: flucytosine[7173](#)

A very low risk of severe toxicity is increased by gene variation. A small proportion of flucytosine is converted to fluorouracil. Patients with this gene variation are more likely to have a reaction to fluorouracil, but generally tolerate low doses (50-75% of the standard fluorouracil dose).

- Be alert to the occurrence of severe side effects, such as leukopaenia, neutropaenia, thrombocytopaenia and diarrhoea
In the majority of cases, side effects of flucytosine occur in the first two to three weeks of the treatment. Flucytosine should be stopped if severe side effects occur.

Literature:

1. Mylan Healthcare LLC. Important risk information: Adapted recommendations for the use of flucytosine (Ancotil, solution for infusion 10 mg/ml, RVG 08533) in patients with dihydropyrimidine dehydrogenase (DPD) deficiency. Direct Healthcare Professional Communication (Orange Hand Letter) 05-06-20.
2. SmPC Ancotil.

Date 15-11-2021

DPD AS 1: flucytosine[7172](#)

A very low risk of severe toxicity is increased by gene variation. A small proportion of flucytosine is converted to fluorouracil. Patients with this gene variation are more likely to react to fluorouracil, but generally tolerate low doses (approximately 50% of the standard fluorouracil dose).

- be alert to the occurrence of severe side effects, such as leukopaenia, neutropaenia, thrombocytopaenia and diarrhoea

In the majority of cases, side effects of flucytosine occur in the first two to three weeks of the treatment. Flucytosine should be stopped if severe side effects occur.

Literature:

1. Mylan Healthcare LLC. Important risk information: Adapted recommendations for the use of flucytosine (Ancotil, solution for infusion 10 mg/ml, RVG 08533) in patients with dihydropyrimidine dehydrogenase (DPD) deficiency. Direct Healthcare Professional Communication (Orange Hand Letter) 05-06-20.
2. SmPC Ancotil.

Date 15-11-2021

DPD FENO: flucytosine

[7171](#)

A very low risk of severe toxicity is increased by gene variation. A small proportion of flucytosine is converted to fluorouracil. Patients with this gene variation are more likely to have a reaction to fluorouracil, but generally tolerate low doses (15-50% of the standard fluorouracil dose).

- be alert to the occurrence of severe side effects, such as leukopaenia, neutropaenia, thrombocytopaenia and diarrhoea.

In the majority of cases, side effects of flucytosine occur in the first two to three weeks of the treatment. Flucytosine should be stopped if severe side effects occur.

Literature:

1. Mylan Healthcare LLC. Important risk information: Adapted recommendations for the use of flucytosine (Ancotil, solution for infusion 10 mg/ml, RVG 08533) in patients with dihydropyrimidine dehydrogenase (DPD) deficiency. Direct Healthcare Professional Communication (Orange Hand Letter) 05-06-20.
2. SmPC Ancotil.

Date 15-11-2021

DPD AS 0: fluorouracil cutaan

[5749](#)

The gene variation increases the risk of severe, potentially fatal toxicity. A reduced conversion of fluorouracil/capecitabine to inactive metabolites means that the normal dose is an overdose.

- avoid fluorouracil

NOTE: If a patient has two different genetic variations that lead to a non-functional DPD enzyme (e.g. *2A and *13), this recommendation only applies if the variations are on a different allele. If both variations are on the same allele, this patient actually has a gene activity score 1, for which no increased risk of severe, potentially fatal toxicity has been found with cutaneous use. These two situations can only be distinguished by determining the enzyme activity (phenotyping). This recommendation only applies if the patient has virtually no enzyme activity.

Literature:

1. Henricks LM et al. Capecitabine-based treatment of a patient with a novel DPYD genotype and complete dihydropyrimidine dehydrogenase deficiency. *Int J Cancer* 2018;142:424-30.
2. Henricks LM et al. Treatment algorithm for homozygous or compound heterozygous DPYD variant allele carriers with low-dose capecitabine. *JCO Precis Oncol* - published online 2017 Oct 6.
3. Kodali S et al. Capecitabine-induced severe toxicity secondary to DPD deficiency and successful treatment with low dose 5-fluorouracil. *J Gastrointest Cancer* 2017;48:66- 69.
4. Lunenburg CA et al. Evaluation of clinical implementation of prospective DPYD genotyping in 5-fluorouracil- or capecitabine-treated patients. *Pharmacogenomics* 2016;17:721-9.
5. Deenen MJ et al. Upfront genotyping of DPYD*2A to individualize fluoropyrimidine therapy: a safety and cost analysis. *J Clin Oncol* 2016;34:227-34.
6. Rosmarin D et al. Genetic markers of toxicity from capecitabine and other fluorouracil-based regimens: investigation in the QUASAR2 study, systematic review, and meta- analysis. *J Clin Oncol* 2014; 32:1031-9.
7. Deenen MJ et al. Relationship between single nucleotide polymorphisms and haplotypes in DPYD and toxicity and efficacy of capecitabine in advanced colorectal cancer. *Clin Cancer Res* 2011; 17:3455-68.
8. Gross E et al. Strong association of a common dihydropyrimidine dehydrogenase gene polymorphism with fluoropyrimidine-related toxicity in cancer patients. *PLoS ONE* 2008;3:e4003.
9. Boisdron-Celle M et al. 5-Fluorouracil-related severe toxicity: a comparison of different methods for the pretherapeutic detection of dihydropyrimidine dehydrogenase deficiency. *Cancer Lett* 2007;249:271-82.
10. Morel A et al. Clinical relevance of different dihydropyrimidine dehydrogenase gene single nucleotide polymorphisms on 5-fluorouracil tolerance. *Mol Cancer Ther* 2006;5:2895-904.
11. Van Kuilenburg AB et al. High prevalence of the IVS14 + 1G>A mutation in the dihydropyrimidine

- dehydrogenase gene of patients with severe 5-fluorouracil-associated toxicity. *Pharmacogenetics* 2002;12:555-8.
12. Raida M et al. Prevalence of a common point mutation in the dihydropyrimidine dehydrogenase (DPD) gene within the 5'-splice donor site of intron 14 in patients with severe 5-fluorouracil (5-FU)-related toxicity compared with controls. *Clin Cancer Res* 2001;7:2832-9.
 13. van Kuilenburg AB et al. Clinical implications of dihydropyrimidine dehydrogenase (DPD) deficiency in patients with severe 5-fluorouracil-associated toxicity: identification of new mutations in the DPD gene. *Clin Cancer Res* 2000;6:4705-12.
 14. Johnson MR et al. Life-threatening toxicity in a dihydropyrimidine dehydrogenase-deficient patient after treatment with topical 5-fluorouracil. *Clin Cancer Res* 1999;5:2006-11.
 15. SPC Efudix crème en Carac cream (VS).

Date 13-05-2019

DPD AS 1,5: fluorouracil/capecitabine

[4647](#)

The gene variation increases the risk of severe, potentially fatal toxicity. A reduced conversion of fluorouracil/capecitabine to inactive metabolites means that the normal dose is an overdose.

- Start with 50% of the standard dose or avoid fluorouracil and capecitabine.
- After starting treatment, the dose should be adjusted based on toxicity and effectiveness. In a study involving 17 patients with genotype *1/2846T, the average dose after titration was 64% of the standard dose. For 51 patients with genotype *1/1236A, the average dose after titration was 74% of the standard dose.
- Tegafur is not an alternative, as this is also metabolised by DPD.

Literature:

1. Kleinjan JP et al. Tolerance-based capecitabine dose escalation after DPYD genotype-guided dosing in heterozygote DPYD variant carriers: a single-center observational study. *Anticancer Drugs* 2019 Jan 8 [Epub ahead of print].
2. Lunenburg CATC et al. Diagnostic and therapeutic strategies for fluoropyrimidine treatment of patients carrying multiple DPYD variants. *Genes (Basel)* 2018;9:E585.
3. Lunenburg CATC et al. Standard fluoropyrimidine dosages in chemoradiation therapy result in an increased risk of severe toxicity in DPYD variant allele carriers. *Eur J Cancer* 2018;104:210-8.
4. Henricks LM et al. DPYD genotype-guided dose individualisation of fluoropyrimidine therapy in patients with cancer: a prospective safety analysis. *Lancet Oncol* 2018;19:1459-67 en persoonlijke communicatie (getitreerde dosis en mediane DPD-activiteit).
5. Madi A et al. Pharmacogenetic analyses of 2183 patients with advanced colorectal cancer; potential role for common dihydropyrimidine dehydrogenase variants in toxicity to chemotherapy. *Eur J Cancer* 2018;102:31-9.
6. Meulendijks D et al. Pretreatment serum uracil concentration as a predictor of severe and fatal fluoropyrimidine-associated toxicity. *Br J Cancer* 2017;116:1415-24.
7. Lunenburg CA et al. Evaluation of clinical implementation of prospective DPYD genotyping in 5-fluorouracil- or capecitabine-treated patients. *Pharmacogenomics* 2016;17:721-9.
8. Lee AM et al. Association between DPYD c.1129-5923 C>G/hapB3 and severe toxicity to 5-fluorouracil-based chemotherapy in stage III colon cancer patients: NCCTG N0147 (Alliance). *Pharmacogenet Genomics* 2016;26:133-7.
9. Meulendijks D et al. Clinical relevance of DPYD variants c.1679T>G, c.1236G>A/HapB3, and c.1601G>A as predictors of severe fluoropyrimidine-associated toxicity: a systematic review and meta-analysis of individual patient data. *Lancet Oncol* 2015;16:1639-50.
10. Lee AM et al. DPYD variants as predictors of 5-fluorouracil toxicity in adjuvant colon cancer treatment (NCCTG N0147). *J Natl Cancer Inst* 2014;106:dju298.
11. Rosmarin D et al. Genetic markers of toxicity from capecitabine and other fluorouracil-based regimens: investigation in the QUASAR2 study, systematic review, and meta-analysis. *J Clin Oncol* 2014; 32:1031-9.
12. Terrazzino S et al. DPYD IVS14+1 G>A and 2846A>T genotyping for the prediction of severe fluoropyrimidine-related toxicity: a meta-analysis. *Pharmacogenomics* 2013; 14:1255-72.
13. Deenen MJ et al. Relationship between single nucleotide polymorphisms and haplotypes in DPYD and toxicity and efficacy of capecitabine in advanced colorectal cancer. *Clin Cancer Res* 2011; 17:3455-68.
14. Kristensen MH et al. Variants in the dihydropyrimidine dehydrogenase, methylenetetrahydrofolate reductase and thymidylate synthase genes predict early toxicity of 5-fluorouracil in colorectal cancer patients. *J Int Med Res* 2010; 38:870-83.
15. Gross E et al. Strong association of a common dihydropyrimidine dehydrogenase gene polymorphism with fluoropyrimidine-related toxicity in cancer patients. *PLoS ONE* 2008;3:e4003.
16. Capitain O et al. The influence of fluorouracil outcome parameters on tolerance and efficacy in patients with advanced colorectal cancer. *Pharmacogenomics J* 2008;8:256-67.
17. Boisdron-Celle M et al. 5-Fluorouracil-related severe toxicity: a comparison of different methods for the pretherapeutic detection of dihydropyrimidine dehydrogenase deficiency. *Cancer Lett* 2007;249:271-82.

18. Cho HJ et al. Thymidylate synthase (TYMS) and dihydropyrimidine dehydrogenase (DPYD) polymorphisms in the Korean population for prediction of 5-fluorouracil-associated toxicity. *Ther Drug Monit* 2007;29:190-6.
19. Morel A et al. Clinical relevance of different dihydropyrimidine dehydrogenase gene single nucleotide polymorphisms on 5-fluorouracil tolerance. *Mol Cancer Ther* 2006;5:2895-904.
20. Yamaguchi K et al. Germline mutation of dihydropyrimidine dehydrogenase gene among a Japanese population in relation to toxicity to 5-fluorouracil. *Jpn J Cancer Res* 2001;92:337-42.
21. van Kuilenburg AB et al. Clinical implications of dihydropyrimidine dehydrogenase (DPD) deficiency in patients with severe 5-fluorouracil-associated toxicity: identification of new mutations in the DPD gene. *Clin Cancer Res* 2000;6:4705-12.
22. SPC's Fluorouracil PCH, Xeloda, Efudix crème, Fluorouracil (VS) en Xeloda (VS).

Date 13-05-2019

DPD AS 1: fluorouracil/capecitabine

[2941](#)

The gene variation increases the risk of severe, potentially fatal toxicity. A reduced conversion of fluorouracil/capecitabine to inactive metabolites means that the normal dose is an overdose.

- Start with 50% of the standard dose or avoid fluorouracil and capecitabine. Adjustment of the subsequent dose should be guided by toxicity and effectiveness. However, in one study involving 17 patients with gene activity 1, the average dose after titration was 57% of the standard dose. Tegafur is not an alternative, as this is also metabolised by DPD.

Literature:

1. Kleinjan JP et al. Tolerance-based capecitabine dose escalation after DPYD genotype-guided dosing in heterozygote DPYD variant carriers: a single-center observational study. *Anticancer Drugs* 2019 Jan 8 [Epub ahead of print].
2. Henricks LM et al. Effectiveness and safety of reduced-dose fluoropyrimidine therapy in patients carrying the DPYD*2A variant: a matched pair analysis. *Int J Cancer* 2018 Nov 28 [Epub ahead of print].
3. Lunenburg CATC et al. Standard fluoropyrimidine dosages in chemoradiation therapy result in an increased risk of severe toxicity in DPYD variant allele carriers. *Eur J Cancer* 2018;104:210-8.
4. Henricks LM et al. DPYD genotype-guided dose individualisation of fluoropyrimidine therapy in patients with cancer: a prospective safety analysis. *Lancet Oncol* 2018;19:1459-67 en persoonlijke communicatie (getitreerde dosis en mediane DPD-activiteit).
5. Madi A et al. Pharmacogenetic analyses of 2183 patients with advanced colorectal cancer; potential role for common dihydropyrimidine dehydrogenase variants in toxicity to chemotherapy. *Eur J Cancer* 2018;102:31-9.
6. Meulendijks D et al. Pretreatment serum uracil concentration as a predictor of severe and fatal fluoropyrimidine-associated toxicity. *Br J Cancer* 2017;116:1415-24.
7. Kodali S et al. Capecitabine-induced severe toxicity secondary to DPD deficiency and successful treatment with low dose 5-fluorouracil. *J Gastrointest Cancer* 2017;48:66- 69.
8. Meulendijks D et al. Patients homozygous for DPYD c.1129-5923C>G/ haplotype B3 have partial DPD deficiency and require a dose reduction when treated with fluoropyrimidines. *Cancer Chemother Pharmacol* 2016;78:875-80.
9. Lunenburg CA et al. Evaluation of clinical implementation of prospective DPYD genotyping in 5-fluorouracil- or capecitabine-treated patients. *Pharmacogenomics* 2016;17:721-9.
10. Deenen MJ et al. Upfront genotyping of DPYD*2A to individualize fluoropyrimidine therapy: a safety and cost analysis. *J Clin Oncol* 2016;34:227-34.
11. Meulendijks D et al. Clinical relevance of DPYD variants c.1679T>G, c.1236G>A/HapB3, and c.1601G>A as predictors of severe fluoropyrimidine-associated toxicity: a systematic review and meta-analysis of individual patient data. *Lancet Oncol* 2015;16:1639-50.
12. Lee AM et al. DPYD variants as predictors of 5-fluorouracil toxicity in adjuvant colon cancer treatment (NCCTG N0147). *J Natl Cancer Inst* 2014;106:dju298.
13. Rosmarin D et al. Genetic markers of toxicity from capecitabine and other fluorouracil-based regimens: investigation in the QUASAR2 study, systematic review, and meta-analysis. *J Clin Oncol* 2014; 32:1031-9.
14. Terrazzino S et al. DPYD IVS14+1 G>A and 2846A>T genotyping for the prediction of severe fluoropyrimidine-related toxicity: a meta-analysis. *Pharmacogenomics* 2013;14:1255-72.
15. Magnani E et al. Fluoropyrimidine toxicity in patients with dihydropyrimidine dehydrogenase splice site variant: the need for further revision of dose and schedule. *Intern Emerg Med* 2013; 8:417-23.
16. Vulsteke C et al. Genetic variability in the multidrug resistance associated protein-1 (ABCC1/MRP1) predicts hematological toxicity in breast cancer patients receiving (neo-)adjuvant chemotherapy with 5-fluorouracil, epirubicin and cyclophosphamide (FEC). *Ann Oncol* 2013; 24:1513-25.
17. van Kuilenburg AB et al. Evaluation of 5-fluorouracil pharmacokinetics in cancer patients with a c.1905+1 G>A mutation in DPYD by means of a Bayesian limited sampling strategy. *Clin Pharmacokinet* 2012;51:163-74.
18. Deenen MJ et al. Relationship between single nucleotide polymorphisms and haplotypes in DPYD and

- toxicity and efficacy of capecitabine in advanced colorectal cancer. *Clin Cancer Res* 2011; 17:3455-68.
19. Gross E et al. Strong association of a common dihydropyrimidine dehydrogenase gene polymorphism with fluoropyrimidine-related toxicity in cancer patients. *PLoS ONE* 2008;3:e4003.
 20. Capitain O et al. The influence of fluorouracil outcome parameters on tolerance and efficacy in patients with advanced colorectal cancer. *Pharmacogenomics J* 2008;8:256-67.
 21. Sulzyc-Bielicka V et al. 5-Fluorouracil toxicity-attributable IVS14 + 1G > A mutation of the dihydropyrimidine dehydrogenase gene in Polish colorectal cancer patients. *Pharmacol Rep* 2008;60:238-42.
 22. Schwab M et al. Role of genetic and nongenetic factors for fluorouracil treatment-related severe toxicity: a prospective clinical trial by the German 5-FU Toxicity Study Group. *J Clin Oncol* 2008;26:2131-8.
 23. Mercier C et al. Prospective phenotypic screening for DPD deficiency prior to 5-FU administration: Decrease in toxicity, not in efficacy. *J Clin Oncol* 2008;26(May 20 suppl):abstr 14556. (meeting abstract)
 24. Jatoi A et al. Paclitaxel, carboplatin, 5-fluorouracil, and radiation for locally advanced esophageal cancer: phase II results of preliminary pharmacologic and molecular efforts to mitigate toxicity and predict outcomes: North Central Cancer Treatment Group (N0044). *Am J Clin Oncol* 2007;30:507-13.
 25. Magné N et al. Dihydropyrimidine dehydrogenase activity and the IVS14+1G>A mutation in patients developing 5FU-related toxicity. *Br J Clin Pharmacol* 2007;64:237- 40.
 26. Saif MW et al. Dihydropyrimidine dehydrogenase deficiency (GPD) in GI malignancies: experience of 4-years. *Pak J Med Sci Q* 2007;23:832-9.
 27. Boisdron-Celle M et al. 5-Fluorouracil-related severe toxicity: a comparison of different methods for the pretherapeutic detection of dihydropyrimidine dehydrogenase deficiency. *Cancer Lett* 2007;249:271-82.
 28. Cho HJ et al. Thymidylate synthase (TYMS) and dihydropyrimidine dehydrogenase (DPYD) polymorphisms in the Korean population for prediction of 5-fluorouracil- associated toxicity. *Ther Drug Monit* 2007;29:190-6.
 29. Salgado J et al. Polymorphisms in the thymidylate synthase and dihydropyrimidine dehydrogenase genes predict response and toxicity to capecitabine-raltitrexed in colorectal cancer. *Oncol Rep* 2007;17:325-8.
 30. Morel A et al. Clinical relevance of different dihydropyrimidine dehydrogenase gene single nucleotide polymorphisms on 5-fluorouracil tolerance. *Mol Cancer Ther* 2006;5:2895-904.
 31. Largillier R et al. Pharmacogenetics of capecitabine in advanced breast cancer patients. *Clin Cancer Res* 2006;12:5496-502.
 32. Salgueiro N et al. Mutations in exon 14 of dihydropyrimidine dehydrogenase and 5-Fluorouracil toxicity in Portuguese colorectal cancer patients. *Genet Med* 2004;6:102- 7.
 33. Van Kuilenburg AB et al. High prevalence of the IVS14 + 1G>A mutation in the dihydropyrimidine dehydrogenase gene of patients with severe 5-fluorouracil-associated toxicity. *Pharmacogenetics* 2002;12:555-8.
 34. Raida M et al. Prevalence of a common point mutation in the dihydropyrimidine dehydrogenase (DPD) gene within the 5'-splice donor site of intron 14 in patients with severe 5-fluorouracil (5-FU)- related toxicity compared with controls. *Clin Cancer Res* 2001;7:2832-9.
 35. van Kuilenburg AB et al. Clinical implications of dihydropyrimidine dehydrogenase (DPD) deficiency in patients with severe 5-fluorouracil-associated toxicity: identification of new mutations in the DPD gene. *Clin Cancer Res* 2000;6:4705-12.
 36. SPC's Fluorouracil PCH, Xeloda, Efudix crème, Fluorouracil (VS) en Xeloda (VS).

Date 13-05-2019

DPD FENO: fluorouracil/capecitabine

[4646](#)

The gene variation increases the risk of severe, potentially fatal toxicity. A reduced conversion of fluorouracil/capecitabine to inactive metabolites means that the normal dose is an overdose.

It is not possible to recommend a dose adjustment for this patient based on the genotype only.

- determine the residual DPD activity in mononuclear cells from peripheral blood and adjust the initial dose based on phenotype and genotype, or avoid fluorouracil and capecitabine.
- Tegafur is not an alternative, as this is also metabolised by DPD.

Literature:

1. Lunenburg CATC et al. Diagnostic and therapeutic strategies for fluoropyrimidine treatment of patients carrying multiple DPYD variants. *Genes (Basel)* 2018;9:E585.
2. Lunenburg CATC et al. Standard fluoropyrimidine dosages in chemoradiation therapy result in an increased risk of severe toxicity in DPYD variant allele carriers. *Eur J Cancer* 2018;104:210-8.
3. Henricks LM et al. DPYD genotype-guided dose individualisation of fluoropyrimidine therapy in patients with cancer: a prospective safety analysis. *Lancet Oncol* 2018;19:1459-67 en persoonlijke communicatie (getitreerde dosis en mediane DPD-activiteit).
4. Henricks LM et al. Treatment algorithm for homozygous or compound heterozygous DPYD variant allele carriers with low-dose capecitabine. *JCO Precis Oncol* 2017 - published online Oct 6.

5. Kodali S et al. Capecitabine-induced severe toxicity secondary to DPD deficiency and successful treatment with low dose 5-fluorouracil. *J Gastrointest Cancer* 2017;48:66- 69.
6. Meulendijks D et al. Patients homozygous for DPYD c.1129-5923C>G/ haplotype B3 have partial DPD deficiency and require a dose reduction when treated with fluoropyrimidines. *Cancer Chemother Pharmacol* 2016;78:875-80.
7. Lunenburg CA et al. Evaluation of clinical implementation of prospective DPYD genotyping in 5-fluorouracil- or capecitabine-treated patients. *Pharmacogenomics* 2016;17:721-9.
8. Lee AM et al. Association between DPYD c.1129-5923 C>G/hapB3 and severe toxicity to 5-fluorouracil-based chemotherapy in stage III colon cancer patients: NCCTG N0147 (Alliance). *Pharmacogenet Genomics* 2016;26:133-7.
9. Deenen MJ et al. Upfront genotyping of DPYD*2A to individualize fluoropyrimidine therapy: a safety and cost analysis. *J Clin Oncol* 2016;34:227-34.
10. Meulendijks D et al. Clinical relevance of DPYD variants c.1679T>G, c.1236G>A/HapB3, and c.1601G>A as predictors of severe fluoropyrimidine-associated toxicity: a systematic review and meta-analysis of individual patient data. *Lancet Oncol* 2015;16:1639-50.
11. Lee AM et al. DPYD variants as predictors of 5-fluorouracil toxicity in adjuvant colon cancer treatment (NCCTG N0147). *J Natl Cancer Inst* 2014;106:dju298.
12. Deenen MJ et al. Relationship between single nucleotide polymorphisms and haplotypes in DPYD and toxicity and efficacy of capecitabine in advanced colorectal cancer. *Clin Cancer Res* 2011; 17:3455-68.
13. Boisdron-Celle M et al. 5-Fluorouracil-related severe toxicity: a comparison of different methods for the pretherapeutic detection of dihydropyrimidine dehydrogenase deficiency. *Cancer Lett* 2007;249:271-82.
14. Morel A et al. Clinical relevance of different dihydropyrimidine dehydrogenase gene single nucleotide polymorphisms on 5-fluorouracil tolerance. *Mol Cancer Ther* 2006;5:2895-904.
15. SPC's Fluorouracil PCH, Xeloda, Efudix crème, Fluorouracil (VS) en Xeloda (VS).

Date 13-05-2019

DPD AS 0: fluorouracil/capecitabine, systemisch

[2940](#)

The gene variation increases the risk of severe, potentially fatal toxicity. A reduced conversion of fluorouracil/capecitabine to inactive metabolites means that the standard dose is a more than 100-fold overdose.

- Avoid fluorouracil and capecitabine
Tegafur is not an alternative, as this is also metabolised by DPD.
- If it is not possible to avoid fluorouracil and capecitabine: determine the residual DPD activity in mononuclear cells from peripheral blood and adjust the initial dose accordingly.
A patient with 0.5% of the normal DPD activity tolerated 0.8% of the standard dose (150 mg capecitabine every 5 days). A patient with undetectable DPD activity tolerated 0.43% of the standard dose (150 mg capecitabine every 5 days with every third dose skipped)

Literature:

1. Henricks LM et al. Capecitabine-based treatment of a patient with a novel DPYD genotype and complete dihydropyrimidine dehydrogenase deficiency. *Int J Cancer* 2018;142:424-30.
2. Henricks LM et al. Treatment algorithm for homozygous or compound heterozygous DPYD variant allele carriers with low-dose capecitabine. *JCO Precis Oncol* - published online 2017 Oct 6.
3. Kodali S et al. Capecitabine-induced severe toxicity secondary to DPD deficiency and successful treatment with low dose 5-fluorouracil. *J Gastrointest Cancer* 2017;48:66- 69.
4. Meulendijks D et al. Patients homozygous for DPYD c.1129-5923C>G/ haplotype B3 have partial DPD deficiency and require a dose reduction when treated with fluoropyrimidines. *Cancer Chemother Pharmacol* 2016;78:875-80.
5. Lunenburg CA et al. Evaluation of clinical implementation of prospective DPYD genotyping in 5-fluorouracil- or capecitabine-treated patients. *Pharmacogenomics* 2016;17:721-9.
6. Deenen MJ et al. Upfront genotyping of DPYD*2A to individualize fluoropyrimidine therapy: a safety and cost analysis. *J Clin Oncol* 2016;34:227-34.
7. Rosmarin D et al. Genetic markers of toxicity from capecitabine and other fluorouracil-based regimens: investigation in the QUASAR2 study, systematic review, and meta- analysis. *J Clin Oncol* 2014; 32:1031-9.
8. Deenen MJ et al. Relationship between single nucleotide polymorphisms and haplotypes in DPYD and toxicity and efficacy of capecitabine in advanced colorectal cancer. *Clin Cancer Res* 2011; 17:3455-68.
9. Gross E et al. Strong association of a common dihydropyrimidine dehydrogenase gene polymorphism with fluoropyrimidine-related toxicity in cancer patients. *PLoS ONE* 2008;3:e4003.
10. Boisdron-Celle M et al. 5-Fluorouracil-related severe toxicity: a comparison of different methods for the pretherapeutic detection of dihydropyrimidine dehydrogenase deficiency. *Cancer Lett* 2007;249:271-82.
11. Morel A et al. Clinical relevance of different dihydropyrimidine dehydrogenase gene single nucleotide polymorphisms on 5-fluorouracil tolerance. *Mol Cancer Ther* 2006;5:2895-904.
12. Van Kuilenburg AB et al. High prevalence of the IVS14 + 1G>A mutation in the dihydropyrimidine dehydrogenase gene of patients with severe 5-fluorouracil-associated toxicity. *Pharmacogenetics* 2002;12:555-8.

13. Raida M et al. Prevalence of a common point mutation in the dihydropyrimidine dehydrogenase (DPD) gene within the 5'-splice donor site of intron 14 in patients with severe 5-fluorouracil (5-FU)- related toxicity compared with controls. Clin Cancer Res 2001;7:2832-9.
14. van Kuilenburg AB et al. Clinical implications of dihydropyrimidine dehydrogenase (DPD) deficiency in patients with severe 5-fluorouracil-associated toxicity: identification of new mutations in the DPD gene. Clin Cancer Res 2000;6:4705-12.
15. Johnson MR et al. Life-threatening toxicity in a dihydropyrimidine dehydrogenase-deficient patient after treatment with topical 5-fluorouracil. Clin Cancer Res 1999;5:2006-11.
16. SPC's Fluorouracil PCH, Xeloda, Efudix crème, Fluorouracil (VS), Xeloda (VS) en Carac cream (VS).

Date 13-05-2019

CYP2D6 IM: fluoxetine

[5611](#)

NO action is needed for this gene-drug interaction.

The ratio of fluoxetine/norfluoxetine increases as a result of the reduced activity of CYP2D6. However, this does not affect the sum of the plasma concentrations of the active substances (fluoxetine and norfluoxetine). There is no effect on adverse events or response.

Literature:

1. Gassó P et al. Effect of CYP2D6, CYP2C9 and ABCB1 genotypes on fluoxetine plasma concentrations and clinical improvement in children and adolescent patients. Pharmacogenomics J 2014;14:457-62.
2. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. Pharmacogenomics J 2014;14:176-81.
3. Scordo MG et al. Influence of CYP2C9, 2C19 and 2D6 genetic polymorphisms on the steady-state plasma concentrations of the enantiomers of fluoxetine and norfluoxetine. Basic Clin Pharmacol Toxicol 2005;97:296-301.
4. Llerena A et al. Effect of CYP2D6 and CYP2C9 genotypes on fluoxetine and norfluoxetine plasma concentrations during steady-state conditions. Eur J Clin Pharmacol 2004;59:869-73.

Date 14-05-2018

CYP2D6 PM: fluoxetine

[5610](#)

NO action is needed for this gene-drug interaction.

The ratio of fluoxetine/norfluoxetine increases as a result of the reduced activity of CYP2D6. However, this does not affect the sum of the plasma concentrations of the active substances (fluoxetine and norfluoxetine). There is insufficient evidence to support an effect on adverse events or response.

Literature:

1. Gassó P et al. Effect of CYP2D6, CYP2C9 and ABCB1 genotypes on fluoxetine plasma concentrations and clinical improvement in children and adolescent patients. Pharmacogenomics J 2014;14:457-62.
2. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. Pharmacogenomics J 2014;14:176-81.
3. Scordo MG et al. Influence of CYP2C9, 2C19 and 2D6 genetic polymorphisms on the steady-state plasma concentrations of the enantiomers of fluoxetine and norfluoxetine. Basic Clin Pharmacol Toxicol 2005;97:296-301.
4. Llerena A et al. Effect of CYP2D6 and CYP2C9 genotypes on fluoxetine and norfluoxetine plasma concentrations during steady-state conditions. Eur J Clin Pharmacol 2004;59:869-73.
5. Roberts RL et al. No evidence of increased adverse drug reactions in cytochrome P450 CYP2D6 poor metabolizers treated with fluoxetine or nortriptyline. Hum Psychopharmacol 2004;19:17-23.
6. Perucca E et al. Fluoxetine-induced movement disorders and deficient CYP2D6 enzyme activity. Mov Disord 1997;12:624-5.
7. SPC Prozac, USA, 30-01-09.

Date 14-05-2018

CYP2D6 UM: fluoxetine

[5612](#)

NO action is needed for this gene-drug interaction.

The ratio of fluoxetine/norfluoxetine decreases as a result of the increased activity of CYP2D6. However, this does not affect the sum of the plasma concentrations of the active substances (fluoxetine and

norfluoxetine). There is no effect on adverse events or response.

Literature:

1. Gassó P et al. Effect of CYP2D6, CYP2C9 and ABCB1 genotypes on fluoxetine plasma concentrations and clinical improvement in children and adolescent patients. *Pharmacogenomics J* 2014;14:457-62.
2. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
3. Scordo MG et al. Influence of CYP2C9, 2C19 and 2D6 genetic polymorphisms on the steady-state plasma concentrations of the enantiomers of fluoxetine and norfluoxetine. *Basic Clin Pharmacol Toxicol* 2005;97:296-301.
4. LLerena A et al. Effect of CYP2D6 and CYP2C9 genotypes on fluoxetine and norfluoxetine plasma concentrations during steady-state conditions. *Eur J Clin Pharmacol* 2004;59:869-73.

Date 14-05-2018

CYP2D6 IM: flupentixol

[2379](#)

This is NOT a gene-drug interaction.

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopenthixol. *Br J Clin Pharmacol* 2021;87:2228-35.

Date 13-09-2021

CYP2D6 PM: flupentixol

[2381](#)

This is NOT a gene-drug interaction.

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopenthixol. *Br J Clin Pharmacol* 2021;87:2228-35.

Date 13-09-2021

CYP2D6 UM: flupentixol

[2380](#)

This is NOT a gene-drug interaction.

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopenthixol. *Br J Clin Pharmacol* 2021;87:2228-35.

Date 13-09-2021

SLCO1B1 521CC: fluvastatine

[3985](#)

NO action is required for this gene-drug interaction.

The gene variation increases the plasma concentration of fluvastatin, but there is insufficient evidence to prove an effect on efficacy or side effects.

Literature:

1. Hirvensalo P et al. Enantiospecific pharmacogenomics of fluvastatin. *Clin Pharmacol Ther* 2019;106:668-80.
2. Mori D et al. Effect of OATP1B1 genotypes on plasma concentrations of endogenous OATP1B1 substrates and drugs, and their association in healthy volunteers. *Drug Metab Pharmacokinet* 2019;34:78-86.
3. Xiang Q et al. The association between the SLCO1B1, apolipoprotein E, and CYP2C9 genes and lipid response to fluvastatin: a meta-analysis. *Pharmacogenet Genomics* 2018;28:261-7.
4. Meyer zu Schwabedissen HE et al. Function-impairing polymorphisms of the hepatic uptake transporter

- SLCO1B1 modify the therapeutic efficacy of statins in a population-based cohort. *Pharmacogenet Genomics* 2015;25:8-18.
5. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. *Pharmacogenet Genomics* 2008;18:921-6.
 6. Couvert P et al. Association between a frequent allele of the gene encoding OATP1B1 and enhanced LDL-lowering response to fluvastatin therapy. *Pharmacogenomics* 2008;9:1217-27.
 7. Singer JB et al. Genetic analysis of fluvastatin response and dyslipidemia in renal transplant recipients. *J Lipid Res* 2007;48:2072-8.
 8. Niemi M et al. SLCO1B1 polymorphism and sex affect the pharmacokinetics of pravastatin but not fluvastatin. *Clin Pharmacol Ther* 2006;80:356-66.
 9. Thompson JF et al. An association study of 43 SNPs in 16 candidate genes with atorvastatin response. *Pharmacogenomics J* 2005;5:352-8.

Date 18-05-2020

SLCO1B1 521TC: fluvastatine

[3984](#)

NO action is required for this gene-drug interaction.

The gene variation increases the plasma concentration of fluvastatin, but there is insufficient evidence to prove an effect on efficacy or side effects.

Literature:

1. Hirvensalo P et al. Enantiospecific pharmacogenomics of fluvastatin. *Clin Pharmacol Ther* 2019;106:668-80.
2. Mori D et al. Effect of OATP1B1 genotypes on plasma concentrations of endogenous OATP1B1 substrates and drugs, and their association in healthy volunteers. *Drug Metab Pharmacokinet* 2019;34:78-86.
3. Xiang Q et al. The association between the SLCO1B1, apolipoprotein E, and CYP2C9 genes and lipid response to fluvastatin: a meta-analysis. *Pharmacogenet Genomics* 2018;28:261-7.
4. Meyer zu Schwabedissen HE et al. Function-impairing polymorphisms of the hepatic uptake transporter SLCO1B1 modify the therapeutic efficacy of statins in a population-based cohort. *Pharmacogenet Genomics* 2015;25:8-18.
5. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. *Pharmacogenet Genomics* 2008;18:921-6.
6. Couvert P et al. Association between a frequent allele of the gene encoding OATP1B1 and enhanced LDL-lowering response to fluvastatin therapy. *Pharmacogenomics* 2008;9:1217-27.
7. Singer JB et al. Genetic analysis of fluvastatin response and dyslipidemia in renal transplant recipients. *J Lipid Res* 2007;48:2072-8.
8. Niemi M et al. SLCO1B1 polymorphism and sex affect the pharmacokinetics of pravastatin but not fluvastatin. *Clin Pharmacol Ther* 2006;80:356-66.
9. Thompson JF et al. An association study of 43 SNPs in 16 candidate genes with atorvastatin response. *Pharmacogenomics J* 2005;5:352-8.

Date 18-05-2020

CYP2C19 IM: fluvoxamine

[3536](#)

This is NOT a gene-drug interaction

Literature:

1. Jan MW et al. Pharmacokinetics of fluvoxamine in relation to CYP2C19 phenotype and genotype. *Drug Metabol Drug Interact* 2002;19:1-11.
2. Spigset O et al. The major fluvoxamine metabolite in urine is formed by CYP2D6. *Eur J Clin Pharmacol* 2001;57:653-8.
3. Spigset O et al. Relationship between fluvoxamine pharmacokinetics and CYP2D6/CYP2C19 phenotype polymorphisms. *Eur J Clin Pharmacol* 1997;52:129-33.

Date 14-05-2018

CYP2C19 PM: fluvoxamine

[3535](#)

This is NOT a gene-drug interaction.

Literature:

1. Jan MW et al. Pharmacokinetics of fluvoxamine in relation to CYP2C19 phenotype and genotype. Drug Metabol Drug Interact 2002;19:1-11.
2. Spigset O et al. The major fluvoxamine metabolite in urine is formed by CYP2D6. Eur J Clin Pharmacol 2001;57:653-8.
3. Spigset O et al. Relationship between fluvoxamine pharmacokinetics and CYP2D6/CYP2C19 phenotype polymorphisms. Eur J Clin Pharmacol 1997;52:129-33.

Date 14-05-2018

CYP2C19 UM: fluvoxamine

[3537](#)

This is NOT a gene-drug interaction.

Literature:

1. Jan MW et al. Pharmacokinetics of fluvoxamine in relation to CYP2C19 phenotype and genotype. Drug Metabol Drug Interact 2002;19:1-11.
2. Spigset O et al. The major fluvoxamine metabolite in urine is formed by CYP2D6. Eur J Clin Pharmacol 2001;57:653-8.
3. Spigset O et al. Relationship between fluvoxamine pharmacokinetics and CYP2D6/CYP2C19 phenotype polymorphisms. Eur J Clin Pharmacol 1997;52:129-33.

Date 14-05-2018

CYP2D6 IM: fluvoxamine

[5608](#)

NO action is needed for this gene-drug interaction.

The plasma concentration of fluvoxamine can increase as a result of the reduced activity of CYP2D6. However, there is insufficient scientific substantiation of an increase in the risk of side effects.

Literature:

1. Suzuki Y et al. CYP2D6 genotype and smoking influence fluvoxamine steady-state concentration in Japanese psychiatric patients: lessons for genotype-phenotype association study design in translational pharmacogenetics. J Psychopharmacol 2011;25:908-14.
2. Sugahara H et al. Effect of smoking and CYP2D6 polymorphisms on the extent of fluvoxamine-alprazolam interaction in patients with psychosomatic disease. Eur J Clin Pharmacol 2009;65:699-704.
3. Suzuki Y et al. Polymorphisms in the 5-hydroxytryptamine 2A receptor and cytochrome P4502D6 genes synergistically predict fluvoxamine-induced side effects in Japanese depressed patients. Neuropsychopharmacology 2006;31:825-31.
4. Gerstenberg G et al. Effects of the CYP2D6 genotype and cigarette smoking on the steady-state plasma concentrations of fluvoxamine and its major metabolite fluvoxamino acid in Japanese depressed patients. Ther Drug Monit 2003;25:463-8.
5. Gerstenberg G et al. Relationship between clinical effects of fluvoxamine and the steady-state plasma concentrations of fluvoxamine and its major metabolite fluvoxamino acid in Japanese depressed patients. Psychopharmacology (Berl) 2003;167:443-8.
6. Ohara K et al. CYP2D6*10 alleles do not determine plasma fluvoxamine concentration/dose ratio in Japanese subjects. Eur J Clin Pharmacol 2003;58:659-61.

Date 14-05-2018

CYP2D6 PM: fluvoxamine

[5607](#)

NO action is needed for this gene-drug interaction.

The plasma concentration of fluvoxamine can increase as a result of the reduced activity of CYP2D6. However, there is no evidence to substantiate an increase in the risk of adverse events.

Literature:

1. Christensen M et al. Low daily 10-mg and 20-mg doses of fluvoxamine inhibit the metabolism of both caffeine (cytochrome P4501A2) and omeprazole (cytochrome P4502C19). Clin Pharmacol Ther 2002;71:141-52.
2. Spigset O et al. Relationship between fluvoxamine pharmacokinetics and CYP2D6/CYP2C19 phenotype polymorphisms. Eur J Clin Pharmacol 1997;52:129-33.

3. Carrillo JA et al. Disposition of fluvoxamine in humans is determined by the polymorphic CYP2D6 and also by the CYP1A2 activity. Clin Pharmacol Ther 1996;60:183-90.
4. SPC's Fevarin en Luvox (VS).

Date 14-05-2018

CYP2D6 UM: fluvoxamine

[5609](#)

NO action is needed for this gene-drug interaction.

The plasma concentration of fluvoxamine can decrease as a result of the increased activity of CYP2D6. However, there is no scientific substantiation of a reduced effectiveness.

Literature:

1. Suzuki Y et al. CYP2D6 genotype and smoking influence fluvoxamine steady-state concentration in Japanese psychiatric patients: lessons for genotype-phenotype association study design in translational pharmacogenetics. J Psychopharmacol 2011;25:908-14.
2. Spigset O et al. Relationship between fluvoxamine pharmacokinetics and CYP2D6/CYP2C19 phenotype polymorphisms. Eur J Clin Pharmacol 1997;52:129-33.
3. Carrillo JA et al. Disposition of fluvoxamine in humans is determined by the polymorphic CYP2D6 and also by the CYP1A2 activity. Clin Pharmacol Ther 1996;60:183-90.

Date 14-05-2018

MTHFR 677CT: foliumzuur

[7164](#)

NO action is required for this gene-drug interaction.

The gene variation has no effect on the treatment with folic acid. Treatment with folic acid decreases the reduction of folate concentrations caused by the gene variation.

Literature:

1. Song Chen MY et al. Defining the plasma folate concentration associated with the red blood cell folate concentration threshold for optimal neural tube defects prevention: a population-based, randomized trial of folic acid supplementation. Am J Clin Nutr 2019;109:1452-61.
2. Jin H et al. An evidence-based approach to globally assess the covariate-dependent effect of the MTHFR single nucleotide polymorphism rs1801133 on blood homocysteine: a systematic review and meta-analysis. Am J Clin Nutr 2018;107:817-25.
3. Du B et al. Genetic polymorphisms of key enzymes in folate metabolism affect the efficacy of folate therapy in patients with hyperhomocysteinaemia. Br J Nutr 2018;119:887-95.
4. Huang X et al. MTHFR gene and serum folate interaction on serum homocysteine lowering: prospect for precision folic acid treatment. Arterioscler Thromb Vasc Biol 2018;38:679-85.
5. den Dekker HT et al. Maternal folic acid use during pregnancy, methylenetetrahydrofolate reductase gene polymorphism, and child's lung function and asthma. Clin Exp Allergy 2018;48:175-85.
6. Shao W et al. Association between MTHFR C677T polymorphism and methotrexate treatment outcome in rheumatoid arthritis patients: a systematic review and meta-analysis. Genet Test Mol Biomarkers 2017;21:275-85.
7. Huo Y et al. Efficacy of folic acid therapy in primary prevention of stroke among adults with hypertension in China: the CSPPT randomized clinical trial. JAMA 2015;313:1325-35.
8. Kondo A et al. C677T mutation in methylenetetrahydrofolate reductase gene and neural tube defects: should Japanese women undergo gene screening before pregnancy? Congenit Anom (Kyoto) 2014;54:30-4.
9. Crider KS et al. MTHFR 677C->T genotype is associated with folate and homocysteine concentrations in a large, population-based, double-blind trial of folic acid supplementation. Am J Clin Nutr 2011;93:1365-72.

Date 07-06-2021

MTHFR 677TT: foliumzuur

[7165](#)

NO action is required for this gene-drug interaction.

The gene variation either has no effect or a positive effect on the treatment with folic acid. Treatment with folic acid decreases the reduction of folate concentrations caused by the gene variation.

Literature:

1. Song Chen MY et al. Defining the plasma folate concentration associated with the red blood cell folate concentration threshold for optimal neural tube defects prevention: a population-based, randomized trial of folic acid supplementation. *Am J Clin Nutr* 2019;109:1452-61.
2. Jin H et al. An evidence-based approach to globally assess the covariate-dependent effect of the MTHFR single nucleotide polymorphism rs1801133 on blood homocysteine: a systematic review and meta-analysis. *Am J Clin Nutr* 2018;107:817-25.
3. Du B et al. Genetic polymorphisms of key enzymes in folate metabolism affect the efficacy of folate therapy in patients with hyperhomocysteinaemia. *Br J Nutr* 2018;119:887-95.
4. Huang X et al. MTHFR gene and serum folate interaction on serum homocysteine lowering: prospect for precision folic acid treatment. *Arterioscler Thromb Vasc Biol* 2018;38:679-85.
5. den Dekker HT et al. Maternal folic acid use during pregnancy, methylenetetrahydrofolate reductase gene polymorphism, and child's lung function and asthma. *Clin Exp Allergy* 2018;48:175-85.
6. Shao W et al. Association between MTHFR C677T polymorphism and methotrexate treatment outcome in rheumatoid arthritis patients: a systematic review and meta-analysis. *Genet Test Mol Biomarkers* 2017;21:275-85.
7. Colson NJ et al. The impact of MTHFR 677 C/T genotypes on folate status markers: a meta-analysis of folic acid intervention studies. *Eur J Nutr* 2017;56:247-60.
8. Huo Y et al. Efficacy of folic acid therapy in primary prevention of stroke among adults with hypertension in China: the CSPPT randomized clinical trial. *JAMA* 2015;313:1325-35.
9. Kondo A et al. C677T mutation in methylenetetrahydrofolate reductase gene and neural tube defects: should Japanese women undergo gene screening before pregnancy? *Congenit Anom (Kyoto)* 2014;54:30-4.
10. Crider KS et al. MTHFR 677C->T genotype is associated with folate and homocysteine concentrations in a large, population-based, double-blind trial of folic acid supplementation. *Am J Clin Nutr* 2011;93:1365-72.

Date 07-06-2021

CYP2D6 IM: gefitinib

[4634](#)

NO action is needed for this gene-drug interaction.

Side effects can occur more frequently, as the gene variation increases the gefitinib plasma concentration. However, the side effects are reversible and manageable, to an extent that adjustment of the therapy in advance is not necessary.

Literature:

1. Hirose T et al. Association of pharmacokinetics and pharmacogenomics with safety and efficacy of gefitinib in patients with EGFR mutation positive advanced non-small cell lung cancer. *Lung Cancer* 2016;93:69-76.
2. Sugiyama E et al. Impact of single nucleotide polymorphisms on severe hepatotoxicity induced by EGFR tyrosine kinase inhibitors in patients with non-small cell lung cancer harboring EGFR mutations. *Lung Cancer* 2015;90:307-13.
3. Kobayashi H et al. Relationship among gefitinib exposure, polymorphisms of its metabolizing enzymes and transporters, and side effects in Japanese patients with non-small-cell lung cancer. *Clin Lung Cancer* 2015;16:274-81.
4. Takimoto T et al. Polymorphisms of CYP2D6 gene and gefitinib-induced hepatotoxicity. *Clinical Lung Cancer* 2013;14:502-7.
5. Suzumura T et al. Reduced CYP2D6 function is associated with gefitinib-induced rash in patients with non-small cell lung cancer. *BMC Cancer* 2012;12:568.
6. Chhun S et al. Gefitinib-phenytoin interaction is not correlated with the C-erythromycin breath test in healthy male volunteers. *Br J Clin Pharmacol* 2009;68:226-37.

Date 19-11-2018

CYP2D6 PM: gefitinib

[4635](#)

NO action is needed for this gene-drug interaction.

The gefitinib plasma concentration may increase due to reduced CYP2D6 activity. However, there is no evidence to suggest that side effects increase to an extent that adjustment of therapy is needed.

Literature:

1. Chhun S et al. Gefitinib-phenytoin interaction is not correlated with the C-erythromycin breath test in healthy male volunteers. *Br J Clin Pharmacol* 2009;68:226-37.
2. Swaisland HC et al. Exploring the relationship between expression of cytochrome P450 enzymes and

- gefitinib pharmacokinetics. Clin Pharmacokinet 2006;45:633-44.
3. SPC Iressa.

Date 19-11-2018

CYP2D6 UM: gefitinib

[4636](#)

NO action is needed for this gene-drug interaction.

The gene variation may lead to a decrease in the gefitinib plasma concentration. In practice, an alternative is only chosen if non-response to gefitinib has been proved. Moreover, dose adjustments guided by the gefitinib plasma concentration are rarely performed in clinical practice as the analytical method is not available in most hospitals.

Literature:

1. Chhun S et al. Gefitinib-phenytoin interaction is not correlated with the C-erythromycin breath test in healthy male volunteers. Br J Clin Pharmacol 2009;68:226-37.
2. Swaisland HC et al. Exploring the relationship between expression of cytochrome P450 enzymes and gefitinib pharmacokinetics. Clin Pharmacokinet 2006;45:633-44.
3. SPC Iressa.

Date 19-11-2018

CYP2C9 IM ANDERS: glibenclamide

[2535](#)

NO action is required for this gene-drug interaction.

The only relevant clinical consequence that was found is an increased effectiveness of glibenclamide without an increase in the frequency and severity of hypoglycaemia.

Literature:

1. Surendiran A et al. Influence of CYP2C9 gene polymorphisms on response to glibenclamide in type 2 diabetes mellitus patients. Eur J Clin Pharmacol 2011;67:797-801.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
3. Yin OQ et al. CYP2C9, but not CYP2C19, polymorphisms affect the pharmacokinetics and pharmacodynamics of glyburide in Chinese subjects. Clin Pharmacol Ther 2005;78:370-7.
4. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.
5. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9 PM ANDERS: glibenclamide

[2536](#)

NO action is required for this gene-drug interaction.

No relevant clinical consequences have been found for the genetic variation.

Literature:

1. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
2. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. Br J Clin Pharmacol 2005;60:103-6.
3. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9*1/*2: glibenclamide

[2530](#)

NO action is required for this gene-drug interaction.

The only relevant clinical consequence that was found is an increased effectiveness of glibenclamide without an increase in frequency and severity of hypoglycaemia for a group of 1 *1/*2 and 15 *1/*3.

Literature:

1. Surendiran A et al. Influence of CYP2C9 gene polymorphisms on response to glibenclamide in type 2 diabetes mellitus patients. Eur J Clin Pharmacol 2011;67:797-801.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288-92.
3. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.
4. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9*1/*3: glibenclamide

[2531](#)

NO action is required for this gene-drug interaction.

The only relevant clinical consequence is an increased effectiveness of glibenclamide without an increase in frequency and severity of hypoglycaemia.

Literature:

1. Surendiran A et al. Influence of CYP2C9 gene polymorphisms on response to glibenclamide in type 2 diabetes mellitus patients. Eur J Clin Pharmacol 2011;67:797-801.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288-92.
3. Yin OQ et al. CYP2C9, but not CYP2C19, polymorphisms affect the pharmacokinetics and pharmacodynamics of glyburide in Chinese subjects. Clin Pharmacol Ther 2005;78:370-7.
4. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.
5. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9*2/*2: glibenclamide

[2532](#)

NO action is required for this gene-drug interaction.

No significant clinical consequences have been found for the genetic variation.

Literature:

1. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
2. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9*2/*3: glibenclamide

[2533](#)

NO action is required for this gene-drug interaction.

No significant kinetic or clinical consequences have been found for this genetic variation.

Literature:

1. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
2. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. Br J Clin Pharmacol 2005;60:103-6.
3. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. Clin Pharmacol Ther 2002;71:286-96.

Date 20-11-2017

CYP2C9*3/*3: glibenclamide

[2534](#)

NO action is required for this gene-drug interaction.

No relevant clinical consequences have been found for this genetic variation.

Literature:

1. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. *Br J Clin Pharmacol* 2005;60:103-6.
2. Kirchheiner J et al. Impact of CYP2C9 amino acid polymorphisms on glyburide kinetics and on the insulin and glucose response in healthy volunteers. *Clin Pharmacol Ther* 2002;71:286-96.

Date 20-11-2017

CYP2C9 IM ANDERS: gliclazide

[2542](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide without significantly increasing the risk of hypoglycaemia.

Literature:

1. Zeng W et al. CYP2C93 variant is associated with antidiabetes efficacy of gliclazide in Chinese type 2 diabetes patients. *J Diabetes Investig* 2016;7:764-8.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
3. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.
4. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. *Pharmacogenomics* 2009;10:1781-7.
5. Xu H et al. Effects of St John's wort and CYP2C9 genotype on the pharmacokinetics and pharmacodynamics of gliclazide. *Br J Pharmacol* 2008;153:1579-86.
6. Zhang Y et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on pharmacokinetics of gliclazide MR in Chinese subjects. *Br J Clin Pharmacol* 2007;64:67-74.

Date 20-11-2017

CYP2C9 PM ANDERS: gliclazide

[2543](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide without significantly increasing the risk of hypoglycaemia.

Literature:

1. Zeng W et al. CYP2C93 variant is associated with antidiabetes efficacy of gliclazide in Chinese type 2 diabetes patients. *J Diabetes Investig* 2016;7:764-8.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
3. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.
4. Xu H et al. Effects of St John's wort and CYP2C9 genotype on the pharmacokinetics and pharmacodynamics of gliclazide. *Br J Pharmacol* 2008;153:1579-86.

Date 20-11-2017

CYP2C9*1/*2: gliclazide

[2537](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide

Literature:

1. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
2. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.
3. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. *Pharmacogenomics* 2009;10:1781-7.
4. Xu H et al. Effects of St John's wort and CYP2C9 genotype on the pharmacokinetics and pharmacodynamics of gliclazide. *Br J Pharmacol* 2008;153:1579-86.

Date 20-11-2017

CYP2C9*1/*3: gliclazide

[2538](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide without significantly increasing the risk of hypoglycaemia.

Literature:

1. Zeng W et al. CYP2C93 variant is associated with antidiabetes efficacy of gliclazide in Chinese type 2 diabetes patients. *J Diabetes Investig* 2016;7:764-8.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
3. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.
4. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. *Pharmacogenomics* 2009;10:1781-7.
5. Xu H et al. Effects of St John's wort and CYP2C9 genotype on the pharmacokinetics and pharmacodynamics of gliclazide. *Br J Pharmacol* 2008;153:1579-86.
6. Zhang Y et al. Influence of CYP2C9 and CYP2C19 genetic polymorphisms on pharmacokinetics of gliclazide MR in Chinese subjects. *Br J Clin Pharmacol* 2007;64:67-74.

Date 20-11-2017

CYP2C9*2/*2: gliclazide

[2539](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide.

Literature:

1. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
2. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.
3. Xu H et al. Effects of St John's wort and CYP2C9 genotype on the pharmacokinetics and pharmacodynamics of gliclazide. *Br J Pharmacol* 2008;153:1579-86.

Date 20-11-2017

CYP2C9*2/*3: gliclazide

[2540](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide.

Literature:

1. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
2. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.

CYP2C9*3/*3: gliclazide

[2541](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of gliclazide without significantly increasing the risk of hypoglycaemia.

Literature:

1. Zeng W et al. CYP2C93 variant is associated with antidiabetes efficacy of gliclazide in Chinese type 2 diabetes patients. *J Diabetes Investig* 2016;7:764-8.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
3. Zhou K et al. Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. *Clin Pharmacol Ther* 2010;87:52-6.

Date 20-11-2017

CYP2C9 IM ANDERS: glimepiride

[2549](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of glimepiride.

Literature:

1. Bhatt D et al. Investigating the role of plasma glucose concentration as a phenotypic marker for CYP2C9 genetic variants, in the diabetic population of Gujarat. *Indian J Pharm Sci* 2014;76:72-7.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. *Eur J Clin Pharmacol* 2011;67:1223-9.
3. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
4. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. *Pharmacogenomics* 2009;10:1781-7.
5. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288- 92.
6. Suzuki K et al. Effect of CYP2C9 genetic polymorphisms on the efficacy and pharmacokinetics of glimepiride in subjects with type 2 diabetes. *Diabetes Res Clin Pract* 2006;72:148-54.
7. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. *Br J Clin Pharmacol* 2005;60:103-6.
8. Wang R et al. Pharmacokinetics of glimepiride and cytochrome P450 2C9 genetic polymorphisms. *Clin Pharmacol Ther* 2005;78:90-2.
9. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. *Clin Pharmacol Ther* 2002;72:326-32.

Date 20-11-2017

CYP2C9 PM ANDERS: glimepiride

[2550](#)

NO action is required for this gene-drug interaction.

Although the genetic variation increases the risk of hypoglycaemia, this risk remains low. This also means that the genetic variation increases the effectiveness. A lack of effectiveness is a much more common problem with sulphonyl urea derivatives than the occurrence of hypoglycaemia.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288- 92.
3. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. *Br J Clin Pharmacol* 2005;60:103-6.
4. Wang R et al. Pharmacokinetics of glimepiride and cytochrome P450 2C9 genetic polymorphisms. *Clin*

Pharmacol Ther 2005;78:90-2.

5. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.

Date 20-11-2017

CYP2C9*1/*2: glimepiride

[2544](#)

NO action is required for this gene-drug interaction.

No significant kinetic or clinical consequences have been found for the genetic variation.

Literature:

1. Bhatt D et al. Investigating the role of plasma glucose concentration as a phenotypic marker for CYP2C9 genetic variants, in the diabetic population of Gujarat. Indian J Pharm Sci 2014;76:72-7.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. Eur J Clin Pharmacol 2011;67:1223-9.
3. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. Pharmacogenomics 2010;11:1517-23.
4. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. Pharmacogenomics 2009;10:1781-7.
5. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
6. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. Br J Clin Pharmacol 2005;60:103-6.
7. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.

Date 20-11-2017

CYP2C9*1/*3: glimepiride

[2545](#)

NO action is required for this gene-drug interaction.

The genetic variation increases the effectiveness of glimepiride.

Literature:

1. Bhatt D et al. Investigating the role of plasma glucose concentration as a phenotypic marker for CYP2C9 genetic variants, in the diabetic population of Gujarat. Indian J Pharm Sci 2014;76:72-7.
2. Gökalp O et al. Mild hypoglycaemic attacks induced by sulphonylureas related to CYP2C9, CYP2C19 and CYP2C8 polymorphisms in routine clinical setting. Eur J Clin Pharmacol 2011;67:1223-9.
3. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. Pharmacogenomics 2010;11:1517-23.
4. Ragia G et al. Presence of CYP2C9*3 allele increases risk for hypoglycemia in Type 2 diabetic patients treated with sulfonylureas. Pharmacogenomics 2009;10:1781-7.
5. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288- 92.
6. Suzuki K et al. Effect of CYP2C9 genetic polymorphisms on the efficacy and pharmacokinetics of glimepiride in subjects with type 2 diabetes. Diabetes Res Clin Pract 2006;72:148-54.
7. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. Br J Clin Pharmacol 2005;60:103-6.
8. Wang R et al. Pharmacokinetics of glimepiride and cytochrome P450 2C9 genetic polymorphisms. Clin Pharmacol Ther 2005;78:90-2.
9. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. Clin Pharmacol Ther 2002;72:326-32.

Date 20-11-2017

CYP2C9*2/*2: glimepiride

[2546](#)

NO action is required for this gene-drug interaction.

No significant clinical effects were observed for this genetic variation.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288- 92.

Date 20-11-2017

CYP2C9*2/*3: glimepiride

[2547](#)

NO action is required for this gene-drug interaction.

Although the genetic variation increases the risk of hypoglycaemia, this risk remains low. This also means that the genetic variation increases the effectiveness. A lack of effectiveness is a much more common problem with sulphonyl urea derivatives than the occurrence of hypoglycaemia.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288- 92.
3. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. *Br J Clin Pharmacol* 2005;60:103-6.
4. Niemi M et al. Glyburide and glimepiride pharmacokinetics in subjects with different CYP2C9 genotypes. *Clin Pharmacol Ther* 2002;72:326-32.

Date 20-11-2017

CYP2C9*3/*3: glimepiride

[2548](#)

NO action is required for this gene-drug interaction.

Although the genetic variation increases the risk of hypoglycaemia, this risk remains low. This also means that the genetic variation increases the effectiveness. A lack of effectiveness is a much more common problem with sulphonyl urea derivatives than the occurrence of hypoglycaemia.

Literature:

1. Holstein A et al. Association between CYP2C9 slow metabolizer genotypes and severe hypoglycaemia on medication with sulphonylurea hypoglycaemic agents. *Br J Clin Pharmacol* 2005;60:103-6.
2. Wang R et al. Pharmacokinetics of glimepiride and cytochrome P450 2C9 genetic polymorphisms. *Clin Pharmacol Ther* 2005;78:90-2.

Date 20-11-2017

CYP2D6 IM: haloperidol

[2397](#)

NO action is required for this gene-drug interaction.

The genetic variation results in a higher plasma concentration, but the effect is small and no clinically significant effects were found.

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopenthixol. *Br J Clin Pharmacol* 2021;87:2228-35.
2. Trogrlić Z et al. Pharmacogenomic response of low dose haloperidol in critically ill adults with delirium. *J Crit Care* 2020;57:203-7.
3. Sychev DA et al. The correlation between CYP2D6 isoenzyme activity and haloperidol efficacy and safety profile in patients with alcohol addiction during the exacerbation of the addiction. *Pharmacogenomics Pers Med* 2016;9:89-95.
4. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. *Eur J Clin*

Pharmacol 2016;72:175-84.

5. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 and personal communication (mean dose-corrected trough concentrations).
6. Panagiotidis G et al. Depot haloperidol treatment in outpatients with schizophrenia on monotherapy: impact of CYP2D6 polymorphism on pharmacokinetics and treatment outcome. Ther Drug Monit 2007;29:417-22.
7. Park JY et al. Combined effects of itraconazole and CYP2D6*10 genetic polymorphism on the pharmacokinetics and pharmacodynamics of haloperidol in healthy subjects. J Clin Psychopharmacol 2006;26:135-42.
8. LLerena A et al. Relationship between haloperidol plasma concentration, debrisoquine metabolic ratio, CYP2D6 and CYP2C9 genotypes in psychiatric patients. Pharmacopsychiatry 2004;37:69-73.
9. Desai M et al. Pharmacokinetics and QT interval pharmacodynamics of oral haloperidol in poor and extensive metabolizers of CYP2D6. Pharmacogenomics J 2003;3:105- 13.
10. Brockmoller J et al. The impact of the CYP2D6 polymorphism on haloperidol pharmacokinetics and on the outcome of haloperidol treatment. Clin Pharmacol Ther 2002;72:438-52.
11. Yasui-Furukori N et al. Effect of the CYP2D6 genotype on prolactin concentration in schizophrenic patients treated with haloperidol. Schizophr Res 2001 1;52:139-42.
12. Pan L et al. Effects of smoking, CYP2D6 genotype, and concomitant drug intake on the steady state plasma concentrations of haloperidol and reduced haloperidol in schizophrenic inpatients. Ther Drug Monit 1999;21:489-97.
13. LLerena A et al. Haloperidol disposition is dependent on the debrisoquine hydroxylation phenotype: increased plasma levels of the reduced metabolite in poor metabolizers. Ther Drug Monit 1992;14:261-4.
14. LLerena A. Haloperidol disposition is dependent on debrisoquine hydroxylation phenotype. Ther Drug Monit 1992;14:92-7.

Date 13-09-2021

CYP2D6 PM: haloperidol

[2398](#)

There are indications for an increased risk of side effects. The genetic variation leads to decreased conversion of haloperidol, resulting in plasma concentrations that are approximately 1.7-fold higher.

- use 60% of the standard

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopenthixol. Br J Clin Pharmacol 2021;87:2228-35.
2. Trogrlić Z et al. Pharmacogenomic response of low dose haloperidol in critically ill adults with delirium. J Crit Care 2020;57:203-7.
3. Šimić I et al. CYP2D6 6/6 genotype and drug interactions as cause of haloperidol-induced extrapyramidal symptoms. Pharmacogenomics 2016;17:1385-9.
4. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. Eur J Clin Pharmacol 2016;72:175-84.
5. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 and personal communication (mean dose-corrected trough concentrations).
6. Butwicka A et al. Neuroleptic malignant syndrome in an adolescent with CYP2D6 deficiency. Eur J Pediatr 2014;173:1639-42.
7. Gassó P et al. Relationship between CYP2D6 genotype and haloperidol pharmacokinetics and extrapyramidal symptoms in healthy volunteers. Pharmacogenomics 2013;14:1551-63.
8. Panagiotidis G et al. Depot haloperidol treatment in outpatients with schizophrenia on monotherapy: impact of CYP2D6 polymorphism on pharmacokinetics and treatment outcome. Ther Drug Monit 2007;29:417-22.
9. LLerena A et al. Relationship between haloperidol plasma concentration, debrisoquine metabolic ratio, CYP2D6 and CYP2C9 genotypes in psychiatric patients. Pharmacopsychiatry 2004;37:69-73.
10. Desai M et al. Pharmacokinetics and QT interval pharmacodynamics of oral haloperidol in poor and extensive metabolizers of CYP2D6. Pharmacogenomics J 2003;3:105- 13.
11. Brockmoller J et al. The impact of the CYP2D6 polymorphism on haloperidol pharmacokinetics and on the outcome of haloperidol treatment. Clin Pharmacol Ther 2002;72:438-52.
12. Yasui-Furukori N et al. Effect of the CYP2D6 genotype on prolactin concentration in schizophrenic patients treated with haloperidol. Schizophr Res 2001 1;52:139-42.
13. Pan L et al. Effects of smoking, CYP2D6 genotype, and concomitant drug intake on the steady state plasma concentrations of haloperidol and reduced haloperidol in schizophrenic inpatients. Ther Drug

Monit 1999;21:489-97.

14. Llerena A et al. Haloperidol disposition is dependent on the debrisoquine hydroxylation phenotype: increased plasma levels of the reduced metabolite in poor metabolizers. Ther Drug Monit 1992;14:261-4.
15. Llerena A. Haloperidol disposition is dependent on debrisoquine hydroxylation phenotype. Ther Drug Monit 1992;14:92-7.
16. SmPC's Haldol en Haldol Decanoas.

Date 13-09-2021

CYP2D6 UM: haloperidol

[2399](#)

There are indications of a risk of reduced effectiveness. The genetic variation leads to an increased conversion of haloperidol, resulting in a plasma concentration that is approximately 40% lower.

- use 1.5 times the standard dose or choose an alternative.

Antipsychotics that are not metabolised by CYP2D6 - or to a much lesser extent - include, for example, flupentixol, penfluridol, quetiapine, olanzapine or clozapine.

Literature:

1. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopenthixol. Eur J Clin Pharmacol 2016;72:175-84.
2. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 and personal communication (mean dose-corrected trough concentrations).
3. Gassó P et al. Relationship between CYP2D6 genotype and haloperidol pharmacokinetics and extrapyramidal symptoms in healthy volunteers. Pharmacogenomics 2013;14:1551-63.
4. Panagiotidis G et al. Depot haloperidol treatment in outpatients with schizophrenia on monotherapy: impact of CYP2D6 polymorphism on pharmacokinetics and treatment outcome. Ther Drug Monit 2007;29:417-22.
5. Brockmoller J et al. The impact of the CYP2D6 polymorphism on haloperidol pharmacokinetics and on the outcome of haloperidol treatment. Clin Pharmacol Ther 2002;72:438-52.

Date 13-09-2021

CYP2C19 IM: imipramine

[2566](#)

NO action is required for this gene-drug interaction.

The genetic variation increases imipramine plasma concentrations, but not imipramine+desipramine plasma concentrations, which govern effectiveness and side effects.

Literature:

1. Schenk PW et al. The CYP2C19*17 genotype is associated with lower imipramine plasma concentrations in a large group of depressed patients. Pharmacogenomics J 2010;10:219-25.
2. Schenk PW et al. Association of graded allele-specific changes in CYP2D6 function with imipramine dose requirement in a large group of depressed patients. Mol Psychiatry 2008;13:597-605.
3. Madsen H et al. Imipramine demethylation in vivo: impact of CYP1A2, CYP2C19, and CYP3A4. Clin Pharmacol Ther 1997;61:319-24.
4. Koyama E et al. Steady-state plasma concentrations of imipramine and desipramine in relation to S-mephenytoin 4-hydroxylation status in Japanese depressive patients. J Clin Psychopharmacol 1996;16:286-93.
5. Madsen H et al. Imipramine metabolism in relation to the sparteine and mephenytoin oxidation polymorphisms--a population study. Br J Clin Pharmacol 1995;39:433-9.
6. Koyama E et al. Metabolic disposition of imipramine in oriental subjects: relation to metoprolol alpha-hydroxylation and S-mephenytoin 4-hydroxylation phenotypes. J Pharmacol Exp Ther 1994;271:860-7.
7. Skjelbo E et al. The N-demethylation of imipramine correlates with the oxidation of S-mephenytoin (S/R-ratio). A population study. Br J Clin Pharmacol 1993;35:331-4.

Date 08-02-2004

CYP2C19 PM: imipramine

[2567](#)

The risk of side effects is increased. The gene variation results in an increase in the plasma concentration

of imipramine+desipramine.

- use 70% of the standard dose and monitor the effect and side effects, or the imipramine and desipramine plasma concentrations to determine the maintenance dose.
- or avoid imipramine
Antidepressants that are not or to a lesser extent metabolised by CYP2C19 include, for example, nortriptyline, fluvoxamine and mirtazapine.

Literature:

1. Schenk PW et al. The CYP2C19*17 genotype is associated with lower imipramine plasma concentrations in a large group of depressed patients. *Pharmacogenomics J* 2010;10:219-25.
2. Schenk PW et al. Association of graded allele-specific changes in CYP2D6 function with imipramine dose requirement in a large group of depressed patients. *Mol Psychiatry* 2008;13:597-605.
3. Morinobu S et al. Effects of genetic defects in the CYP2C19 gene on the N-demethylation of imipramine, and clinical outcome of imipramine therapy. *Psychiatry Clin Neurosci* 1997;51:253-7.
4. Madsen H et al. Imipramine demethylation in vivo: impact of CYP1A2, CYP2C19, and CYP3A4. *Clin Pharmacol Ther* 1997;61:319-24.
5. Koyama E et al. Steady-state plasma concentrations of imipramine and desipramine in relation to S-mephenytoin 4-hydroxylation status in Japanese depressive patients. *J Clin Psychopharmacol* 1996;16:286-93.
6. Madsen H et al. Imipramine metabolism in relation to the sparteine and mephenytoin oxidation polymorphisms--a population study. *Br J Clin Pharmacol* 1995;39:433-9.
7. Koyama E et al. Metabolic disposition of imipramine in oriental subjects: relation to metoprolol alpha-hydroxylation and S-mephenytoin 4-hydroxylation phenotypes. *J Pharmacol Exp Ther* 1994;271:860-7.
8. Skjelbo E et al. The N-demethylation of imipramine correlates with the oxidation of S-mephenytoin (S/R-ratio). A population study. *Br J Clin Pharmacol* 1993;35:331-4.
9. Skjelbo E et al. The mephenytoin oxidation polymorphism is partially responsible for the N-demethylation of imipramine. *Clin Pharmacol Ther* 1991;49:18-23.

Date 08-02-2024

CYP2C19 UM: imipramine

[2568](#)

NO action is required for this gene-drug interaction.

The genetic variation decreases imipramine plasma concentrations, but not imipramine+desipramine plasma concentrations, which govern effectiveness and side effects.

Literature:

1. Schenk PW et al. The CYP2C19*17 genotype is associated with lower imipramine plasma concentrations in a large group of depressed patients. *Pharmacogenomics J* 2010;10:219-25.

Date 08-02-2024

CYP2D6 IM: imipramine

[2392](#)

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of imipramine and desipramine.

- use 70% of the standard dose and monitor the effect and side effects or the plasma concentrations of imipramine and desipramine in order to set the maintenance.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. *JAMA Netw Open* 2023;6:e2312443.
2. Schliessbach J et al. Effect of single-dose imipramine on chronic low-back and experimental pain. A randomized controlled trial. *PLoS One* 2018;13:e0195776.
3. Schenk PW et al. Association of graded allele-specific changes in CYP2D6 function with imipramine dose requirement in a large group of depressed patients. *Mol Psychiatry* 2008;13:597-605.
4. Sindrup SH et al. Nonlinear kinetics of imipramine in low and medium plasma level ranges. *Ther Drug Monit* 1990;12:445-9.
5. Brosten K et al. Imipramine demethylation and hydroxylation: impact of the sparteine oxidation phenotype. *Clin Pharmacol Ther* 1986;40:543-9.

Date 08-02-2024

The risk of side effects may be increased, because the gene variation leads to increased plasma concentrations of imipramine and the active metabolite desipramine.

- use 30% of the standard dose and monitor the effect and side effects or the plasma concentrations of imipramine and desipramine in order to set the maintenance dose.

Literature:

1. Schenk PW et al. Association of graded allele-specific changes in CYP2D6 function with imipramine dose requirement in a large group of depressed patients. *Mol Psychiatry* 2008;13:597-605.
2. Koyama E et al. Metabolic disposition of imipramine in oriental subjects: relation to metoprolol alpha-hydroxylation and S-mephenytoin 4"-hydroxylation phenotypes. *J Pharmacol Exp Ther* 1994;271:860-7.
3. Sindrup SH et al. Nonlinear kinetics of imipramine in low and medium plasma level ranges. *Ther Drug Monit* 1990;12:445-9.
4. Balant-Gorgia AE et al. High blood concentrations of imipramine or clomipramine and therapeutic failure: a case report study using drug monitoring data. *Ther Drug Monit* 1989;11:415-20.
5. Brosen K et al. Imipramine demethylation and hydroxylation: impact of the sparteine oxidation phenotype. *Clin Pharmacol Ther* 1986;40:543-9.
6. Brosen K et al. Steady-state concentrations of imipramine and its metabolites in relation to the sparteine/debrisoquine polymorphism. *Eur J Clin Pharmacol* 1986;30:679- 84.
7. SmPC Tofranil-PM (VS).

Date 08-02-2024

The risk of ineffectiveness and cardiotoxic side effects may be increased. The gene variation leads to reduced plasma concentrations of imipramine and the active metabolite desipramine and to increased plasma concentrations of the potentially cardiotoxic hydroxy metabolites.

- use 1.7 times the standard dose and monitor the effect and side effects or the plasma concentrations of imipramine and desipramine in order to set the maintenance dose
- if a dose increase is not wanted due to the potentially cardiotoxic hydroxy metabolites: avoid imipramine. Antidepressants that are not metabolised by CYP2D6 - or to a lesser extent - include, for example, citalopram and sertraline.

Literature:

1. Schenk PW et al. Association of graded allele-specific changes in CYP2D6 function with imipramine dose requirement in a large group of depressed patients. *Mol Psychiatry* 2008;13:597-605.
2. Sindrup SH et al. Nonlinear kinetics of imipramine in low and medium plasma level ranges. *Ther Drug Monit* 1990;12:445-9.

Date 08-02-2024

NO action is needed for this gene-drug interaction.

This genetic variation (IM) is more common in Western populations than the wild-type (*1/*1). This means that treatment is largely geared to patients with this genetic variation. Adjustment of the treatment is therefore not useful.

Literature:

1. Yang Y et al. UGT1A1*6 and UGT1A1*28 polymorphisms are correlated with irinotecan-induced toxicity: A meta-analysis. *Asia Pac J Clin Oncol* 2018;14:e479-e489.
2. Chen X et al. UGT1A1 polymorphisms with irinotecan-induced toxicities and treatment outcome in Asians with lung cancer: a meta-analysis. *Cancer Chemother Pharmacol* 2017;79:1109-1117.
3. Chen YJ et al. The association of UGT1A1*6 and UGT1A1*28 with irinotecan-induced neutropenia in Asians: a meta-analysis. *Biomarkers*. 2014;19:56-62.
4. Goetz MP et al. UGT1A1 genotype-guided phase I study of irinotecan, oxaliplatin, and capecitabine. *Invest New Drugs* 2013;31:1559-67.
5. Denlinger CS et al. Pharmacokinetic analysis of irinotecan plus bevacizumab in patients with advanced solid tumors. *Cancer Chemother Pharmacol* 2009;65:97-105.
6. Minami H et al. Irinotecan pharmacokinetics/pharmacodynamics and UGT1A genetic polymorphisms in

- Japanese: roles of UGT1A16 and 28. *Pharmacogenet Genomics* 2007;17:497-504.
7. de Jong FA et al. Prophylaxis of irinotecan-induced diarrhea with neomycin and potential role for UGT1A1*28 genotype screening: a double-blind, randomized, placebo- controlled study. *Oncologist* 2006;11:944-54.
 8. Han JY et al. Comprehensive analysis of UGT1A polymorphisms predictive for pharmacokinetics and treatment outcome in patients with non-small-cell lung cancer treated with irinotecan and cisplatin. *J Clin Oncol* 2006;24:2237-44.
 9. Paoluzzi L et al. Influence of genetic variants in UGT1A1 and UGT1A9 on the in vivo glucuronidation of SN-38. *J Clin Pharmacol* 2004;44:854-60.
 10. Sai K et al. UGT1A1 haplotypes associated with reduced glucuronidation and increased serum bilirubin in irinotecan-administered Japanese patients with cancer. *Clin Pharmacol Ther* 2004;75:501-15.
 11. Innocenti F et al. Genetic variants in the UDP-glucuronosyl-transferase 1A1 gene predict the risk of severe neutropenia of irinotecan. *J Clin Oncol* 2004;22:1382-8.
 12. Iyer L et al. UGT1A1*28 polymorphism as a determinant of irinotecan disposition and toxicity. *Pharmacogenomics J* 2002;2:43-7.
 13. Ando Y et al. Polymorphisms of UDP-glucuronosyl-transferase gene and irinotecan toxicity: a pharmacogenetic analysis. *Cancer Res* 2000;60:6921-6.

Date 07-06-2021

UGT1A1 PM ANDERS: irinotecan

[2449](#)

Serious, life-threatening adverse events occur more often in patients with this genetic variation. The genetic variation reduces conversion of irinotecan to inactive metabolites.

- Start with 70% of the standard dose

If the patient tolerates this initial dose, the dose can be increased, guided by the neutrophil count.

Literature:

1. Yang Y et al. UGT1A1*6 and UGT1A1*28 polymorphisms are correlated with irinotecan-induced toxicity: A meta-analysis. *Asia Pac J Clin Oncol* 2018;14:e479-e489.
2. Chen X et al. UGT1A1 polymorphisms with irinotecan-induced toxicities and treatment outcome in Asians with lung cancer: a meta-analysis. *Cancer Chemother Pharmacol* 2017;79:1109-1117.
3. Han FF et al. Associations between UGT1A1*6 or UGT1A1*6/*28 polymorphisms and irinotecan-induced neutropenia in Asian cancer patients. *Cancer Chemother Pharmacol* 2014;73:779-88.
4. Chen YJ et al. The association of UGT1A1*6 and UGT1A1*28 with irinotecan-induced neutropenia in Asians: a meta-analysis. *Biomarkers*. 2014;19:56-62.
5. Goetz MP et al. UGT1A1 genotype-guided phase I study of irinotecan, oxaliplatin, and capecitabine. *Invest New Drugs* 2013;31:1559-67.
6. Hu ZY et al. Dose-dependent association between UGT1A1*28 polymorphism and irinotecan-induced diarrhoea: a meta-analysis. *Eur J Cancer* 2010;46:1856-65.
7. Denlinger CS et al. Pharmacokinetic analysis of irinotecan plus bevacizumab in patients with advanced solid tumors. *Cancer Chemother Pharmacol* 2009;65:97-105.
8. Minami H et al. Irinotecan pharmacokinetics/pharmacodynamics and UGT1A genetic polymorphisms in Japanese: roles of UGT1A1*6 and 28. *Pharmacogenet Genomics* 2007;17:497-504.
9. de Jong FA et al. Prophylaxis of irinotecan-induced diarrhea with neomycin and potential role for UGT1A1*28 genotype screening: a double-blind, randomized, placebo- controlled study. *Oncologist* 2006;11:944-54.
10. Han JY et al. Comprehensive analysis of UGT1A polymorphisms predictive for pharmacokinetics and treatment outcome in patients with non-small-cell lung cancer treated with irinotecan and cisplatin. *J Clin Oncol* 2006;24:2237-44.
11. Paoluzzi L et al. Influence of genetic variants in UGT1A1 and UGT1A9 on the in vivo glucuronidation of SN-38. *J Clin Pharmacol* 2004;44:854-60.
12. Sai K et al. UGT1A1 haplotypes associated with reduced glucuronidation and increased serum bilirubin in irinotecan-administered Japanese patients with cancer. *Clin Pharmacol Ther* 2004;75:501-15.
13. Innocenti F et al. Genetic variants in the UDP-glucuronosyl-transferase 1A1 gene predict the risk of severe neutropenia of irinotecan. *J Clin Oncol* 2004;22:1382-8.
14. Iyer L et al. UGT1A1*28 polymorphism as a determinant of irinotecan disposition and toxicity. *Pharmacogenomics J* 2002;2:43-7.
15. Ando Y et al. Polymorphisms of UDP-glucuronosyl-transferase gene and irinotecan toxicity: a pharmacogenetic analysis. *Cancer Res* 2000;60:6921-6.

Date 07-06-2021

UGT1A1*1/*28: irinotecan

[2450](#)

NO action is needed for this gene-drug interaction.

This genetic variation (*1/*28) is more common in Western populations than the wild-type (*1/*1). This means that treatment is largely geared to patients with this genetic variation. Adjustment of the treatment is therefore not useful.

Literature:

1. Yang Y et al. UGT1A1*6 and UGT1A1*28 polymorphisms are correlated with irinotecan-induced toxicity: A meta-analysis. *Asia Pac J Clin Oncol* 2018;14:e479-e489.
2. Tejpar S et al. Clinical and pharmacogenetic determinants of 5-fluorouracil/ leucovorin/irinotecan toxicity: results of the PETACC-3 trial. *Eur J Cancer*. 2018;99:66-77.
3. Chen X et al. UGT1A1 polymorphisms with irinotecan-induced toxicities and treatment outcome in Asians with lung cancer: a meta-analysis. *Cancer Chemother Pharmacol* 2017;79:1109-1117.
4. Liu XH et al. Predictive value of UGT1A1*28 polymorphism in irinotecan-based chemotherapy. *J Cancer* 2017;8:691-703.
5. Dias MM et al. The effect of the UGT1A1*28 allele on survival after irinotecan-based chemotherapy: a collaborative meta-analysis. *Pharmacogenomics J* 2014;14:424-31.
6. Chen YJ et al. The association of UGT1A1*6 and UGT1A1*28 with irinotecan-induced neutropenia in Asians: a meta-analysis. *Biomarkers*. 2014;19:56-62.
7. Liu X et al. Association of UGT1A1*28 polymorphisms with irinotecan-induced toxicities in colorectal cancer: a meta-analysis in Caucasians. *Pharmacogenomics J* 2014;14:120-9.
8. Goetz MP et al. UGT1A1 genotype-guided phase I study of irinotecan, oxaliplatin, and capecitabine. *Invest New Drugs* 2013;31:1559-67.
9. Liu X et al. Association between UGT1A1*28 polymorphisms and clinical outcomes of irinotecan-based chemotherapies in colorectal cancer: a meta-analysis in Caucasians. *PLoS One* 2013;8:e58489.
10. Dias MM et al. Impact of the UGT1A1*28 allele on response to irinotecan: a systematic review and meta-analysis. *Pharmacogenomics* 2012;13:889-99.
11. Hu ZY et al. Dose-dependent association between UGT1A1*28 genotype and irinotecan-induced neutropenia: low doses also increase risk. *Clin Cancer Res* 2010;16:3832- 42.
12. Hu ZY et al. Dose-dependent association between UGT1A1*28 polymorphism and irinotecan-induced diarrhoea: a meta-analysis. *Eur J Cancer* 2010;46:1856-65.
13. Denlinger CS et al. Pharmacokinetic analysis of irinotecan plus bevacizumab in patients with advanced solid tumors. *Cancer Chemother Pharmacol* 2009;65:97- 105. Kweekel DM et al. UGT1A1*28 genotype and irinotecan dosage in patients with metastatic colorectal cancer: a Dutch Colorectal Cancer Group study. *Br J Cancer* 2008;99:275-82.
14. Liu CY et al. UGT1A1*28 polymorphism predicts irinotecan-induced severe toxicities without affecting treatment outcome and survival in patients with metastatic colorectal carcinoma. *Cancer* 2008;112:1932-40.
15. Lankisch TO et al. Gilbert's Syndrome and irinotecan toxicity: combination with UDP-glucuronosyl-transferase 1A7 variants increases risk. *Cancer Epidemiol Biomarkers Prev* 2008;17:695-701.
16. Minami H et al. Irinotecan pharmacokinetics/pharmacodynamics and UGT1A genetic polymorphisms in Japanese: roles of UGT1A16 and 28. *Pharmacogenet Genomics* 2007;17:497-504.
17. Stewart CF et al. UGT1A1 promoter genotype correlates with SN-38 pharmacokinetics, but not severe toxicity in patients receiving low-dose irinotecan. *J Clin Oncol* 2007;25:2594-600.
18. Côté JF et al. UGT1A1 polymorphism can predict hematologic toxicity in patients treated with irinotecan. *Clin Cancer Res* 2007;13:3269-75.
19. Ramchandani RP et al. The role of SN-38 exposure, UGT1A1*28 polymorphism, and baseline bilirubin level in predicting severe irinotecan toxicity. *J Clin Pharmacol* 2007;47:78-86.
20. Zárate Romero R et al. Potential application of GSTT1-null genotype in predicting toxicity associated to 5-fluorouracil irinotecan and leucovorin regimen in advanced stage colorectal cancer patients. *Oncol Rep* 2006;16:497-503.
21. de Jong FA et al. Prophylaxis of irinotecan-induced diarrhea with neomycin and potential role for UGT1A1*28 genotype screening: a double-blind, randomized, placebo- controlled study. *Oncologist* 2006;11:944-54.
22. Toffoli G et al. The role of UGT1A1*28 polymorphism in the pharmacodynamics and pharmacokinetics of irinotecan in patients with metastatic colorectal cancer. *J Clin Oncol* 2006;24:3061-8.
23. Han JY et al. Comprehensive analysis of UGT1A polymorphisms predictive for pharmacokinetics and treatment outcome in patients with non-small-cell lung cancer treated with irinotecan and cisplatin. *J Clin Oncol* 2006;24:2237-44.
24. McLeod HL et al. UGT1A1*28, toxicity and outcome in advanced colorectal cancer: results from Trial N9741. *J Clin Oncol* 2006;24 (suppl. abstr. 3520).
25. Massacesi C et al. Uridine diphosphate glucuronosyl transferase 1A1 promoter polymorphism predicts the risk of gastrointestinal toxicity and fatigue induced by irinotecan-based chemotherapy. *Cancer* 2006;106:1007-16.
26. Wright MA et al. A phase I pharmacologic and pharmacogenetic trial of sequential 24-hour infusion of irinotecan followed by leucovorin and a 48-hour infusion of fluorouracil in adult patients with solid tumors. *Clin Cancer Res* 2005;11:4144-50.
27. Kweekel DM et al. Ondersteuning van de chemotherapiekeuze. *Pharm Weekblad* 2005;20:685-7.
28. Steiner M et al. 5-fluorouracil/irinotecan induced lethal toxicity as a result of a combined pharmacogenetic syndrome: report of a case. *J Clin Pathol* 2005;58:553-5.
29. Soepenberg O et al. Phase I pharmacokinetic, food effect, and pharmacogenetic study of oral irinotecan given as semisolid matrix capsules in patients with solid tumors. *Clin Cancer Res* 2005;11:1504-11.

30. Zhou Q et al. Pharmacogenetic profiling across the irinotecan pathway in Asian patients with cancer. *Br J Clin Pharmacol* 2005;59:415-24.
31. Marcuello E et al. UGT1A1 gene variations and irinotecan treatment in patients with metastatic colorectal cancer. *Br J Cancer* 2004;91:678-82.
32. Rouits E et al. Relevance of different UGT1A1 polymorphisms in irinotecan-induced toxicity: a molecular and clinical study of 75 patients. *Clin Cancer Res* 2004;10:5151- 9.
33. Paoluzzi L et al. Influence of genetic variants in UGT1A1 and UGT1A9 on the in vivo glucuronidation of SN-38. *J Clin Pharmacol* 2004;44:854-60.
34. Sai K et al. UGT1A1 haplotypes associated with reduced glucuronidation and increased serum bilirubin in irinotecan-administered Japanese patients with cancer. *Clin Pharmacol Ther* 2004;75:501-15.
35. Innocenti F et al. Genetic variants in the UDP-glucuronosyl-transferase 1A1 gene predict the risk of severe neutropenia of irinotecan. *J Clin Oncol* 2004;22:1382-8.
36. Font A et al. Weekly regimen of irinotecan/docetaxel in previously treated non-small cell lung cancer patients and correlation with uridine diphosphate glucuronosyl- transferase 1A1 (UGT1A1) polymorphism. *Invest New Drugs* 2003;21:435-43.
37. Mathijssen RH et al. Irinotecan pathway genotype analysis to predict pharmacokinetics. *Clin Cancer Res* 2003;9:3246-53.
38. Iyer L et al. UGT1A1*28 polymorphism as a determinant of irinotecan disposition and toxicity. *Pharmacogenomics J* 2002;2:43-7.
39. Ando Y et al. Polymorphisms of UDP-glucuronosyl-transferase gene and irinotecan toxicity: a pharmacogenetic analysis. *Cancer Res* 2000;60:6921-6.
40. Wasserman E et al. Severe CPT-11 toxicity in patients with Gilbert's syndrome: two case reports. *Ann Oncol* 1997;8:1049-51.

Date 07-06-2021

UGT1A1*28/*28: irinotecan

[2451](#)

Serious, life-threatening adverse events occur more often in patients with this genetic variation. The genetic variation reduces conversion of irinotecan to inactive metabolites.

- Start with 70% of the standard dose

If the patient tolerates this initial dose, the dose can be increased, guided by the neutrophil count.

Literature:

1. Yang Y et al. UGT1A1*6 and UGT1A1*28 polymorphisms are correlated with irinotecan-induced toxicity: A meta-analysis. *Asia Pac J Clin Oncol* 2018;14:e479-e489.
2. Tejpar S et al. Clinical and pharmacogenetic determinants of 5-fluorouracil/ leucovorin/irinotecan toxicity: results of the PETACC-3 trial. *Eur J Cancer*. 2018;99:66-77.
3. Chen X et al. UGT1A1 polymorphisms with irinotecan-induced toxicities and treatment outcome in Asians with lung cancer: a meta-analysis. *Cancer Chemother Pharmacol* 2017;79:1109-1117.
4. Liu XH et al. Predictive value of UGT1A1*28 polymorphism in irinotecan-based chemotherapy. *J Cancer* 2017;8:691-703.
5. Lu CY et al. Clinical implication of UGT1A1 promoter polymorphism for irinotecan dose escalation in metastatic colorectal cancer patients treated with bevacizumab combined with FOLFIRI in the first-line setting. *Transl Oncol* 2015;8:474-9.
6. Dias MM et al. The effect of the UGT1A1*28 allele on survival after irinotecan-based chemotherapy: a collaborative meta-analysis. *Pharmacogenomics J* 2014;14:424-31.
7. Han FF et al. Associations between UGT1A16 or UGT1A16/*28 polymorphisms and irinotecan-induced neutropenia in Asian cancer patients. *Cancer Chemother Pharmacol* 2014;73:779-88.
8. Chen YJ et al. The association of UGT1A16 and UGT1A128 with irinotecan-induced neutropenia in Asians: a meta-analysis. *Biomarkers*. 2014;19:56-62.
9. Liu X et al. Association of UGT1A1*28 polymorphisms with irinotecan-induced toxicities in colorectal cancer: a meta-analysis in Caucasians. *Pharmacogenomics J* 2014;14:120-9.
10. Goetz MP et al. UGT1A1 genotype-guided phase I study of irinotecan, oxaliplatin, and capecitabine. *Invest New Drugs* 2013;31:1559-67.
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12. Dias MM et al. Impact of the UGT1A1*28 allele on response to irinotecan: a systematic review and meta-analysis. *Pharmacogenomics* 2012;13:889-99.
13. Hu ZY et al. Dose-dependent association between UGT1A1*28 genotype and irinotecan-induced neutropenia: low doses also increase risk. *Clin Cancer Res* 2010;16:3832- 42.
14. Hu ZY et al. Dose-dependent association between UGT1A1*28 polymorphism and irinotecan-induced diarrhoea: a meta-analysis. *Eur J Cancer* 2010;46:1856-65.
15. Denlinger CS et al. Pharmacokinetic analysis of irinotecan plus bevacizumab in patients with advanced solid tumors. *Cancer Chemother Pharmacol* 2009;65:97-105.
16. Kweekel DM et al. UGT1A1*28 genotype and irinotecan dosage in patients with metastatic colorectal cancer: a Dutch Colorectal Cancer Group study. *Br J Cancer* 2008;99:275-82.
17. Liu CY et al. UGT1A1*28 polymorphism predicts irinotecan-induced severe toxicities without affecting treatment outcome and survival in patients with metastatic colorectal carcinoma. *Cancer*

2008;112:1932-40.

18. Lankisch TO et al. Gilbert's Syndrome and irinotecan toxicity: combination with UDP-glucuronosyl-transferase 1A7 variants increases risk. *Cancer Epidemiol Biomarkers Prev* 2008;17:695-701.
19. Hoskins JM et al. UGT1A1*28 genotype and irinotecan-induced neutropenia: dose matters. *J Natl Cancer Inst* 2007;99:1290-5.
20. Minami H et al. Irinotecan pharmacokinetics/pharmacodynamics and UGT1A genetic polymorphisms in Japanese: roles of UGT1A16 and 28. *Pharmacogenet Genomics* 2007;17:497-504.
21. Stewart CF et al. UGT1A1 promoter genotype correlates with SN-38 pharmacokinetics, but not severe toxicity in patients receiving low-dose irinotecan. *J Clin Oncol* 2007;25:2594-600.
22. Côté JF et al. UGT1A1 polymorphism can predict hematologic toxicity in patients treated with irinotecan. *Clin Cancer Res* 2007;13:3269-75.
23. Ramchandani RP et al. The role of SN-38 exposure, UGT1A1*28 polymorphism, and baseline bilirubin level in predicting severe irinotecan toxicity. *J Clin Pharmacol* 2007;47:78-86.
24. de Jong FA et al. Prophylaxis of irinotecan-induced diarrhea with neomycin and potential role for UGT1A1*28 genotype screening: a double-blind, randomized, placebo- controlled study. *Oncologist* 2006;11:944-54.
25. Toffoli G et al. The role of UGT1A1*28 polymorphism in the pharmacodynamics and pharmacokinetics of irinotecan in patients with metastatic colorectal cancer. *J Clin Oncol* 2006;24:3061-8.
26. McLeod HL et al. UGT1A1*28, toxicity and outcome in advanced colorectal cancer: results from Trial N9741. *J Clin Oncol* 2006;24 (suppl. abstr. 3520).
27. Massacesi C et al. Uridine diphosphate glucuronosyl transferase 1A1 promoter polymorphism predicts the risk of gastrointestinal toxicity and fatigue induced by irinotecan-based chemotherapy. *Cancer* 2006;106:1007-16.
28. Kweekel DM et al. Ondersteuning van de chemotherapiekeuze. *Pharm Weekblad* 2005;20:685-7.
29. Soepenberg O et al. Phase I pharmacokinetic, food effect, and pharmacogenetic study of oral irinotecan given as semisolid matrix capsules in patients with solid tumors. *Clin Cancer Res* 2005;11:1504-11.
30. Zhou Q et al. Pharmacogenetic profiling across the irinotecan pathway in Asian patients with cancer. *Br J Clin Pharmacol* 2005;59:415-24.
31. Carlini LE et al. UGT1A7 and UGT1A9 polymorphisms predict response and toxicity in colorectal cancer patients treated with capecitabine/ irinotecan. *Clin Cancer Res* 2005;11:1226-36.
32. Kitagawa C et al. Genetic polymorphism in the phenobarbital-responsive enhancer module of the UDP-glucuronosyltransferase 1A1 gene and irinotecan toxicity. *Pharmacogenet Genomics* 2005;15:35-41.
33. Marcuello E et al. UGT1A1 gene variations and irinotecan treatment in patients with metastatic colorectal cancer. *Br J Cancer* 2004;91:678-82.
34. Rouits E et al. Relevance of different UGT1A1 polymorphisms in irinotecan-induced toxicity: a molecular and clinical study of 75 patients. *Clin Cancer Res* 2004;10:5151- 9.
35. Paoluzzi L et al. Influence of genetic variants in UGT1A1 and UGT1A9 on the in vivo glucuronidation of SN-38. *J Clin Pharmacol* 2004;44:854-60.
36. Sai K et al. UGT1A1 haplotypes associated with reduced glucuronidation and increased serum bilirubin in irinotecan-administered Japanese patients with cancer. *Clin Pharmacol Ther* 2004;75:501-15.
37. Innocenti F et al. Genetic variants in the UDP-glucuronosyl-transferase 1A1 gene predict the risk of severe neutropenia of irinotecan. *J Clin Oncol* 2004;22:1382-8.
38. Font A et al. Weekly regimen of irinotecan/docetaxel in previously treated non-small cell lung cancer patients and correlation with uridine diphosphate glucuronosyl- transferase 1A1 (UGT1A1) polymorphism. *Invest New Drugs* 2003;21:435-43.
39. Mathijssen RH et al. Irinotecan pathway genotype analysis to predict pharmacokinetics. *Clin Cancer Res* 2003;9:3246-53.
40. Iyer L et al. UGT1A1*28 polymorphism as a determinant of irinotecan disposition and toxicity. *Pharmacogenomics J* 2002;2:43-7.
41. Ando Y et al. Polymorphisms of UDP-glucuronosyl-transferase gene and irinotecan toxicity: a pharmacogenetic analysis. *Cancer Res* 2000;60:6921-6.
42. Wasserman E et al. Severe CPT-11 toxicity in patients with Gilbert's syndrome: two case reports. *Ann Oncol* 1997;8:1049-51.
43. SmPC's Campto en Camptosar (VS).

Date 07-06-2021

CYP2D6 IM: kinidine

[2923](#)

This is NOT a gene-drug interaction.

Literature:

1. Nielsen F et al. Lack of relationship between quinidine pharmacokinetics and the sparteine oxidation polymorphism. *Eur J Clin Pharmacol* 1995;48:501-4.
2. Brøsen K et al. Quinidine kinetics after a single oral dose in relation to the sparteine oxidation polymorphism in man. *Br J Clin Pharmacol* 1990;29:248-53.
3. Mikus G et al. Pharmacokinetics and metabolism of quinidine in extensive and poor metabolisers of sparteine. *Eur J Clin Pharmacol* 1986;31:69-72.

Date 12-09-2022

CYP2D6 PM: kinidine

[2922](#)

This is NOT a gene-drug interaction.

Literature:

1. Nielsen F et al. Lack of relationship between quinidine pharmacokinetics and the sparteine oxidation polymorphism. Eur J Clin Pharmacol 1995;48:501-4.
2. Brøsen K et al. Quinidine kinetics after a single oral dose in relation to the sparteine oxidation polymorphism in man. Br J Clin Pharmacol 1990;29:248-53.
3. Mikus G et al. Pharmacokinetics and metabolism of quinidine in extensive and poor metabolisers of sparteine. Eur J Clin Pharmacol 1986;31:69-72.

Date 12-09-2022

CYP2D6 UM: kinidine

[2924](#)

This is NOT a gene-drug interaction.

Literature:

1. Nielsen F et al. Lack of relationship between quinidine pharmacokinetics and the sparteine oxidation polymorphism. Eur J Clin Pharmacol 1995;48:501-4.
2. Brøsen K et al. Quinidine kinetics after a single oral dose in relation to the sparteine oxidation polymorphism in man. Br J Clin Pharmacol 1990;29:248-53.
3. Mikus G et al. Pharmacokinetics and metabolism of quinidine in extensive and poor metabolisers of sparteine. Eur J Clin Pharmacol 1986;31:69-72.

Date 12-09-2022

HLA-B*1502: lamotrigine

[6399](#)

The life-threatening cutaneous side effect Stevens-Johnson Syndrome/Toxic Epidermal Necrolysis (SJS/TEN) occurs more often in patients with this genetic variation. Based on the estimated risk for all patients and the increase by a factor 3.6 for patients with this genetic variation, the risk of lamotrigine-induced SJS/TEN in patients with HLA-B*1502 is estimated at 0.4%.

- carefully weigh the risk of SJS/TEN against the benefits
 - avoid lamotrigine if an alternative is available
- Carbamazepine carries a much higher risk of SJS/TEN in these patients and is therefore not an alternative. A similar risk has been reported for phenytoin as for lamotrigine. The same applies to oxcarbazepine, but the most severe forms (SJS/TEN overlap and TEN) have not been observed with oxcarbazepine.
- if it is not possible to avoid these products, advise the patient to report any rash immediately

Literature:

1. Sukasem C et al. Spectrum of cutaneous adverse reactions to aromatic antiepileptic drugs and human leukocyte antigen genotypes in Thai patients and meta-analysis. Pharmacogenomics J 2021;21:682-90.
2. Sabourirad S et al. Investigating the association of lamotrigine and phenytoin-induced Stevens-Johnson syndrome/Toxic Epidermal Necrolysis with HLA-B*1502 in Iranian population. Exp Dermatol 2021;30:284-7.
3. Deng Y et al. Association between HLA alleles and lamotrigine-induced cutaneous adverse drug reactions in Asian populations: a meta-analysis. Seizure 2018;60:163-71.
4. Shi YW et al. HLA-A*24:02 as a common risk factor for antiepileptic drug-induced cutaneous adverse reactions. Neurology 2017;88:2183-2191.
5. Zeng T et al. Association of HLA-B*1502 allele with lamotrigine-induced Stevens-Johnson syndrome and toxic epidermal necrolysis in Han Chinese subjects: a meta-analysis. Int J Dermatol 2015;54:488-93.
6. Kwan PK et al. Association between HLA-B*15:02 allele and antiepileptic drug-induced severe cutaneous reactions in Hong Kong Chinese: a population-based study. Hong Kong Med J 2014;20 Suppl 7:16-8.
7. Wang W et al. Genetic predictors of Stevens-Johnson syndrome and toxic epidermal necrolysis induced by aromatic antiepileptic drugs among the Chinese Han population. Epilepsy Behav 2014;37:16-9.
8. Bloch KM et al. Pharmacogenetics of antiepileptic drug-induced hypersensitivity. Pharmacogenomics

2014;15:857-68.

9. Cheung YK et al. HLA-B alleles associated with severe cutaneous reactions to antiepileptic drugs in Han Chinese. *Epilepsia* 2013;54:1307-14.
10. Hung SI et al. Common risk allele in aromatic antiepileptic-drug induced Stevens-Johnson syndrome and toxic epidermal necrolysis in Han Chinese. *Pharmacogenomics* 2010;11:349-56.

Date 23-05-2022

CYP2C19 IM: lansoprazol

2502

NO action is needed for this gene-drug interaction.

The higher plasma concentration of lansoprazole results in an increase in the therapeutic effectiveness, without an increase in the incidence of side effects.

Literature:

1. Lang JE et al. Lansoprazole is associated with worsening asthma control in children with the CYP2C19 poor metabolizer phenotype. *Ann Am Thorac Soc* 2015 Jun;12:878- 85.
2. Li CY et al. A correlative study of polymorphisms of CYP2C19 and MDR1 C3435T with the pharmacokinetic profiles of lansoprazole and its main metabolites following single oral administration in healthy adult Chinese subjects. *Eur J Drug Metab Pharmacokinet* 2014;39:121-8.
3. Lima JJ et al. Association of CYP2C19 polymorphisms and lansoprazole-associated respiratory adverse effects in children. *J Pediatr* 2013;163:686-91.
4. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
5. Zhang D et al. Effects of CYP2C19 polymorphism on the pharmacokinetics of lansoprazole and its main metabolites in healthy Chinese subjects. *Xenobiotica* 2011;41:511- 7.
6. Tamura T et al. Improvements in *Helicobacter pylori* eradication rates through clinical CYP2C19 genotyping. *Nagoya J Med Sci* 2011;73:25-31.
7. Xu HR et al. The effect of CYP2C19 activity on pharmacokinetics of lansoprazole and its active metabolites in healthy subjects. *Pharm Biol* 2010;48:947-52.
8. Lee JH et al. The influence of CYP2C19 polymorphism on eradication of *Helicobacter pylori*: a prospective randomized study of lansoprazole and rabeprazole. *Gut Liver* 2010;4:201-6.
9. Furuta T et al. CYP2C19 genotype is associated with symptomatic recurrence of GERD during maintenance therapy with low-dose lansoprazole. *Eur J Clin Pharmacol* 2009;65:693-8.
10. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
11. Hunfeld NG et al. Effect of CYP2C19 *and* 17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752-60.
12. Sakurai Y et al. Population pharmacokinetics and proton pump inhibitory effects of intravenous lansoprazole in healthy Japanese males. *Biol Pharm Bull* 2007;30:2238-43.
13. Kawamura M et al. Cytochrome P450 2C19 polymorphism influences the preventive effect of lansoprazole on the recurrence of erosive reflux esophagitis. *J Gastroenterol Hepatol* 2007;22:222-6.
14. Furuta T et al. Effect of concomitant dosing of famotidine with lansoprazole on gastric acid secretion in relation to CYP2C19 genotype status. *Aliment Pharmacol Ther* 2005;22:67-74.
15. Kawamura M et al. Study Group of GERD. The effects of lansoprazole on erosive reflux oesophagitis are influenced by CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2003;17:965-73.
16. Furuta T et al. Effect of cytochrome P450 2C19 genotypic differences on cure rates for gastroesophageal reflux disease by lansoprazole. *Clin Pharmacol Ther* 2002;72:453-60.
17. Shirai N et al. Comparison of lansoprazole and famotidine for gastric acid inhibition during the daytime and night-time in different CYP2C19 genotype groups. *Aliment Pharmacol Ther* 2002;16:837-46.
18. Furuta T et al. Effect of high-dose lansoprazole on intragastric pH in subjects who are homozygous extensive metabolizers of cytochrome P450 2C19. *Clin Pharmacol Ther* 2001;70:484-92.
19. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
20. Howden CW et al. Dose-response evaluation of the antisecretory effect of continuous infusion intravenous lansoprazole regimens over 48 h. *Aliment Pharmacol Ther* 2006;23:975-84.
21. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
22. Furuta T et al. Effect of MDR1 C3435T polymorphism on cure rates of *Helicobacter pylori* infection by triple therapy with lansoprazole, amoxicillin and clarithromycin in relation to CYP 2C19 genotypes and 23S rRNA genotypes of *H. pylori*. *Aliment Pharmacol Ther* 2007;26:693-703.
23. Sugimoto M et al. Evidence that the degree and duration of acid suppression are related to *Helicobacter pylori* eradication by triple therapy. *Helicobacter* 2007;12:317- 23.
24. Furuta T et al. Pharmacogenomics-based tailored versus standard therapeutic regimen for eradication of *H. pylori*. *Clin Pharmacol Ther* 2007;81:521-8.
25. Padol S et al. The effect of CYP2C19 polymorphisms on *H. pylori* eradication rate in dual and triple first-line PPI therapies: a meta-analysis. *Am J Gastroenterol* 2006;101:1467-75.

26. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of *Helicobacter pylori* by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.
27. Furuta T et al. Influence of CYP2C19 polymorphism and *Helicobacter pylori* genotype determined from gastric tissue samples on response to triple therapy for *H pylori* infection. *Clin Gastroenterol Hepatol* 2005;3:564-73.
28. Furuta T et al. Polymorphism of interleukin-1beta affects the eradication rates of *Helicobacter pylori* by triple therapy. *Clin Gastroenterol Hepatol* 2004;2:22-30.
29. Kawabata H et al. Effect of different proton pump inhibitors, differences in CYP2C19 genotype and antibiotic resistance on the eradication rate of *Helicobacter pylori* infection by a 1-week regimen of proton pump inhibitor, amoxicillin and clarithromycin. *Aliment Pharmacol Ther* 2003;17:259-64.
30. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of *Helicobacter pylori* infection with lansoprazole- or rabeprazole-based triple therapy in Japan. *Eur J Gastroenterol Hepatol* 2003;15:27-33.
31. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for *Helicobacter pylori* infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. *Clin Pharmacol Ther* 2001;69:158-68.
32. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
33. Qiao HL et al. Pharmacokinetics of three proton pump inhibitors in Chinese subjects in relation to the CYP2C19 genotype. *Eur J Clin Pharmacol* 2006;62:107-12.
34. Miura M et al. Pharmacokinetic differences between the enantiomers of lansoprazole and its metabolite, 5-hydroxylansoprazole, in relation to CYP2C19 genotypes. *Eur J Clin Pharmacol* 2004;60:623-8.
35. Ieiri I et al. Comparison of the kinetic disposition of and serum gastrin change by lansoprazole versus rabeprazole during an 8-day dosing scheme in relation to CYP2C19 polymorphism. *Eur J Clin Pharmacol* 2001;57:485-92.
36. Sakai T et al. CYP2C19 genotype and pharmacokinetics of three proton pump inhibitors in healthy subjects. *Pharm Res* 2001;18:721-7.
37. Katsuki H et al. Genetic polymorphism of CYP2C19 and lansoprazole pharmacokinetics in Japanese subjects. *Eur J Clin Pharmacol* 1997;52:391-6.

Date 05-03-2018

CYP2C19 PM: lansoprazol

[2503](#)

NO action is needed for this gene-drug interaction.

The higher plasma concentration of lansoprazole results in an increase in the therapeutic effectiveness, without an increase in the incidence of side effects.

Literature:

1. Liou JM et al. Sequential therapy for 10 days versus triple therapy for 14 days in the eradication of *Helicobacter pylori* in the community and hospital populations: a randomised trial. *Gut* 2016;65:1784-1792.
2. Liou JM et al. Levofloxacin sequential therapy vs levofloxacin triple therapy in the second-line treatment of *Helicobacter pylori*: a randomized trial. *Am J Gastroenterol* 2016;111:381-7.
3. Lang JE et al. Lansoprazole is associated with worsening asthma control in children with the CYP2C19 poor metabolizer phenotype. *Ann Am Thorac Soc* 2015 Jun;12:878- 85.
4. Li CY et al. A correlative study of polymorphisms of CYP2C19 and MDR1 C3435T with the pharmacokinetic profiles of lansoprazole and its main metabolites following single oral administration in healthy adult Chinese subjects. *Eur J Drug Metab Pharmacokinet* 2014;39:121-8.
5. Lima JJ et al. Association of CYP2C19 polymorphisms and lansoprazole-associated respiratory adverse effects in children. *J Pediatr* 2013;163:686-91.
6. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
7. Zhang D et al. Effects of CYP2C19 polymorphism on the pharmacokinetics of lansoprazole and its main metabolites in healthy Chinese subjects. *Xenobiotica* 2011;41:511- 7.
8. Tamura T et al. Improvements in *Helicobacter pylori* eradication rates through clinical CYP2C19 genotyping. *Nagoya J Med Sci* 2011;73:25-31.
9. Xu HR et al. The effect of CYP2C19 activity on pharmacokinetics of lansoprazole and its active metabolites in healthy subjects. *Pharm Biol* 2010;48:947-52.
10. Lee JH et al. The influence of CYP2C19 polymorphism on eradication of *Helicobacter pylori*: a prospective randomized study of lansoprazole and rabeprazole. *Gut Liver* 2010;4:201-6.
11. Furuta T et al. CYP2C19 genotype is associated with symptomatic recurrence of GERD during maintenance therapy with low-dose lansoprazole. *Eur J Clin Pharmacol* 2009;65:693-8.
12. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
13. Sakurai Y et al. Population pharmacokinetics and proton pump inhibitory effects of intravenous

- lansoprazole in healthy Japanese males. *Biol Pharm Bull* 2007;30:2238-43.
14. Kawamura M et al. Cytochrome P450 2C19 polymorphism influences the preventive effect of lansoprazole on the recurrence of erosive reflux esophagitis. *J Gastroenterol Hepatol* 2007;22:222-6.
 15. Furuta T et al. Effect of concomitant dosing of famotidine with lansoprazole on gastric acid secretion in relation to CYP2C19 genotype status. *Aliment Pharmacol Ther* 2005;22:67-74.
 16. Kawamura M et al. Study Group of GERD. The effects of lansoprazole on erosive reflux oesophagitis are influenced by CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2003;17:965-73.
 17. Furuta T et al. Effect of cytochrome P4502C19 genotypic differences on cure rates for gastroesophageal reflux disease by lansoprazole. *Clin Pharmacol Ther* 2002;72:453-60.
 18. Shirai N et al. Comparison of lansoprazole and famotidine for gastric acid inhibition during the daytime and night-time in different CYP2C19 genotype groups. *Aliment Pharmacol Ther* 2002;16:837-46.
 19. Furuta T et al. Effect of high-dose lansoprazole on intragastric pH in subjects who are homozygous extensive metabolizers of cytochrome P4502C19. *Clin Pharmacol Ther* 2001;70:484-92.
 20. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
 21. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
 22. Furuta T et al. Effect of MDR1 C3435T polymorphism on cure rates of *Helicobacter pylori* infection by triple therapy with lansoprazole, amoxicillin and clarithromycin in relation to CYP 2C19 genotypes and 23S rRNA genotypes of *H. pylori*. *Aliment Pharmacol Ther* 2007;26:693-703.
 23. Sugimoto M et al. Evidence that the degree and duration of acid suppression are related to *Helicobacter pylori* eradication by triple therapy. *Helicobacter* 2007;12:317-23.
 24. Furuta T et al. Pharmacogenomics-based tailored versus standard therapeutic regimen for eradication of *H. pylori*. *Clin Pharmacol Ther* 2007;81:521-8.
 25. Padol S et al. The effect of CYP2C19 polymorphisms on *H. pylori* eradication rate in dual and triple first-line PPI therapies: a meta-analysis. *Am J Gastroenterol* 2006;101:1467-75.
 26. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of *Helicobacter pylori* by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.
 27. Furuta T et al. Influence of CYP2C19 polymorphism and *Helicobacter pylori* genotype determined from gastric tissue samples on response to triple therapy for *H. pylori* infection. *Clin Gastroenterol Hepatol* 2005;3:564-73.
 28. Furuta T et al. Polymorphism of interleukin-1 β affects the eradication rates of *Helicobacter pylori* by triple therapy. *Clin Gastroenterol Hepatol* 2004;2:22-30.
 29. Kawabata H et al. Effect of different proton pump inhibitors, differences in CYP2C19 genotype and antibiotic resistance on the eradication rate of *Helicobacter pylori* infection by a 1-week regimen of proton pump inhibitor, amoxicillin and clarithromycin. *Aliment Pharmacol Ther* 2003;17:259-64.
 30. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of *Helicobacter pylori* infection with lansoprazole- or rabeprazole-based triple therapy in Japan. *Eur J Gastroenterol Hepatol* 2003;15:27-33.
 31. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for *Helicobacter pylori* infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. *Clin Pharmacol Ther* 2001;69:158-68.
 32. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
 33. Qiao HL et al. Pharmacokinetics of three proton pump inhibitors in Chinese subjects in relation to the CYP2C19 genotype. *Eur J Clin Pharmacol* 2006;62:107-12.
 34. Miura M et al. Pharmacokinetic differences between the enantiomers of lansoprazole and its metabolite, 5-hydroxylansoprazole, in relation to CYP2C19 genotypes. *Eur J Clin Pharmacol* 2004;60:623-8.
 35. Hu YR et al. Pharmacokinetics of lansoprazole in Chinese healthy subjects in relation to CYP2C19 genotypes. *Acta Pharmacol Sin* 2004;25:986-90.
 36. Ieiri I et al. Comparison of the kinetic disposition of and serum gastrin change by lansoprazole versus rabeprazole during an 8-day dosing scheme in relation to CYP2C19 polymorphism. *Eur J Clin Pharmacol* 2001;57:485-92.
 37. Sakai T et al. CYP2C19 genotype and pharmacokinetics of three proton pump inhibitors in healthy subjects. *Pharm Res* 2001;18:721-7.
 38. Katsuki H et al. Genetic polymorphism of CYP2C19 and lansoprazole pharmacokinetics in Japanese subjects. *Eur J Clin Pharmacol* 1997;52:391-6.
 39. SPC Prezal.

Date 05-03-2018

CYP2C19 UM: lansoprazol

[2504](#)

The genetic variation may reduce lansoprazole plasma concentrations and therefore lansoprazole effectiveness.

Recommendation:

- For *Helicobacter pylori* ERADICATION THERAPY:

- Use a 4-fold higher dose
 - Advise the patient to contact their doctor if symptoms of dyspepsia persist
- OTHER INDICATIONS:
- Be alert to reduced effectiveness
 - If necessary, use a 4-fold higher dose
 - Advise the patient to report persisting symptoms of dyspepsia

Literature:

1. Liou JM et al. Sequential therapy for 10 days versus triple therapy for 14 days in the eradication of *Helicobacter pylori* in the community and hospital populations: a randomised trial. *Gut* 2016;65:1784-1792.
2. Liou JM et al. Levofloxacin sequential therapy vs levofloxacin triple therapy in the second-line treatment of *Helicobacter pylori*: a randomized trial. *Am J Gastroenterol* 2016;111:381-7.
3. Lang JE et al. Lansoprazole is associated with worsening asthma control in children with the CYP2C19 poor metabolizer phenotype. *Ann Am Thorac Soc* 2015 Jun;12:878- 85.
4. Li CY et al. A correlative study of polymorphisms of CYP2C19 and MDR1 C3435T with the pharmacokinetic profiles of lansoprazole and its main metabolites following single oral administration in healthy adult Chinese subjects. *Eur J Drug Metab Pharmacokinet* 2014;39:121-8.
5. Lima JJ et al. Association of CYP2C19 polymorphisms and lansoprazole-associated respiratory adverse effects in children. *J Pediatr* 2013;163:686-91.
6. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
7. Zhang D et al. Effects of CYP2C19 polymorphism on the pharmacokinetics of lansoprazole and its main metabolites in healthy Chinese subjects. *Xenobiotica* 2011;41:511- 7.
8. Tamura T et al. Improvements in *Helicobacter pylori* eradication rates through clinical CYP2C19 genotyping. *Nagoya J Med Sci* 2011;73:25-31.
9. Xu HR et al. The effect of CYP2C19 activity on pharmacokinetics of lansoprazole and its active metabolites in healthy subjects. *Pharm Biol* 2010;48:947-52.
10. Lee JH et al. The influence of CYP2C19 polymorphism on eradication of *Helicobacter pylori*: a prospective randomized study of lansoprazole and rabeprazole. *Gut Liver* 2010;4:201-6.
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12. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
13. Hunfeld NG et al. Effect of CYP2C19*2 and *17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752-60.
14. Sakurai Y et al. Population pharmacokinetics and proton pump inhibitory effects of intravenous lansoprazole in healthy Japanese males. *Biol Pharm Bull* 2007;30:2238-43.
15. Kawamura M et al. Cytochrome P450 2C19 polymorphism influences the preventive effect of lansoprazole on the recurrence of erosive reflux esophagitis. *J Gastroenterol Hepatol* 2007;22:222-6.
16. Furuta T et al. Effect of concomitant dosing of famotidine with lansoprazole on gastric acid secretion in relation to CYP2C19 genotype status. *Aliment Pharmacol Ther* 2005;22:67-74.
17. Kawamura M et al. Study Group of GERD. The effects of lansoprazole on erosive reflux oesophagitis are influenced by CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2003;17:965-73.
18. Furuta T et al. Effect of cytochrome P4502C19 genotypic differences on cure rates for gastroesophageal reflux disease by lansoprazole. *Clin Pharmacol Ther* 2002;72:453-60.
19. Shirai N et al. Comparison of lansoprazole and famotidine for gastric acid inhibition during the daytime and night-time in different CYP2C19 genotype groups. *Aliment Pharmacol Ther* 2002;16:837-46.
20. Furuta T et al. Effect of high-dose lansoprazole on intragastric pH in subjects who are homozygous extensive metabolizers of cytochrome P4502C19. *Clin Pharmacol Ther* 2001;70:484-92.
21. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
22. Howden CW et al. Dose-response evaluation of the antisecretory effect of continuous infusion intravenous lansoprazole regimens over 48 h. *Aliment Pharmacol Ther* 2006;23:975-84.
23. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
24. Furuta T et al. Effect of MDR1 C3435T polymorphism on cure rates of *Helicobacter pylori* infection by triple therapy with lansoprazole, amoxicillin and clarithromycin in relation to CYP 2C19 genotypes and 23S rRNA genotypes of *H. pylori*. *Aliment Pharmacol Ther* 2007;26:693-703.
25. Sugimoto M et al. Evidence that the degree and duration of acid suppression are related to *Helicobacter pylori* eradication by triple therapy. *Helicobacter* 2007;12:317- 23.
26. Furuta T et al. Pharmacogenomics-based tailored versus standard therapeutic regimen for eradication of *H. pylori*. *Clin Pharmacol Ther* 2007;81:521-8.
27. Padol S et al. The effect of CYP2C19 polymorphisms on *H. pylori* eradication rate in dual and triple first-line PPI therapies: a meta-analysis. *Am J Gastroenterol* 2006;101:1467-75.
28. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of *Helicobacter pylori* by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.

29. Furuta T et al. Influence of CYP2C19 polymorphism and Helicobacter pylori genotype determined from gastric tissue samples on response to triple therapy for H pylori infection. Clin Gastroenterol Hepatol 2005;3:564-73.
30. Furuta T et al. Polymorphism of interleukin-1beta affects the eradication rates of Helicobacter pylori by triple therapy. Clin Gastroenterol Hepatol 2004;2:22-30.
31. Kawabata H et al. Effect of different proton pump inhibitors, differences in CYP2C19 genotype and antibiotic resistance on the eradication rate of Helicobacter pylori infection by a 1-week regimen of proton pump inhibitor, amoxicillin and clarithromycin. Aliment Pharmacol Ther 2003;17:259-64.
32. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of Helicobacter pylori infection with lansoprazole- or rabeprazole-based triple therapy in Japan. Eur J Gastroenterol Hepatol 2003;15:27-33.
33. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for Helicobacter pylori infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. Clin Pharmacol Ther 2001;69:158-68.
34. Inaba T et al. Helicobacter pylori infection: CYP2C19 genotype and serum ferritin. J Gastroenterol Hepatol 2002;17:748-53.
35. Qiao HL et al. Pharmacokinetics of three proton pump inhibitors in Chinese subjects in relation to the CYP2C19 genotype. Eur J Clin Pharmacol 2006;62:107-12.
36. Miura M et al. Pharmacokinetic differences between the enantiomers of lansoprazole and its metabolite, 5-hydroxylansoprazole, in relation to CYP2C19 genotypes. Eur J Clin Pharmacol 2004;60:623-8.
37. Hu YR et al. Pharmacokinetics of lansoprazole in Chinese healthy subjects in relation to CYP2C19 genotypes. Acta Pharmacol Sin 2004;25:986-90.
38. Ieiri I et al. Comparison of the kinetic disposition of and serum gastrin change by lansoprazole versus rabeprazole during an 8-day dosing scheme in relation to CYP2C19 polymorphism. Eur J Clin Pharmacol 2001;57:485-92.
39. Sakai T et al. CYP2C19 genotype and pharmacokinetics of three proton pump inhibitors in healthy subjects. Pharm Res 2001;18:721-7.
40. Katsuki H et al. Genetic polymorphism of CYP2C19 and lansoprazole pharmacokinetics in Japanese subjects. Eur J Clin Pharmacol 1997;52:391-6.
41. SPC Prezal.

Date 05-03-2018

CYP2C19 IM: mavacamten

[8211](#)

NO action is required for this gene-drug interaction.

Although the plasma concentration of mavacamten may increase due to the reduced CYP2C19 activity, this does not appear to lead to an increase in side effects.

Literature:

SmPC Camzyos (NL en VS).

Date 06-11-2023

CYP2C19 PM: mavacamten

[8209](#)

The risk of serious side effects, such as heart failure (decrease in left ventricular ejection fraction (LVEF)), may be increased. The gene variation can lead to a three times higher exposure to mavacamten.

- NO CYP3A4 inhibitor as comedication:
 - start with 2.5 mg/day and give a maximum of 5 mg/day
(This corresponds to half the normal starting dose and one third of the normal maximum dose.)
- MODERATE or WEAK CYP3A4 inhibitor as comedication:
 - give a maximum of 2.5 mg/day
(This corresponds to half the normal starting dose and one-sixth of the normal maximum dose when using a moderate or weak CYP3A4 inhibitor).
- STRONG CYP3A4 inhibitor as comedication:
 - Mavacamten is contraindicated.
 - avoid mavacamten

Literature:

1. Perera V et al. Effects of omeprazole and verapamil on the pharmacokinetics, safety, and tolerability of mavacamten: two drug-drug interaction studies in healthy participants. Clin Pharmacol Drug Dev 2023

Date 06-11-2023

CYP2C19 UM: mavacamten

[8210](#)

NO action is required for this gene-drug interaction.

Although the plasma concentration of mavacamten may decrease due to increased CYP2C19 activity, this does not appear to reduce its effectiveness.

Literatuur:

1. SmPC Camzyos

Date 06-11-2023

MTHFR 677CT: methotrexaat

[5253](#)

This is NOT a gene-drug interaction.

Literature:

1. Huang J et al. Are gene polymorphisms related to adverse events of methotrexate in patients with rheumatoid arthritis? A retrospective cohort study based on an updated meta-analysis. *Ther Adv Chronic Dis* 2020;11:2040622320916026.
2. Yao P et al. The influence of MTHFR genetic polymorphisms on adverse reactions after methotrexate in patients with hematological malignancies: a meta-analysis. *Hematology* 2019;24:10-9.
3. Zhu C et al. Associations between the C677T and A1298C polymorphisms of MTHFR and the toxicity of methotrexate in childhood malignancies: a meta-analysis. *Pharmacogenomics J* 2018;18:450-9.
4. Shao W et al. Association between MTHFR C677T polymorphism and methotrexate treatment outcome in rheumatoid arthritis patients: a systematic review and meta- analysis. *Genet Test Mol Biomarkers* 2017;21:275-85.
5. Qiu Q et al. Polymorphisms and pharmacogenomics for the clinical efficacy of methotrexate in patients with rheumatoid arthritis: a systematic review and meta-analysis. *Sci Rep* 2017;7:44015.
6. Qiu Q et al. Polymorphisms and pharmacogenomics for the toxicity of methotrexate monotherapy in patients with rheumatoid arthritis: a systematic review and meta- analysis. *Medicine (Baltimore)* 2017;96:e6337.
7. Chen Y et al. Are gene polymorphisms related to treatment outcomes of methotrexate in patients with rheumatoid arthritis? A systematic review and meta-analysis. *Pharmacogenomics* 2017;18:175-95.
8. Song GG et al. Association of the MTHFR C677T and A1298C polymorphisms with methotrexate toxicity in rheumatoid arthritis: a meta-analysis. *Clin Rheumatol* 2014;33:1715-24.
9. Hagleitner MM et al. The role of the MTHFR 677C>T polymorphism in methotrexate-induced liver toxicity: a meta-analysis in patients with cancer. *Pharmacogenomics J* 2014;14:115-9.
10. Morgan MD et al. MTHFR functional genetic variation and methotrexate treatment response in rheumatoid arthritis: a meta-analysis. *Pharmacogenomics* 2014;15:467-75.
11. Owen SA et al. MTHFR gene polymorphisms and outcome of methotrexate treatment in patients with rheumatoid arthritis: analysis of key polymorphisms and meta- analysis of C677T and A1298C polymorphisms. *Pharmacogenomics J* 2013;13:137-47.
12. Yang L et al. Impact of methylenetetrahydrofolate reductase (MTHFR) polymorphisms on methotrexate-induced toxicities in acute lymphoblastic leukemia: a meta- analysis. *Tumour Biol* 2012;33:1445-54.
13. Spyridopoulou KP et al. Methylene tetrahydrofolate reductase gene polymorphisms and their association with methotrexate toxicity: a meta-analysis. *Pharmacogenet Genomics* 2012;22:117-33.
14. Fisher MC et al. Meta-analysis of methylenetetrahydrofolate reductase (MTHFR) polymorphisms affecting methotrexate toxicity. *J Rheumatol* 2009;36:539-45.

Date 07-06-2021

MTHFR 677TT: methotrexaat

[5254](#)

This is NOT a gene-drug interaction.

Literature:

1. Huang J et al. Are gene polymorphisms related to adverse events of methotrexate in patients with rheumatoid arthritis? A retrospective cohort study based on an updated meta-analysis. *Ther Adv Chronic Dis* 2020;11:2040622320916026.
2. Yao P et al. The influence of MTHFR genetic polymorphisms on adverse reactions after methotrexate in patients with hematological malignancies: a meta-analysis. *Hematology* 2019;24:10-9.
3. Zhu C et al. Associations between the C677T and A1298C polymorphisms of MTHFR and the toxicity of methotrexate in childhood malignancies: a meta-analysis. *Pharmacogenomics J* 2018;18:450-9.
4. Shao W et al. Association between MTHFR C677T polymorphism and methotrexate treatment outcome in rheumatoid arthritis patients: a systematic review and meta-analysis. *Genet Test Mol Biomarkers* 2017;21:275-85.
5. Qiu Q et al. Polymorphisms and pharmacogenomics for the clinical efficacy of methotrexate in patients with rheumatoid arthritis: a systematic review and meta-analysis. *Sci Rep* 2017;7:44015.
6. Qiu Q et al. Polymorphisms and pharmacogenomics for the toxicity of methotrexate monotherapy in patients with rheumatoid arthritis: a systematic review and meta-analysis. *Medicine (Baltimore)* 2017;96:e6337.
7. Chen Y et al. Are gene polymorphisms related to treatment outcomes of methotrexate in patients with rheumatoid arthritis? A systematic review and meta-analysis. *Pharmacogenomics* 2017;18:175-95.
8. Song GG et al. Association of the MTHFR C677T and A1298C polymorphisms with methotrexate toxicity in rheumatoid arthritis: a meta-analysis. *Clin Rheumatol* 2014;33:1715-24.
9. Hagleitner MM et al. The role of the MTHFR 677C>T polymorphism in methotrexate-induced liver toxicity: a meta-analysis in patients with cancer. *Pharmacogenomics J* 2014;14:115-9.
10. Morgan MD et al. MTHFR functional genetic variation and methotrexate treatment response in rheumatoid arthritis: a meta-analysis. *Pharmacogenomics* 2014;15:467-75.
11. Lopez-Lopez E et al. A systematic review and meta-analysis of MTHFR polymorphisms in methotrexate toxicity prediction in pediatric acute lymphoblastic leukemia. *Pharmacogenomics J* 2013;13:498-506.
12. Owen SA et al. MTHFR gene polymorphisms and outcome of methotrexate treatment in patients with rheumatoid arthritis: analysis of key polymorphisms and meta-analysis of C677T and A1298C polymorphisms. *Pharmacogenomics J* 2013;13:137-47.
13. Yang L et al. Impact of methylenetetrahydrofolate reductase (MTHFR) polymorphisms on methotrexate-induced toxicities in acute lymphoblastic leukemia: a meta-analysis. *Tumour Biol* 2012;33:1445-54.
14. Spyridopoulou KP et al. Methylene tetrahydrofolate reductase gene polymorphisms and their association with methotrexate toxicity: a meta-analysis. *Pharmacogenet Genomics* 2012;22:117-33.
15. Fisher MC et al. Meta-analysis of methylenetetrahydrofolate reductase (MTHFR) polymorphisms affecting methotrexate toxicity. *J Rheumatol* 2009;36:539-45.

Date 07-06-2021

COMT Met/Met: methylfenidaat

[5931](#)

This is NOT a gene-drug interaction.

Literature:

1. Fageera W et al. COMT by DRD3 epistatic interaction in modulating behaviors in children with ADHD: a pharmaco-dynamic behavioral approach. *J Atten Disord* 2021;25:1720-30.
2. Myer NM et al. Pharmacogenetics predictors of methylphenidate efficacy in childhood ADHD. *Mol Psychiatry* 2018;23:1929-36.
3. Pagerols M et al. Pharmacogenetics of methylphenidate response and tolerability in attention-deficit/hyperactivity disorder. *Pharmacogenomics J* 2017;17:98-104.
4. Unal D et al. Genetic variations in attention deficit hyperactivity disorder subtypes and treatment resistant cases. *Psychiatry Investig* 2016;13:427-33.
5. Park S et al. Catechol-O-methyl-transferase Val158Met polymorphism and a response of hyperactive-impulsive symptoms to methylphenidate: a replication study from South Korea. *J Psychopharmacol* 2014;28:671-6.
6. Contini V et al. No significant association between genetic variants in 7 candidate genes and response to methylphenidate treatment in adult patients with ADHD. *J Clin Psychopharmacol* 2012;32:820-3.
7. Froehlich TE et al. Pharmacogenetic predictors of methylphenidate dose-response in attention-deficit/hyperactivity disorder. *J Am Acad Child Adolesc Psychiatry* 2011;50:1129-1139.
8. Salatino-Oliveira A et al. Catechol-O-methyltransferase Valine158Methionine polymorphism moderates methylphenidate effects on oppositional symptoms in boys with attention-deficit/hyperactivity disorder. *Biol Psychiatry* 2011;70:216-21.
9. McGough JJ et al. A candidate gene analysis of methylphenidate response in attention-deficit/hyperactivity disorder. *J Am Acad Child Adolesc Psychiatry* 2009;48:1155-64.
10. Kereszturi E et al. Catechol-O-methyl-transferase Val158Met polymorphism is associated with methylphenidate response in ADHD children. *Am J Med Genet B Neuropsychiatr Genet* 2008;147B:1431-5.
11. Sengupta S et al. COMT Val108/158Met polymorphism and the modulation of task-oriented behavior in children with ADHD. *Neuropsychopharmacology* 2008;33:3069-77.
12. Cheon KA et al. Association of the catechol-O-methyltransferase polymorphism with methylphenidate response in a classroom setting in children with attention-deficit hyperactivity disorder. *Int Clin*

Date 31-01-2022

COMT Val/Met: methylfenidaat

[5930](#)

This is NOT a gene-drug interaction.

Literature:

1. Fageera W et al. COMT by DRD3 epistatic interaction in modulating behaviors in children with ADHD: a pharmaco-dynamic behavioral approach. *J Atten Disord* 2021;25:1720-30.
2. Myer NM et al. Pharmacogenetics predictors of methylphenidate efficacy in childhood ADHD. *Mol Psychiatry* 2018;23:1929-36.
3. Pagerols M et al. Pharmacogenetics of methylphenidate response and tolerability in attention-deficit/hyperactivity disorder. *Pharmacogenomics J* 2017;17:98-104.
4. Unal D et al. Genetic variations in attention deficit hyperactivity disorder subtypes and treatment resistant cases. *Psychiatry Investig* 2016;13:427-33.
5. Park S et al. Catechol-O-methyl-transferase Val158Met polymorphism and a response of hyperactive-impulsive symptoms to methylphenidate: a replication study from South Korea. *J Psychopharmacol* 2014;28:671-6.
6. Contini V et al. No significant association between genetic variants in 7 candidate genes and response to methylphenidate treatment in adult patients with ADHD. *J Clin Psychopharmacol* 2012;32:820-3.
7. Froehlich TE et al. Pharmacogenetic predictors of methylphenidate dose-response in attention-deficit/hyperactivity disorder. *J Am Acad Child Adolesc Psychiatry* 2011;50:1129-1139.
8. Salatino-Oliveira A et al. Catechol-O-methyltransferase Valine158Methionine polymorphism moderates methylphenidate effects on oppositional symptoms in boys with attention-deficit/hyperactivity disorder. *Biol Psychiatry* 2011;70:216-21.
9. McGough JJ et al. A candidate gene analysis of methylphenidate response in attention-deficit/hyperactivity disorder. *J Am Acad Child Adolesc Psychiatry* 2009;48:1155-64.
10. Kereszturi E et al. Catechol-O-methyl-transferase Val158Met polymorphism is associated with methylphenidate response in ADHD children. *Am J Med Genet B Neuropsychiatr Genet* 2008;147B:1431-5.
11. Sengupta S et al. COMT Val108/158Met polymorphism and the modulation of task-oriented behavior in children with ADHD. *Neuropsychopharmacology* 2008;33:3069-77.
12. Cheon KA et al. Association of the catechol-O-methyltransferase polymorphism with methylphenidate response in a classroom setting in children with attention-deficit hyperactivity disorder. *Int Clin Psychopharmacol* 2008;23:291-8.

Date 31-01-2022

CYP2D6 IM: methylfenidaat

[2917](#)

This is NOT a gene-drug interaction.

Literature:

1. DeVane CL et al. Single-dose pharmacokinetics of methylphenidate in CYP2D6 extensive and poor metabolizers. *J Clin Psychopharmacol* 2000;20:347-9.

Date 31-01-2022

CYP2D6 PM: methylfenidaat

[2916](#)

This is NOT a gene-drug interaction.

Literature:

1. DeVane CL et al. Single-dose pharmacokinetics of methylphenidate in CYP2D6 extensive and poor metabolizers. *J Clin Psychopharmacol* 2000;20:347-9.

Date 31-01-2022

CYP2D6 UM: methylfenidaat

[2918](#)

This is NOT a gene-drug interaction.

Literature:

1. DeVane CL et al. Single-dose pharmacokinetics of methylphenidate in CYP2D6 extensive and poor metabolizers. *J Clin Psychopharmacol* 2000;20:347-9.

Date 31-01-2022

CYP2D6 IM: metoprolol

2400

The gene variation reduces the conversion of metoprolol to inactive metabolites. However, the clinical consequences are limited mainly to the occurrence of asymptomatic bradycardia.

Recommendation:

- If a GRADUAL REDUCTION in HEART RATE is desired, or in the event of SYMPTOMATIC BRADYCARDIA:
 - use smaller steps in dose titration and/or prescribe no more than 50% of the standard dose
- OTHER CASES:
 - no action required

Literature:

1. Chen J et al. Impact of the CYP2D6 genotype on metoprolol tolerance and adverse events in elderly Chinese patients with cardiovascular diseases. *Front Pharmacol* 2022;13:876392.
2. Meloche M et al. Leveraging large observational studies to discover genetic determinants of drug concentrations: a proof-of-concept study. *Clin Transl Sci* 2022;15:1063- 73.
3. Meloche M et al. CYP2D6 polymorphism and its impact on the clinical response to metoprolol: a systematic review and meta-analysis. *Br J Clin Pharmacol* 2020;86:1015-33.
4. Chen L et al. The association of ADRB1 and CYP2D6 polymorphisms with antihypertensive effects and analysis of their contribution to hypertension risk. *Am J Med Sci* 2018;355:235-9.
5. Gao X et al. Impact of CYP2D6 and ADRB1 polymorphisms on heart rate of post-PCI patients treated with metoprolol. *Pharmacogenomics* 2017 Nov 2 (online ahead of print).
6. Hamadeh IS et al. Impact of CYP2D6 polymorphisms on clinical efficacy and tolerability of metoprolol tartrate. *Clin Pharmacol Ther* 2014;96:175-81.
7. Batty JA et al. An investigation of CYP2D6 genotype and response to metoprolol CR/XL during dose titration in patients with heart failure: a MERIT-HF substudy. *Clin Pharmacol Ther* 2014;95:321-30.
8. Rau T et al. Impact of the CYP2D6 genotype on the clinical effects of metoprolol: a prospective longitudinal study. *Clin Pharmacol Ther* 2009;85:269-72.
9. Bijl MJ et al. Genetic variation in the CYP2D6 gene is associated with a lower heart rate and blood pressure in beta-blocker users. *Clin Pharmacol Ther* 2009;85:45-50.
10. Goryachkina K et al. CYP2D6 is a major determinant of metoprolol disposition and effects in hospitalized Russian patients treated for acute myocardial infarction. *Eur J Clin Pharmacol* 2008;64:1163-73.
11. Yuan H et al. Effects of polymorphism of the beta(1) adrenoreceptor and CYP2D6 on the therapeutic effects of metoprolol. *J Int Med Res* 2008;36:1354-62.
12. Jin SK et al. Influence of CYP2D6*10 on the pharmacokinetics of metoprolol in healthy Korean volunteers. *J Clin Pharm Ther* 200;33:567-73.
13. Ismail R et al. The relevance of CYP2D6 genetic polymorphism on chronic metoprolol therapy in cardiovascular patients. *J Clin Pharm Ther* 2006;31:99-109.
14. Terra SG et al. Beta1-adrenergic receptor polymorphisms and left ventricular remodeling changes in response to beta-blocker therapy. *Clin Pharmacol Ther* 2005;77:127- 137.
15. Nozawa T et al. Influence of CYP2D6 genotype on metoprolol plasma concentration and beta-adrenergic inhibition during long-term treatment: a comparison with bisoprolol. *J Cardiovasc Pharmacol* 2005;46:713-20.
16. Fux R et al. Impact of CYP2D6 genotype on adverse effects during treatment with metoprolol: a prospective clinical study. *Clin Pharmacol Ther* 2005;78:378-87.
17. Zineh I et al. Pharmacokinetics and CYP2D6 genotypes do not predict metoprolol adverse events or efficacy in hypertension. *Clin Pharmacol Ther* 2004;76:536-44.
18. Taguchi M et al. Effect of CYP2D6*10 on pharmacokinetic variability of routinely administered metoprolol in middle-aged and elderly Japanese patients. *Eur J Clin Pharmacol* 2003;59:385-8.
19. Rau T et al. Effect of the CYP2D6 genotype on metoprolol metabolism persists during long-term treatment. *Pharmacogenetics* 2002;12:465-72.
20. Huang JD et al. Pharmacokinetics of metoprolol enantiomers in Chinese subjects of major CYP2D6 genotypes. *Clin Pharmacol Ther* 1999;65:402-7.
21. Koytchev R et al. Influence of the cytochrome P4502D6*4 allele on the pharmacokinetics of controlled-release metoprolol. *Eur J Clin Pharmacol* 1998;54:469-74.

Date 12-09-2022

The gene variation reduces the conversion of metoprolol to inactive metabolites. However, the clinical consequences are limited mainly to the occurrence of asymptomatic bradycardia.

Recommendation:

- If a GRADUAL REDUCTION in HEART RATE is desired, or in the event of SYMPTOMATIC BRADYCARDIA:
 - use smaller steps in dose titration and/or prescribe no more than 25% of the standard dose
- OTHER CASES:
 - no action required

Literature:

1. Meloche M et al. Leveraging large observational studies to discover genetic determinants of drug concentrations: a proof-of-concept study. *Clin Transl Sci* 2022;15:1063- 73.
2. Meloche M et al. CYP2D6 polymorphism and its impact on the clinical response to metoprolol: a systematic review and meta-analysis. *Br J Clin Pharmacol* 2020;86:1015- 33.
3. Hamadeh IS et al. Impact of CYP2D6 polymorphisms on clinical efficacy and tolerability of metoprolol tartrate. *Clin Pharmacol Ther* 2014;96:175-81.
4. Batty JA et al. An investigation of CYP2D6 genotype and response to metoprolol CR/XL during dose titration in patients with heart failure: a MERIT-HF substudy. *Clin Pharmacol Ther* 2014;95:321-30.
5. Rau T et al. Impact of the CYP2D6 genotype on the clinical effects of metoprolol: a prospective longitudinal study. *Clin Pharmacol Ther* 2009;85:269-72.
6. Bijl MJ et al. Genetic variation in the CYP2D6 gene is associated with a lower heart rate and blood pressure in beta-blocker users. *Clin Pharmacol Ther* 2009;85:45-50.
7. Goryachkina K et al. CYP2D6 is a major determinant of metoprolol disposition and effects in hospitalized Russian patients treated for acute myocardial infarction. *Eur J Clin Pharmacol* 2008;64:1163-73.
8. Yuan H et al. Effects of polymorphism of the beta(1) adrenoceptor and CYP2D6 on the therapeutic effects of metoprolol. *J Int Med Res* 2008;36:1354-62.
9. Seeringer A et al. Enantiospecific pharmacokinetics of metoprolol in CYP2D6 ultra-rapid metabolizers and correlation with exercise-induced heart rate. *Eur J Clin Pharmacol* 2008;64:883-8.
10. Ismail R et al. The relevance of CYP2D6 genetic polymorphism on chronic metoprolol therapy in cardiovascular patients. *J Clin Pharm Ther* 2006;31:99-109.
11. Terra SG et al. Beta1-adrenergic receptor polymorphisms and left ventricular remodeling changes in response to beta-blocker therapy. *Clin Pharmacol Ther* 2005;77:127- 137.
12. Fux R et al. Impact of CYP2D6 genotype on adverse effects during treatment with metoprolol: a prospective clinical study. *Clin Pharmacol Ther* 2005;78:378-87.
13. Zineh I et al. Pharmacokinetics and CYP2D6 genotypes do not predict metoprolol adverse events or efficacy in hypertension. *Clin Pharmacol Ther* 2004;76:536-44.
14. Kirchheiner J et al. Impact of the ultrarapid metabolizer genotype of cytochrome P450 2D6 on metoprolol pharmacokinetics and pharmacodynamics. *Clin Pharmacol Ther* 2004;76:302-12.
15. Wuttke H et al. Increased frequency of cytochrome P450 2D6 poor metabolizers among patients with metoprolol-associated adverse effects. *Clin Pharmacol Ther* 2002;72:429-37.
16. Rau T et al. Effect of the CYP2D6 genotype on metoprolol metabolism persists during long-term treatment. *Pharmacogenetics* 2002;12:465-72.
17. Laurent-Kenesi MA et al. Influence of CYP2D6-dependent metabolism on the steady-state pharmacokinetics and pharmacodynamics of metoprolol and nicardipine, alone and in combination. *Br J Clin Pharmacol* 1993;36:531-8.
18. Lewis RV et al. Influence of debrisoquine oxidation phenotype on exercise tolerance and subjective fatigue after metoprolol and atenolol in healthy subjects. *Br J Clin Pharmacol* 1991;31:391-8.
19. Clark DWJ et al. Adverse effects from metoprolol are not generally associated with oxidation status. *Br J Clin Pharmacol* 1984;18:965-966.
20. Lennard MS et al. Differential stereoselective metabolism of metoprolol in extensive and poor debrisoquin metabolizers. *Clin Pharmacol Ther* 1983;34:732-7.
21. SmPC Toprol-XL (VS).

Date 12-09-2022

The gene variation increases the conversion of metoprolol to inactive metabolites. This can increase the dose requirement. However, with a target dose of 200 mg/day, there was no effect on the blood pressure and hardly any effect on the reduction of the heart rate.

Recommendation:

- use the maximum dose for the relevant indication as a target dose
- if the effectiveness is still insufficient: increase the dose based on effectiveness and side effects to 2.5 times the standard dose or select an alternative.

Possible alternatives include:

- HEART FAILURE: bisoprolol or carvedilol.

Bisoprolol: advantage: not metabolised by CYP2D6; disadvantage: elimination depends on the kidney function.

Carvedilol: advantage: elimination does not depend on the kidney function; disadvantage: is metabolised (to a lesser extent than metoprolol) by CYP2D6.

- OTHER INDICATIONS: atenolol or bisoprolol. Neither is metabolised by CYP2D6.

Literature:

1. Meloche M et al. Leveraging large observational studies to discover genetic determinants of drug concentrations: a proof-of-concept study. Clin Transl Sci 2022;15:1063-73.
2. Meloche M et al. CYP2D6 polymorphism and its impact on the clinical response to metoprolol: a systematic review and meta-analysis. Br J Clin Pharmacol 2020;86:1015- 33.
3. Hamadeh IS et al. Impact of CYP2D6 polymorphisms on clinical efficacy and tolerability of metoprolol tartrate. Clin Pharmacol Ther 2014;96:175-81.
4. Goryachkina K et al. CYP2D6 is a major determinant of metoprolol disposition and effects in hospitalized Russian patients treated for acute myocardial infarction. Eur J Clin Pharmacol 2008;64:1163-73.
5. Seeringer A et al. Enantiospecific pharmacokinetics of metoprolol in CYP2D6 ultra-rapid metabolizers and correlation with exercise-induced heart rate. Eur J Clin Pharmacol 2008;64:883-8.
6. Ismail R et al. The relevance of CYP2D6 genetic polymorphism on chronic metoprolol therapy in cardiovascular patients. J Clin Pharm Ther 2006;31:99-109.
7. Fux R et al. Impact of CYP2D6 genotype on adverse effects during treatment with metoprolol: a prospective clinical study. Clin Pharmacol Ther 2005;78:378-87.
8. Kirchheiner J et al. Impact of the ultrarapid metabolizer genotype of cytochrome P450 2D6 on metoprolol pharmacokinetics and pharmacodynamics. Clin Pharmacol Ther 2004;76:302-12.

Date 12-09-2022

CYP2C19 IM: mirtazapine

[3533](#)

This is NOT a gene-drug interaction.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022 Jul 15. Online ahead of print.
2. Grasmäder K et al. Population pharmacokinetic analysis of mirtazapine. Eur J Clin Pharmacol 2004;60:473-80.

Date 14-11-2022

CYP2C19 PM: mirtazapine

[3532](#)

This is NOT a gene-drug interaction.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022 Jul 15. Online ahead of print.
2. Johnson M et al. A poor metabolizer for cytochromes P450 2D6 and 2C19: a case report on antidepressant treatment. CNS Spectr 2006;11:757-60.

Date 14-11-2022

CYP2C19 UM: mirtazapine

[3534](#)

This is NOT a gene-drug interaction.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022 Jul 15. Online ahead of print.

CYP2D6 IM: mirtazapine[2588](#)

NO action is required for this gene-drug interaction.

There is insufficient evidence to suggest that the higher plasma concentration of mirtazapine results in an increase in the side effects or efficacy.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022 Jul 15. Online ahead of print.
2. Zastrozhin MS et al. The Influence of concentration of micro-RNA hsa-miR-370-3p and CYP2D6*4 on equilibrium concentration of mirtazapine in patients with major depressive disorder. *Psychopharmacol Bull* 2020;50:58-75.
3. Zastrozhin MS et al. Effects of CYP2D6 activity on the efficacy and safety of mirtazapine in patients with depressive disorders and comorbid alcohol use disorder. *Can J Physiol Pharmacol* 2019;97:781-5.
4. Hayashi Y et al. Factors affecting steady-state plasma concentrations of enantiomeric mirtazapine and its desmethylated metabolites in Japanese psychiatric patients. *Pharmacopsychiatry* 2015;48:279-85.
5. Okubo M et al. Effects of cytochrome P450 2D6 and 3A5 genotypes and possible coadministered medicines on the metabolic clearance of antidepressant mirtazapine in Japanese patients. *Biochem Pharmacol* 2015;93:104-9.
6. Jaquenoud Sirot E et al. Multicenter study on the clinical effectiveness, pharmacokinetics, and pharmacogenetics of mirtazapine in depression. *J Clin Psychopharmacol* 2012;32:622-9.
7. Borobia AM et al. Influence of sex and CYP2D6 genotype on mirtazapine disposition, evaluated in Spanish healthy volunteers. *Pharmacol Res* 2009;59:393-8.
8. Lind AB et al. Steady-state concentrations of mirtazapine, N-desmethyilmirtazapine, 8-hydroxymirtazapine and their enantiomers in relation to cytochrome P450 2D6 genotype, age and smoking behaviour. *Clin Pharmacokinet* 2009;48:63-70.
9. Grasmader K et al. Population pharmacokinetic analysis of mirtazapine. *Eur J Clin Pharmacol* 2004;60:473-80.
10. Murphy GM Jr et al. Pharmacogenetics of antidepressant medication intolerance. *Am J Psychiatry* 2003;160:1830-5.

Date 14-11-2022

CYP2D6 PM: mirtazapine[2587](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of mirtazapine does not result - or hardly results - in an increase in the side effects.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022 Jul 15. Online ahead of print.
2. Milosavljevic F et al. Association of CYP2C19 and CYP2D6 poor and intermediate metabolizer status with antidepressant and antipsychotic exposure: a systematic review and meta-analysis. *JAMA Psychiatry* 2021;78:270-80.
3. Jaquenoud Sirot E et al. Multicenter study on the clinical effectiveness, pharmacokinetics, and pharmacogenetics of mirtazapine in depression. *J Clin Psychopharmacol* 2012;32:622-9.
4. Ramaekers JG et al. Residual effects of esmirtazapine on actual driving performance: overall findings and an exploratory analysis into the role of CYP2D6 phenotype. *Psychopharmacology* 2011;215:321-32.
5. Borobia AM et al. Influence of sex and CYP2D6 genotype on mirtazapine disposition, evaluated in Spanish healthy volunteers. *Pharmacol Res* 2009;59:393-8.
6. Lind AB et al. Steady-state concentrations of mirtazapine, N-desmethyilmirtazapine, 8-hydroxymirtazapine and their enantiomers in relation to cytochrome P450 2D6 genotype, age and smoking behaviour. *Clin Pharmacokinet* 2009;48:63-70.
7. Brockmoller J et al. Pharmacokinetics of mirtazapine: enantioselective effects of the CYP2D6 ultra rapid metabolizer genotype and correlation with adverse effects. *Clin Pharmacol Ther* 2007;81:699-707.
8. Johnson M et al. A poor metabolizer for cytochromes P450 2D6 and 2C19: a case report on antidepressant treatment. *CNS Spectr* 2006;11:757-60.
9. Stephan PL et al. Adverse drug reactions following nonresponse in a depressed patient with CYP2D6 deficiency and low CYP 3A4/5 activity. *Pharmacopsychiatry* 2006;39:150-2.
10. Kirchheiner J et al. Impact of the CYP2D6 ultrarapid metabolizer genotype on mirtazapine pharmacokinetics and adverse events in healthy volunteers. *J Clin Psychopharmacol* 2004;24:647-52.

11. Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. Eur J Clin Pharmacol 2004;60:329-36.
12. Murphy GM Jr et al. Pharmacogenetics of antidepressant medication intolerance. Am J Psychiatry 2003;160:1830-5.

Date 14-11-2022

CYP2D6 UM: mirtazapine

[2589](#)

NO action is required for this gene-drug interaction.

The effect on the plasma concentration of mirtazapine is small. No effect has been demonstrated with regard to effectiveness or side effects.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. Pharmacopsychiatry 2022 Jul 15. Online ahead of print.
2. Jaquenoud Sirot E et al. Multicenter study on the clinical effectiveness, pharmacokinetics, and pharmacogenetics of mirtazapine in depression. J Clin Psychopharmacol 2012;32:622-9.
3. Lind AB et al. Steady-state concentrations of mirtazapine, N-desmethyilmirtazapine, 8-hydroxymirtazapine and their enantiomers in relation to cytochrome P450 2D6 genotype, age and smoking behaviour. Clin Pharmacokinet 2009;48:63-70.
4. Brockmoller J et al. Pharmacokinetics of mirtazapine: enantioselective effects of the CYP2D6 ultra rapid metabolizer genotype and correlation with adverse effects. Clin Pharmacol Ther 2007;81:699-707.
5. Kirchheiner J et al. Impact of the CYP2D6 ultrarapid metabolizer genotype on mirtazapine pharmacokinetics and adverse events in healthy volunteers. J Clin Psychopharmacol 2004;24:647-52.
6. Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. Eur J Clin Pharmacol 2004;60:329-36.

Date 14-11-2022

CYP2C19 IM: moclobemide

[2581](#)

NO action is needed for this gene-drug interaction.

Although the moclobemide plasma concentration may increase as a result of the decreased CYP2C19 activity, this does not lead to an increased incidence of side effects, in as far as is known.

Literature:

1. Gram LF et al. Moclobemide, a substrate of CYP2C19 and an inhibitor of CYP2C19, CYP2D6, and CYP1A2: a panel study. Clin Pharmacol Ther 1995;57:670-7.
2. SmPC Moclobemide Mylan.

Date 14-11-2022

CYP2C19 PM: moclobemide

[2582](#)

NO action is needed for this gene-drug interaction.

Although the moclobemide plasma concentration may increase as a result of the decreased CYP2C19 activity, this does not lead to an increased incidence of side effects, in as far as is known.

Literature:

1. Yu KS et al. Effect of omeprazole on the pharmacokinetics of moclobemide according to the genetic polymorphism of CYP2C19. Clin Pharmacol Ther 2001;69:266-73.
2. Gram LF et al. Moclobemide, a substrate of CYP2C19 and an inhibitor of CYP2C19, CYP2D6, and CYP1A2: a panel study. Clin Pharmacol Ther 1995;57:670-7.
3. SmPC Moclobemide Mylan.

Date 14-11-2022

CYP2C19 UM: moclobemide

[2583](#)

NO action is needed for this gene-drug interaction.

Although the moclobemide plasma concentration may decrease as a result of increased CYP2C19 activity, this does not lead to increased effectiveness, in as far as is known.

Literature:

1. Gram LF et al. Moclobemide, a substrate of CYP2C19 and an inhibitor of CYP2C19, CYP2D6, and CYP1A2: a panel study. Clin Pharmacol Ther 1995;57:670-7.
2. SmPC Moclobemide Mylan.

Date 14-11-2022

CYP2D6 IM: nortriptyline

[2403](#)

The risk of side effects may be increased, because the gene variation leads to an increased plasma concentration of nortriptyline.

- use 60% of the standard dose and monitor the effect and side effects or the plasma concentration of nortriptyline in order to set the maintenance dose.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor metabolizer phenotype. Ther Drug Monit 2021;43:672-80 en persoonlijke communicatie (gemiddelde dosisgecorrigeerde serumconcentraties).
3. van der Schans J et al. Effects of pharmacogenetic screening for CYP2D6 among elderly starting therapy with nortriptyline or venlafaxine: a pragmatic randomized controlled trial (CYSCE Trial). J Clin Psychopharmacol 2019;39:583-90.
4. Berm E et al. Relation between CYP2D6 genotype, phenotype and therapeutic drug concentrations among nortriptyline and venlafaxine users in old age psychiatry. Pharmacopsychiatry 2016;49:186-190.
5. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. Psychopharmacology (Berl) 2015;232:2609-17.
6. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. J Psychopharmacol 2014;28:133-41.
7. Lee SY et al. Sequence-based CYP2D6 genotyping in the Korean population. Ther Drug Monit 2006;28:382-7.
8. Lee S et al. A case report of a poor metabolizer of CYP2D6 presented with unusual responses to nortriptyline medication. J Korean Med Sci 2004;19:750-2.
9. Dalen P et al. Disposition of debrisoquine and nortriptyline in Korean subjects in relation to CYP2D6 genotypes, and comparison with Caucasians. Br J Clin Pharmacol 2003;55:630-4.
10. Murphy GM et al. CYP2D6 genotyping with oligonucleotide microarrays and nortriptyline concentrations in geriatric depression. Neuropsychopharmacol 2001;25:737-43.
11. Kvist EE et al. Quantitative pharmacogenetics of nortriptyline: a novel approach. Clin Pharmacokinet 2001;40:869-77.
12. Morita S et al. Steady-state plasma levels of nortriptyline and its hydroxylated metabolites in Japanese patients: impact of CYP2D6 genotype on the hydroxylation of nortriptyline. J Clin Psychopharmacol 2000;20:141-9.
13. Yue QJ et al. Pharmacokinetics of nortriptyline and its 10-hydroxymetabolite in Chinese subjects of different CYP2D6 genotypes. Clin Pharmacol Ther 1998;64:384-90.
14. Chen S et al. The cytochrome P450 2D6 (CYP2D6) enzyme polymorphism: screening costs and influence on clinical outcomes in psychiatry. Clin Pharmacol Ther 1996;60:522-34

Date 08-02-2024

CYP2D6 PM: nortriptyline

[2404](#)

The risk of side effects may be increased, because the gene variation leads to an increased plasma concentration of nortriptyline.

- use 40% of the standard dose and monitor the effect and side effects or the plasma concentration of nortriptyline in order to set the maintenance dose.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. JAMA Netw Open 2023;6:e2312443.
2. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor

- metabolizer phenotype. *Ther Drug Monit* 2021;43:672-80 and personal communication (mean dose-corrected serum concentrations).
3. van der Schans J et al. Effects of pharmacogenetic screening for CYP2D6 among elderly starting therapy with nortriptyline or venlafaxine: a pragmatic randomized controlled trial (CYSCE Trial). *J Clin Psychopharmacol* 2019;39:583-90.
 4. Berm E et al. Relation between CYP2D6 genotype, phenotype and therapeutic drug concentrations among nortriptyline and venlafaxine users in old age psychiatry. *Pharmacopsychiatry* 2016;49:186-190.
 5. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. *Psychopharmacology (Berl)* 2015;232:2609-17.
 6. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. *J Psychopharmacol* 2014;28:133-41.
 7. Roberts et al. No evidence of increased adverse drug reactions in cytochrome P450 CYP2D6 poor metabolizers treated with fluoxetine or nortriptyline. *Hum Psychopharmacol* 2004 Jan;19:17-23.
 8. Kvist EE et al. Quantitative pharmacogenetics of nortriptyline: a novel approach. *Clin Pharmacokinet* 2001;40:869-77.
 9. Dalen P et al. 10-Hydroxylation of nortriptyline in white persons with 0, 1, 2, 3, and 13 functional CYP2D6 genes. *Clin Pharmacol Ther* 1998;63:444-52.
 10. Dahl M et al. Steady-state plasma levels of nortriptyline and its 10-hydroxymetabolite: relationship to the CYP2D6 genotype. *Psychopharmacol* 1996;123:315-9.
 11. Chen S et al. The cytochrome P450 2D6 (CYP2D6) enzyme polymorphism: screening costs and influence on clinical outcomes in psychiatry. *Clin Pharmacol Ther* 1996;60:522-34.
 12. Bertilsson L et al. Slow hydroxylation of nortriptyline and concomitant poor debrisoquine hydroxylation: clinical implications. *Lancet* 1981;1:560-1.
 13. SmPC Pamelor (USA).

Date 08-02-2024

CYP2D6 UM: nortriptyline

[2405](#)

The risk of ineffectiveness and cardiotoxic effects may be increased. The gene variation leads to a decrease in the plasma concentration of nortriptyline and an increase in the plasma concentration of the cardiotoxic metabolite Z-10-hydroxynortriptyline.

- use 1.7 times the standard dose and monitor the effect and side effects or the plasma concentration of nortriptyline and be alert to an increase in the plasma concentration of the cardiotoxic metabolite Z-10-hydroxynortriptyline

Plasma concentrations of Z-hydroxynortriptyline exceeding 40 ng/mL are considered toxic.

- if a dose increase is not wanted due to the cardiotoxic hydroxy metabolite: avoid nortriptyline
Antidepressants that are not metabolised via CYP2D6 - or to a lesser extent - include, for example, citalopram and sertraline.

Literature:

1. Vos CF et al. Effectiveness of genotype-specific tricyclic antidepressant dosing in patients with major depressive disorder: a randomized clinical trial. *JAMA Netw Open* 2023;6:e2312443.
2. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor metabolizer phenotype. *Ther Drug Monit* 2021;43:672-80 and personal communication (mean dose-corrected serum concentrations).
3. van der Schans J et al. Effects of pharmacogenetic screening for CYP2D6 among elderly starting therapy with nortriptyline or venlafaxine: a pragmatic randomized controlled trial (CYSCE Trial). *J Clin Psychopharmacol* 2019;39:583-90.
4. Hodgson K et al. Exploring the role of drug-metabolising enzymes in antidepressant side effects. *Psychopharmacology (Berl)* 2015;232:2609-17.
5. Hodgson K et al. Genetic differences in cytochrome P450 enzymes and antidepressant treatment response. *J Psychopharmacol* 2014;28:133-41.
6. Lee SY et al. Sequence-based CYP2D6 genotyping in the Korean population. *Ther Drug Monit* 2006;28:382-7.
7. Kvist EE et al. Quantitative pharmacogenetics of nortriptyline: a novel approach. *Clin Pharmacokinet* 2001;40:869-77.
8. Dalen P et al. 10-Hydroxylation of nortriptyline in white persons with 0, 1, 2, 3, and 13 functional CYP2D6 genes. *Clin Pharmacol Ther* 1998;63:444-52.
9. Bertilsson L et al. Molecular basis for rational megaprescribing in ultrarapid hydroxylators of debrisoquine. *Lancet* 1993;341:63.

Date 08-02-2024

CYP1A2 IM: olanzapine

[4437](#)

This is NOT a gene-drug interaction.

Literature:

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Date 13-09-2021

CYP1A2 NM: olanzapine

[4434](#)

This is NOT a gene-drug interaction.

Literature:

10. Koller D et al. Safety and cardiovascular effects of multiple-dose administration of aripiprazole and olanzapine in a randomised clinical trial. *Hum Psychopharmacol* 2021;36:1-12.
11. Yan P et al. Association of the genetic polymorphisms of metabolizing enzymes, transporters, target receptors and their interactions with treatment response to olanzapine in chinese han schizophrenia patients. *Psychiatry Res* 2020;293:113470.
12. Koller D et al. The effects of aripiprazole and olanzapine on pupillary light reflex and its relationship with pharmacogenetics in a randomized multiple-dose trial. *Br J Clin Pharmacol* 2020;86:2051-62 en persoonlijke communicatie (supplementaire files).
13. Hattori S et al. The association of genetic polymorphisms in CYP1A2, UGT1A4, and ABCB1 with autonomic nervous system dysfunction in schizophrenia patients treated with olanzapine. *BMC Psychiatry* 2020;20:72.
14. Djordjevic N et al. Cigarette smoking and heavy coffee consumption affecting response to olanzapine: The role of genetic polymorphism. *World J Biol Psychiatry* 2020;21:29-52.
15. Na Takuathung M et al. Impact of CYP1A2 genetic polymorphisms on pharmacokinetics of antipsychotic drugs: a systematic review and meta-analysis. *Acta Psychiatr Scand* 2019;139:15-25.
16. Czerwensky F et al. CYP1A2*1D and *1F polymorphisms have a significant impact on olanzapine serum concentrations. *Ther Drug Monit* 2015; 37:152-60.
17. Looman NMG et al. Associatie van genetische variatie in CYP1A2 en UGT1A4 met metabole stoornissen bij gebruikers van clozapine en olanzapine. *PW Wetenschappelijk Platform* 2013; 7:a1310.
18. Söderberg MM et al. Influence of CYP1A1/CYP1A2 and AHR polymorphisms on systemic olanzapine exposure. *Pharmacogenet Genomics* 2013;23:279-85.
19. Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
20. Skogh E et al. High correlation between serum and cerebrospinal fluid olanzapine concentrations in patients with schizophrenia or schizoaffective disorder medicating with oral olanzapine as the only antipsychotic drug. *J Clin Psychopharmacol* 2011;31:4-9.
21. Ghotbi R et al. Carriers of the UGT1A4 142T>G gene variant are predisposed to reduced olanzapine exposure--an impact similar to male gender or smoking in schizophrenic patients. *Eur J Clin Pharmacol* 2010;66:465-74.
22. Nozawa M et al. The relationship between the response of clinical symptoms and plasma olanzapine concentration, based on pharmacogenetics: Juntendo University Schizophrenia Projects (JUSP). *Ther Drug Monit* 2008;30:35-40.
23. Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.

Date 13-09-2021

CYP1A2 PM: olanzapine

[4438](#)

This is NOT a gene-drug interaction.

Literature:

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Date 13-09-2021

CYP1A2*1A/*1F: olanzapine

[4433](#)

This is NOT a gene-drug interaction.

Literature:

1. Yan P et al. Association of the genetic polymorphisms of metabolizing enzymes, transporters, target receptors and their interactions with treatment response to olanzapine in chinese han schizophrenia

- patients. *Psychiatry Res* 2020;293:113470.
- Hattori S et al. The association of genetic polymorphisms in CYP1A2, UGT1A4, and ABCB1 with autonomic nervous system dysfunction in schizophrenia patients treated with olanzapine. *BMC Psychiatry* 2020;20:72.
 - Na Takuathung M et al. Impact of CYP1A2 genetic polymorphisms on pharmacokinetics of antipsychotic drugs: a systematic review and meta-analysis. *Acta Psychiatr Scand* 2019;139:15-25.
 - Czerwensky F et al. CYP1A2*1D and *1F polymorphisms have a significant impact on olanzapine serum concentrations. *Ther Drug Monit* 2015; 37:152-60.
 - Looman NMG et al. Associatie van genetische variatie in CYP1A2 en UGT1A4 met metabole stoornissen bij gebruikers van clozapine en olanzapine. *PW Wetenschappelijk Platform* 2013; 7:a1310.
 - Söderberg MM et al. Influence of CYP1A1/CYP1A2 and AHR polymorphisms on systemic olanzapine exposure. *Pharmacogenet Genomics* 2013;23:279-85.
 - Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
 - Skogh E et al. High correlation between serum and cerebrospinal fluid olanzapine concentrations in patients with schizophrenia or schizoaffective disorder medicating with oral olanzapine as the only antipsychotic drug. *J Clin Psychopharmacol* 2011;31:4-9.
 - Ghotbi R et al. Carriers of the UGT1A4 142T>G gene variant are predisposed to reduced olanzapine exposure--an impact similar to male gender or smoking in schizophrenic patients. *Eur J Clin Pharmacol* 2010;66:465-74.
 - Nozawa M et al. The relationship between the response of clinical symptoms and plasma olanzapine concentration, based on pharmacogenetics: Juntendo University Schizophrenia Projects (JUSP). *Ther Drug Monit* 2008;30:35-40.
 - Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.

Date 13-09-2021

CYP 1A2*1C-heterozygoot: olanzapine

[4435](#)

This is NOT a gene-drug interaction.

Literature:

- Koller D et al. Safety and cardiovascular effects of multiple-dose administration of aripiprazole and olanzapine in a randomised clinical trial. *Hum Psychopharmacol* 2021;36:1-12.
- Yan P et al. Association of the genetic polymorphisms of metabolizing enzymes, transporters, target receptors and their interactions with treatment response to olanzapine in chinese han schizophrenia patients. *Psychiatry Res* 2020;293:113470.
- Koller D et al. The effects of aripiprazole and olanzapine on pupillary light reflex and its relationship with pharmacogenetics in a randomized multiple-dose trial. *Br J Clin Pharmacol* 2020;86:2051-62 en persoonlijke communicatie (supplementaire files).
- Hattori S et al. The association of genetic polymorphisms in CYP1A2, UGT1A4, and ABCB1 with autonomic nervous system dysfunction in schizophrenia patients treated with olanzapine. *BMC Psychiatry* 2020;20:72.
- Looman NMG et al. Associatie van genetische variatie in CYP1A2 en UGT1A4 met metabole stoornissen bij gebruikers van clozapine en olanzapine. *PW Wetenschappelijk Platform* 2013; 7:a1310.
- Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
- Nozawa M et al. The relationship between the response of clinical symptoms and plasma olanzapine concentration, based on pharmacogenetics: Juntendo University Schizophrenia Projects (JUSP). *Ther Drug Monit* 2008;30:35-40.
- Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.

Date 13-09-2021

CYP1A2*1C/*1C: olanzapine

[4436](#)

This is NOT a gene-drug interaction.

Literature:

- Yan P et al. Association of the genetic polymorphisms of metabolizing enzymes, transporters, target receptors and their interactions with treatment response to olanzapine in chinese han schizophrenia patients. *Psychiatry Res* 2020;293:113470.
- Hattori S et al. The association of genetic polymorphisms in CYP1A2, UGT1A4, and ABCB1 with autonomic nervous system dysfunction in schizophrenia patients treated with olanzapine. *BMC Psychiatry* 2020;20:72.

3. Nozawa M et al. The relationship between the response of clinical symptoms and plasma olanzapine concentration, based on pharmacogenetics: Juntendo University Schizophrenia Projects (JUSP). *Ther Drug Monit* 2008;30:35-40.
4. Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.

Date 13-09-2021

CYP2D6 IM: olanzapine

[2406](#)

This is NOT a gene-drug interaction.

Literature:

1. Zubiaur P et al. Impact of polymorphisms in transporter and metabolizing enzyme genes on olanzapine pharmacokinetics and safety in healthy volunteers. *Biomed Pharmacother* 2021;133:111087.
2. Miroshnichenko II et al. Therapeutic drug monitoring of olanzapine and cytochrome P450 genotyping in nonsmoking subjects. *Ther Drug Monit* 2020;42:325-9.
3. Djordjevic N et al. Cigarette smoking and heavy coffee consumption affecting response to olanzapine: The role of genetic polymorphism. *World J Biol Psychiatry* 2020;21:29-52.
4. Okubo M et al. Individual differences in in vitro and in vivo metabolic clearances of the antipsychotic drug olanzapine from non-smoking and smoking Japanese subjects genotyped for cytochrome P4502D6 and flavincontaining monooxygenase 3. *Hum Psychopharmacol* 2016;31:83-92.
5. Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
6. Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.
7. Nozawa M et al. The relationship between the response of clinical symptoms and plasma olanzapine concentration, based on pharmacogenetics: Juntendo University Schizophrenia Projects (JUSP). *Ther Drug Monit* 2008;30:35-40.
8. Iwahashi K. Olanzapine metabolism by CYP1A2/CYP2D6 and hyperglycaemia. *Acta Neuropsychiatrica* 2004;16:229-230.
9. Ellingrod VL et al. CYP2D6 polymorphisms and atypical antipsychotic weight gain. *Psychiatr Genet* 2002;12:55-8.

Date 13-09-2021

CYP2D6 PM: olanzapine

[2407](#)

This is NOT a gene-drug interaction.

Literature:

1. Zubiaur P et al. Impact of polymorphisms in transporter and metabolizing enzyme genes on olanzapine pharmacokinetics and safety in healthy volunteers. *Biomed Pharmacother* 2021;133:111087.
2. Djordjevic N et al. Cigarette smoking and heavy coffee consumption affecting response to olanzapine: The role of genetic polymorphism. *World J Biol Psychiatry* 2020;21:29-52.
3. Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
4. Skogh E et al. High correlation between serum and cerebrospinal fluid olanzapine concentrations in patients with schizophrenia or schizoaffective disorder medicating with oral olanzapine as the only antipsychotic drug. *J Clin Psychopharmacol* 2011;31:4-9.
5. Thomas P et al. Correlates of response to olanzapine in a North Indian schizophrenia sample. *Psychiatry Res* 2008;161:275-83.
6. Carrillo JA et al. Role of the smoking-induced cytochrome P450 (CYP)1A2 and polymorphic CYP2D6 in steady-state concentration of olanzapine. *J Clin Psychopharmacol* 2003;23:119-27.
7. Hagg S et al. Olanzapine disposition in humans is unrelated to CYP1A2 and CYP2D6 phenotypes. *Eur J Clin Pharmacol* 2001;57:493-7.

Date 13-09-2021

CYP2D6 UM: olanzapine

[2408](#)

This is NOT a gene-drug interaction.

Literature:

1. Zubiaur P et al. Impact of polymorphisms in transporter and metabolizing enzyme genes on olanzapine pharmacokinetics and safety in healthy volunteers. *Biomed Pharmacother* 2021;133:111087.
2. Cabaleiro T et al. Polymorphisms influencing olanzapine metabolism and adverse effects in healthy subjects. *Hum Psychopharmacol* 2013;28:205-14.
3. Skogh E et al. High correlation between serum and cerebrospinal fluid olanzapine concentrations in patients with schizophrenia or schizoaffective disorder medicating with oral olanzapine as the only antipsychotic drug. *J Clin Psychopharmacol* 2011;31:4-9.

Date 13-09-2021

CYP2C19 IM: omeprazol

2505

NO action is required for this gene-drug interaction.

The higher plasma concentration of omeprazole results in an increase in the therapeutic effectiveness, without an increase in the side effects.

Literature:

1. Park S et al. Effects of CYP2C19 genetic polymorphisms on PK/PD responses of omeprazole in Korean healthy volunteers. *J Korean Med Sci* 2017;32:729-736.
2. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of H. pylori infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
3. Wang L et al. Ilaprazole for the treatment of duodenal ulcer: a randomized, double-blind and controlled phase III trial. *Curr Med Res Opin* 2012;28:101-9.
4. Zendejdel N et al. Role of cytochrome P450 2C19 genetic polymorphisms in the therapeutic efficacy of omeprazole in Iranian patients with erosive reflux esophagitis. *Arch Iran Med* 2010;13:406-12.
5. Helsby NA et al. Omeprazole-induced acute interstitial nephritis is not related to CYP2C19 genotype or CYP2C19 phenotype. *Br J Clin Pharmacol* 2010;69:516-9.
6. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
7. Hunfeld NG et al. Effect of CYP2C19 *and* 17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752-60.
8. Ohkusa T et al. Effect of CYP2C19 polymorphism on the safety and efficacy of omeprazole in Japanese patients with recurrent reflux esophagitis. *Aliment Pharmacol Ther* 2005;21:1331-9.
9. Roh HK et al. Omeprazole treatment of Korean patients: effects on gastric pH and gastrin release in relation to CYP2C19 geno- and phenotypes. *Basic Clin Pharmacol Toxicol* 2004;95:112-9.
10. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
11. Sagar M et al. Effects of omeprazole on intragastric pH and plasma gastrin are dependent on the CYP2C19 polymorphism. *Gastroenterology* 2000;119:670-6.
12. Furuta T et al. CYP2C19 genotype status and effect of omeprazole on intragastric pH in humans. *Clin Pharmacol Ther* 1999;65:552-61.
13. Shimatani T et al. Effect of omeprazole 10 mg on intragastric pH in three different CYP2C19 genotypes, compared with omeprazole 20 mg and lafutidine 20 mg, a new H₂-receptor antagonist. *Aliment Pharmacol Ther* 2003;18:1149-1157.
14. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.
15. Sugimoto M et al. Initial 48-hour acid inhibition by intravenous infusion of omeprazole, famotidine, or both in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2006;80:539-48.
16. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
17. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for Helicobacter pylori eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
18. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of Helicobacter pylori by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.
19. Gawronska-Szklarz B et al. Effect of CYP2C19 and MDR1 polymorphisms on cure rate in patients with acid-related disorders with Helicobacter pylori infection. *Eur J Clin Pharmacol* 2005;61:375-9.
20. Sheu BS et al. Esomeprazole 40 mg twice daily in triple therapy and the efficacy of Helicobacter pylori eradication related to CYP2C19 metabolism. *Aliment Pharmacol Ther* 2005;21:283-8.
21. Furuta T et al. Polymorphism of interleukin-1 β affects the eradication rates of Helicobacter pylori by triple therapy. *Clin Gastroenterol Hepatol* 2004;2:22-30.
22. Sapone A et al. The clinical role of cytochrome p450 genotypes in Helicobacter pylori management. *Am J Gastroenterol* 2003;98:1010-5.
23. Miwa H et al. Clarithromycin resistance, but not CYP2C-19 polymorphism, has a major impact on

treatment success in 7-day treatment regimen for cure of *H. pylori* infection: a multiple logistic regression analysis. *Dig Dis Sci* 2001;46:2445-50.

24. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for *Helicobacter pylori* infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxicillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
25. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for *Helicobacter pylori* infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. *Clin Pharmacol Ther* 2001;69:158-68.
26. Aoyama N et al. Sufficient effect of 1-week omeprazole and amoxicillin dual treatment for *Helicobacter pylori* eradication in cytochrome P450 2C19 poor metabolizers. *J Gastroenterol* 1999;34 Suppl 11:80-3.
27. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
28. Hu XP et al. Effects of CYP2C19 genetic polymorphism on the pharmacokinetics and pharmacodynamics of omeprazole in Chinese people. *J Clin Pharm Ther* 2007;32:517- 24.
29. SmPC Prilosec (VS).

Date 05-03-2018

CYP2C19 PM: omeprazol

[2506](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of omeprazole results in an increase in the therapeutic effectiveness, without an increase in the side effects.

Literature:

1. Park S et al. Effects of CYP2C19 genetic polymorphisms on PK/PD responses of omeprazole in Korean healthy volunteers. *J Korean Med Sci* 2017;32:729-736.
2. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
3. Wang L et al. Ilaprazole for the treatment of duodenal ulcer: a randomized, double-blind and controlled phase III trial. *Curr Med Res Opin* 2012;28:101-9.
4. Helsby NA et al. Omeprazole-induced acute interstitial nephritis is not related to CYP2C19 genotype or CYP2C19 phenotype. *Br J Clin Pharmacol* 2010;69:516-9.
5. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
6. Ohkusa T et al. Effect of CYP2C19 polymorphism on the safety and efficacy of omeprazole in Japanese patients with recurrent reflux esophagitis. *Aliment Pharmacol Ther* 2005;21:1331-9.
7. Roh HK et al. Omeprazole treatment of Korean patients: effects on gastric pH and gastrin release in relation to CYP2C19 geno- and phenotypes. *Basic Clin Pharmacol Toxicol* 2004;95:112-9.
8. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
9. Sagar M et al. Effects of omeprazole on intragastric pH and plasma gastrin are dependent on the CYP2C19 polymorphism. *Gastroenterology* 2000;119:670-6.
10. Furuta T et al. CYP2C19 genotype status and effect of omeprazole on intragastric pH in humans. *Clin Pharmacol Ther* 1999;65:552-61.
11. Shimatani T et al. Effect of omeprazole 10 mg on intragastric pH in three different CYP2C19 genotypes, compared with omeprazole 20 mg and lafutidine 20 mg, a new H₂-receptor antagonist. *Aliment Pharmacol Ther* 2003;18:1149–1157.
12. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.
13. Sugimoto M et al. Initial 48-hour acid inhibition by intravenous infusion of omeprazole, famotidine, or both in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2006;80:539-48.
14. Ji S et al. Comparison of the efficacy of rabeprazole 10 mg and omeprazole 20 mg for the healing rapidity of peptic ulcer diseases. *J Gastroenterol Hepatol* 2006;21:1381- 7.
15. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
16. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
17. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of *Helicobacter pylori* by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.
18. Sheu BS et al. Esomeprazole 40 mg twice daily in triple therapy and the efficacy of *Helicobacter pylori* eradication related to CYP2C19 metabolism. *Aliment Pharmacol Ther* 2005;21:283-8.
19. Furuta T et al. Polymorphism of interleukin-1beta affects the eradication rates of *Helicobacter pylori* by triple therapy. *Clin Gastroenterol Hepatol* 2004;2:22-30.
20. Sapone A et al. The clinical role of cytochrome p450 genotypes in *Helicobacter pylori* management. *Am J Gastroenterol* 2003;98:1010-5.

21. Miwa H et al. Clarithromycin resistance, but not CYP2C19 polymorphism, has a major impact on treatment success in 7-day treatment regimen for cure of H. pylori infection: a multiple logistic regression analysis. *Dig Dis Sci* 2001;46:2445-50.
22. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for Helicobacter pylori infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxicillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
23. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for Helicobacter pylori infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. *Clin Pharmacol Ther* 2001;69:158-68.
24. Tanigawara Y et al. CYP2C19 genotype-related efficacy of omeprazole for the treatment of infection caused by Helicobacter pylori. *Clin Pharmacol Ther* 1999;66:528-34.
25. Aoyama N et al. Sufficient effect of 1-week omeprazole and amoxicillin dual treatment for Helicobacter pylori eradication in cytochrome P450 2C19 poor metabolizers. *J Gastroenterol* 1999;34 Suppl 11:80-3.
26. Inaba T et al. Helicobacter pylori infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
27. Hu XP et al. Effects of CYP2C19 genetic polymorphism on the pharmacokinetics and pharmacodynamics of omeprazole in Chinese people. *J Clin Pharm Ther* 2007;32:517- 24.
28. SmPC's Losec en Prilosec (VS).

Date 05-03-2018

CYP2C19 UM: omeprazol

[2507](#)

The genetic variation may lead to a reduced omeprazole plasma concentration and therefore reduced effectiveness.

Recommendation:

- For Helicobacter pylori ERADICATION THERAPY:
 - use a 3-fold higher dose
 - advise the patient to contact their doctor if symptoms of dyspepsia persist
- OTHER INDICATIONS:
 - be alert to reduced effectiveness
 - if necessary, use a 3-fold higher dose
 - advise the patient to report persisting symptoms of dyspepsia

Literature:

1. Park S et al. Effects of CYP2C19 genetic polymorphisms on PK/PD responses of omeprazole in Korean healthy volunteers. *J Korean Med Sci* 2017;32:729-736.
2. Chwiesko A et al. Effects of different omeprazole dosing on gastric pH in non-variceal upper gastrointestinal bleeding: a randomized prospective study. *J Dig Dis* 2016;17:588-599.
3. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of H. pylori infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
4. Dury S et al. Agranulocytosis induced by proton pump inhibitors. *J Clin Gastroenterol* 2012;46:859.
5. Wang L et al. Ilaprazole for the treatment of duodenal ulcer: a randomized, double-blind and controlled phase III trial. *Curr Med Res Opin* 2012;28:101-9.
6. Zendehdel N et al. Role of cytochrome P450 2C19 genetic polymorphisms in the therapeutic efficacy of omeprazole in Iranian patients with erosive reflux esophagitis. *Arch Iran Med* 2010;13:406-12.
7. Hellsby NA et al. Omeprazole-induced acute interstitial nephritis is not related to CYP2C19 genotype or CYP2C19 phenotype. *Br J Clin Pharmacol* 2010;69:516-9.
8. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
9. Hunfeld NG et al. Effect of CYP2C19*2 and 17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752-60.
10. Ohkusa T et al. Effect of CYP2C19 polymorphism on the safety and efficacy of omeprazole in Japanese patients with recurrent reflux esophagitis. *Aliment Pharmacol Ther* 2005;21:1331-9.
11. Roh HK et al. Omeprazole treatment of Korean patients: effects on gastric pH and gastrin release in relation to CYP2C19 geno- and phenotypes. *Basic Clin Pharmacol Toxicol* 2004;95:112-9.
12. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
13. Sagar M et al. Effects of omeprazole on intragastric pH and plasma gastrin are dependent on the CYP2C19 polymorphism. *Gastroenterology* 2000;119:670-6.
14. Furuta T et al. CYP2C19 genotype status and effect of omeprazole on intragastric pH in humans. *Clin Pharmacol Ther* 1999;65:552-61.
15. Shimatani T et al. Effect of omeprazole 10 mg on intragastric pH in three different CYP2C19 genotypes, compared with omeprazole 20 mg and lafutidine 20 mg, a new H₂-receptor antagonist. *Aliment Pharmacol Ther* 2003;18:1149-1157.
16. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.

17. Sugimoto M et al. Initial 48-hour acid inhibition by intravenous infusion of omeprazole, famotidine, or both in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2006;80:539-48.
18. Ji S et al. Comparison of the efficacy of rabeprazole 10 mg and omeprazole 20 mg for the healing rapidity of peptic ulcer diseases. *J Gastroenterol Hepatol* 2006;21:1381- 7.
19. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
20. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
21. Sugimoto M et al. Influences of proinflammatory and anti-inflammatory cytokine polymorphisms on eradication rates of clarithromycin-sensitive strains of *Helicobacter pylori* by triple therapy. *Clin Pharmacol Ther* 2006;80:41-50.
22. Gawronska-Szklarz B et al. Effect of CYP2C19 and MDR1 polymorphisms on cure rate in patients with acid-related disorders with *Helicobacter pylori* infection. *Eur J Clin Pharmacol* 2005;61:375-9.
23. Sheu BS et al. Esomeprazole 40 mg twice daily in triple therapy and the efficacy of *Helicobacter pylori* eradication related to CYP2C19 metabolism. *Aliment Pharmacol Ther* 2005;21:283-8.
24. Furuta T et al. Polymorphism of interleukin-1beta affects the eradication rates of *Helicobacter pylori* by triple therapy. *Clin Gastroenterol Hepatol* 2004;2:22-30.
25. Sapone A et al. The clinical role of cytochrome p450 genotypes in *Helicobacter pylori* management. *Am J Gastroenterol* 2003;98:1010-5.
26. Miwa H et al. Clarithromycin resistance, but not CYP2C-19 polymorphism, has a major impact on treatment success in 7-day treatment regimen for cure of *H. pylori* infection: a multiple logistic regression analysis. *Dig Dis Sci* 2001;46:2445-50.
27. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for *Helicobacter pylori* infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxicillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
28. Furuta T et al. Effect of genotypic differences in CYP2C19 on cure rates for *Helicobacter pylori* infection by triple therapy with a proton pump inhibitor, amoxicillin, and clarithromycin. *Clin Pharmacol Ther* 2001;69:158-68.
29. Tanigawara Y et al. CYP2C19 genotype-related efficacy of omeprazole for the treatment of infection caused by *Helicobacter pylori*. *Clin Pharmacol Ther* 1999;66:528-34.
30. Aoyama N et al. Sufficient effect of 1-week omeprazole and amoxicillin dual treatment for *Helicobacter pylori* eradication in cytochrome P450 2C19 poor metabolizers. *J Gastroenterol* 1999;34 Suppl 11:80-3.
31. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
32. Rocha A et al. Investigation of the in vivo activity of CYP3A in Brazilian volunteers: comparison of midazolam and omeprazole as drug markers. *Eur J Clin Pharmacol* 2008;64:901-6.
33. Baldwin RM et al. Increased omeprazole metabolism in carriers of the CYP2C19*17 allele; a pharmacokinetic study in healthy volunteers. *Br J Clin Pharmacol* 2008;65:767-74.
34. Hu XP et al. Effects of CYP2C19 genetic polymorphism on the pharmacokinetics and pharmacodynamics of omeprazole in Chinese people. *J Clin Pharm Ther* 2007;32:517- 24.
35. Sim SC et al. A common novel CYP2C19 gene variant causes ultrarapid drug metabolism relevant for the drug response to proton pump inhibitors and antidepressants. *Clin Pharmacol Ther* 2006;79:103-13.
36. SmPC's Losec en Prilosec (VS).

Date 05-03-2018

HLA-B*1502: oxcarbazepine

6400

Stevens-Johnson syndrome, the severe cutaneous side effect that can potentially result in permanent damage, occurs more often in patients with this genetic variation. The calculated risk of oxcarbazepine-induced SJS in patients with HLA-B*1502 is 0.73%.

- carefully weigh the risk of SJS against the benefits
- avoid oxcarbazepine if an alternative is available

Carbamazepine carries a 10-fold higher risk of SJS/TEN in these patients and is therefore not an alternative.

In these patients, phenytoin and lamotrigine carry a similar risk of SJS/TEN as oxcarbazepine, but more severe forms of SJS/TEN (SJS/TEN overlap and TEN) are also observed with these medicines.

Therefore, they are also not suitable as alternatives.

- if it is not possible to avoid oxcarbazepine, advise the patient to report any rash immediately

Literature:

1. Lee KH et al. Reducing severe cutaneous adverse and type B adverse drug reactions using pre-stored human leukocyte antigen genotypes. *Clin Transl Allergy* 2022;12:e12098.
2. Sukasem C et al. Spectrum of cutaneous adverse reactions to aromatic antiepileptic drugs and human leukocyte antigen genotypes in Thai patients and meta-analysis. *Pharmacogenomics J* 2021;21:682-90.
3. Liu H et al. Association of the HLA-B*15:02 allele with pure cervical lymphadenopathy induced by

carbamazepine and oxcarbazepine: a case report and literature review. *Basic Clin Pharmacol Toxicol* 2021;128:348-51.

4. Liu Y et al. Association between HLA-B*15:02 and oxcarbazepine-induced cutaneous adverse reaction: a meta-analysis. *Pharmacogenomics* 2018;19:547-52.
5. Tangamornsuksan W et al. Association between HLA genotypes and oxcarbazepine-induced cutaneous adverse drug reactions: a systematic review and meta-analysis. *J Pharm Pharm Sci* 2018;21:1-18.
6. Chen CB et al. Risk and association of HLA with oxcarbazepine-induced cutaneous adverse reactions in Asians. *Neurology* 2017;88:78-86.
7. Sun D et al. Association of HLA-B*1502 and *1511 allele with antiepileptic drug-induced Stevens-Johnson syndrome in central China. *J Huazhong Univ Sci Technolog Med Sci* 2014;34:146-50.
8. Amstutz U et al. HLA-A*31:01 and HLA-B*15:02 as genetic markers for carbamazepine hypersensitivity in children. *Clin Pharmacol Ther* 2013;94:142-9.
9. Wal P et al. Genetic predisposition to oxcarbazepine induced Stevens-Johnson syndrome. *Indian J Crit Care Med* 2011;15:173-5.
10. Hung SI et al. Common risk allele in aromatic antiepileptic-drug induced Stevens-Johnson syndrome and toxic epidermal necrolysis in Han Chinese. *Pharmacogenomics* 2010;11:349-56.
11. Shankarkumar U et al. HLA B*1502 allele association with oxcarbamazepine-induced skin reactions in epilepsy patient from India. *Epilepsia* 2009;50:1837-8.
12. Lin LC et al. Oxcarbazepine-induced Stevens-Johnson syndrome: a case report. *Kaohsiung J Med Sci* 2009;25:82-6.
13. SmPC's Trileptal (NL) en Oxtellar XR (VS).

Date 23-05-2022

CYP2D6 IM: oxycodon

[2418](#)

NO action is required for this gene-drug interaction.

The reduced conversion of oxycodone to the more active metabolite oxymorphone does not result in reduced analgesia for patients.

Literature:

1. Cajanus K et al. Analgesic plasma concentrations of oxycodone after surgery for breast cancer-which factors matter? *Clin Pharmacol Ther* 2017 Jun 23 [Epub ahead of print].
2. Stamer UM et al. CYP2D6 genotype dependent oxycodone metabolism in postoperative patients. *PloS One* 2013;8:e60239.
3. Naito T et al. CYP3A5*3 affects plasma disposition of noroxycodone and dose escalation in cancer patients receiving oxycodone. *J Clin Pharmacol* 2011;51:1529-38.
4. Lemberg KK et al. Does co-administration of paroxetine change oxycodone analgesia: an interaction study in chronic pain patients. *Scan Jour Pain* 2010;1;24-33.
5. Comer SD et al. Abuse liability of oxycodone as a function of pain and drug use history. *Drug Alcohol Depend* 2010;109:130-8.
6. Jannetto PJ et al. Utilization of pharmacogenomics and therapeutic drug monitoring for opioid pain management. *Pharmacogenomics* 2009;10:1157-67.

Date 20-11-2017

CYP2D6 PM: oxycodon

[2417](#)

NO action is required for this gene-drug interaction.

The reduced conversion of oxycodone to the more active metabolite oxymorphone does not result in reduced analgesia in patients.

Literature:

1. Cajanus K et al. Analgesic plasma concentrations of oxycodone after surgery for breast cancer-which factors matter? *Clin Pharmacol Ther* 2017 Jun 23 [Epub ahead of print].
2. Lam J et al. Putative association of ABCB1 2677G>T/A with oxycodone-induced central nervous system depression in breastfeeding mothers. *Ther Drug Monit* 2013;35:466-72.
3. Stamer UM et al. CYP2D6 genotype dependent oxycodone metabolism in postoperative patients. *PloS One* 2013;8:e60239.
4. Andreassen TN et al. Do CYP2D6 genotypes reflect oxycodone requirements for cancer patients treated for cancer pain? A cross-sectional multicentre study. *Eur J Clin Pharmacol* 2012;68:55-64.
5. Zwisler ST et al. Impact of CYP2D6 genotype on post-operative intravenous oxycodone analgesia. *Acta Anaesthesiol Scan* 2010;54:232-40.
6. Samer CF et al. Genetic polymorphisms and drug interactions modulating CYP2D6 and CYP3A activities have a major effect on oxycodone analgesic efficacy and safety. *Br J Pharmacol* 2010;16:919-30.

7. Comer SD et al. Abuse liability of oxycodone as a function of pain and drug use history. *Drug Alcohol Depend* 2010;109:130-8.
8. Jannetto PJ et al. Utilization of pharmacogenomics and therapeutic drug monitoring for opioid pain management. *Pharmacogenomics* 2009;10:1157-67.
9. Zwisler ST et al. The hypoalgesic effect of oxycodone in human experimental pain models in relation to the CYP2D6 oxidation polymorphism. *Basic Clin Pharmacol Toxicol* 2009;104:335-44.
10. Foster A et al. Complicated pain management in a CYP450 2D6 poor metabolizer. *Pain Pract* 2007;7:352-6.
11. Susce MT et al. Response to hydrocodone, codeine and oxycodone in a CYP2D6 poor metabolizer. *Prog Neuropsychopharmacol Biol Psychiatry* 2006;30:1356-8.
12. Maddocks I et al. Attenuation of morphine-induced delirium in palliative care by substitution with infusion of oxycodone. *J Pain Symptom Manage* 1996;12:182-9.

CYP2D6 UM: oxycodon

[2419](#)

NO action is required for this gene-drug interaction.

The increased conversion of oxycodone to the more active metabolite oxymorphone does not result in an increase in side effects in patients.

Literature:

1. Cajanus K et al. Analgesic plasma concentrations of oxycodone after surgery for breast cancer-which factors matter? Clin Pharmacol Ther 2017 Jun 23 [Epub ahead of print].
2. Lam J et al. Putative association of ABCB1 2677G>T/A with oxycodone-induced central nervous system depression in breastfeeding mothers. Ther Drug Monit 2013;35:466-72.
3. Stamer UM et al. CYP2D6 genotype dependent oxycodone metabolism in postoperative patients. PloS One 2013;8:e60239.
4. Andreassen TN et al. Do CYP2D6 genotypes reflect oxycodone requirements for cancer patients treated for cancer pain? A cross-sectional multicentre study. Eur J Clin Pharmacol 2012;68:55-64.
5. Lemberg KK et al. Does co-administration of paroxetine change oxycodone analgesia: an interaction study in chronic pain patients. Scan Jour Pain 2010;1;24-33.
6. Samer CF et al. Genetic polymorphisms and drug interactions modulating CYP2D6 and CYP3A activities have a major effect on oxycodone analgesic efficacy and safety. Br J Pharmacol 2010;16:919-30.
7. de Leon J et al. Adverse drug reactions to oxycodone and hydrocodone in CYP2D6 ultrarapid metabolizers. J Clin Psychopharmacol 2003;23:420-1.

Date 20-11-2017

CYP3A4 IM: paclitaxel

[7050](#)

NO action is required for this gene-drug interaction.

The genetic variation has a slight effect on the metabolism of paclitaxel, and there is insufficient evidence of an increase in adverse events or reduced efficacy.

Literature:

1. Lam SW et al. Genotypes of CYP2C8 and FGD4 and their association with peripheral neuropathy or early dose reduction in paclitaxel-treated breast cancer patients. Br J Cancer 2016;115:1335-42.
2. Apellániz-Ruiz M et al. Whole-exome sequencing reveals defective CYP3A4 variants predictive of paclitaxel dose-limiting neuropathy. Clin Cancer Res 2015;21:322-8.
3. Assis J et al. Influence of CYP3A4 genotypes in the outcome of serous ovarian cancer patients treated with first-line chemotherapy: implication of a CYP3A4 activity profile. Int J Clin Exp Med 2013;6:552-61.
4. de Graan AJ et al. CYP3A4*22 genotype and systemic exposure affect paclitaxel-induced neurotoxicity. Clin Cancer Res 2013;19:3316-24.
5. Nakajima Y et al. Impact of the haplotype CYP3A4*16B harboring the Thr185Ser substitution on paclitaxel metabolism in Japanese patients with cancer. Clin Pharmacol Ther 2006;80:179-91.
6. Nakajima M et al. Pharmacokinetics of paclitaxel in ovarian cancer patients and genetic polymorphisms of CYP2C8, CYP3A4, and MDR1. J Clin Pharmacol 2005;45: 674- 82.

Date 04-11-2019

CYP3A4 PM: paclitaxel

[7051](#)

NO action is required for this gene-drug interaction.

The genetic variation has a slight effect on the metabolism of paclitaxel, and there is insufficient evidence of an increase in adverse events or reduced efficacy.

Literature:

1. Lam SW et al. Genotypes of CYP2C8 and FGD4 and their association with peripheral neuropathy or early dose reduction in paclitaxel-treated breast cancer patients. Br J Cancer 2016;115:1335-42.
2. Assis J et al. Influence of CYP3A4 genotypes in the outcome of serous ovarian cancer patients treated with first-line chemotherapy: implication of a CYP3A4 activity profile. Int J Clin Exp Med 2013;6:552-61.
3. de Graan AJ et al. CYP3A4*22 genotype and systemic exposure affect paclitaxel-induced neurotoxicity. Clin Cancer Res 2013;19:3316-24.

CYP2C19 IM: pantoprazol[2508](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of pantoprazole results in an increase in the therapeutic effectiveness, without an increase in the side effects.

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Ormeci A et al. Effect of cytochrome P450 2C19 polymorphisms on the *Helicobacter pylori* eradication rate following two-week triple therapy with pantoprazole or rabeprazole. *Eur Rev Med Pharmacol Sci* 2016;20:879-85.
3. Hsu PI et al. A randomized controlled study comparing reverse hybrid therapy and standard triple therapy for *Helicobacter pylori* infection. *Medicine (Baltimore)* 2015;94:e2104.
4. Román M et al. Evaluation of the relationship between polymorphisms in CYP2C19 and the pharmacokinetics of omeprazole, pantoprazole and rabeprazole. *Pharmacogenomics* 2014;15:1893-901.
5. Gawrońska-Szklarz B et al. CYP2C19 polymorphism affects single-dose pharmacokinetics of oral pantoprazole in healthy volunteers. *Eur J Clin Pharmacol* 2012;68:1267- 74.
6. Sheu BS et al. CYP2C19 genotypes determine the efficacy of on-demand therapy of pantoprazole for reflux esophagitis as Los-Angeles grades C and D. *J Gastroenterol Hepatol* 2012;27:104-9.
7. Thacker DL et al. Stereoselective pharmacokinetics of stable isotope (+/-)-[13C]-pantoprazole: Implications for a rapid screening phenotype test of CYP2C19 activity. *Chirality* 2011;23:904-9.
8. Chen WY et al. Double-dosed pantoprazole accelerates the sustained symptomatic response in overweight and obese patients with reflux esophagitis in Los Angeles grades A and B. *Am J Gastroenterol* 2010;105:1046-52.
9. Gawrońska-Szklarz B et al. Effects of CYP2C19, MDR1, and interleukin 1-B gene variants on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxicillin, and metronidazole. *Eur J Clin Pharmacol* 2010;66:681-7.
10. Hunfeld NG et al. A comparison of the acid-inhibitory effects of esomeprazole and pantoprazole in relation to pharmacokinetics and CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2010;31:150-9.
11. Hunfeld NG et al. Effect of CYP2C19 2 and 17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752- 60.
12. Choi KD et al. Optimal dose of intravenous pantoprazole in patients with peptic ulcer bleeding requiring endoscopic hemostasis in Korea. *J Gastroenterol Hepatol* 2009;24:1617-24.
13. Oh JH et al. Low-dose intravenous pantoprazole for optimal inhibition of gastric acid in Korean patients. *J Gastroenterol Hepatol* 2007;22:1429-34.
14. Oh JH et al. Effects of CYP2C19 and MDR1 genotype on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxycillin and clarithromycin. *J Gastroenterol Hepatol* 2009;24:294-8.
15. Kang JM et al. Effect of the CYP2C19 polymorphism on the eradication rate of *Helicobacter pylori* infection by 7-day triple therapy with regular proton pump inhibitor dosage. *J Gastroenterol Hepatol* 2008;23:1287-91.
16. Kurzawski M et al. Effect of CYP2C19*17 gene variant on *Helicobacter pylori* eradication in peptic ulcer patients. *Eur J Clin Pharmacol* 2006;62:877-80.
17. Gawronska-Szklarz B et al. Effect of CYP2C19 and MDR1 polymorphisms on cure rate in patients with acid-related disorders with *Helicobacter pylori* infection. *Eur J Clin Pharmacol* 2005;61:375-9.
18. Kearns GL et al. Single-dose pharmacokinetics of oral and intravenous pantoprazole in children and adolescents. *J Clin Pharmacol* 2008;48:1356-65.

Date 05-03-2018

CYP2C19 PM: pantoprazol[2509](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of pantoprazole results in an increase in the therapeutic effectiveness, without an increase in the side effects.

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Ormeci A et al. Effect of cytochrome P450 2C19 polymorphisms on the *Helicobacter pylori* eradication

rate following two-week triple therapy with pantoprazole or rabeprazole. *Eur Rev Med Pharmacol Sci* 2016;20:879-85.

3. Hsu PI et al. A randomized controlled study comparing reverse hybrid therapy and standard triple therapy for *Helicobacter pylori* infection. *Medicine (Baltimore)* 2015;94:e2104.
4. Gawrońska-Szklarz B et al. CYP2C19 polymorphism affects single-dose pharmacokinetics of oral pantoprazole in healthy volunteers. *Eur J Clin Pharmacol* 2012;68:1267- 74.
5. Sheu BS et al. CYP2C19 genotypes determine the efficacy of on-demand therapy of pantoprazole for reflux esophagitis as Los-Angeles grades C and D. *J Gastroenterol Hepatol* 2012;27:104-9.
6. Thacker DL et al. Stereoselective pharmacokinetics of stable isotope (+/-)-[13C]-pantoprazole: Implications for a rapid screening phenotype test of CYP2C19 activity. *Chirality* 2011;23:904-9.
7. Chen WY et al. Double-dosed pantoprazole accelerates the sustained symptomatic response in overweight and obese patients with reflux esophagitis in Los Angeles grades A and B. *Am J Gastroenterol* 2010;105:1046-52.
8. Gawrońska-Szklarz B et al. Effects of CYP2C19, MDR1, and interleukin 1-B gene variants on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxicillin, and metronidazole. *Eur J Clin Pharmacol* 2010;66:681-7.
9. Tseng PH et al. A comparative study of proton-pump inhibitor tests for Chinese reflux patients in relation to the CYP2C19 genotypes. *J Clin Gastroenterol* 2009;43:920-5.
10. Hunfeld NG et al. Effect of CYP2C19 2 and 17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752- 60.
11. Choi KD et al. Optimal dose of intravenous pantoprazole in patients with peptic ulcer bleeding requiring endoscopic hemostasis in Korea. *J Gastroenterol Hepatol* 2009;24:1617-24.
12. Oh JH et al. Low-dose intravenous pantoprazole for optimal inhibition of gastric acid in Korean patients. *J Gastroenterol Hepatol* 2007;22:1429-34.
13. Oh JH et al. Effects of CYP2C19 and MDR1 genotype on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxycillin and clarithromycin. *J Gastroenterol Hepatol* 2009;24:294-8.
14. Kang JM et al. Effect of the CYP2C19 polymorphism on the eradication rate of *Helicobacter pylori* infection by 7-day triple therapy with regular proton pump inhibitor dosage. *J Gastroenterol Hepatol* 2008;23:1287-91.
15. Kurzawski M et al. Effect of CYP2C19*17 gene variant on *Helicobacter pylori* eradication in peptic ulcer patients. *Eur J Clin Pharmacol* 2006;62:877-80.
16. Kearns GL et al. Single-dose pharmacokinetics of oral and intravenous pantoprazole in children and adolescents. *J Clin Pharmacol* 2008;48:1356-65.
17. SPC's Pantozol en Protonix I.V. (VS).

Date 05-03-2018

CYP2C19 UM: pantoprazol

[2510](#)

The genetic variation may lead to reduced pantoprazole plasma concentrations and therefore reduced pantoprazole effectiveness.

Recommendation:

- For *Helicobacter pylori* ERADICATION THERAPY:
 - use a 5-fold higher dose
 - advise the patient to contact their doctor if symptoms of dyspepsia persist
- OTHER INDICATIONS:
 - be alert to reduced effectiveness
 - if necessary, use a 5-fold higher dose
 - advise the patient to report persisting symptoms of dyspepsia

Literature:

1. Deshpande N et al. Rapid and ultra-rapid metabolizers with CYP2C19*17 polymorphism do not respond to standard therapy with proton pump inhibitors. *Meta Gene* 2016;9:159-64.
2. Ormeci A et al. Effect of cytochrome P450 2C19 polymorphisms on the *Helicobacter pylori* eradication rate following two-week triple therapy with pantoprazole or rabeprazole. *Eur Rev Med Pharmacol Sci* 2016;20:879-85.
3. Hsu PI et al. A randomized controlled study comparing reverse hybrid therapy and standard triple therapy for *Helicobacter pylori* infection. *Medicine (Baltimore)* 2015;94:e2104.
4. Román M et al. Evaluation of the relationship between polymorphisms in CYP2C19 and the pharmacokinetics of omeprazole, pantoprazole and rabeprazole. *Pharmacogenomics* 2014;15:1893-901.
5. Gawrońska-Szklarz B et al. CYP2C19 polymorphism affects single-dose pharmacokinetics of oral pantoprazole in healthy volunteers. *Eur J Clin Pharmacol* 2012;68:1267- 74.
6. Sheu BS et al. CYP2C19 genotypes determine the efficacy of on-demand therapy of pantoprazole for reflux esophagitis as Los-Angeles grades C and D. *J Gastroenterol Hepatol* 2012;27:104-9.

7. Thacker DL et al. Stereoselective pharmacokinetics of stable isotope (+/-)-[13C]-pantoprazole: Implications for a rapid screening phenotype test of CYP2C19 activity. *Chirality* 2011;23:904-9.
8. Chen WY et al. Double-dosed pantoprazole accelerates the sustained symptomatic response in overweight and obese patients with reflux esophagitis in Los Angeles grades A and B. *Am J Gastroenterol* 2010;105:1046-52.
9. Gawrońska-Szklarz B et al. Effects of CYP2C19, MDR1, and interleukin 1-B gene variants on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxicillin, and metronidazole. *Eur J Clin Pharmacol* 2010;66:681-7.
10. Hunfeld NG et al. A comparison of the acid-inhibitory effects of esomeprazole and pantoprazole in relation to pharmacokinetics and CYP2C19 polymorphism. *Aliment Pharmacol Ther* 2010;31:150-9.
11. Tseng PH et al. A comparative study of proton-pump inhibitor tests for Chinese reflux patients in relation to the CYP2C19 genotypes. *J Clin Gastroenterol* 2009;43:920-5.
12. Hunfeld NG et al. Effect of CYP2C19*2 and *17 mutations on pharmacodynamics and kinetics of proton pump inhibitors in Caucasians. *Br J Clin Pharmacol* 2008;65:752-60.
13. Choi KD et al. Optimal dose of intravenous pantoprazole in patients with peptic ulcer bleeding requiring endoscopic hemostasis in Korea. *J Gastroenterol Hepatol* 2009;24:1617-24.
14. Oh JH et al. Low-dose intravenous pantoprazole for optimal inhibition of gastric acid in Korean patients. *J Gastroenterol Hepatol* 2007;22:1429-34.
15. Oh JH et al. Effects of CYP2C19 and MDR1 genotype on the eradication rate of *Helicobacter pylori* infection by triple therapy with pantoprazole, amoxycillin and clarithromycin. *J Gastroenterol Hepatol* 2009;24:294-8.
16. Kang JM et al. Effect of the CYP2C19 polymorphism on the eradication rate of *Helicobacter pylori* infection by 7-day triple therapy with regular proton pump inhibitor dosage. *J Gastroenterol Hepatol* 2008;23:1287-91.
17. Kurzawski M et al. Effect of CYP2C19*17 gene variant on *Helicobacter pylori* eradication in peptic ulcer patients. *Eur J Clin Pharmacol* 2006;62:877-80.
18. Gawronska-Szklarz B et al. Effect of CYP2C19 and MDR1 polymorphisms on cure rate in patients with acid-related disorders with *Helicobacter pylori* infection. *Eur J Clin Pharmacol* 2005;61:375-9.
19. Kearns GL et al. Single-dose pharmacokinetics of oral and intravenous pantoprazole in children and adolescents. *J Clin Pharmacol* 2008;48:1356-65.
20. SPC's Pantozol en Protonix I.V. (VS).

Date 05-03-2018

CYP2D6 IM: paroxetine

[2409](#)

NO action is needed for this gene-drug interaction.

The plasma concentration of paroxetine can increase as a result of the reduced activity of CYP2D6. However, studies did not find any clinical effects.

Literature:

1. Janssen PK et al. Nonresponders to daily paroxetine and another SSRI in men with lifelong premature ejaculation: a pharmacokinetic dose-escalation study for a rare phenomenon. *Korean J Urol* 2014;55:599-607.
2. Saruwatari J et al. Possible impact of the CYP2D6*10 polymorphism on the nonlinear pharmacokinetic parameter estimates of paroxetine in Japanese patients with major depressive disorders. *Pharmgenomics Pers Med* 2014;7:121-7.
3. Murata Y et al. Severe sleepiness and excess sleep duration induced by paroxetine treatment is a beneficial pharmacological effect, not an adverse reaction. *J Affect Disord* 2013;150:1209-12.
4. Murata Y et al. Effects of the serotonin 1A, 2A, 2C, 3A, and 3B and serotonin transporter gene polymorphisms on the occurrence of paroxetine discontinuation syndrome. *J Clin Psychopharmacol* 2010;30:11-7.
5. Ververs FF et al. Effect of cytochrome P450 2D6 genotype on maternal paroxetine plasma concentrations during pregnancy. *Clin Pharmacokinet* 2009;48:677-83.
6. Van Nieuwerburgh FC et al. Response to serotonin reuptake inhibitors in OCD is not influenced by common CYP2D6 polymorphisms. *Int J Psychiatry Clin Pract* 2009;13:345-348.
7. Gex-Fabry M et al. CYP2D6 and ABCB1 genetic variability: influence on paroxetine plasma level and therapeutic response. *Ther Drug Monit* 2008;30:474-82.
8. Kuhn UD et al. Reboxetine and cytochrome P450--comparison with paroxetine treatment in humans. *Int J Clin Pharmacol Ther* 2007;45:36-46.
9. Sugai T et al. The effect of 5-hydroxytryptamine 3A and 3B receptor genes on nausea induced by paroxetine. *Pharmacogenomics J* 2006;6:351-6.
10. Findling RL et al. Multiple dose pharmacokinetics of paroxetine in children and adolescents with major depressive disorder or obsessive-compulsive disorder. *Neuropsychopharmacology* 2006;31:1274-85.
11. Feng Y et al. Paroxetine: population pharmacokinetic analysis in late-life depression using sparse concentration sampling. *Br J Clin Pharmacol* 2006;61:558-69.
12. Ueda M et al. The impact of CYP2D6 genotypes on the plasma concentration of paroxetine in Japanese psychiatric patients. *Prog Neuro-psychopharmacol Biol Psychiatry* 2006;30:486-91.

13. Sawamura K et al. Effects of dosage and CYP2D6-mutated allele on plasma concentration of paroxetine. Eur J Clin Pharmacol 2004;60:553-7.
14. Murphy G et al. Pharmacogenetics of antidepressant medication intolerance. Am J Psychiatry 2003;160:1830-5.
15. Ozdemir V et al. Paroxetine steady-state plasma concentration in relation to CYP2D6 genotype in extensive metabolizers. J Clin Psychopharmacol 1999;19:472-5.

Date 14-05-2018

CYP2D6 PM: paroxetine

[2410](#)

NO action is needed for this gene-drug interaction.

The plasma concentration of paroxetine can increase as a result of the reduced activity of CYP2D6. However, studies did not find any clinical effects.

Literature:

1. Ververs FF et al. Effect of cytochrome P450 2D6 genotype on maternal paroxetine plasma concentrations during pregnancy. Clin Pharmacokinet 2009;48:677-83.
2. Van Nieuwerburgh FC et al. Response to serotonin reuptake inhibitors in OCD is not influenced by common CYP2D6 polymorphisms. Int J Psychiatry Clin Pract 2009;13:345-348.
3. Gex-Fabry M et al. CYP2D6 and ABCB1 genetic variability: influence on paroxetine plasma level and therapeutic response. Ther Drug Monit 2008;30:474-82.
4. Kuhn UD et al. Reboxetine and cytochrome P450--comparison with paroxetine treatment in humans. Int J Clin Pharmacol Ther 2007;45:36-46.
5. Findling RL et al. Multiple dose pharmacokinetics of paroxetine in children and adolescents with major depressive disorder or obsessive-compulsive disorder. Neuropsychopharmacology 2006;31:1274-85.
6. Feng Y et al. Paroxetine: population pharmacokinetic analysis in late-life depression using sparse concentration sampling. Br J Clin Pharmacol 2006;61:558-69.
7. Sawamura K et al. Effects of dosage and CYP2D6-mutated allele on plasma concentration of paroxetine. Eur J Clin Pharmacol 2004;60:553-7.
8. Charlier C et al. Polymorphisms in the CYP 2D6 gene: association with plasma concentrations of fluoxetine and paroxetine. Ther Drug Monit 2003;25:738-42.
9. Murphy G et al. Pharmacogenetics of antidepressant medication intolerance. Am J Psychiatry 2003;160:1830-5.
10. Sindrup SH et al. Pharmacokinetics of the selective serotonin reuptake inhibitor paroxetine: nonlinearity and relation to the sparteine oxidation polymorphism. Clin Pharmacol Ther 1992;51:288-95.
11. Sindrup SH et al. The relationship between paroxetine and the sparteine oxidation polymorphism. Clin Pharmacol Ther 1992;51:278-87.

Date 14-05-2018

CYP2D6 UM: paroxetine

[2411](#)

Efficacy will probably be lacking. The genetic variation increases the conversion of paroxetine.

It is not possible to offer substantiated advice for dose adjustment based on the literature.

- avoid paroxetine

Antidepressants that are not metabolised by CYP2D6, or to a lesser extent, include for example citalopram or sertraline.

Literature:

1. Gex-Fabry M et al. CYP2D6 and ABCB1 genetic variability: influence on paroxetine plasma level and therapeutic response. Ther Drug Monit 2008;30:474-82.
2. Findling RL et al. Multiple dose pharmacokinetics of paroxetine in children and adolescents with major depressive disorder or obsessive-compulsive disorder. Neuropsychopharmacology 2006;31:1274-85.
3. Feng Y et al. Paroxetine: population pharmacokinetic analysis in late-life depression using sparse concentration sampling. Br J Clin Pharmacol 2006;61:558-69.
4. Güzey C et al. Low serum concentrations of paroxetine in CYP2D6 ultrarapid metabolizers. J Clin Psychopharmacol 2006;26:211-2.
5. Charlier C et al. Polymorphisms in the CYP 2D6 gene: association with plasma concentrations of fluoxetine and paroxetine. Ther Drug Monit 2003;25:738-42.
6. Murphy G et al. Pharmacogenetics of antidepressant medication intolerance. Am J Psychiatry 2003;160:1830-5.

Date 14-05-2018

The risk of QT-prolongation – and thereby also the risk of torsade de points – is theoretically increased, because the genetic variation results in an increase in the plasma concentration of pimoziide. The elevated plasma concentration and associated theoretical increased risk of QT elongation can be negated by following the dose recommendations provided below.

- use no more than the following doses (80% of the standard maximum dose):
 - 12 years and older: 16 mg/day
 - younger than 12 years: 0.08 mg/kg per day to a maximum of 3 mg/day

Literature:

1. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimoziide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 en persoonlijke communicatie (gemiddelde dosisgecorrigeerde pimozidedalconcentraties).
2. Nucci G et al. Population pharmacokinetic modelling of pimoziide and its relation to CYP2D6 genotype. Poster presented at the annual meeting of population approach group in Europe 2007.

Date 13-09-2021

The risk of QT-prolongation – and thereby also the risk of torsade de points – is theoretically increased, because the genetic variation results in an increase in the plasma concentration of pimoziide. The elevated plasma concentration and associated theoretical increased risk of QT elongation can be negated by following the dose recommendations provided below.

- use no more than the following doses (50% of the standard maximum dose):
 - 12 years and older: 10 mg/day
 - younger than 12 years: 0.05 mg/kg per day to a maximum of 2 mg/day

Literature:

1. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimoziide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 en persoonlijke communicatie (gemiddelde dosisgecorrigeerde pimozidedalconcentraties).
2. Nucci G et al. Population pharmacokinetic modelling of pimoziide and its relation to CYP2D6 genotype. Poster presented at the annual meeting of population approach group in Europe 2007.
3. Desta Z et al. Effect of clarithromycin on the pharmacokinetics and pharmacodynamics of pimoziide in healthy poor and extensive metabolizers of cytochrome P450 2D6 (CYP2D6). Clin Pharmacol Ther 1999;65:10-20.
4. Pharmacogenetic changes to the FDA-approved Orap (pimoziide) label include adult and pediatric dosing recommendations for CYP2D6 poor metabolizers. FDA- nieuwsbericht 27-09-11.
5. SmPC Orap (NL en VS).

Date 13-09-2021

NO action is required for this gene-drug interaction.

This gene variation can result in lower pimoziide concentrations. However, there is no evidence of reduced effectiveness.

Literature:

1. van der Weide K et al. The influence of the CYP3A4*22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimoziide, and risperidone in psychiatric patients. J Clin Psychopharmacol 2015;35:228-36 en persoonlijke communicatie (gemiddelde dosisgecorrigeerde pimozidedalconcentraties).

Date 13-09-2021

This is NOT a gene-drug interaction.

Literature:

1. Lee CR et al. Clinical outcomes and sustainability of using CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *Circ Genom Precis Med* 2018;11:e002069.
2. Ogawa H et al. Effects of CYP2C19 allelic variants on inhibition of platelet aggregation and major adverse cardiovascular events in Japanese patients with acute coronary syndrome: The PRASFIT-ACS study. *J Cardiol* 2016;68:29-36.
3. Doll JA et al. Impact of CYP2C19 metabolizer status on patients with ACS treated with prasugrel versus clopidogrel. *J Am Coll Cardiol* 2016;67:936-47.
4. Varenhorst C et al. Genetic variation of CYP2C19 affects both pharmacokinetic and pharmacodynamic responses to clopidogrel but not prasugrel in aspirin-treated patients with coronary artery disease. *Eur Heart J* 2009;30:1744-52.
5. Mega JL et al. Cytochrome P450 genetic polymorphisms and the response to prasugrel: relationship to pharmacokinetic, pharmacodynamic, and clinical outcomes. *Circulation* 2009;119:2553-60.
6. Brandt JT et al. Common polymorphisms of CYP2C19 and CYP2C9 affect the pharmacokinetic and pharmacodynamic response to clopidogrel but not prasugrel. *J Thromb Haemost* 2007;5:2429-36.
7. SPC Efient (NL en VS).

Date 19-11-2018

CYP2C19 PM: prasugrel

[2934](#)

This is NOT a gene-drug interaction.

Literature:

1. Lee CR et al. Clinical outcomes and sustainability of using CYP2C19 genotype-guided antiplatelet therapy after percutaneous coronary intervention. *Circ Genom Precis Med* 2018;11:e002069.
2. Deiman BA et al. Reduced number of cardiovascular events and increased cost-effectiveness by genotype-guided antiplatelet therapy in patients undergoing percutaneous coronary interventions in the Netherlands. *Neth Heart J* 2016;24:589-99.
3. Ogawa H et al. Effects of CYP2C19 allelic variants on inhibition of platelet aggregation and major adverse cardiovascular events in Japanese patients with acute coronary syndrome: The PRASFIT-ACS study. *J Cardiol* 2016;68:29-36.
4. Doll JA et al. Impact of CYP2C19 metabolizer status on patients with ACS treated with prasugrel versus clopidogrel. *J Am Coll Cardiol* 2016;67:936-47.
5. Varenhorst C et al. Genetic variation of CYP2C19 affects both pharmacokinetic and pharmacodynamic responses to clopidogrel but not prasugrel in aspirin-treated patients with coronary artery disease. *Eur Heart J* 2009;30:1744-52.
6. Mega JL et al. Cytochrome P450 genetic polymorphisms and the response to prasugrel: relationship to pharmacokinetic, pharmacodynamic, and clinical outcomes. *Circulation* 2009;119:2553-60.
7. Brandt JT et al. Common polymorphisms of CYP2C19 and CYP2C9 affect the pharmacokinetic and pharmacodynamic response to clopidogrel but not prasugrel. *J Thromb Haemost* 2007;5:2429-36.
8. SPC Efient (NL en VS).

Date 19-11-2018

CYP2C19 UM: prasugrel

[2936](#)

This is NOT a gene-drug interaction.

Literature:

1. Mega JL et al. Cytochrome P450 genetic polymorphisms and the response to prasugrel: relationship to pharmacokinetic, pharmacodynamic, and clinical outcomes. *Circulation* 2009;119:2553-60.
2. SPC Efient (NL en VS).

Date 19-11-2018

SLC01B1 521TC: pravastatin

[8208](#)

NO action is required for this gene-drug interaction.

The gene variation reduces the transport of pravastatin into the liver, but no clinically significant consequences (increase in myopathy or clinically significant reduction in LDL-cholesterol lowering) have

been observed.

Literature:

1. Jessop JP et al. Pharmacogenetic testing in a 70-year-old woman with polypharmacy and multiple comorbidities: a case report. *Am J Case Rep* 2023;24: e938850.
2. Yee SW et al. Organic anion transporter polypeptide 1B1 polymorphism modulates the extent of drug-drug interaction and associated biomarker levels in healthy volunteers. *Clin Transl Sci* 2019;12:388-99.
3. Khine H et al. Statin-associated muscle symptoms and SLCO1B1 rs 4149056 genotype in patients with familial hypercholesterolemia. *Am Heart J* 2016;179:1-9.
4. Akao H et al. Genetic variation at the SLCO1B1 gene locus and low density lipoprotein cholesterol lowering response to pravastatin in the elderly. *Atherosclerosis* 2012;220:413-7.
5. Martin NG et al. The effects of a single nucleotide polymorphism in SLCO1B1 on the pharmacodynamics of pravastatin. *Br J Clin Pharmacol.* 2012;73:303-6.
6. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. *J Am Coll Cardiol* 2009;54:1609-16.
7. Suwannakul S et al. Pharmacokinetic interaction between pravastatin and olmesartan in relation to SLCO1B1 polymorphism. *J Hum Genet* 2008;53:899-904.
8. Zhang W et al. SLCO1B1 521T-->C functional genetic polymorphism and lipid-lowering efficacy of multiple-dose pravastatin in Chinese coronary heart disease patients. *Br J Clin Pharmacol.* 2007;64:346-52.
9. Niemi M et al. SLCO1B1 polymorphism and sex affect the pharmacokinetics of pravastatin but not fluvastatin. *Clin Pharmacol Ther* 2006;80:356-66.

Date 16-05-2023

SLCO1B1 521CC: pravastatin

[8207](#)

NO action is required for this gene-drug interaction.

The gene variation reduces the transport of pravastatin into the liver, but no clinically significant consequences (increase in myopathy or clinically significant reduction in LDL-cholesterol lowering) have been observed.

Literature:

1. Yee SW et al. Organic anion transporter polypeptide 1B1 polymorphism modulates the extent of drug-drug interaction and associated biomarker levels in healthy volunteers. *Clin Transl Sci* 2019;12:388-99.
2. Akao H et al. Genetic variation at the SLCO1B1 gene locus and low density lipoprotein cholesterol lowering response to pravastatin in the elderly. *Atherosclerosis* 2012;220:413-7.
3. Martin NG et al. The effects of a single nucleotide polymorphism in SLCO1B1 on the pharmacodynamics of pravastatin. *Br J Clin Pharmacol.* 2012;73:303-6.
4. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. *J Am Coll Cardiol* 2009;54:1609-16.
5. Deng JW et al. The effect of SLCO1B1*15 on the disposition of pravastatin and pitavastatin is substrate dependent: the contribution of transporting activity changes by SLCO1B1*15. *Pharmacogenet Genomics* 2008;18:424-33.
6. Suwannakul S et al. Pharmacokinetic interaction between pravastatin and olmesartan in relation to SLCO1B1 polymorphism. *J Hum Genet* 2008;53:899-904.
7. Niemi M et al. SLCO1B1 polymorphism and sex affect the pharmacokinetics of pravastatin but not fluvastatin. *Clin Pharmacol Ther* 2006;80:356-66.

Date 16-5-2023

CYP2D6 IM: propafenon

[2427](#)

Genetic variation increases the sum of the plasma concentrations of propafenone and the active metabolite 5-hydroxypropafenone. This may increase the risk of side effects.

Recommendation:

It is not possible to offer adequately substantiated recommendations for dose adjustment based on the literature.

- Either guide the dose by therapeutic drug monitoring, perform an ECG and be alert to side effects
- Or choose an alternative

Antiarrhythmic drugs that are hardly if at all metabolised by CYP2D6 include, for example, sotalol, disopyramide, quinidine and amiodarone.

Literature:

1. Sunthakar SD et al. Influence of CYP2D6 genetic variation on adverse events with propafenone in the pediatric and young adult population. Clin Transl Sci 2022 May 5 [online ahead of print].
2. Doki K et al. Effect of CYP2D6 genetic polymorphism on peak propafenone concentration: no significant effect of CYP2D6*10. Pharmacogenomics 2020;21:1279-88.
3. Mörike K et al. Propafenone for the prevention of atrial tachyarrhythmias after cardiac surgery: a randomized, double-blind placebo-controlled trial. Clin Pharmacol Ther 2008;84:104-10.
4. Chen B et al. Influence of CYP2D6*10B genotype on pharmacokinetics of propafenone enantiomers in Chinese subjects. Acta Pharmacol Sin 2003;24:1277-80.
5. Cai WM et al. Effect of CYP2D6*10 genotype on propafenone pharmacodynamics in Chinese patients with ventricular arrhythmia. Acta Pharmacol Sin 2002;23:1040-4.
6. Cai WM et al. Simultaneous modeling of pharmacokinetics and pharmacodynamics of propafenone in healthy subjects. Acta Pharmacol Sin 2001;22:956-60.

Date 12-09-2022

CYP2D6 PM: propafenon

[2426](#)

Genetic variation increases the sum of the plasma concentrations of propafenone and the active metabolite 5-hydroxypropafenone. This increases the risk of side effects.

Recommendation:

- Reduce the dose to 30% of the standard dose, perform an ECG and monitor plasma concentrations

Literature:

1. Sunthakar SD et al. Influence of CYP2D6 genetic variation on adverse events with propafenone in the pediatric and young adult population. Clin Transl Sci 2022 May 5 [online ahead of print].
2. Mörike K et al. Propafenone for the prevention of atrial tachyarrhythmias after cardiac surgery: a randomized, double-blind placebo-controlled trial. Clin Pharmacol Ther 2008;84:104-10.
3. Jazwinska-Tarnawska E et al. The influence of CYP2D6 polymorphism on the antiarrhythmic efficacy of propafenone in patients with paroxysmal atrial fibrillation during 3 months propafenone prophylactic treatment. Int J Clin Pharmacol Ther 2001;39:288-92.
4. Chow MS et al. Evaluation of CYP2D6 oxidation of dextromethorphan and propafenone in a Chinese population with atrial fibrillation. J Clin Pharmacol 2001;41:92-6.
5. Labbe L et al. Pharmacokinetic and pharmacodynamic interaction between mexiletine and propafenone in human beings. Clin Pharmacol Ther 2000;68:44-57.
6. Dilger K et al. Consequences of rifampicin treatment on propafenone disposition in extensive and poor metabolizers of CYP2D6. Pharmacogenetics 1999;9:551-9.
7. Cai WM et al. The influence of CYP2D6 activity on the kinetics of propafenone enantiomers in Chinese subjects. Br J Clin Pharmacol 1999;47:553-6.
8. Morike K et al. Propafenone in a usual dose produces severe side-effects: the impact of genetically determined metabolic status on drug therapy. J Intern Med 1995;238:469-72.
9. Morike KE et al. Quinidine-enhanced beta-blockade during treatment with propafenone in extensive metabolizer human subjects. Clin Pharmacol Ther 1994;55:28-34.
10. Lee JT et al. The role of genetically determined polymorphic drug metabolism in the beta-blockade produced by propafenone. N Engl J Med 1990;21:1764-8.
11. Siddoway LA et al. Polymorphism of propafenone metabolism and disposition in man: clinical and pharmacokinetic consequences. Circulation 1987;75:785-91.
12. SmPC Rytmonorm.
13. SmPC Rhythmol SR (VS).

Date 12-09-2022

CYP2D6 UM: propafenon

[2428](#)

Genetic variation decreases the sum of the plasma concentrations of propafenone and the active metabolite 5-hydroxypropafenone. This increases the risk of reduced or no efficacy.

Recommendation:

It is not possible to offer adequately substantiated recommendations for dose adjustment based on the literature.

- Either monitor plasma concentrations, perform an ECG and be alert to reduced efficacy of the therapy.
- Or choose an alternative

Antiarrhythmic drugs that are hardly if at all metabolised by CYP2D6 include, for example, sotalol, disopyramide, quinidine and amiodarone.

Literature:

1. Sunthakar SD et al. Influence of CYP2D6 genetic variation on adverse events with propafenone in the pediatric and young adult population. Clin Transl Sci 2022 May 5 [online ahead of print].
2. Mörike K et al. Propafenone for the prevention of atrial tachyarrhythmias after cardiac surgery: a randomized, double-blind placebo-controlled trial. Clin Pharmacol Ther 2008;84:104-10.
3. Jazwinska-Tarnawska E et al. The influence of CYP2D6 polymorphism on the antiarrhythmic efficacy of propafenone in patients with paroxysmal atrial fibrillation during 3 months propafenone prophylactic treatment. Int J Clin Pharmacol Ther 2001;39:288-92.

Date 12-09-2022

CYP2D6 IM: quetiapine

[2795](#)

This is NOT a gene-drug interaction.

Literature:

1. Stäubli CK et al. Severe adverse drug reactions to quetiapine in two patients carrying CYP2D6*4 variants: a case report. Int J Mol Sci 2021;22:6480.
2. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. Pharmacogenomics J 2016;16:357-65.
3. Bakken GV et al. Impact of genetic variability in CYP2D6, CYP3A5, and ABCB1 on serum concentrations of quetiapine and N-desalkylquetiapine in psychiatric patients. Ther Drug Monit 2015;37:256-61.
4. Kato D et al. Delirium resolving upon switching from risperidone to quetiapine: implication of CYP2D6 genotype. Psychosomatics 2005;46:374-5.

Date 13-09-2021

CYP2D6 PM: quetiapine

[2794](#)

This is NOT a gene-drug interaction.

Literature:

1. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. Pharmacogenomics J 2016;16:357-65.
2. Bakken GV et al. Impact of genetic variability in CYP2D6, CYP3A5, and ABCB1 on serum concentrations of quetiapine and N-desalkylquetiapine in psychiatric patients. Ther Drug Monit 2015;37:256-61.

Date 13-09-2021

CYP2D6 UM: quetiapine

[2796](#)

This is NOT a gene-drug interaction.

Literature:

1. Bakken GV et al. Impact of genetic variability in CYP2D6, CYP3A5, and ABCB1 on serum concentrations of quetiapine and N-desalkylquetiapine in psychiatric patients. Ther Drug Monit 2015;37:256-61.
2. Khazaal Y et al. Use of high doses of quetiapine in bipolar disorder episodes are not linked to high activity of cytochrome P450 3A4 and/or cytochrome P450 2D6. Psychiatr Q 2013;84:329-35.

Date 13-09-2021

CYP3A4 IM: quetiapine

[5606](#)

NO action is needed for this gene-drug interaction.

This gene variation reduces the conversion of quetiapine to inactive metabolites and a metabolite with antidepressant effect. However, the effect on the plasma concentration of quetiapine is limited (20% increase)

and it is not known whether this has any clinical consequences. The relationship between the plasma concentration and clinical effect is weak for quetiapine.

Literature:

1. van der Weide K et al. The influence of the CYP3A4*22 polymorphism on serum concentration of quetiapine in psychiatric patients. J Clin Psychopharmacol 2014;34:256-60. En persoonlijke communicatie.

Date 13-09-2021

CYP3A4 PM: quetiapine

[5605](#)

The plasma concentration of quetiapine is 3.2-fold higher in these patients. In addition, the formation of the active metabolite N-desalkylquetiapine, which is probably responsible for the antidepressant effect, should be reduced. The gene variation results in reduced activity of the enzyme CYP3A4, which converts quetiapine to N-desalkylquetiapine and an inactive metabolite.

- indication DEPRESSION

- choose an alternative

Aripiprazole appears to be less dependent on CYP3A4 for metabolism. Olanzapine is not metabolised by CYP3A4.

- OTHER INDICATIONS

- use 30% of the standard dose

Literature:

1. van der Weide K et al. The influence of the CYP3A4*22 polymorphism on serum concentration of quetiapine in psychiatric patients. J Clin Psychopharmacol 2014;34:256-60. And personal communication.

Date 13-09-2021

CYP2C19 IM: rabeprazole

[2513](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of rabeprazole does not result in an increase in side effects.

Literature:

1. Nakamura K et al. Limited effect of rebamipide in addition to proton pump inhibitor (PPI) in the treatment of post-endoscopic submucosal dissection gastric ulcers: a randomized controlled trial comparing PPI plus rebamipide combination therapy with PPI monotherapy. Gut Liver 2016;10:917-924.
2. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of H. pylori infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. PLoS One 2013;8:e62162.
3. Kinoshita Y et al. Randomised clinical trial: a multicentre, double-blind, placebo-controlled study on the efficacy and safety of rabeprazole 5 mg or 10 mg once daily in patients with non-erosive reflux disease. Aliment Pharmacol Ther 2011;33:213-24.
4. Lay CS et al. Correlation of CYP2C19 genetic polymorphisms with Helicobacter pylori eradication in patients with cirrhosis and peptic ulcer. J Chin Med Assoc 2010;73:188-93.
5. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. Hepatogastroenterology 2009;56:703-6.
6. Yamano HO et al. Plasma concentration of rabeprazole after 8-week administration in gastroesophageal reflux disease patients and intragastric pH elevation. J Gastroenterol Hepatol 2008;23:534-40.
7. Lee YC et al. Influence of cytochrome P450 2C19 genetic polymorphism and dosage of rabeprazole on accuracy of proton-pump inhibitor testing in Chinese patients with gastroesophageal reflux disease. J Gastroenterol Hepatol 2007;22:1286-92.
8. Li ZS et al. Effect of esomeprazole and rabeprazole on intragastric pH in healthy Chinese: an open, randomized crossover trial. J Gastroenterol Hepatol 2007;22:815-20.
9. Ariizumi K et al. Therapeutic effects of 10 mg/day rabeprazole administration on reflux esophagitis was not influenced by the CYP2C19 polymorphism. J Gastroenterol Hepatol 2006;21:1428-34.
10. Hu YM et al. Pharmacodynamic and kinetic effect of rabeprazole on serum gastrin level in relation to CYP2C19 polymorphism in Chinese Hans. World J Gastroenterol 2006;12:4750-3.
11. Sugimoto M et al. Comparison of an increased dosage regimen of rabeprazole versus a concomitant dosage regimen of famotidine with rabeprazole for nocturnal gastric acid inhibition in relation to

- cytochrome P450 2C19 genotypes. *Clin Pharmacol Ther* 2005;77:302-11.
12. Sugimoto M et al. Different dosage regimens of rabeprazole for nocturnal gastric acid inhibition in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2004;76:290-301.
 13. Shimatani T et al. Rabeprazole 10 mg twice daily is superior to 20 mg once daily for night-time gastric acid suppression. *Aliment Pharmacol Ther* 2004;19:113-22.
 14. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
 15. Horai Y et al. Pharmacodynamic effects and kinetic disposition of rabeprazole in relation to CYP2C19 genotypes. *Aliment Pharmacol Ther* 2001;15:793-803.
 16. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
 17. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.
 18. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
 19. Yang JC et al. Pharmacokinetic- pharmacodynamic analysis of the role of CYP2C19 genotypes in short-term rabeprazole-based triple therapy against *Helicobacter pylori*. *Br J Clin Pharmacol* 2009;67:503-10.
 20. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
 21. Kuwayama H et al. Rabeprazole-based eradication therapy for *Helicobacter pylori*: a large-scale study in Japan. *Aliment Pharmacol Ther* 2007;25:1105-13.
 22. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of *Helicobacter pylori* infection with lansoprazole- or rabeprazole-based triple therapy in Japan. *Eur J Gastroenterol Hepatol* 2003;15:27-33.
 23. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for *Helicobacter pylori* infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxycillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
 24. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
 25. SPC Pariet.

Date 05-03-2018

CYP2C19 PM: rabeprazol

[2514](#)

NO action is required for this gene-drug interaction.

The higher plasma concentration of rabeprazole does not result in an increase in side effects.

Literature:

1. Nakamura K et al. Limited effect of rebamipide in addition to proton pump inhibitor (PPI) in the treatment of post-endoscopic submucosal dissection gastric ulcers: a randomized controlled trial comparing PPI plus rebamipide combination therapy with PPI monotherapy. *Gut Liver* 2016;10:917-924.
2. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
3. Kinoshita Y et al. Randomised clinical trial: a multicentre, double-blind, placebo- controlled study on the efficacy and safety of rabeprazole 5 mg or 10 mg once daily in patients with non-erosive reflux disease. *Aliment Pharmacol Ther* 2011;33:213-24.
4. Lay CS et al. Correlation of CYP2C19 genetic polymorphisms with *Helicobacter pylori* eradication in patients with cirrhosis and peptic ulcer. *J Chin Med Assoc* 2010;73:188-93.
5. Tseng PH et al. A comparative study of proton-pump inhibitor tests for Chinese reflux patients in relation to the CYP2C19 genotypes. *J Clin Gastroenterol* 2009;43:920-5.
6. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
7. Yamano HO et al. Plasma concentration of rabeprazole after 8-week administration in gastroesophageal reflux disease patients and intragastric pH elevation. *J Gastroenterol Hepatol* 2008;23:534-40.
8. Lee YC et al. Influence of cytochrome P450 2C19 genetic polymorphism and dosage of rabeprazole on accuracy of proton-pump inhibitor testing in Chinese patients with gastroesophageal reflux disease. *J Gastroenterol Hepatol* 2007;22:1286-92.
9. Li ZS et al. Effect of esomeprazole and rabeprazole on intragastric pH in healthy Chinese: an open, randomized crossover trial. *J Gastroenterol Hepatol* 2007;22:815-20.
10. Ariizumi K et al. Therapeutic effects of 10 mg/day rabeprazole administration on reflux esophagitis was not influenced by the CYP2C19 polymorphism. *J Gastroenterol Hepatol* 2006;21:1428-34.
11. Hu YM et al. Pharmacodynamic and kinetic effect of rabeprazole on serum gastrin level in relation to CYP2C19 polymorphism in Chinese Hans. *World J Gastroenterol* 2006;12:4750-3.
12. Sugimoto M et al. Comparison of an increased dosage regimen of rabeprazole versus a concomitant

- dosage regimen of famotidine with rabeprazole for nocturnal gastric acid inhibition in relation to cytochrome P450 2C19 genotypes. *Clin Pharmacol Ther* 2005;77:302-11.
13. Sugimoto M et al. Different dosage regimens of rabeprazole for nocturnal gastric acid inhibition in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2004;76:290-301.
 14. Shimatani T et al. Rabeprazole 10 mg twice daily is superior to 20 mg once daily for night-time gastric acid suppression. *Aliment Pharmacol Ther* 2004;19:113-22.
 15. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
 16. Horai Y et al. Pharmacodynamic effects and kinetic disposition of rabeprazole in relation to CYP2C19 genotypes. *Aliment Pharmacol Ther* 2001;15:793-803.
 17. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
 18. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.
 19. Ji S et al. Comparison of the efficacy of rabeprazole 10 mg and omeprazole 20 mg for the healing rapidity of peptic ulcer diseases. *J Gastroenterol Hepatol* 2006;21: 1381- 7.
 20. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
 21. Yang JC et al. Pharmacokinetic- pharmacodynamic analysis of the role of CYP2C19 genotypes in short-term rabeprazole-based triple therapy against *Helicobacter pylori*. *Br J Clin Pharmacol* 2009;67:503-10.
 22. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
 23. Kuwayama H et al. Rabeprazole-based eradication therapy for *Helicobacter pylori*: a large-scale study in Japan. *Aliment Pharmacol Ther* 2007;25:1105-13.
 24. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of *Helicobacter pylori* infection with lansoprazole- or rabeprazole-based triple therapy in Japan. *Eur J Gastroenterol Hepatol* 2003;15:27-33.
 25. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for *Helicobacter pylori* infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxycillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
 26. Hokari K et al. Efficacy of triple therapy with rabeprazole for *Helicobacter pylori* infection and CYP2C19 genetic polymorphism. *Aliment Pharmacol Ther* 2001;15:1479- 84.
 27. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
 28. SPC's Pariet en Aciphex (VS).

Date 05-03-2018

CYP2C19 UM: rabeprazol

[2515](#)

NO action is required for this gene-drug interaction.

There is currently insufficient information about this gene variation to recommend any action. Moreover, the fact that there are no differences in effectiveness between PM and EM patients also makes differences in effectiveness between UM and EM patients less likely.

Literature:

1. Nakamura K et al. Limited effect of rebamipide in addition to proton pump inhibitor (PPI) in the treatment of post-endoscopic submucosal dissection gastric ulcers: a randomized controlled trial comparing PPI plus rebamipide combination therapy with PPI monotherapy. *Gut Liver* 2016;10:917-924.
2. Tang HL et al. Effects of CYP2C19 loss-of-function variants on the eradication of *H. pylori* infection in patients treated with proton pump inhibitor-based triple therapy regimens: a meta-analysis of randomized clinical trials. *PLoS One* 2013;8:e62162.
3. Kinoshita Y et al. Randomised clinical trial: a multicentre, double-blind, placebo- controlled study on the efficacy and safety of rabeprazole 5 mg or 10 mg once daily in patients with non-erosive reflux disease. *Aliment Pharmacol Ther* 2011;33:213-24.
4. Lay CS et al. Correlation of CYP2C19 genetic polymorphisms with *Helicobacter pylori* eradication in patients with cirrhosis and peptic ulcer. *J Chin Med Assoc* 2010;73:188-93.
5. Tseng PH et al. A comparative study of proton-pump inhibitor tests for Chinese reflux patients in relation to the CYP2C19 genotypes. *J Clin Gastroenterol* 2009;43:920-5.
6. Saitoh T et al. Influences of CYP2C19 polymorphism on recurrence of reflux esophagitis during proton pump inhibitor maintenance therapy. *Hepatogastroenterology* 2009;56:703-6.
7. Yamano HO et al. Plasma concentration of rabeprazole after 8-week administration in gastroesophageal reflux disease patients and intragastric pH elevation. *J Gastroenterol Hepatol* 2008;23:534-40.
8. Lee YC et al. Influence of cytochrome P450 2C19 genetic polymorphism and dosage of rabeprazole on accuracy of proton-pump inhibitor testing in Chinese patients with gastroesophageal reflux disease. *J Gastroenterol Hepatol* 2007;22:1286-92.

9. Li ZS et al. Effect of esomeprazole and rabeprazole on intragastric pH in healthy Chinese: an open, randomized crossover trial. *J Gastroenterol Hepatol* 2007;22:815-20.
10. Ariizumi K et al. Therapeutic effects of 10 mg/day rabeprazole administration on reflux esophagitis was not influenced by the CYP2C19 polymorphism. *J Gastroenterol Hepatol* 2006;21:1428-34.
11. Hu YM et al. Pharmacodynamic and kinetic effect of rabeprazole on serum gastrin level in relation to CYP2C19 polymorphism in Chinese Hans. *World J Gastroenterol* 2006;12:4750-3.
12. Sugimoto M et al. Comparison of an increased dosage regimen of rabeprazole versus a concomitant dosage regimen of famotidine with rabeprazole for nocturnal gastric acid inhibition in relation to cytochrome P450 2C19 genotypes. *Clin Pharmacol Ther* 2005;77:302-11.
13. Sugimoto M et al. Different dosage regimens of rabeprazole for nocturnal gastric acid inhibition in relation to cytochrome P450 2C19 genotype status. *Clin Pharmacol Ther* 2004;76:290-301.
14. Shimatani T et al. Rabeprazole 10 mg twice daily is superior to 20 mg once daily for night-time gastric acid suppression. *Aliment Pharmacol Ther* 2004;19:113-22.
15. Shirai N et al. Effects of CYP2C19 genotypic differences in the metabolism of omeprazole and rabeprazole on intragastric pH. *Aliment Pharmacol Ther* 2001;15:1929-37.
16. Horai Y et al. Pharmacodynamic effects and kinetic disposition of rabeprazole in relation to CYP2C19 genotypes. *Aliment Pharmacol Ther* 2001;15:793-803.
17. Adachi K et al. CYP2C19 genotype status and intragastric pH during dosing with lansoprazole or rabeprazole. *Aliment Pharmacol Ther* 2000;14:1259-66.
18. Ando T et al. Endoscopic analysis of gastric ulcer after one week's treatment with omeprazole and rabeprazole in relation to CYP2C19 genotype. *Dig Dis Sci* 2008;53:933- 7.
19. Ji S et al. Comparison of the efficacy of rabeprazole 10 mg and omeprazole 20 mg for the healing rapidity of peptic ulcer diseases. *J Gastroenterol Hepatol* 2006;21: 1381- 7.
20. Ando T et al. A comparative study on endoscopic ulcer healing of omeprazole versus rabeprazole with respect to CYP2C19 genotypic differences. *Dig Dis Sci* 2005;50:1625-31.
21. Yang JC et al. Pharmacokinetic- pharmacodynamic analysis of the role of CYP2C19 genotypes in short-term rabeprazole-based triple therapy against *Helicobacter pylori*. *Br J Clin Pharmacol* 2009;67:503-10.
22. Zhao F et al. Effect of CYP2C19 genetic polymorphisms on the efficacy of proton pump inhibitor-based triple therapy for *Helicobacter pylori* eradication: a meta-analysis. *Helicobacter* 2008;13:532-41.
23. Kuwayama H et al. Rabeprazole-based eradication therapy for *Helicobacter pylori*: a large-scale study in Japan. *Aliment Pharmacol Ther* 2007;25:1105-13.
24. Miki I et al. Impact of clarithromycin resistance and CYP2C19 genetic polymorphism on treatment efficacy of *Helicobacter pylori* infection with lansoprazole- or rabeprazole-based triple therapy in Japan. *Eur J Gastroenterol Hepatol* 2003;15:27-33.
25. Dojo M et al. Effects of CYP2C19 gene polymorphism on cure rates for *Helicobacter pylori* infection by triple therapy with proton pump inhibitor (omeprazole or rabeprazole), amoxicillin and clarithromycin in Japan. *Dig Liver Dis* 2001;33:671-5.
26. Hokari K et al. Efficacy of triple therapy with rabeprazole for *Helicobacter pylori* infection and CYP2C19 genetic polymorphism. *Aliment Pharmacol Ther* 2001;15:1479- 84.
27. Inaba T et al. *Helicobacter pylori* infection: CYP2C19 genotype and serum ferritin. *J Gastroenterol Hepatol* 2002;17:748-53.
28. SPC's Pariet en Aciphex (VS).

Date 05-03-2018

HLA-B44 negatief: ribavirine

[2755](#)

This is NOT a gene-drug interaction.

Literature:

1. Vidal-Castiñeira JR et al. Diversity of killer cell immunoglobulin-like receptor (KIR) genotypes and KIR2DL2/3 variants in HCV treatment outcome. *PLoS One* 2014;9:e99426.
2. Vidal-Castiñeira JR et al. A predictive model of treatment outcome in patients with chronic HCV infection using IL28B and PD-1 genotyping. *J Hepatol* 2012;56:1230-8.
3. Romero-Gómez M et al. HLA class I B44 is associated with sustained response to interferon + ribavirin therapy in patients with chronic hepatitis C. *Am J Gastroenterol* 2003;98:1621-6.

Date 13-05-2019

CYP2D6 IM: risperidon

[2383](#)

NO action is needed for this gene-drug interaction.

There is little evidence to support an increase in side effects caused by the gene variation. The gene variation may lead to a decrease in the required maintenance dose. However, as the effect on the dose is smaller than that of the normal biological variation, action is not useful.

Literature:

1. Ganoci L et al. ABCB1, ABCG2 and CYP2D6 polymorphism effects on disposition and response to long-acting risperidone. *Prog Neuropsychopharmacol Biol Psychiatry* 2021;104:110042.
2. Cui Y et al. CYP2D6 genotype-based dose recommendations for risperidone in Asian people. *Front Pharmacol* 2020;11:936.
3. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6:418-26.
4. Oshikoya KA et al. CYP2D6 genotype and adverse events to risperidone in children and adolescents. *Pediatr Res* 2019;85:602-6.
5. Schoretsanitis G et al. Prolactin levels: sex differences in the effects of risperidone, 9-hydroxyrisperidone levels, CYP2D6 and ABCB1 variants. *Pharmacogenomics* 2018;19:815-823.
6. Kaur G et al. Identification of genetic correlates of response to risperidone: findings of a multicentric schizophrenia study from India. *Asian J Psychiatr* 2017;29:174-82.
7. Ivaturi V et al. Exposure-response analysis after subcutaneous administration of RBP-7000, a once-a-month long-acting Atrigel formulation of risperidone. *Br J Clin Pharmacol* 2017;83:1476-98.
8. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. *Pharmacogenomics J* 2016;16:357-65.
9. Sukasem C et al. Impact of pharmacogenetic markers of CYP2D6 and DRD2 on prolactin response in risperidone-treated Thai children and adolescents with autism spectrum disorders. *J Clin Psychopharmacol* 2016;36:141-6.
10. Dos Santos-Júnior A et al. Pharmacogenetics of risperidone and cardiovascular risk in children and adolescents. *Int J Endocrinol* 2016;2016:5872423.
11. dos Santos Júnior A et al. Hyperprolactinemia in children and adolescents with use of risperidone: clinical and molecular genetics aspects. *J Child Adolesc Psychopharmacol* 2015;25:738-48.
12. Vandenberghe F et al. Genetics-based population pharmacokinetics and pharmacodynamics of risperidone in a psychiatric cohort. *Clin Pharmacokinet* 2015;54:1259-72.
13. van der Weide K et al. The influence of the CYP3A4 *22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.
14. Suzuki Y et al. Effect of risperidone metabolism and P-glycoprotein gene polymorphism on QT interval in patients with schizophrenia. *Pharmacogenomics J* 2014;14:452- 6.
15. Almoguera B et al. CYP2D6 poor metabolizer status might be associated with better response to risperidone treatment. *Pharmacogenet Genomics* 2013 ;23:627-30.
16. Almoguera B et al. Association of common genetic variants with risperidone adverse events in a Spanish schizophrenic population. *Pharmacogenomics J* 2013; 13:197-204. PubMed PMID: 22212732.
17. Mas S et al. Intuitive pharmacogenetics: spontaneous risperidone dosage is related to CYP2D6, CYP3A5 and ABCB1 genotypes. *Pharmacogenomics J* 2012; 12:255-9.
18. Jovanović N et al. The role of CYP2D6 and ABCB1 pharmacogenetics in drug-naïve patients with first-episode schizophrenia treated with risperidone. *Eur J Clin Pharmacol* 2010; 66:1109-17.
19. Novalbos J et al. Effects of CYP2D6 genotype on the pharmacokinetics, pharmacodynamics, and safety of risperidone in healthy volunteers. *J Clin Psychopharmacol* 2010;30:504-11.
20. Wang L et al. Serum prolactin levels, plasma risperidone levels, polymorphism of cytochrome P450 2D6 and clinical response in patients with schizophrenia. *J Psychopharmacol* 2007;21:837-42.
21. de Leon J et al. A study of genetic (CYP2D6 and ABCB1) and environmental (drug inhibitors and inducers) variables that may influence plasma risperidone levels. *Pharmacopsychiatry* 2007;40:93-102.
22. Cho HY et al. Pharmacokinetics and bioequivalence evaluation of risperidone in healthy male subjects with different CYP2D6 genotypes. *Arch Pharm Res* 2006;29:525-33.
23. Lane HY et al. Risperidone-related weight gain: genetic and nongenetic predictors. *J Clin Psychopharmacol* 2006;26:128-34.
24. Riedel M et al. Risperidone plasma levels, clinical response and side-effects. *Eur Arch Psychiatry Clin Neurosci* 2005;255:261-8.
25. Kato D et al. Delirium resolving upon switching from risperidone to quetiapine: implication of CYP2D6 genotype. *Psychosomatics* 2005;46:374-5.
26. Kakihara S et al. Prediction of response to risperidone treatment with respect to plasma concentrations of risperidone, catecholamine metabolites, and polymorphism of cytochrome P450 2D6. *Int Clin Psychopharmacol* 2005;20:71-8.
27. de Leon J et al. The CYP2D6 poor metabolizer phenotype may be associated with risperidone adverse drug reactions and discontinuation. *J Clin Psychiatry* 2005;66:15-27.
28. Llerena A et al. QTc interval, CYP2D6 and CYP2C9 genotypes and risperidone plasma concentrations. *J Psychopharmacol* 2004;18:189-93.
29. Yasui-Furukori N et al. Effects of various factors on steady-state plasma concentrations of risperidone and 9-hydroxyrisperidone: lack of impact of MDR-1 genotypes. *Br J Clin Pharmacol* 2004;57:569-75.
30. Roh HK et al. Risperidone metabolism in relation to CYP2D6*10 allele in Korean schizophrenic patients. *Eur J Clin Pharmacol* 2001;57:671-5.
31. Scordo MG et al. Cytochrome P450 2D6 genotype and steady state plasma levels of risperidone and 9-hydroxyrisperidone. *Psychopharmacology* 1999;147:300-5.
32. Bork JA et al. A pilot study on risperidone metabolism: the role of cytochromes P450 2D6 and 3A. *J Clin Psychiatry* 1999;60:469-76.

The percentage of patients with therapy failure increased from 16% to 26%. The gene variation increases the plasma concentration of risperidone plus the active metabolite and increases the proportion of risperidone in this ratio, which is more effective at crossing the blood-brain barrier.

- use 67% of the standard dose
- if problematic side effects originating in the central nervous system occur despite this reduced dose, then reduce the dose further to 50% of the standard dose

Literature:

1. Ganoci L et al. ABCB1, ABCG2 and CYP2D6 polymorphism effects on disposition and response to long-acting risperidone. *Prog Neuropsychopharmacol Biol Psychiatry* 2021;104:110042.
2. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6:418-26.
3. Oshikoya KA et al. CYP2D6 genotype and adverse events to risperidone in children and adolescents. *Pediatr Res* 2019;85:602-6.
4. Schoretsanitis G et al. Prolactin levels: sex differences in the effects of risperidone, 9-hydroxyrisperidone levels, CYP2D6 and ABCB1 variants. *Pharmacogenomics* 2018;19:815-823.
5. Kaur G et al. Identification of genetic correlates of response to risperidone: findings of a multicentric schizophrenia study from India. *Asian J Psychiatr* 2017;29:174-82.
6. Ivaturi V et al. Exposure-response analysis after subcutaneous administration of RBP-7000, a once-a-month long-acting Atrigel formulation of risperidone. *Br J Clin Pharmacol* 2017;83:1476-98.
7. Xu Q et al. Association studies of genomic variants with treatment response to risperidone, clozapine, quetiapine and chlorpromazine in the Chinese Han population. *Pharmacogenomics J* 2016;16:357-65.
8. Dos Santos-Júnior A et al. Pharmacogenetics of risperidone and cardiovascular risk in children and adolescents. *Int J Endocrinol* 2016;2016:5872423.
9. dos Santos Júnior A et al. Hyperprolactinemia in children and adolescents with use of risperidone: clinical and molecular genetics aspects. *J Child Adolesc Psychopharmacol* 2015;25:738-48.
10. Vandenberghe F et al. Genetics-based population pharmacokinetics and pharmacodynamics of risperidone in a psychiatric cohort. *Clin Pharmacokinet* 2015;54:1259-72.
11. van der Weide K et al. The influence of the CYP3A4 *22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.
12. Suzuki Y et al. Effect of risperidone metabolism and P-glycoprotein gene polymorphism on QT interval in patients with schizophrenia. *Pharmacogenomics J* 2014;14:452- 6.
13. Gassó P et al. Effect of CYP2D6 on risperidone pharmacokinetics and extrapyramidal symptoms in healthy volunteers: results from a pharmacogenetic clinical trial. *Pharmacogenomics* 2014;15:17-28.
14. Almoguera B et al. CYP2D6 poor metabolizer status might be associated with better response to risperidone treatment. *Pharmacogenet Genomics* 2013 ;23:627-30.
15. Almoguera B et al. Association of common genetic variants with risperidone adverse events in a Spanish schizophrenic population. *Pharmacogenomics J* 2013; 13:197-204. PubMed PMID: 22212732.
16. Mas S et al. Intuitive pharmacogenetics: spontaneous risperidone dosage is related to CYP2D6, CYP3A5 and ABCB1 genotypes. *Pharmacogenomics J* 2012; 12:255-9.
17. Novalbos J et al. Effects of CYP2D6 genotype on the pharmacokinetics, pharmacodynamics, and safety of risperidone in healthy volunteers. *J Clin Psychopharmacol* 2010;30:504-11.
18. Jovanović N et al. The role of CYP2D6 and ABCB1 pharmacogenetics in drug-naïve patients with first-episode schizophrenia treated with risperidone. *Eur J Clin Pharmacol* 2010; 66:1109-17.
19. de Leon J et al. A study of genetic (CYP2D6 and ABCB1) and environmental (drug inhibitors and inducers) variables that may influence plasma risperidone levels. *Pharmacopsychiatry* 2007;40:93-102.
20. de Leon J et al. Polymorphic variations in GSTM1, GSTT1, PgP, CYP2D6, CYP3A5, and dopamine D2 and D3 receptors and their association with tardive dyskinesia in severe mental illness. *J Clin Psychopharmacol* 2005;25:448-56.
21. de Leon J et al. The CYP2D6 poor metabolizer phenotype may be associated with risperidone adverse drug reactions and discontinuation. *J Clin Psychiatry* 2005;66:15-27.
22. Llerena A et al. QTc interval, CYP2D6 and CYP2C9 genotypes and risperidone plasma concentrations. *J Psychopharmacol* 2004;18:189-93.
23. Kohnke MD et al. Cytochrome P450 2D6 deficiency and its clinical relevance in a patient treated with risperidone. *Pharmacopsychiatry* 2002;35(3):116-8.
24. Scordo MG et al. Cytochrome P450 2D6 genotype and steady state plasma levels of risperidone and 9-hydroxyrisperidone. *Psychopharmacology* 1999;147:300-5.
25. Bork JA et al. A pilot study on risperidone metabolism: the role of cytochromes P450 2D6 and 3A. *J Clin Psychiatry* 1999;60:469-76.
26. SmPC's Risperdal (NL en VS) en Risperdal Consta (NL).

Date 13-09-2021

The percentage of patients with therapy failure increases from 16% to 37%. The gene variation leads to a high ratio of the active metabolite (9-hydroxyrisperidone (paliperidone)) compared to risperidone, which crosses the blood-brain barrier more effectively.

- choose an alternative or titrate the dose according to the maximum dose for the active metabolite (paliperidone) (oral 12 mg/day for adults and children from 15 years of age weighing at least 51 kg and 6 mg/day for children from 15 years of age weighing less than 51 kg; intramuscular 75 mg per 2 weeks)

Literature:

1. Jukic MM et al. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. *Lancet Psychiatry* 2019;6:418-26.
2. Oshikoya KA et al. CYP2D6 genotype and adverse events to risperidone in children and adolescents. *Pediatr Res* 2019;85:602-6.
3. Schoretsanis G et al. Prolactin levels: sex differences in the effects of risperidone, 9-hydroxyrisperidone levels, CYP2D6 and ABCB1 variants. *Pharmacogenomics* 2018;19:815-823.
4. van der Weide K et al. The influence of the CYP3A4 *22 polymorphism and CYP2D6 polymorphisms on serum concentrations of aripiprazole, haloperidol, pimozide, and risperidone in psychiatric patients. *J Clin Psychopharmacol* 2015;35:228-36.
5. Gassó P et al. Effect of CYP2D6 on risperidone pharmacokinetics and extrapyramidal symptoms in healthy volunteers: results from a pharmacogenetic clinical trial. *Pharmacogenomics* 2014;15:17-28.
6. Almoguera B et al. CYP2D6 poor metabolizer status might be associated with better response to risperidone treatment. *Pharmacogenet Genomics* 2013 ;23:627-30.
7. Almoguera B et al. Association of common genetic variants with risperidone adverse events in a Spanish schizophrenic population. *Pharmacogenomics J* 2013; 13:197-204. PubMed PMID: 22212732.
8. Mas S et al. Intuitive pharmacogenetics: spontaneous risperidone dosage is related to CYP2D6, CYP3A5 and ABCB1 genotypes. *Pharmacogenomics J* 2012; 12:255-9.
9. Novalbos J et al. Effects of CYP2D6 genotype on the pharmacokinetics, pharmacodynamics, and safety of risperidone in healthy volunteers. *J Clin Psychopharmacol* 2010;30:504-11.
10. de Leon J et al. A study of genetic (CYP2D6 and ABCB1) and environmental (drug inhibitors and inducers) variables that may influence plasma risperidone levels. *Pharmacopsychiatry* 2007;40:93-102.
11. de Leon J et al. The CYP2D6 poor metabolizer phenotype may be associated with risperidone adverse drug reactions and discontinuation. *J Clin Psychiatry* 2005;66:15-27.
12. Llerena A et al. QTc interval, CYP2D6 and CYP2C9 genotypes and risperidone plasma concentrations. *J Psychopharmacol* 2004;18:189-93.
13. Guzey C et al. Risperidone metabolism and the impact of being a cytochrome P450 2D6 ultrarapid metabolizer. *J Clin Psychiatry* 2000;61:600-1.
14. Scordo MG et al. Cytochrome P450 2D6 genotype and steady state plasma levels of risperidone and 9-hydroxyrisperidone. *Psychopharmacology* 1999;147:300-5.

Date 13-09-2021

SLCO1B1 521TC: rosuvastatine

8206

The risk of myopathy can be elevated. The genetic variation may lead to reduced rosuvastatin transport to the liver, which may increase rosuvastatin plasma concentrations.

Patient has ADDITIONAL SIGNIFICANT RISK FACTORS for statin-induced myopathy:

- keep the rosuvastatin dose as low as possible (e.g., by adding ezetimibe).
- advise the patient to report muscle symptoms

Patient has NO additional significant risk factors for statin-induced myopathy:

- advise the patient to report muscle symptoms

Risk factors for statin-induced myopathy are included in the table 'Risk group' in the last part of the risk analysis for rosuvastatin.

Literature:

1. Lehtisalo M et al. A comprehensive pharmacogenomic study indicates roles for SLCO1B1, ABCG2 and SLCO2B1 in rosuvastatin pharmacokinetics. *Br J Clin Pharmacol*. 2023;89:242-52.
2. Merćep I et al. Loss of function polymorphisms in SLCO1B1 (c.521T>C, rs4149056) and ABCG2 (c.421C>A, rs2231142) genes are associated with adverse events of rosuvastatin: a case-control study. *Eur J Clin Pharmacol* 2022;78:227-36.
3. Xiang Q et al. Correlation between single-nucleotide polymorphisms and statin-induced myopathy: a mixed-effects model meta-analysis. *Eur J Clin Pharmacol* 2021;77:569-81.
4. Zhang D et al. Effects of ABCG2 and SLCO1B1 gene variants on inflammation markers in patients with hypercholesterolemia and diabetes mellitus treated with rosuvastatin. *Eur J Clin Pharmacol* 2020;76:939-46.
5. Bai X et al. Effects of SLCO1B1 and GATM gene variants on rosuvastatin-induced myopathy are

unrelated to high plasma exposure of rosuvastatin and its metabolites. *Acta Pharmacol Sin* 2019;40:492-99.

6. Xiang Q et al. Association between SLCO1B1 T521C polymorphism and risk of statin-induced myopathy: a meta-analysis. *Pharmacogenomics J* 2018;18:721-9.
7. Danik JS et al. Lack of association between SLCO1B1 polymorphisms and clinical myalgia following rosuvastatin therapy. *Am Heart J* 2013;165:1008-14.
8. Bailey KM et al. Hepatic metabolism and transporter gene variants enhance response to rosuvastatin in patients with acute myocardial infarction: the GEOSTAT-1 Study. *Circ Cardiovasc Genet* 2010;3:276-85.
9. Pasanen MK et al. Different effects of SLCO1B1 polymorphism on the pharmacokinetics of atorvastatin and rosuvastatin. *Clin Pharmacol Ther* 2007;82:726-33.

Date 16-05-2023

SLCO1B1 521CC: rosuvastatine

[8205](#)

The risk of myopathy can be elevated. The genetic variation may lead to reduced rosuvastatin transport to the liver, which may increase rosuvastatin plasma concentrations.

Patient has ADDITIONAL SIGNIFICANT RISK FACTORS for statin-induced myopathy:

- keep the rosuvastatin dose as low as possible (e.g., by adding ezetimibe).
- advise the patient to report muscle symptoms

Patient has NO additional significant risk factors for statin-induced myopathy:

- advise the patient to report muscle symptoms

Risk factors for statin-induced myopathy are included in the table 'Risk group' in the last part of the risk analysis for rosuvastatin.

Literature:

1. Lehtisalo M et al. A comprehensive pharmacogenomic study indicates roles for SLCO1B1, ABCG2 and SLCO2B1 in rosuvastatin pharmacokinetics. *Br J Clin Pharmacol*. 2023;89:242-52.
2. Mercép I et al. Loss of function polymorphisms in SLCO1B1 (c.521T>C, rs4149056) and ABCG2 (c.421C>A, rs2231142) genes are associated with adverse events of rosuvastatin: a case-control study. *Eur J Clin Pharmacol* 2022;78:227-36.
3. Xiang Q et al. Correlation between single-nucleotide polymorphisms and statin-induced myopathy: a mixed-effects model meta-analysis. *Eur J Clin Pharmacol* 2021;77:569-81.
4. Zhang D et al. Effects of ABCG2 and SLCO1B1 gene variants on inflammation markers in patients with hypercholesterolemia and diabetes mellitus treated with rosuvastatin. *Eur J Clin Pharmacol* 2020;76:939-46.
5. Bai X et al. Effects of SLCO1B1 and GATM gene variants on rosuvastatin-induced myopathy are unrelated to high plasma exposure of rosuvastatin and its metabolites. *Acta Pharmacol Sin* 2019;40:492-99.
6. Xiang Q et al. Association between SLCO1B1 T521C polymorphism and risk of statin-induced myopathy: a meta-analysis. *Pharmacogenomics J* 2018;18:721-9.
7. Danik JS et al. Lack of association between SLCO1B1 polymorphisms and clinical myalgia following rosuvastatin therapy. *Am Heart J* 2013;165:1008-14.
8. Bailey KM et al. Hepatic metabolism and transporter gene variants enhance response to rosuvastatin in patients with acute myocardial infarction: the GEOSTAT-1 Study. *Circ Cardiovasc Genet* 2010;3:276-85.
9. Pasanen MK et al. Different effects of SLCO1B1 polymorphism on the pharmacokinetics of atorvastatin and rosuvastatin. *Clin Pharmacol Ther* 2007;82:726-33.
10. SmPCs Crestor (NL and USA).

Date 16-05-2023

CYP2C19 IM: sertraline

[2593](#)

NO action is needed for this gene-drug interaction.

The gene variation has a minor effect on the sertraline plasma concentration. No effect on side effects was found.

Literature:

1. Saiz-Rodríguez M et al. Effect of polymorphisms on the pharmacokinetics, pharmacodynamics and safety of sertraline in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:501-511.
2. AIOLaby RR et al. Molecular biomarkers predictive of sertraline treatment response in young children with fragile X syndrome. *Brain Dev* 2017;39:483-492.
3. Yuce-Artun N et al. Influence of CYP2B6 and CYP2C19 polymorphisms on sertraline metabolism in major depression patients. *Int J Clin Pharm* 2016;38:388-94.

- Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
- Rudberg I et al. Serum concentrations of sertraline and N-desmethyl sertraline in relation to CYP2C19 genotype in psychiatric patients. *Eur J Clin Pharmacol* 2008;64:1181-8.
- Wang JH et al. Pharmacokinetics of sertraline in relation to genetic polymorphism of CYP2C19. *Clin Pharmacol Ther* 2001;70:42-7.

Date 14-05-2018

CYP2C19 PM: sertraline

[2594](#)

The risk of side effects is increased. The gene variation leads to increased plasma concentrations of sertraline

- Do not give doses exceeding 75 mg/day
- Guide the dose by response and side effects and/or sertraline plasma concentration.

Literature:

- AIOLaby RR et al. Molecular biomarkers predictive of sertraline treatment response in young children with fragile X syndrome. *Brain Dev* 2017;39:483-492.
- Yuce-Artun N et al. Influence of CYP2B6 and CYP2C19 polymorphisms on sertraline metabolism in major depression patients. *Int J Clin Pharm* 2016;38:388-94.
- Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
- Rudberg I et al. Serum concentrations of sertraline and N-desmethyl sertraline in relation to CYP2C19 genotype in psychiatric patients. *Eur J Clin Pharmacol* 2008;64:1181-8.
- Grasmader K et al. Impact of polymorphisms of cytochrome-P450 isoenzymes 2C9, 2C19 and 2D6 on plasma concentrations and clinical effects of antidepressants in a naturalistic clinical setting. *Eur J Clin Pharmacol* 2004;60:329-36.
- Wang JH et al. Pharmacokinetics of sertraline in relation to genetic polymorphism of CYP2C19. *Clin Pharmacol Ther* 2001;70:42-7.
- SPC Zoloft.

Date 14-05-2018

CYP2C19 UM: sertraline

[2595](#)

NO action is needed for this gene-drug interaction.

The gene variation has a negligible effect on the plasma concentration of sertraline. Moreover, no significant effect on response and side effects has been found.

Literature:

- AIOLaby RR et al. Molecular biomarkers predictive of sertraline treatment response in young children with fragile X syndrome. *Brain Dev* 2017;39:483-492.
- Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
- Rudberg I et al. Serum concentrations of sertraline and N-desmethyl sertraline in relation to CYP2C19 genotype in psychiatric patients. *Eur J Clin Pharmacol* 2008;64:1181-8.

Date 14-05-2018

CYP2D6 IM: sertraline

[3539](#)

This is NOT a gene-drug interaction.

Literature:

- Saiz-Rodríguez M et al. Effect of polymorphisms on the pharmacokinetics, pharmacodynamics and safety of sertraline in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:501-511.
- AIOLaby RR et al. Molecular biomarkers predictive of sertraline treatment response in young children with fragile X syndrome. *Brain Dev* 2017;39:483-492.
- Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.

Date 14-05-2018

This is NOT a gene-drug interaction.

Literature:

1. Saiz-Rodríguez M et al. Effect of polymorphisms on the pharmacokinetics, pharmacodynamics and safety of sertraline in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:501-511.
2. AIOlaby RR et al. Molecular biomarkers predictive of sertraline treatment response in young children with fragile X syndrome. *Brain Dev* 2017;39:483-492.
3. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
4. Hamelin BA et al. The disposition of fluoxetine but not sertraline is altered in poor metabolizers of debrisoquin. *Clin Pharmacol Ther* 1996;60:512-21.

Date 14-05-2018

This is NOT a gene-drug interaction.

Literature:

1. Saiz-Rodríguez M et al. Effect of polymorphisms on the pharmacokinetics, pharmacodynamics and safety of sertraline in healthy volunteers. *Basic Clin Pharmacol Toxicol* 2018;122:501-511.
2. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.

Date 14-05-2018

When using simvastatin 80 mg/day, the risk of myopathy is increased 30-fold to 18% and the risk of severe myopathy is increased 48-fold to 12%. When using 40 mg/day, this risk is increased 7-fold to 1% and 11-fold to 0.68% respectively. The gene variation leads to reduced simvastatin transport to the liver, which increases the simvastatin plasma concentration and therefore the risk of side effects.

- Choose an alternative

Consider any additional risk factors for statin-induced myopathy.

Atorvastatin is affected less severely by the SLCO1B1 gene variation, but is also affected by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem. Use of atorvastatin is not recommended for patients with additional risk factors for statin-induced myopathy.

Rosuvastatin and pravastatin are influenced to a lesser extent by the SLCO1B1 gene variation. They are also not influenced by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem.

Fluvastatin is not significantly influenced by the SLCO1B1 gene variation or CYP3A4 inhibitors.

Literature:

1. Xiang Q et al. Association between SLCO1B1 T521C polymorphism and risk of statin-induced myopathy: a meta-analysis. *Pharmacogenomics J* 2018;18:721-9.
2. Wu X et al. Associations of the SLCO1B1 polymorphisms with hepatic function, baseline lipid levels, and lipid-lowering response to simvastatin in patients with hyperlipidemia. *Clin Appl Thromb Hemost* 2018;24:240S-247S.
3. Kitzmiller JP et al. Candidate-gene study of functional polymorphisms in SLCO1B1 and CYP3A4/5 and the cholesterol-lowering response to simvastatin. *Clin Transl Sci* 2017;10:172-7.
4. Jiang J et al. Association between SLCO1B1 -521T>C and -388A>G polymorphisms and risk of statin-induced adverse drug reactions: a meta-analysis. *Springerplus* 2016;5:1368.
5. Hou Q et al. Association between SLCO1B1 gene T521C polymorphism and statin-related myopathy risk: a meta-analysis of case-control studies. *Medicine (Baltimore)* 2015;94:e1268.
6. Luzum JA et al. Individual and combined associations of genetic variants in CYP3A4, CYP3A5, and SLCO1B1 with simvastatin and simvastatin acid plasma concentrations. *J Cardiovasc Pharmacol* 2015;66:80-5.
7. Dou Y et al. Meta-analysis of the SLCO1B1 c.521T>C variant reveals slight influence on the lipid-lowering efficacy of statins. *Ann Lab Med* 2015;35:329-35.
8. de Keyser CE et al. The SLCO1B1 c.521T>C polymorphism is associated with dose decrease or switching during statin therapy in the Rotterdam Study. *Pharmacogenet Genomics* 2014;24:43-51.
9. Carr DF et al. SLCO1B1 genetic variant associated with statin-induced myopathy: a proof-of-concept study using the Clinical Practice Research Datalink. *Clin Pharmacol Ther* 2013;94:695-701.
10. Hopewell JC et al. Impact of common genetic variation on response to simvastatin therapy among 18

- 705 participants in the Heart Protection Study. *Eur Heart J* 2013;34:982-92.
11. Hu M et al. Intronic variants in SLCO1B1 related to statin-induced myopathy are associated with the low-density lipoprotein cholesterol response to statins in Chinese patients with hyperlipidaemia. *Pharmacogenet Genomics* 2012;22:803-6.
 12. Brunham LR et al. Differential effect of the rs4149056 variant in SLCO1B1 on myopathy associated with simvastatin and atorvastatin. *Pharmacogenomics J* 2012;12:233-7.
 13. Sortica VA et al. SLCO1B1 gene variability influences lipid-lowering efficacy on simvastatin therapy in Southern Brazilians. *Clin Chem Lab Med* 2012;50:441-8.
 14. Bailey KM et al. Hepatic metabolism and transporter gene variants enhance response to rosuvastatin in patients with acute myocardial infarction: the GEOSTAT-1 Study. *Circ Cardiovasc Genet* 2010;3:276-85.
 15. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. *J Am Coll Cardiol* 2009;54:1609-16.
 16. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. *Pharmacogenet Genomics* 2008;18:921-6.
 17. SEARCH Collaborative Group. SLCO1B1 variants and statin-induced myopathy -- a genomewide study. *N Engl J Med* 2008;359:789-99.
 18. Pasanen MK et al. SLCO1B1 polymorphism markedly affects the pharmacokinetics of simvastatin acid. *Pharmacogenet Genomics* 2006;16:873-9.
 19. Ramsey LB et al. The clinical pharmacogenetics implementation consortium guideline for SLCO1B1 and simvastatin-induced myopathy: 2014 update. *Clin Pharmacol Ther* 2014;96:423-8.
 20. SmPC Zocor.

Date 18-05-2020

SLCO1B1 521TC: simvastatine

[3980](#)

When using simvastatin 80 mg/day, the risk of myopathy is increased 5-fold to 3% for moderately severe to severe myopathy and 1.3% for severe myopathy. When using 40 mg/day, this risk is increased 2.6-fold to 0.39% and 0.17% respectively. The gene variation may lead to reduced simvastatin transport to the liver, which may increase simvastatin plasma concentrations and therefore the risk of side effects.

- Choose an alternative

Consider any additional risk factors for statin-induced myopathy.

Atorvastatin is affected less severely by the SLCO1B1 gene variation, but is also affected by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem. Use of atorvastatin is not recommended for patients with additional risk factors for statin-induced myopathy.

Rosuvastatin and pravastatin are influenced to a lesser extent by the SLCO1B1 gene variation. They are also not influenced by CYP3A4 inhibitors such as amiodarone, verapamil and diltiazem.

Fluvastatin is not significantly influenced by the SLCO1B1 gene variation or CYP3A4 inhibitors.

- If an alternative is not an option:

- Avoid simvastatin doses exceeding 40 mg/day
- Advise the patient to contact their doctor in the event of muscle symptoms.

Literature:

1. Xiang Q et al. Association between SLCO1B1 T521C polymorphism and risk of statin-induced myopathy: a meta-analysis. *Pharmacogenomics J* 2018;18:721-9.
2. Wu X et al. Associations of the SLCO1B1 polymorphisms with hepatic function, baseline lipid levels, and lipid-lowering response to simvastatin in patients with hyperlipidemia. *Clin Appl Thromb Hemost* 2018;24:240S-247S.
3. Kitzmiller JP et al. Candidate-gene study of functional polymorphisms in SLCO1B1 and CYP3A4/5 and the cholesterol-lowering response to simvastatin. *Clin Transl Sci* 2017;10:172-7.
4. Jiang J et al. Association between SLCO1B1 -521T>C and -388A>G polymorphisms and risk of statin-induced adverse drug reactions: a meta-analysis. *Springerplus* 2016;5:1368.
5. Hou Q et al. Association between SLCO1B1 gene T521C polymorphism and statin-related myopathy risk: a meta-analysis of case-control studies. *Medicine (Baltimore)* 2015;94:e1268.
6. Luzum JA et al. Individual and combined associations of genetic variants in CYP3A4, CYP3A5, and SLCO1B1 with simvastatin and simvastatin acid plasma concentrations. *J Cardiovasc Pharmacol* 2015;66:80-5.
7. Dou Y et al. Meta-analysis of the SLCO1B1 c.521T>C variant reveals slight influence on the lipid-lowering efficacy of statins. *Ann Lab Med* 2015;35:329-35.
8. de Keyser CE et al. The SLCO1B1 c.521T>C polymorphism is associated with dose decrease or switching during statin therapy in the Rotterdam Study. *Pharmacogenet Genomics* 2014;24:43-51.
9. Carr DF et al. SLCO1B1 genetic variant associated with statin-induced myopathy: a proof-of-concept study using the Clinical Practice Research Datalink. *Clin Pharmacol Ther* 2013;94:695-701.
10. Hopewell JC et al. Impact of common genetic variation on response to simvastatin therapy among 18 705 participants in the Heart Protection Study. *Eur Heart J* 2013;34:982-92.
11. Hu M et al. Intronic variants in SLCO1B1 related to statin-induced myopathy are associated with the

low-density lipoprotein cholesterol response to statins in Chinese patients with hyperlipidaemia. Pharmacogenet Genomics 2012;22:803-6.

12. Brunham LR et al. Differential effect of the rs4149056 variant in SLCO1B1 on myopathy associated with simvastatin and atorvastatin. Pharmacogenomics J 2012;12:233- 7.
13. Sortica VA et al. SLCO1B1 gene variability influences lipid-lowering efficacy on simvastatin therapy in Southern Brazilians. Clin Chem Lab Med 2012;50:441-8.
14. Bailey KM et al. Hepatic metabolism and transporter gene variants enhance response to rosuvastatin in patients with acute myocardial infarction: the GEOSTAT-1 Study. Circ Cardiovasc Genet 2010;3:276-85.
15. Voora D et al. The SLCO1B1*5 genetic variant is associated with statin-induced side effects. J Am Coll Cardiol 2009;54:1609-16.
16. Pasanen MK et al. Polymorphism of the hepatic influx transporter organic anion transporting polypeptide 1B1 is associated with increased cholesterol synthesis rate. Pharmacogenet Genomics 2008;18:921-6.
17. SEARCH Collaborative Group. SLCO1B1 variants and statin-induced myopathy -- a genomewide study. N Engl J Med 2008;359:789-99.
18. Pasanen MK et al. SLCO1B1 polymorphism markedly affects the pharmacokinetics of simvastatin acid. Pharmacogenet Genomics 2006;16:873-9.
19. Ramsey LB et al. The clinical pharmacogenetics implementation consortium guideline for SLCO1B1 and simvastatin-induced myopathy: 2014 update. Clin Pharmacol Ther 2014;96:423-8.
20. SmPC Zocor.

Date 18-05-2020

CYP2C9 IM OTHER: siponimod

[7117](#)

Theoretically, the risk of adverse reactions is increased, as the gene variation results in higher plasma concentrations of siponimod.

- use 50% of the normal maintenance dose
 - reconsider the choice and the potential benefit of siponimod if the patient is also using a moderate CYP3A4 inducer, such as modafinil, or a strong CYP3A4 inducer
- For the comparable gene variation *1/*3, the moderate or strong CYP3A4 inducer results in a reduction in the exposure of siponimod by 49%, according to a pharmacokinetic model.

Literature:

1. Gardin A et al. Siponimod pharmacokinetics, safety, and tolerability in combination with the potent CYP3A4 inhibitor itraconazole in healthy subjects with different CYP2C9 genotypes. Eur J Clin Pharmacol 2019;75:1565-74.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9 PM OTHER: siponimod

[7118](#)

Siponimod is contraindicated in patients with the comparable gene variation *3/*3. Theoretically, the risk of adverse reactions is greatly increased, as the gene variation results in much higher plasma concentrations of siponimod.

- avoid siponimod

Literature:

1. Gardin A et al. Effect of fluconazole coadministration and CYP2C9 genetic polymorphism on siponimod pharmacokinetics in healthy subjects. Clin Pharmacokinet 2019;58:349-61.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9*1/*2: siponimod

[7112](#)

NO action is required for this gene-drug interaction.

The gene variation can slightly increase the exposure to siponimod. However, the effect is too small to expect any impact on efficacy or adverse reactions

Literature:

1. Gardin A et al. Siponimod pharmacokinetics, safety, and tolerability in combination with the potent CYP3A4 inhibitor itraconazole in healthy subjects with different CYP2C9 genotypes. Eur J Clin Pharmacol 2019;75:1565-74.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9*1/*3: siponimod

[7114](#)

Theoretically, the risk of adverse reactions is increased, as the gene variation results in higher plasma concentrations of siponimod.

- use 50% of the normal maintenance dose
 - reconsider the choice and the potential benefit of siponimod if the patient is also using a moderate CYP3A4 inducer, such as modafinil, or a strong CYP3A4 inducer
- For this gene variation, a moderate or strong CYP3A4 inducer results in a reduction in the exposure of siponimod by 49%, according to a pharmacokinetic model.

Literature:

1. Gardin A et al. Siponimod pharmacokinetics, safety, and tolerability in combination with the potent CYP3A4 inhibitor itraconazole in healthy subjects with different CYP2C9 genotypes. Eur J Clin Pharmacol 2019;75:1565-74.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9*2/*2: siponimod

[7113](#)

NO action is required for this gene-drug interaction.

The gene variation can slightly increase the exposure to siponimod. However, the effect is too small to expect any impact on efficacy or adverse reactions.

Literature:

1. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9*2/*3: siponimod

[7115](#)

Theoretically, the risk of adverse reactions is increased, as the gene variation results in higher plasma concentrations of siponimod.

- use 50% of the normal maintenance dose
 - reconsider the choice and the potential benefit of siponimod if the patient is also using a moderate CYP3A4 inducer, such as modafinil, or a strong CYP3A4 inducer
- For this genetic variation, a moderate or strong CYP3A4 inducer results in a reduction in the exposure of siponimod by 49%, according to a pharmacokinetic model.

Literature:

1. Gardin A et al. Effect of fluconazole coadministration and CYP2C9 genetic polymorphism on siponimod pharmacokinetics in healthy subjects. Clin Pharmacokinet 2019;58:349-61.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2C9*3/*3: siponimod

[7116](#)

Siponimod is contraindicated in patients with this gene variation. Theoretically, the risk of adverse reactions is greatly increased, as the gene variation results in much higher plasma concentrations of siponimod.

- avoid siponimod

Literature:

1. Gardin A et al. Effect of fluconazole coadministration and CYP2C9 genetic polymorphism on siponimod pharmacokinetics in healthy subjects. Clin Pharmacokinet 2019;58:349-61.
2. SmPC Mayzent (NL en VS).

Date 6-11-2023

CYP2D6 IM: sotalol

[2929](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2D6 PM: sotalol

[2928](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP2D6 UM: sotalol

[2930](#)

This is NOT a gene-drug interaction.

Literature:

-

Date 12-09-2022

CYP3A5 heterozygote expresser: tacrolimus

[2763](#)

An increase of the initial dose can result in an increased chance of reaching a tacrolimus concentration within the target range before the start of therapeutic drug monitoring. However, there is no direct evidence that this results in improved clinical results. The genetic variation results in increased conversion of tacrolimus to inactive metabolites and therefore in a higher required dose.

- Indications OTHER than liver transplantation:

- Use 1.5 times the initial dose that would yield the desired result in non-expressers

Adjustment of the dose should then be based on therapeutic drug monitoring.

For example: A Dutch study found a median trough concentration for tacrolimus of 14.7 ng/mL after 3 days at an initial dose of 0.15 mg/kg twice daily for 29 kidney transplant patients who were heterozygous expressers. Their target value was 10-15 ng/mL.

- LIVER transplantation:

In addition to the patient's genotype, the metabolism of tacrolimus is also determined by the genotype of the transplanted liver.

- LIVER is also of the genotype HETEROZYGOUS EXPRESSER:

- Use 1.5 times the normal initial dose

Adjustment of the dose should then be based on therapeutic drug monitoring.

- LIVER has a DIFFERENT genotype:

There is insufficient evidence in the literature to support a dose recommendation.

Literature:

1. Teng H et al. HDL-C and creatinine levels at 1 month are associated with patient 12-month survival rate after kidney transplantation. Pharmacogenet Genomics 2024;34:33-42.
2. Lenain R et al. Impact of tacrolimus daily dose limitation in renal transplant recipients expressing CYP3A5: a retrospective study. J Pers Med 2021;11:1002.
3. Yang H et al. Clinical impact of the adaptation of initial tacrolimus dosing to the CYP3A5 genotype after kidney transplantation: systematic review and meta-analysis of randomized controlled trials. Clin Pharmacokinet 2021;60:877-85.

4. Khan AR et al. CYP3A5 gene polymorphisms and their impact on dosage and trough concentration of tacrolimus among kidney transplant patients: a systematic review and meta-analysis. *Pharmacogenomics J* 2020;20:553-62.
5. Prasad N et al. Melding pharmacogenomic effect of MDR1 and CYP3A5 gene polymorphism on tacrolimus dosing in renal transplant recipients in Northern India. *Kidney Int Rep* 2019;5:28-38.
6. Largeau B et al. Comparison of tacrolimus starting doses based on CYP3A5 phenotype or genotype in kidney transplant recipients. *Prog Transplant* 2019;29:300-8.
7. Fernando ME et al. Influence of CYP3A5 and ABCB1 polymorphism on tacrolimus drug dosing in South Indian renal allograft recipients. *Indian J Nephrol* 2019;29:261-6.
8. Seibert SR et al. Tacrolimus trough and dose intra-patient variability and CYP3A5 genotype: effects on acute rejection and graft failure in European American and African American kidney transplant recipients. *Clin Transplant* 2018;32: e13424.
9. Liu F et al. Long-term influence of CYP3A5, CYP3A4, ABCB1, and NR1I2 polymorphisms on tacrolimus concentration in Chinese renal transplant recipients. *Genet Test Mol Biomarkers* 2017;21:663-73.
10. Pallet N et al. Long-term clinical impact of adaptation of initial tacrolimus dosing to CYP3A5 genotype. *Am J Transplant* 2016;16:2670-5.
11. Shuker N et al. A randomized controlled trial comparing the efficacy of Cyp3a5 genotype-based with body-weight-based tacrolimus dosing after living donor kidney transplantation. *Am J Transplant* 2016;16:2085-96.
12. De Meyer M et al. Pharmacogenetic-based strategy using de novo tacrolimus once daily after kidney transplantation: prospective pilot study. *Pharmacogenomics* 2016;17:1019-27.
13. Yaowakulpatana K et al. Impact of CYP3A5 polymorphism on trough concentrations and outcomes of tacrolimus minimization during the early period after kidney transplantation. *Eur J Clin Pharmacol* 2016;72:277-83.
14. Pulk RA et al. Multigene predictors of tacrolimus exposure in kidney transplant recipients. *Pharmacogenomics* 2015;16:841-54.
15. Wang L et al. Benefits of minimizing immunosuppressive dosage according to cytochrome P450 3A5 genotype in liver transplant patients: findings from a single-center study. *Genet Mol Res* 2015;14:3191-9.
16. Rojas L et al. Effect of CYP3A5*3 on kidney transplant recipients treated with tacrolimus: a systematic review and meta-analysis of observational studies. *Pharmacogenomics J* 2015;15:38-48.
17. Buendia JA et al. Effects of combinational CYP3A5 6986A>G polymorphism in graft liver and native intestine on the pharmacokinetics of tacrolimus in liver transplant patients: a meta-analysis. *Ther Drug Monit* 2014;36:442-7.
18. Uesugi M et al. Impact of cytochrome P450 3A5 polymorphism in graft livers on the frequency of acute cellular rejection in living-donor liver transplantation. *Pharmacogenet Genomics* 2014;24:356-66.
19. Terrazzino S et al. The effect of CYP3A5 6986A>G and ABCB1 3435C>T on tacrolimus dose-adjusted trough levels and acute rejection rates in renal transplant patients: a systematic review and meta-analysis. *Pharmacogenet Genomics* 2012;22:642-5.
20. Tang HL et al. Lower tacrolimus daily dose requirements and acute rejection rates in the CYP3A5 non-expressors than expressors. *Pharmacogenet Genomics* 2011;21:713-20.
21. Thervet E et al. Optimization of initial tacrolimus dose using pharmacogenetic testing. *Clin Pharmacol Ther* 2010; 87: 721-726.
22. Satoh S et al. Lack of tacrolimus circadian pharmacokinetics and CYP3A5 pharmacogenetics in the early and maintenance stages in Japanese renal transplant recipients. *Br J Clin Pharmacol* 2008;66:207-14.
23. Klauke B et al. No association between single nucleotide polymorphisms and the development of nephrotoxicity after orthotopic heart transplantation. *J Heart Lung Transplant* 2008;27:741-5.
24. Fukudo M et al. Impact of MDR1 and CYP3A5 on the oral clearance of tacrolimus and tacrolimus-related renal dysfunction in adult living-donor liver transplant patients. *Pharmacogenet Genomics* 2008;18:413-23.
25. Hesselink DA et al. CYP3A5 genotype is not associated with a higher risk of acute rejection in tacrolimus-treated renal transplant recipients. *Pharmacogenet Genomics* 2008;18:339-48.
26. Kuypers DR et al. CYP3A5 and CYP3A4 but not MDR1 single-nucleotide polymorphisms determine long-term tacrolimus disposition and drug-related nephrotoxicity in renal recipients. *Clin Pharmacol Ther* 2007;82:711-25.
27. Renders L et al. CYP3A5 genotype markedly influences the pharmacokinetics of tacrolimus and sirolimus in kidney transplant recipients. *Clin Pharmacol Ther* 2007;81:228-34.
28. Mourad M et al. The influence of genetic polymorphisms of cytochrome P450 3A5 and ABCB1 on starting dose- and weight-standardized tacrolimus trough concentrations after kidney transplantation in relation to renal function. *Clin Chem Lab Med* 2006;44:1192-8.
29. Roy JN et al. Cyp3A4, Cyp3A5, and MDR-1 genetic influences on tacrolimus pharmacokinetics in renal transplant recipients. *Pharmacogenet Genomics* 2006;16:659-65.
30. Cheung CY et al. Influence of different allelic variants of the CYP3A and ABCB1 genes on the tacrolimus pharmacokinetic profile of Chinese renal transplant recipients. *Pharmacogenomics* 2006;7:563-74.
31. Uesugi M et al. Effect of intestinal CYP3A5 on postoperative tacrolimus trough levels in living-donor liver transplant recipients. *Pharmacogenet Genomics* 2006;16:119-27.
32. Zhang X et al. Influence of CYP3A5 and MDR1 polymorphisms on tacrolimus concentration in the early stage after renal transplantation. *Clin Transplant* 2005;19:638-43.
33. Tada H et al. Impact of CYP3A5 and MDR1(ABCB1) C3435T polymorphisms on the pharmacokinetics of tacrolimus in renal transplant recipients. *Transplant Proc* 2005;37:1730-2.
34. Macphee IA et al. Tacrolimus pharmacogenetics: the CYP3A5*1 allele predicts low dose-normalized tacrolimus blood concentrations in whites and South Asians. *Transplantation* 2005;79:499-502.
35. Hesselink DA et al. Genetic polymorphisms of the CYP3A4, CYP3A5, and MDR-1 genes and

Date 23-05-2024

CYP3A5 homozygote expresser: tacrolimus

[2762](#)

An increase of the initial dose can result in an increased chance of reaching a tacrolimus concentration within the target range before the start of therapeutic drug monitoring. However, there is no direct evidence that this results in improved clinical results. The genetic variation results in an increased conversion of tacrolimus to inactive metabolites and therefore a higher required dose.

- Indications OTHER than liver transplantation:

- Use 2.5 times the initial dose that would yield the desired result in non-expressers

Adjustment of the dose should then be based on therapeutic drug monitoring.

For example: A Dutch study found a median trough concentration for tacrolimus of 9.4 ng/mL after 3 days at an initial dose of 0.15 mg/kg twice daily for 5 kidney transplant patients who were homozygous expressers. Their target value was 10-15 ng/mL.

- LIVER transplantation:

In addition to the patient's genotype, the metabolism of tacrolimus is also determined by the genotype of the transplanted liver.

- LIVER is also of the genotype HOMOZYGOUS EXPRESSER:

- Use 2.5 times the normal initial dose

Adjustment of the dose should then be based on therapeutic drug monitoring.

- LIVER has a DIFFERENT genotype:

There is insufficient evidence in the literature to support a dose recommendation.

Literature:

1. Teng H et al. HDL-C and creatinine levels at 1 month are associated with patient 12-month survival rate after kidney transplantation. Pharmacogenet Genomics 2024;34:33-42.
2. Lenain R et al. Impact of tacrolimus daily dose limitation in renal transplant recipients expressing CYP3A5: a retrospective study. J Pers Med 2021;11:1002.
3. Yang H et al. Clinical impact of the adaptation of initial tacrolimus dosing to the CYP3A5 genotype after kidney transplantation: systematic review and meta-analysis of randomized controlled trials. Clin Pharmacokinet 2021;60:877-85.
4. Khan AR et al. CYP3A5 gene polymorphisms and their impact on dosage and trough concentration of tacrolimus among kidney transplant patients: a systematic review and meta-analysis. Pharmacogenomics J 2020;20:553-62.
5. Prasad N et al. Melding pharmacogenomic effect of MDR1 and CYP3A5 gene polymorphism on tacrolimus dosing in renal transplant recipients in Northern India. Kidney Int Rep 2019;5:28-38.
6. Largeau B et al. Comparison of tacrolimus starting doses based on CYP3A5 phenotype or genotype in kidney transplant recipients. Prog Transplant 2019;29:300-8.
7. Fernando ME et al. Influence of CYP3A5 and ABCB1 polymorphism on tacrolimus drug dosing in South Indian renal allograft recipients. Indian J Nephrol 2019;29:261-6.
8. Seibert SR et al. Tacrolimus trough and dose intra-patient variability and CYP3A5 genotype: effects on acute rejection and graft failure in European American and African American kidney transplant recipients. Clin Transplant 2018;32: e13424.
9. Liu F et al. Long-term influence of CYP3A5, CYP3A4, ABCB1, and NR1I2 polymorphisms on tacrolimus concentration in Chinese renal transplant recipients. Genet Test Mol Biomarkers 2017;21:663-73.
10. Pallet N et al. Long-term clinical impact of adaptation of initial tacrolimus dosing to CYP3A5 genotype. Am J Transplant 2016;16:2670-5.
11. Shuker N et al. A randomized controlled trial comparing the efficacy of Cyp3a5 genotype-based with body-weight-based tacrolimus dosing after living donor kidney transplantation. Am J Transplant 2016;16:2085-96.
12. De Meyer M et al. Pharmacogenetic-based strategy using de novo tacrolimus once daily after kidney transplantation: prospective pilot study. Pharmacogenomics 2016;17:1019-27.
13. Yaowakulpatana K et al. Impact of CYP3A5 polymorphism on trough concentrations and outcomes of tacrolimus minimization during the early period after kidney transplantation. Eur J Clin Pharmacol 2016;72:277-83.
14. Pulk RA et al. Multigene predictors of tacrolimus exposure in kidney transplant recipients. Pharmacogenomics 2015;16:841-54.
15. Wang L et al. Benefits of minimizing immunosuppressive dosage according to cytochrome P450 3A5 genotype in liver transplant patients: findings from a single-center study. Genet Mol Res 2015;14:3191-9.
16. Rojas L et al. Effect of CYP3A5*3 on kidney transplant recipients treated with tacrolimus: a systematic review and meta-analysis of observational studies. Pharmacogenomics J 2015;15:38-48.
17. Buendia JA et al. Effects of combinational CYP3A5 6986A>G polymorphism in graft liver and native intestine on the pharmacokinetics of tacrolimus in liver transplant patients: a meta-analysis. Ther Drug Monit 2014;36:442-7.

18. Uesugi M et al. Impact of cytochrome P450 3A5 polymorphism in graft livers on the frequency of acute cellular rejection in living-donor liver transplantation. *Pharmacogenet Genomics* 2014;24:356-66.
19. Terrazzino S et al. The effect of CYP3A5 6986A>G and ABCB1 3435C>T on tacrolimus dose-adjusted trough levels and acute rejection rates in renal transplant patients: a systematic review and meta-analysis. *Pharmacogenet Genomics* 2012;22:642-5.
20. Tang HL et al. Lower tacrolimus daily dose requirements and acute rejection rates in the CYP3A5 non-expressers than expressers. *Pharmacogenet Genomics* 2011;21:713-20.
21. Thervet E et al. Optimization of initial tacrolimus dose using pharmacogenetic testing. *Clin Pharmacol Ther* 2010; 87: 721-726.
22. Satoh S et al. Lack of tacrolimus circadian pharmacokinetics and CYP3A5 pharmacogenetics in the early and maintenance stages in Japanese renal transplant recipients. *Br J Clin Pharmacol* 2008;66:207-14.
23. Klauke B et al. No association between single nucleotide polymorphisms and the development of nephrotoxicity after orthotopic heart transplantation. *J Heart Lung Transplant* 2008;27:741-5.
24. Fukudo M et al. Impact of MDR1 and CYP3A5 on the oral clearance of tacrolimus and tacrolimus-related renal dysfunction in adult living-donor liver transplant patients. *Pharmacogenet Genomics* 2008;18:413-23.
25. Hesselink DA et al. CYP3A5 genotype is not associated with a higher risk of acute rejection in tacrolimus-treated renal transplant recipients. *Pharmacogenet Genomics* 2008;18:339-48.
26. Kuypers DR et al. CYP3A5 and CYP3A4 but not MDR1 single-nucleotide polymorphisms determine long-term tacrolimus disposition and drug-related nephrotoxicity in renal recipients. *Clin Pharmacol Ther* 2007;82:711-25.
27. Renders L et al. CYP3A5 genotype markedly influences the pharmacokinetics of tacrolimus and sirolimus in kidney transplant recipients. *Clin Pharmacol Ther* 2007;81:228-34.
28. Mourad M et al. The influence of genetic polymorphisms of cytochrome P450 3A5 and ABCB1 on starting dose- and weight-standardized tacrolimus trough concentrations after kidney transplantation in relation to renal function. *Clin Chem Lab Med* 2006;44:1192-8.
29. Roy JN et al. Cyp3A4, Cyp3A5, and MDR-1 genetic influences on tacrolimus pharmacokinetics in renal transplant recipients. *Pharmacogenet Genomics* 2006;16:659-65.
30. Cheung CY et al. Influence of different allelic variants of the CYP3A and ABCB1 genes on the tacrolimus pharmacokinetic profile of Chinese renal transplant recipients. *Pharmacogenomics* 2006;7:563-74.
31. Uesugi M et al. Effect of intestinal CYP3A5 on postoperative tacrolimus trough levels in living-donor liver transplant recipients. *Pharmacogenet Genomics* 2006;16:119-27.
32. Zhang X et al. Influence of CYP3A5 and MDR1 polymorphisms on tacrolimus concentration in the early stage after renal transplantation. *Clin Transplant* 2005;19:638-43.
33. Tada H et al. Impact of CYP3A5 and MDR1(ABCB1) C3435T polymorphisms on the pharmacokinetics of tacrolimus in renal transplant recipients. *Transplant Proc* 2005;37:1730-2.
34. Macphee IA et al. Tacrolimus pharmacogenetics: the CYP3A5*1 allele predicts low dose-normalized tacrolimus blood concentrations in whites and South Asians. *Transplantation* 2005;79:499-502.
35. Hesselink DA et al. Genetic polymorphisms of the CYP3A4, CYP3A5, and MDR-1 genes and pharmacokinetics of the calcineurin inhibitors cyclosporine and tacrolimus. *Clin Pharmacol Ther* 2003;74:245-54.

Date 23-05-2024

CYP2D6 IM: tamoxifen

[2433](#)

This gene variation reduces the conversion of tamoxifen to the active metabolite endoxifen. This can result in reduced effectiveness.

Recommendation:

- select an alternative or measure the endoxifen concentration and increase the dose if necessary by a factor of 1.5-2
- Aromatase inhibitors are a possible alternative for post-menopausal women.
- if TAMOXIFEN is selected: avoid co-medication with CYP2D6 inhibitors such as paroxetine and fluoxetine

Literature:

1. Welzen ME et al. The effect of tamoxifen dose increment in patients with impaired CYP2D6 activity. *Ther Drug Monit* 2015;37:501-7.
2. Martinez de Dueñas E et al. Adjusting the dose of tamoxifen in patients with early breast cancer and CYP2D6 poor metabolizer phenotype. *Breast* 2014;23:400-6.
3. Province MA et al. CYP2D6 genotype and adjuvant tamoxifen: meta-analysis of heterogeneous study populations. *Clin Pharmacol Ther* 2014;95:216-27.
4. Jung JA et al. Association between CYP2D6 genotypes and the clinical outcomes of adjuvant tamoxifen for breast cancer: a meta-analysis. *Pharmacogenomics* 2014;15:49- 60.
5. Cronin-Fenton DP et al. Metabolism and transport of tamoxifen in relation to its effectiveness: new perspectives on an ongoing controversy. *Future Oncol* 2014;10:107-22.
6. Lum DW et al. CYP2D6 genotype and tamoxifen response for breast cancer: a systematic review and meta-analysis. *PLoS One* 2013;8:e76648.
7. Zeng Z et al. CYP2D6 polymorphisms influence tamoxifen treatment outcomes in breast cancer

- patients: a meta-analysis. *Cancer Chemother Pharmacol* 2013;72:287-303.
8. Regan MM et al. CYP2D6 genotype and tamoxifen response in postmenopausal women with endocrine-responsive breast cancer: the breast international group 1-98 trial. *J Natl Cancer Inst* 2012;104:441-51.
 9. Rae JM et al. CYP2D6 and UGT2B7 genotype and risk of recurrence in tamoxifen-treated breast cancer patients. *J Natl Cancer Inst* 2012;104:452-60.
 10. Park IH et al. Lack of any association between functionally significant CYP2D6 polymorphisms and clinical outcomes in early breast cancer patients receiving adjuvant tamoxifen treatment. *Breast Cancer Res Treat* 2012;131:455-61.
 11. Kiyotani K et al. Dose-adjustment study of tamoxifen based on CYP2D6 genotypes in Japanese breast cancer patients. *Breast Cancer Res Treat* 2012;131:137-45.
 12. Barginear MF et al. Increasing tamoxifen dose in breast cancer patients based on CYP2D6 genotypes and endoxifen levels: effect on active metabolite isomers and the antiestrogenic activity score. *Clin Pharmacol Ther* 2011;90:605-11.
 13. Irvin WJ Jr et al. Genotype-guided tamoxifen dosing increases active metabolite exposure in women with reduced CYP2D6 metabolism: a multicenter study. *J Clin Oncol* 2011;29:3232-9.
 14. Lash TL et al. CYP2D6 inhibition and breast cancer recurrence in a population-based study in Denmark. *J Natl Cancer Inst* 2011;103:489-500.
 15. Thompson AM et al. Comprehensive CYP2D6 genotype and adherence affect outcome in breast cancer patients treated with tamoxifen monotherapy. *Breast Cancer Res Treat* 2011;125:279-87.
 16. Stingl JC et al. Impact of CYP2D6 *4 genotype on progression free survival in tamoxifen breast cancer treatment. *Curr Med Res Opin* 2010;26:2535-42.
 17. Lammers LA et al. The impact of CYP2D6-predicted phenotype on tamoxifen treatment outcome in patients with metastatic breast cancer. *Br J Cancer* 2010;103:765-71.
 18. Schroth W et al. CYP2D6 polymorphisms as predictors of outcome in breast cancer patients treated with tamoxifen: expanded polymorphism coverage improves risk stratification. *Clin Cancer Res* 2010;16:4468-77.
 19. Seruga B et al. Cytochrome P450 2D6 and outcomes of adjuvant tamoxifen therapy: results of a meta-analysis. *Breast Cancer Res Treat* 2010;122:609-17.
 20. Kiyotani K et al. Lessons for pharmacogenomics studies: association study between CYP2D6 genotype and tamoxifen response. *Pharmacogenet Genomics* 2010;20:565-8.
 21. Abraham JE et al. CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. *Breast Cancer Res* 2010;12:R64.
 22. Schroth W et al. Association between CYP2D6 polymorphisms and outcomes among women with early stage breast cancer treated with tamoxifen. *JAMA* 2009;302:1429- 36.
 23. Gjerde J et al. Effects of CYP2D6 and SULT1A1 genotypes including SULT1A1 gene copy number on tamoxifen metabolism. *Ann Oncol* 2008;19:56-61.
 24. Schroth W et al. Breast cancer treatment outcome with adjuvant tamoxifen relative to patient CYP2D6 and CYP2C19 genotypes. *J Clin Oncol* 2007;25:5187-93.
 25. Lim HS et al. Clinical implications of CYP2D6 genotypes predictive of tamoxifen pharmacokinetics in metastatic breast cancer. *J Clin Oncol* 2007;25:3837-45.
 26. Gonzalez-Santiago S et al. CYP2D6*4 polymorphism as blood predictive biomarker of breast cancer relapse in patients receiving adjuvant tamoxifen. *J Clin Oncol* 2007;25(18S):590.
 27. Wegman P et al. Genetic variants of CYP3A5, CYP2D6, SULT1A1, UGT2B15 and tamoxifen response in postmenopausal patients with breast cancer. *Breast Cancer Res* 2007;9:R7.
 28. Goetz MP et al. The impact of cytochrome P450 2D6 metabolism in women receiving adjuvant tamoxifen. *Breast Cancer Res Treat* 2007;101:113-21.
 29. Borges S et al. Quantitative effect of CYP2D6 genotype and inhibitors on tamoxifen metabolism: implication for optimization of breast cancer treatment. *Clin Pharmacol Ther* 2006;80:61-74.
 30. Nowell SA et al. Association of genetic variation in tamoxifen-metabolizing enzymes with overall survival and recurrence of disease in breast cancer patients. *Breast Cancer Res Treat* 2005;91:249-58.
 31. Jin Y et al. CYP2D6 genotype, antidepressant use, and tamoxifen metabolism during adjuvant breast cancer treatment. *J Natl Cancer Inst* 2005;97:30-9.
 32. Wegman P et al. Genotype of metabolic enzymes and the benefit of tamoxifen in postmenopausal breast cancer patients. *Breast Cancer Res* 2005;7:R284-90.

Date 09-11-2015

CYP2D6 PM: tamoxifen

[2432](#)

This gene variation reduces the conversion of tamoxifen to the active metabolite endoxifen. This can result in reduced effectiveness.

Recommendation:

- select an alternative or increase the dose to 40 mg/day and monitor the endoxifen concentration
- Studies have demonstrated that PM can achieve an adequate endoxifen concentration when the dose is increased to 40-60 mg/day.
- Aromatase inhibitors are a possible alternative for post-menopausal women.

Literature:

1. Welzen ME et al. The effect of tamoxifen dose increment in patients with impaired CYP2D6 activity. *Ther Drug Monit* 2015;37:501-7.
2. Martinez de Dueñas E et al. Adjusting the dose of tamoxifen in patients with early breast cancer and CYP2D6 poor metabolizer phenotype. *Breast* 2014;23:400-6.
3. Province MA et al. CYP2D6 genotype and adjuvant tamoxifen: meta-analysis of heterogeneous study populations. *Clin Pharmacol Ther* 2014;95:216-27.
4. Jung JA et al. Association between CYP2D6 genotypes and the clinical outcomes of adjuvant tamoxifen for breast cancer: a meta-analysis. *Pharmacogenomics* 2014;15:49- 60.
5. Cronin-Fenton DP et al. Metabolism and transport of tamoxifen in relation to its effectiveness: new perspectives on an ongoing controversy. *Future Oncol* 2014;10:107-22.
6. Lum DW et al. CYP2D6 genotype and tamoxifen response for breast cancer: a systematic review and meta-analysis. *PLoS One* 2013;8:e76648.
7. Zeng Z et al. CYP2D6 polymorphisms influence tamoxifen treatment outcomes in breast cancer patients: a meta-analysis. *Cancer Chemother Pharmacol* 2013;72:287-303.
8. Regan MM et al. CYP2D6 genotype and tamoxifen response in postmenopausal women with endocrine-responsive breast cancer: the breast international group 1-98 trial. *J Natl Cancer Inst* 2012;104:441-51.
9. Rae JM et al. CYP2D6 and UGT2B7 genotype and risk of recurrence in tamoxifen-treated breast cancer patients. *J Natl Cancer Inst* 2012;104:452-60.
10. Barginear MF et al. Increasing tamoxifen dose in breast cancer patients based on CYP2D6 genotypes and endoxifen levels: effect on active metabolite isomers and the antiestrogenic activity score. *Clin Pharmacol Ther* 2011;90:605-11.
11. Irvin WJ Jr et al. Genotype-guided tamoxifen dosing increases active metabolite exposure in women with reduced CYP2D6 metabolism: a multicenter study. *J Clin Oncol* 2011;29:3232-9.
12. Lash TL et al. CYP2D6 inhibition and breast cancer recurrence in a population-based study in Denmark. *J Natl Cancer Inst* 2011;103:489-500.
13. Thompson AM et al. Comprehensive CYP2D6 genotype and adherence affect outcome in breast cancer patients treated with tamoxifen monotherapy. *Breast Cancer Res Treat* 2011;125:279-87.
14. Stingl JC et al. Impact of CYP2D6 *4 genotype on progression free survival in tamoxifen breast cancer treatment. *Curr Med Res Opin* 2010;26:2535-42.
15. Lammers LA et al. The impact of CYP2D6-predicted phenotype on tamoxifen treatment outcome in patients with metastatic breast cancer. *Br J Cancer* 2010;103:765-71.
16. Schroth W et al. CYP2D6 polymorphisms as predictors of outcome in breast cancer patients treated with tamoxifen: expanded polymorphism coverage improves risk stratification. *Clin Cancer Res* 2010;16:4468-77.
17. Seruga B et al. Cytochrome P450 2D6 and outcomes of adjuvant tamoxifen therapy: results of a meta-analysis. *Breast Cancer Res Treat* 2010;122:609-17.
18. Kiyotani K et al. Lessons for pharmacogenomics studies: association study between CYP2D6 genotype and tamoxifen response. *Pharmacogenet Genomics* 2010;20:565-8.
19. Abraham JE et al. CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. *Breast Cancer Res* 2010;12:R64.
20. Schroth W et al. Association between CYP2D6 polymorphisms and outcomes among women with early stage breast cancer treated with tamoxifen. *JAMA* 2009;302:1429- 36.
21. Gjerde J et al. Effects of CYP2D6 and SULT1A1 genotypes including SULT1A1 gene copy number on tamoxifen metabolism. *Ann Oncol* 2008;19:56-61.
22. Schroth W et al. Breast cancer treatment outcome with adjuvant tamoxifen relative to patient CYP2D6 and CYP2C19 genotypes. *J Clin Oncol* 2007;25:5187-93.
23. Gonzalez-Santiago S et al. CYP2D6*4 polymorphism as blood predictive biomarker of breast cancer relapse in patients receiving adjuvant tamoxifen. *J Clin Oncol* 2007;25(18S):590.
24. Wegman P et al. Genetic variants of CYP3A5, CYP2D6, SULT1A1, UGT2B15 and tamoxifen response in postmenopausal patients with breast cancer. *Breast Cancer Res* 2007;9:R7.
25. Goetz MP et al. The impact of cytochrome P450 2D6 metabolism in women receiving adjuvant tamoxifen. *Breast Cancer Res Treat* 2007;101:113-21.
26. Bonanni B et al. Polymorphism in the CYP2D6 tamoxifen-metabolizing gene influences clinical effect but not hot flashes: data from the Italian Tamoxifen Trial. *J Clin Oncol* 2006;24:3708-9.
27. Borges S et al. Quantitative effect of CYP2D6 genotype and inhibitors on tamoxifen metabolism: implication for optimization of breast cancer treatment. *Clin Pharmacol Ther* 2006;80:61-74.
28. Goetz MP et al. Pharmacogenetics of tamoxifen biotransformation is associated with clinical outcomes of efficacy and hot flashes. *J Clin Oncol* 2005;23:9312-8.
29. Nowell SA et al. Association of genetic variation in tamoxifen-metabolizing enzymes with overall survival and recurrence of disease in breast cancer patients. *Breast Cancer Res Treat* 2005;91:249-58.
30. Jin Y et al. CYP2D6 genotype, antidepressant use, and tamoxifen metabolism during adjuvant breast cancer treatment. *J Natl Cancer Inst* 2005;97:30-9.
31. Wegman P et al. Genotype of metabolic enzymes and the benefit of tamoxifen in postmenopausal breast cancer patients. *Breast Cancer Res* 2005;7:R284-90.
32. SPC Tamoxifen PCH.

NO action is needed for this gene-drug interaction.

As a result of the genetic variation, the plasma concentration of the active metabolites 4-hydroxytamoxifen and endoxifen can increase. However, there is no evidence that this results in an increase in the side effects.

Literature:

1. Martinez de Dueñas E et al. Adjusting the dose of tamoxifen in patients with early breast cancer and CYP2D6 poor metabolizer phenotype. *Breast* 2014;23:400-6.
2. Schroth W et al. CYP2D6 polymorphisms as predictors of outcome in breast cancer patients treated with tamoxifen: expanded polymorphism coverage improves risk stratification. *Clin Cancer Res* 2010;16:4468-77.
3. Gjerde J et al. Effects of CYP2D6 and SULT1A1 genotypes including SULT1A1 gene copy number on tamoxifen metabolism. *Ann Oncol* 2008;19:56-61.
4. Lim HS et al. Clinical implications of CYP2D6 genotypes predictive of tamoxifen pharmacokinetics in metastatic breast cancer. *J Clin Oncol* 2007;25:3837-45.

Date 09-11-2015

DPD AS 0: tegafur**[2942](#)**

The gene variation increases the risk of severe, possibly fatal toxicity. A reduced conversion of tegafur to inactive metabolites means that the normal dose is an overdose.

- avoid tegafur

Fluorouracil and capecitabine are not suitable alternatives, as these are also metabolised by DPD.

- If it is not possible to avoid tegafur: start with a very low dose and adjust the initial dose based on toxicity and efficacy. A substantiated recommendation for dose reduction cannot be made based on the literature. The recommendation for fluorouracil and capecitabine is to determine the residual DPD activity in mononuclear cells from peripheral blood and to adjust the initial dose accordingly. A patient with 0.5% of the normal DPD activity tolerated 0.8% of the standard capecitabine dose (150 mg every 5 days). A patient with undetectable DPD activity tolerated 0.43% of the standard capecitabine dose (150 mg every 5 days with every third dose skipped)

Literature:

1. Deenen MJ et al. Standard-dose tegafur combined with uracil is not safe treatment after severe toxicity from 5-fluorouracil or capecitabine. *Ann Intern Med* 2010;153:767-8.
2. SPC Teysuno.

Date 13-05-2019

DPD AS 1,5: tegafur**[4645](#)**

The gene variation increases the risk of severe, possibly fatal toxicity. A reduced conversion of tegafur into inactive metabolites means that the normal dose is an overdose.

- Avoid tegafur or start with a low dose and adjust the initial dose based on toxicity and efficacy

Fluorouracil and capecitabine are not alternatives, as these are also metabolised by DPD.

It is not possible to offer substantiated advice for dose reduction based on the literature.

For fluorouracil and capecitabine, starting with 50 % of the standard dose is recommended and the dose should then be adjusted based on toxicity and effectiveness.

In one study, the average dose of fluorouracil/capecitabine after titration was 64% of the standard dose for 17 patients with genotype *1/2846T and 74% of the standard dose for 51 patients with genotype *1/1236A.

Literature:

1. Cubero DI et al. Tegafur-uracil is a safe alternative for the treatment of colorectal cancer in patients with partial dihydropyrimidine dehydrogenase deficiency: a proof of principle. *Ther Adv Med Oncol* 2012;4:167-72.
2. Deenen MJ et al. Standard-dose tegafur combined with uracil is not safe treatment after severe toxicity from 5-fluorouracil or capecitabine. *Ann Intern Med* 2010;153:767-8.
3. SPC Teysuno.

DPD AS 1: tegafur

[2943](#)

The gene variation increases the risk of severe, possibly fatal toxicity. A reduced conversion of tegafur into inactive metabolites means that the normal dose is an overdose.

- Avoid tegafur or start with a low dose and adjust the initial dose based on toxicity and efficacy
- Fluorouracil and capecitabine are not alternatives, as these are also metabolised by DPD.
It is not possible to offer substantiated advice for dose reduction based on the literature.
For fluorouracil and capecitabine, starting with 50% of the standard dose is recommended.

Literature:

1. Cubero DI et al. Tegafur-uracil is a safe alternative for the treatment of colorectal cancer in patients with partial dihydropyrimidine dehydrogenase deficiency: a proof of principle. *Ther Adv Med Oncol* 2012;4:167-72.
2. Deenen MJ et al. Standard-dose tegafur combined with uracil is not safe treatment after severe toxicity from 5-fluorouracil or capecitabine. *Ann Intern Med* 2010;153:767-8.
3. SPC Teysuno.

Date 13-05-2019

DPD FENO: tegafur

[4644](#)

The gene variation increases the risk of severe, possibly fatal toxicity. A reduced conversion of tegafur to inactive metabolites means that the normal dose is an overdose.

- Avoid tegafur or start with a low dose and adjust the initial dose based on toxicity and efficacy
- Fluorouracil and capecitabine are not alternatives, as these are also metabolised by DPD.
It is not possible to offer substantiated advice for dose reduction based on the literature.
For fluorouracil and capecitabine, it is recommended to determine the residual DPD activity in mononuclear cells from peripheral blood and adjust the initial dose based on phenotype and genotype.

Literature:

1. Cubero DI et al. Tegafur-uracil is a safe alternative for the treatment of colorectal cancer in patients with partial dihydropyrimidine dehydrogenase deficiency: a proof of principle. *Ther Adv Med Oncol* 2012;4:167-72.
2. Deenen MJ et al. Standard-dose tegafur combined with uracil is not safe treatment after severe toxicity from 5-fluorouracil or capecitabine. *Ann Intern Med* 2010;153:767-8.
3. SPC Teysuno.

Date 13-05-2019

CYP2C19 IM: ticagrelor

[3542](#)

This is NOT a gene-drug interaction.

Literature:

1. Rath PC et al. A study on the impact of CYP2C19 genotype and platelet reactivity assay on patients undergoing PCI. *Indian Heart J* 2015;67:114-21.
2. Steg PG et al. Stent thrombosis with ticagrelor versus clopidogrel in patients with acute coronary syndromes: an analysis from the prospective, randomized PLATO trial. *Circulation* 2013;128:1055-65.
3. Tantry US et al. First analysis of the relation between CYP2C19 genotype and pharmacodynamics in patients treated with ticagrelor versus clopidogrel: the ONSET/OFFSET and RESPOND genotype studies. *Circ Cardiovasc Genet* 2010;3:556-66.
4. Wallentin L et al. Effect of CYP2C19 and ABCB1 single nucleotide polymorphisms on outcomes of treatment with ticagrelor versus clopidogrel for acute coronary syndromes: a genetic substudy of the PLATO trial. *Lancet* 2010;376:1320-8.
5. SPC's Brilique (NL) en Brilinta (VS).

Date 19-11-2018

CYP2C19 PM: ticagrelor

[3541](#)

This is NOT a gene-drug interaction.

Literature:

1. Zhong Z et al. Effect of cytochrome P450 2C19 polymorphism on adverse cardiovascular events after drug-eluting stent implantation in a large Hakka population with acute coronary syndrome receiving clopidogrel in southern China. *Eur J Clin Pharmacol* 2018;74:423-31.
2. Shen DL et al. Clinical value of CYP2C19 genetic testing for guiding the antiplatelet therapy in a Chinese population. *J Cardiovasc Pharmacol* 2016;67:232-6.
3. Xiong R et al. A randomized controlled trial to assess the efficacy and safety of doubling dose clopidogrel versus ticagrelor for the treatment of acute coronary syndrome in patients with CYP2C19*2 homozygotes. *Int J Clin Exp Med* 2015;8:13310-6.
4. Rath PC et al. A study on the impact of CYP2C19 genotype and platelet reactivity assay on patients undergoing PCI. *Indian Heart J* 2015;67:114-21.
5. Steg PG et al. Stent thrombosis with ticagrelor versus clopidogrel in patients with acute coronary syndromes: an analysis from the prospective, randomized PLATO trial. *Circulation* 2013;128:1055-65.
6. Tantry US et al. First analysis of the relation between CYP2C19 genotype and pharmacodynamics in patients treated with ticagrelor versus clopidogrel: the ONSET/OFFSET and RESPOND genotype studies. *Circ Cardiovasc Genet* 2010;3:556-66.
7. Wallentin L et al. Effect of CYP2C19 and ABCB1 single nucleotide polymorphisms on outcomes of treatment with ticagrelor versus clopidogrel for acute coronary syndromes: a genetic substudy of the PLATO trial. *Lancet* 2010;376:1320-8.
8. SPC's Brilique (NL) en Brilinta (VS).

Date 19-11-2018

CYP2C19 UM: ticagrelor

[3543](#)

This is NOT a gene-drug interaction.

Literature:

1. Rath PC et al. A study on the impact of CYP2C19 genotype and platelet reactivity assay on patients undergoing PCI. *Indian Heart J* 2015;67:114-21.
2. Steg PG et al. Stent thrombosis with ticagrelor versus clopidogrel in patients with acute coronary syndromes: an analysis from the prospective, randomized PLATO trial. *Circulation* 2013;128:1055-65.
3. Tantry US et al. First analysis of the relation between CYP2C19 genotype and pharmacodynamics in patients treated with ticagrelor versus clopidogrel: the ONSET/OFFSET and RESPOND genotype studies. *Circ Cardiovasc Genet* 2010;3:556-66.

Date 19-11-2018

NUDT15 IM: tioguanine

[6956](#)

Grade ≥ 2 leukopenia occurs in an estimated 40% of these patients with normal therapy. The gene variation increases the amount of the fully activated metabolite of tioguanine.

- IMMUNOSUPPRESSION:

- start with 50% of the normal dose

Adjustment of the initial dose should be guided by toxicity (monitoring of the blood count) and effectiveness.

Monitoring should be performed at an increased frequency.

NOTE: The percentage of 50% is based on the analogy with azathioprine and 6-mercaptopurine, that form the same active metabolite as thioguanine.

NOTE: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

- LEUKAEMIA:

- start with 50% of the normal tioguanine dose or start with the normal dose and reduce to 50% if side effects necessitate a dose reduction

It is not known whether dose reduction in advance results in the same efficacy as dose reduction based on toxicity.

Adjustment of the initial dose should be guided by toxicity (monitoring of blood count) and effectiveness. Monitoring should be performed at an increased frequency.

NOTE: The percentage of 50% is based on the analogy with azathioprine and 6-mercaptopurine, that form the same active metabolite as thioguanine.

NOTE: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

NOTE: more stringent dose reductions are necessary if the patient is also TPMT IM or TPMT PM.

Literature:

1. Yu N et al. Prevalence of NUDT15 genetic variants and incidence of thiopurine-induced leukopenia in inflammatory bowel disease: a systematic review and meta-analysis. *J Crohns Colitis* 2023;jjad107.
2. Wang CW et al. Implementation of NUDT15 genotyping to prevent azathioprine-induced leukopenia for patients with autoimmune disorders in Chinese population. *Clin Pharmacol Ther* 2022;112:1079-87.
3. Maeda T et al. Long-term efficacy and tolerability of dose-adjusted thiopurine treatment in maintaining remission in inflammatory bowel disease patients with NUDT15 heterozygosity. *Intest Res* 2022;20:90-100.
4. Chao K et al. Randomised clinical trial: dose optimising strategy by NUDT15 genotyping reduces leucopenia during thiopurine treatment of Crohn's disease. *Aliment Pharmacol Ther* 2021;54:1124-1133.
5. Mao X et al. Effects of TPMT, NUDT15, and ITPA genetic variants on 6-mercaptopurine toxicity for pediatric patients with acute lymphoblastic leukemia in Yunnan of China. *Front Pediatr* 2021;9:719803.
6. Tanaka Y et al. An international retrospective study for tolerability of 6-mercaptopurine on NUDT15 bi-allelic variants in children with acute lymphoblastic leukemia. *Haematologica* 2021;106:2026-9.
7. Wang DS et al. Childhood acute lymphoblastic leukemia mercaptopurine intolerance is associated with NUDT15 variants. *Pediatr Res* 2021;89: 217-22.
8. van Gennep S et al. Systematic review with meta-analysis: risk factors for thiopurine-induced leukopenia in IBD. *Aliment Pharmacol Ther* 2019;50:484-506.
9. Wang R et al. Association between the c.415C > T, c.52G > A, and 36_37insGGAGTC polymorphisms of NUDT 15 and thiopurine-induced leukopenia, thiopurine intolerance, and severe hair loss: an updated meta-analysis. *Drug Des Devel Ther* 2019;13:2729-44.
10. Park Y et al. Star allele-based haplotyping versus gene-wise variant burden scoring for predicting 6-mercaptopurine intolerance in pediatric acute lymphoblastic leukemia patients. *Front Pharmacol* 2019;10:654.
11. Liu Y et al. Associations between the NUDT15 R139C polymorphism and susceptibility to thiopurine-induced leukopenia in Asians: a meta-analysis. *Onco Targets Ther* 2018;11:8309-17.
12. Zhu Y et al. Combination of common and novel rare NUDT15 variants improves predictive sensitivity of thiopurine-induced leukopenia in children with acute lymphoblastic leukemia. *Haematologica* 2018;103:e293-e295.
13. Zhang AL et al. Association of NUDT15 c.415C>T allele and thiopurine-induced leukocytopenia in Asians: a systematic review and meta-analysis. *Ir J Med Sci* 2018;187:145-153.
14. Yi ES et al. NUDT15 variants cause hematopoietic toxicity with low 6-TGN levels in children with acute lymphoblastic leukemia. *Cancer Res Treat* 2018;50:872-82.
15. Kim H et al. APEX1 polymorphism and mercaptopurine-related early onset neutropenia in pediatric acute lymphoblastic leukemia. *Cancer Res Treat* 2018;50:823-34.
16. Chao K et al. Combined detection of NUDT15 variants could highly predict thiopurine-induced leukopenia in Chinese patients with inflammatory bowel disease: a multicenter analysis. *Inflamm Bowel Dis* 2017;23:1592-9.
17. Yin D et al. Impact of NUDT15 polymorphisms on thiopurines-induced myelotoxicity and thiopurines tolerance dose. *Oncotarget* 2017;8:13575-85.
18. Liang DC et al. NUDT15 gene polymorphism related to mercaptopurine intolerance in Taiwan Chinese children with acute lymphoblastic leukemia. *Pharmacogenomics J* 2016;16:536-9.
19. Zhu X et al. NUDT15 polymorphisms are better than thiopurine S-methyltransferase as predictor of risk for thiopurine-induced leukopenia in Chinese patients with Crohn's disease. *Aliment Pharmacol Ther* 2016;44:967-75.
20. Moriyama T et al. NUDT15 polymorphisms alter thiopurine metabolism and hematopoietic toxicity. *Nat Genet* 2016;48:367-73.
21. Yang JJ et al. Inherited NUDT15 variant is a genetic determinant of mercaptopurine intolerance in children with acute lymphoblastic leukemia. *J Clin Oncol* 2015;33:1235-42.
22. Lennard L et al. Thiopurine dose intensity and treatment outcome in childhood lymphoblastic leukaemia: the influence of thiopurine methyltransferase pharmacogenetics. *Br J Haematol.* 2015;169:228-40. PubMed PMID: 25441457.
23. Yang SK et al. A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. *Nat Genet* 2014;46:1017-20.
24. SmPCs Lanvis (NL) and Tabloid (USA)

Date 25-9-2023

NUDT15 PM: tioguanine

[6957](#)

Grade ≥ 2 leukopaenia occurs in an estimated 95% of these patients with standard therapy. The genetic variation increases the concentration of the fully activated metabolite of tioguanine.

- avoid tioguanine
 - if it is not possible to avoid tioguanine: use 10% of the standard dose and advise patients to report symptoms of myelosuppression (such as severe sore throat in combination with fever, regular nosebleeds and tendency to bruising)
- Adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and effectiveness. Monitoring should be performed at an increased frequency.
- NOTE: The percentage of 10% is based on the analogy with azathioprine and 6-mercaptopurine and the

analogy with TPMT, for which the gene variants have a comparable effect on toxicity to those of NUDT15. For NUDT15 PM, a percentage of < 20% was calculated for azathioprine and 6-mercaptopurine, but there were insufficient data available to calculate the exact percentage.

NOTE: Dose adjustment based on the total of 6-TGN metabolites is not possible for these patients, as they develop toxicity within the therapeutic range that applies for patients without gene variants.

NOTE: more stringent dose reductions are necessary if the patient is also TPMT IM or TPMT PM.

Literature:

1. Yu N et al. Prevalence of NUDT15 genetic variants and incidence of thiopurine-induced leukopenia in inflammatory bowel disease: a systematic review and meta-analysis. *J Crohns Colitis* 2023;jjad107.
2. Wang CW et al. Implementation of NUDT15 genotyping to prevent azathioprine-induced leukopenia for patients with autoimmune disorders in Chinese population. *Clin Pharmacol Ther* 2022;112:1079-87.
3. Chao K et al. Randomised clinical trial: dose optimising strategy by NUDT15 genotyping reduces leucopenia during thiopurine treatment of Crohn's disease. *Aliment Pharmacol Ther* 2021;54:1124-1133.
4. Mao X et al. Effects of TPMT, NUDT15, and ITPA genetic variants on 6-mercaptopurine toxicity for pediatric patients with acute lymphoblastic leukemia in Yunnan of China. *Front Pediatr* 2021;9:719803.
5. Tanaka Y et al. An international retrospective study for tolerability of 6-mercaptopurine on NUDT15 bi-allelic variants in children with acute lymphoblastic leukemia. *Haematologica* 2021;106:2026-9.
6. Wang DS et al. Childhood acute lymphoblastic leukemia mercaptopurine intolerance is associated with NUDT15 variants. *Pediatr Res* 2021;89: 217-22.
7. van Gennep S et al. Systematic review with meta-analysis: risk factors for thiopurine-induced leukopenia in IBD. *Aliment Pharmacol Ther* 2019;50:484-506.
8. Wang R et al. Association between the c.415C > T, c.52G > A, and 36_37insGGAGTC polymorphisms of NUDT 15 and thiopurine-induced leukopenia, thiopurine intolerance, and severe hair loss: an updated meta-analysis. *Drug Des Devel Ther* 2019;13:2729-44.
9. Park Y et al. Star allele-based haplotyping versus gene-wise variant burden scoring for predicting 6-mercaptopurine intolerance in pediatric acute lymphoblastic leukemia patients. *Front Pharmacol* 2019;10:654.
10. Liu Y et al. Associations between the NUDT15 R139C polymorphism and susceptibility to thiopurine-induced leukopenia in Asians: a meta-analysis. *Onco Targets Ther* 2018;11:8309-17.
11. Zhu Y et al. Combination of common and novel rare NUDT15 variants improves predictive sensitivity of thiopurine-induced leukopenia in children with acute lymphoblastic leukemia. *Haematologica* 2018;103:e293-e295.
12. Zhang AL et al. Association of NUDT15 c.415C>T allele and thiopurine-induced leukocytopenia in Asians: a systematic review and meta-analysis. *Ir J Med Sci* 2018;187:145-153.
13. Yi ES et al. NUDT15 variants cause hematopoietic toxicity with low 6-TGN levels in children with acute lymphoblastic leukemia. *Cancer Res Treat* 2018;50:872-82.
14. Kim H et al. APEX1 polymorphism and mercaptopurine-related early onset neutropenia in pediatric acute lymphoblastic leukemia. *Cancer Res Treat* 2018;50:823-34.
15. Chao K et al. Combined detection of NUDT15 variants could highly predict thiopurine-induced leukopenia in Chinese patients with inflammatory bowel disease: a multicenter analysis. *Inflamm Bowel Dis* 2017;23:1592-9.
16. Yin D et al. Impact of NUDT15 polymorphisms on thiopurines-induced myelotoxicity and thiopurines tolerance dose. *Oncotarget* 2017;8:13575-85.
17. Liang DC et al. NUDT15 gene polymorphism related to mercaptopurine intolerance in Taiwan Chinese children with acute lymphoblastic leukemia. *Pharmacogenomics J* 2016;16:536-9.
18. Zhu X et al. NUDT15 polymorphisms are better than thiopurine S-methyltransferase as predictor of risk for thiopurine-induced leukopenia in Chinese patients with Crohn's disease. *Aliment Pharmacol Ther* 2016;44:967-75.
19. Moriyama T et al. NUDT15 polymorphisms alter thiopurine metabolism and hematopoietic toxicity. *Nat Genet* 2016;48:367-73.
20. Yang JJ et al. Inherited NUDT15 variant is a genetic determinant of mercaptopurine intolerance in children with acute lymphoblastic leukemia. *J Clin Oncol* 2015;33:1235-42.
21. Yang SK et al. A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. *Nat Genet* 2014;46:1017-20.
22. SmPCs Lanvis (NL) and Tabloid (USA).

Date 25-9-2023

TPMT IM: tioguanine

[2560](#)

The risk of serious adverse events such as myelosuppression is increased. The genetic variation increases the concentration of the active metabolites of tioguanine.

- IMMUNOSUPPRESSION:

- Start with 75% of the standard dose

Adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and efficacy.

- LEUKAEMIA:

- start with 75% of the standard tioguanine dose, or start with the standard dose and reduce to 75% if side effects necessitate a dose reduction It is not known whether dose reduction in advance results in the same efficacy as dose reduction based on toxicity.

The initial dose should be adjusted based on toxicity (monitoring of the blood counts) and efficacy.

Note: more stringent dose reductions are necessary if the patient is also NUDT15 IM or NUDT15 PM.

Literature:

1. McAtee CL et al. Treatment-related sinusoidal obstruction syndrome in children with de novo acute lymphoblastic leukemia during intensification. *Cancer Chemother Pharmacol* 2017;80:1261-4.
2. Lennard L et al. Thiopurine dose intensity and treatment outcome in childhood lymphoblastic leukaemia: the influence of thiopurine methyltransferase pharmacogenetics. *Br J Haematol* 2015;169:228-40.
3. Wray L et al. TPMT and MTHFR genotype is not associated with altered risk of thioguanine-related sinusoidal obstruction syndrome in pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group. *Pediatr Blood Cancer* 2014;61:2086-8.
4. Lennard L et al. The thiopurine methyltransferase genetic polymorphism is associated with thioguanine-related veno-occlusive disease of the liver in children with acute lymphoblastic leukemia. *Clin Pharmacol Ther* 2006;80:375-83.
5. Standen GR et al. Heterozygosity for the thiopurine methyltransferase *3A allele in an acute non-lymphoblastic leukaemia patient with delayed marrow regeneration following H-DAT chemotherapy. *Br J Haematol* 2001;112:1089.
6. Teml A et al. A prospective, open-label trial of 6-thioguanine in patients with ulcerative or indeterminate colitis. *Scand J Gastroenterol* 2005;40:1205-13.
7. Herrlinger KR et al. Thioguanine-nucleotides do not predict efficacy of tioguanine in Crohn's disease. *Aliment Pharmacol Ther* 2004;19:1269-76.

Date 04-11-2019

TPMT PM: tioguanine

[2561](#)

The risk of serious, life-threatening adverse events such as myelosuppression is strongly increased. The genetic variation increases the concentration of the active metabolites of tioguanine.

- Choose an alternative or use 6-7% of the standard dose
Any adjustment of the initial dose should be guided by toxicity (monitoring of blood counts) and effectiveness.
- If the dose is decreased: advise patients to seek medical attention when symptoms of myelosuppression (such as severe sore throat in combination with fever, regular nosebleeds and tendency to bruising) develop

Literature:

1. van der Burg M and Gerding MN. Pancytopenie bij tioguaninegebruik. *Ned Tijdschr Geneeskd* 2018;162:D2839.
2. Lennard L et al. Thiopurine dose intensity and treatment outcome in childhood lymphoblastic leukaemia: the influence of thiopurine methyltransferase pharmacogenetics. *Br J Haematol* 2015;169:228-40.
3. Wray L et al. TPMT and MTHFR genotype is not associated with altered risk of thioguanine-related sinusoidal obstruction syndrome in pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group. *Pediatr Blood Cancer* 2014;61:2086-8.
4. Mares WG et al. Safe 6-thioguanine therapy of a TPMT deficient Crohn's disease patient by using therapeutic drug monitoring. *J Crohns Colitis* 2009;3:128-30.
5. McBride KL et al. Severe 6-thioguanine-induced marrow aplasia in a child with acute lymphoblastic leukemia and inherited thiopurine methyltransferase deficiency. *J Pediatr Hematol Oncol* 2000;22:441-5.
6. SmPC's Lanvis (NL) and Tabloid (VS).

Date 04-11-2019

CYP2C9 IM ANDERS: tolbutamide

[2556](#)

NO action is required for this gene-drug interaction.

There is insufficient evidence to state that the increased tolbutamide plasma concentration has any clinical consequences.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. *Clin Pharmacol Ther* 2009;86:54-61.
3. Becker ML et al. Cytochrome P450 2C9 2 and 3 polymorphisms and the dose and effect of sulfonylurea

- in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288-92.
- Chen K et al. Relationship of P450 2C9 genetic polymorphisms in Chinese and the pharmacokinetics of tolbutamide. J Clin Pharm Ther 2005;30:241-9.
 - Jetter A et al. Cytochrome P450 2C9 phenotyping using low-dose tolbutamide. Eur J Clin Pharmacol 2004;60:165-71.
 - Lee CR et al. Tolbutamide, flurbiprofen, and losartan as probes of CYP2C9 activity in humans. J Clin Pharmacol 2003;43:84-91.
 - Lee CR et al. Evaluation of cytochrome P450 2C9 metabolic activity with tolbutamide in CYP2C91 heterozygotes. Clin Pharmacol Ther 2002;72:562-71.
 - Shon JH et al. Effects of CYP2C19 and CYP2C9 genetic polymorphisms on the disposition of and blood glucose lowering response to tolbutamide in humans. Pharmacogenetics 2002;12:111-9.
 - Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. Pharmacogenetics 2002;12:101-9.

Date 20-11-2017

CYP2C9 PM ANDERS: tolbutamide

[2557](#)

NO action is required for this gene-drug interaction.

No clinical consequences of the increased tolbutamide plasma concentration were observed.

Literature:

- Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. Pharmacogenomics 2010;11:1517-23.
- Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. Clin Pharmacol Ther 2009;86:54-61.
- Becker ML et al. Cytochrome P450 2C9 2 and 3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288-92.
- Chen K et al. Relationship of P450 2C9 genetic polymorphisms in Chinese and the pharmacokinetics of tolbutamide. J Clin Pharm Ther 2005;30:241-9.
- Jetter A et al. Cytochrome P450 2C9 phenotyping using low-dose tolbutamide. Eur J Clin Pharmacol 2004;60:165-71.
- Lee CR et al. Evaluation of cytochrome P450 2C9 metabolic activity with tolbutamide in CYP2C91 heterozygotes. Clin Pharmacol Ther 2002;72:562-71.
- Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. Pharmacogenetics 2002;12:101-9.

Date 20-11-2017

CYP2C9*1/*2: tolbutamide

[2551](#)

NO action is required for this gene-drug interaction.

No clinical consequences of the increased tolbutamide plasma concentration were observed.

Literature:

- Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. Pharmacogenomics 2010;11:1517-23.
- Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. Clin Pharmacol Ther 2009;86:54-61.
- Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. Clin Pharmacol Ther 2008;83:288-92.
- Jetter A et al. Cytochrome P450 2C9 phenotyping using low-dose tolbutamide. Eur J Clin Pharmacol 2004;60:165-71.
- Lee CR et al. Tolbutamide, flurbiprofen, and losartan as probes of CYP2C9 activity in humans. J Clin Pharmacol 2003;43:84-91.
- Lee CR et al. Evaluation of cytochrome P450 2C9 metabolic activity with tolbutamide in CYP2C91 heterozygotes. Clin Pharmacol Ther 2002;72:562-71.
- Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. Pharmacogenetics 2002;12:101-9.

Date 20-11-2017

CYP2C9*1/*3: tolbutamide

[2552](#)

NO action is required for this gene-drug interaction.

There is insufficient evidence to state that the increased tolbutamide plasma concentration has any clinical consequences.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. *Clin Pharmacol Ther* 2009;86:54-61.
3. Becker ML et al. Cytochrome P450 2C9 2 and 3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288-92.
4. Chen K et al. Relationship of P450 2C9 genetic polymorphisms in Chinese and the pharmacokinetics of tolbutamide. *J Clin Pharm Ther* 2005;30:241-9.
5. Jetter A et al. Cytochrome P450 2C9 phenotyping using low-dose tolbutamide. *Eur J Clin Pharmacol* 2004;60:165-71.
6. Lee CR et al. Tolbutamide, flurbiprofen, and losartan as probes of CYP2C9 activity in humans. *J Clin Pharmacol* 2003;43:84-91.
7. Lee CR et al. Evaluation of cytochrome P450 2C9 metabolic activity with tolbutamide in CYP2C91 heterozygotes. *Clin Pharmacol Ther* 2002;72:562-71.
8. Shon JH et al. Effects of CYP2C19 and CYP2C9 genetic polymorphisms on the disposition of and blood glucose lowering response to tolbutamide in humans. *Pharmacogenetics* 2002;12:111-9.
9. Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. *Pharmacogenetics* 2002;12:101-9.

Date 20-11-2017

CYP2C9*2/*2: tolbutamide

[2553](#)

NO action is required for this gene-drug interaction.

No clinical consequences of the increased tolbutamide plasma concentration were observed.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288-92.
3. Jetter A et al. Cytochrome P450 2C9 phenotyping using low-dose tolbutamide. *Eur J Clin Pharmacol* 2004;60:165-71.
4. Lee CR et al. Evaluation of cytochrome P450 2C9 metabolic activity with tolbutamide in CYP2C91 heterozygotes. *Clin Pharmacol Ther* 2002;72:562-71.
5. Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. *Pharmacogenetics* 2002;12:101-9.

Date 20-11-2017

CYP2C9*2/*3: tolbutamide

[2554](#)

NO action is required for this gene-drug interaction.

No clinical consequences of the increased tolbutamide plasma concentration were observed.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. *Clin Pharmacol Ther* 2009;86:54-61.
3. Becker ML et al. Cytochrome P450 2C9 2 and 3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288-92.
4. Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. *Pharmacogenetics* 2002;12:101-9.

CYP2C9*3/*3: tolbutamide

2555

NO action is required for this gene-drug interaction.

No clinical consequences of the increased tolbutamide plasma concentration were observed.

Literature:

1. Swen JJ et al. Effect of CYP2C9 polymorphisms on prescribed dose and time-to-stable dose of sulfonylureas in primary care patients with Type 2 diabetes mellitus. *Pharmacogenomics* 2010;11:1517-23.
2. Vormfelde SV et al. Relative impact of genotype and enzyme induction on the metabolic capacity of CYP2C9 in healthy volunteers. *Clin Pharmacol Ther* 2009;86:54-61.
3. Becker ML et al. Cytochrome P450 2C9 *2 and *3 polymorphisms and the dose and effect of sulfonylurea in type II diabetes mellitus. *Clin Pharmacol Ther* 2008;83:288-92.
4. Chen K et al. Relationship of P450 2C9 genetic polymorphisms in Chinese and the pharmacokinetics of tolbutamide. *J Clin Pharm Ther* 2005;30:241-9.
5. Kirchheiner J et al. Impact of CYP2C9 and CYP2C19 polymorphisms on tolbutamide kinetics and the insulin and glucose response in healthy volunteers. *Pharmacogenetics* 2002;12:101-9.

Date 20-11-2017

CYP2D6 IM: tramadol

2421

The genetic variation reduces the conversion of tramadol to a metabolite with a higher activity. This can result in reduced analgesia.

Recommendation:

It is not possible to provide a specific recommendation for dose adjustment, because the total analgesic effect changes when the ratio between the mother compound and the active metabolite changes.

- be alert to a reduced effectiveness
 - in the case of inadequate effectiveness:
 - try a dose increase
 - if this does not work: choose an alternative
- Do not select codeine, as this is also metabolised by CYP2D6. Morphine is not metabolised by CYP2D6. Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in analgesia in patients.
- if no alternative is selected: advise the patient to report inadequate analgesia

Literature:

1. Seripa D et al. Role of CYP2D6 polymorphisms in the outcome of postoperative pain treatment. *Pain Med* 2015;16:2012-23.
2. Dong H et al. Effect of the CYP2D6 gene polymorphism on postoperative analgesia of tramadol in Han nationality nephrectomy patients. *Eur J Clin Pharmacol* 2015;71:681-6.
3. Zhao Q et al. A logistic equation to determine the validity of tramadol from related gene polymorphisms and psychological factors. *Pharmacogenomics* 2014;15:487-95.
4. Matouskova O et al. Pupillometry in healthy volunteers as a biomarker of tramadol efficacy. *J Clin Pharm Ther* 2011;36:513-7.
5. Rauers NI et al. Antagonistic effects of ondansetron and tramadol? A randomized placebo and active drug controlled study. *J Pain* 2010;11:1274-81.
6. Kim E et al. Adverse events in analgesic treatment with tramadol associated with CYP2D6 extensive-metaboliser and OPRM1 high-expression variants. *Ann Rheum Dis* 2010;69:1889-90.
7. Allegaert K et al. Postmenstrual age and CYP2D6 polymorphisms determine tramadol O-demethylation in critically ill neonates and infants. *Pediatr Res* 2008;63:674-9.
8. Stamer UM et al. Concentrations of tramadol and O-desmethyiltramadol enantiomers in different CYP2D6 genotypes. *Clin Pharmacol Ther* 2007;82:41-7.
9. Slanar O et al. Miotic action of tramadol is determined by CYP2D6 genotype. *Physiol Res* 2007;56:129-36.
10. Wang G et al. Effect of the CYP2D6*10 C188T polymorphism on postoperative tramadol analgesia in a Chinese population. *Eur J Clin Pharmacol* 2006;62:927-31.
11. Borlak J et al. A rapid and simple CYP2D6 genotyping assay: case study with the analgetic tramadol. *Metabolism* 2003;52:1439-43.
12. Gan SH et al. Correlation of tramadol pharmacokinetics and CYP2D6*10 genotype in Malaysian subjects. *J Pharm Biomed Anal* 2002;30:189-195.
13. Abdel-Rahman SM et al. Concordance between tramadol and dextromethorphan parent/metabolite ratios: the influence of CYP2D6 and non-CYP2D6 pathways on biotransformation. *J Clin Pharmacol* 2002;42:24-9.

CYP2D6 PM: tramadol

2420

The genetic variation reduces the conversion of tramadol to a metabolite with a higher activity. This can result in reduced analgesia.

Recommendation:

It is not possible to provide a specific recommendation for dose adjustment, because the total analgesic effect changes when the ratio between the mother compound and the active metabolite changes.

- be alert to a reduced effectiveness
- in the case of inadequate effectiveness:
 - try a dose increase.

- if this does not work: choose an alternative

Do not select codeine, as this is also metabolised by CYP2D6. Morphine is not metabolised by CYP2D6. Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in analgesia in patients.

- if no alternative is selected: advise the patient to report inadequate analgesia

Literature:

1. Seripa D et al. Role of CYP2D6 polymorphisms in the outcome of postoperative pain treatment. *Pain Med* 2015;16:2012-23.
2. Matouskova O et al. Pupillometry in healthy volunteers as a biomarker of tramadol efficacy. *J Clin Pharm Ther* 2011;36:513-7.
3. Rauers NI et al. Antagonistic effects of ondansetron and tramadol? A randomized placebo and active drug controlled study. *J Pain* 2010;11:1274-81.
4. Halling J et al. CYP2D6 polymorphism in relation to tramadol metabolism: a study of faroese patients. *Ther Drug Monit* 2008;30:271-5.
5. Allegaert K et al. Postmenstrual age and CYP2D6 polymorphisms determine tramadol O-demethylation in critically ill neonates and infants. *Pediatr Res* 2008;63:674-9.
6. Kirchheiner J et al. Effects of the CYP2D6 gene duplication on the pharmacokinetics and pharmacodynamics of tramadol. *J Clin Psychopharmacol* 2008;28:78-83.
7. Stamer UM et al. Concentrations of tramadol and O-desmethyiltramadol enantiomers in different CYP2D6 genotypes. *Clin Pharmacol Ther* 2007;82:41-7.
8. García-Quetglas E et al. Pharmacokinetics of tramadol enantiomers and their respective phase I metabolites in relation to CYP2D6 phenotype. *Pharmacol Res* 2007;55:122-30.
9. Slanar O et al. Miotic action of tramadol is determined by CYP2D6 genotype. *Physiol Res* 2007;56:129-36.
10. Pedersen RS et al. Enantioselective pharmacokinetics of tramadol in CYP2D6 extensive and poor metabolizers. *Eur J Clin Pharmacol* 2006;62:513-21.
11. Enggaard TP et al. The analgesic effect of tramadol after intravenous injection in healthy volunteers in relation to CYP2D6. *Anesth Analg* 2006;102:146-50.
12. Fliegert F et al. The effects of tramadol on static and dynamic pupillometry in healthy subjects--the relationship between pharmacodynamics, pharmacokinetics and CYP2D6 metaboliser status. *Eur J Clin Pharmacol* 2005;61:257-66.
13. Borlak J et al. A rapid and simple CYP2D6 genotyping assay: case study with the analgetic tramadol. *Metabolism* 2003;52:1439-43.
14. Stamer UM et al. Impact of CYP2D6 genotype on postoperative tramadol analgesia. *Pain* 2003;105:231-8.
15. Abdel-Rahman SM et al. Concordance between tramadol and dextromethorphan parent/metabolite ratios: the influence of CYP2D6 and non-CYP2D6 pathways on biotransformation. *J Clin Pharmacol* 2002;42:24-9.
16. Paar WD et al. Polymorphic CYP2D6 mediates O-demethylation of the opioid analgesic tramadol. *Eur J Clin Pharmacol* 1997;53:235-9.
17. Poulsen L et al. The hypoalgesic effect of tramadol in relation to CYP2D6. *Clin Pharmacol Ther* 1996;60:636-44.
18. SPC Ultram (VS).

CYP2D6 UM: tramadol

2422

The genetic variation increases the conversion of tramadol to a metabolite with a stronger opioid effect. This can result in an increase in potentially life-threatening side effects.

Recommendation:

As the total analgesic effect changes when the ratio between the mother compound and the active

metabolite changes, the effect of a dose reduction cannot be predicted with certainty.

- select an alternative

Do not choose codeine, as it is contra-indicated for CYP2D6 UM. Morphine is not metabolised by CYP2D6. Oxycodone is metabolised by CYP2D6 to a limited extent, but this does not result in differences in side effects in patients.

- if an alternative is not possible:

- use 40% of the standard dose
- advise the patient to report side effects (such as drowsiness, confusion, constipation, nausea and vomiting, respiratory depression or urine retention).

Literature:

1. Seripa D et al. Role of CYP2D6 polymorphisms in the outcome of postoperative pain treatment. *Pain Med* 2015;16:2012-23.
2. Orliaguet G et al. A case of respiratory depression in a child with ultrarapid CYP2D6 metabolism after tramadol. *Pediatrics* 2015;135:e753-5.
3. Saarikoski T et al. Effects of terbinafine and itraconazole on the pharmacokinetics of orally administered tramadol. *Eur J Clin Pharmacol* 2015;71:321-7.
4. Rauers NI et al. Antagonistic effects of ondansetron and tramadol? A randomized placebo and active drug controlled study. *J Pain* 2010;11:1274-81.
5. Stamer UM et al. Respiratory depression with tramadol in a patient with renal impairment and CYP2D6 gene duplication. *Anesth Analg* 2008;107:926-9.
6. Allegaert K et al. Postmenstrual age and CYP2D6 polymorphisms determine tramadol O-demethylation in critically ill neonates and infants. *Pediatr Res* 2008;63:674-9.
7. Kirchheiner J et al. Effects of the CYP2D6 gene duplication on the pharmacokinetics and pharmacodynamics of tramadol. *J Clin Psychopharmacol* 2008;28:78-83.
8. Stamer UM et al. Concentrations of tramadol and O-desmethytramadol enantiomers in different CYP2D6 genotypes. *Clin Pharmacol Ther* 2007;82:41-7.
9. Gleason PP et al. Debilitating reaction following the initial dose of tramadol. *Ann Pharmacother* 1997;31:1150-2.
10. SPC Ultram (VS).

Date 20-11-2017

CYP2D6 IM: venlafaxine

[2386](#)

There are indications of an increased risk of side effects and a reduced chance of efficacy.

The gene variation reduces the conversion of venlafaxine to the active metabolite O-desmethylvenlafaxine, whilst an association between high O-desmethylvenlafaxine/venlafaxine ratios and response without side effects was found.

It is not possible to offer adequately substantiated advice for dose reduction based on the literature.

- avoid venlafaxine

Antidepressants that are not metabolised by CYP2D6 - or to a lesser extent - include, for example, duloxetine, mirtazapine, (es)citalopram and sertraline.

- if it is not possible to avoid venlafaxine and side effects occur:

- reduce the dose
 - monitor the effect and side effects or check the plasma concentrations of venlafaxine and O-desmethylvenlafaxine
- It is not known whether it is possible to reduce the dose to such an extent that the side effects disappear, while the effectiveness is maintained. In general, it is assumed that the effectiveness is determined by the sum of the plasma concentrations of venlafaxine and O-desmethylvenlafaxine. However, the side effects do not appear to be related to this sum.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and anti-depressant treatment response. *Pharmacopsychiatry* 2022 Jul 15. Online ahead of print.
2. Austin-Zimmerman I et al. The influence of CYP2D6 and CYP2C19 genetic variation on diabetes mellitus risk in people taking antidepressants and antipsychotics. *Genes (Basel)* 2021;12:1758.
3. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor metabolizer phenotype. *Ther Drug Monit* 2021;43:672-80.
4. Kringen MK et al. The influence of combined CYP2D6 and CYP2C19 genotypes on venlafaxine and O-desmethylvenlafaxine concentrations in a large patient cohort. *J Clin Psychopharmacol* 2020;40:137-44.
5. Lin XQ et al. The associations between CYP2D6 metabolizer status and pharmacokinetics and clinical outcomes of venlafaxine: a systematic review and meta-analysis. *Pharmacopsychiatry* 2019;52:222-31.
6. Watanabe Y et al. Factors impacting the efficacy of venlafaxine extended release 75-225 mg/day in patients with major depressive disorder: exploratory post hoc subgroup analyses of a randomized, double-blind, placebo-controlled study in Japan. *Neuropsychiatr Dis Treat* 2018;14:1261-72.

7. Taranu A et al. Should a routine genotyping of CYP2D6 and CYP2C19 genetic polymorphisms be recommended to predict venlafaxine efficacy in depressed patients treated in psychiatric settings? *Pharmacogenomics* 2017;18:639-50.
8. Berm E et al. Relation between CYP2D6 genotype, phenotype and therapeutic drug concentrations among nortriptyline and venlafaxine users in old age psychiatry. *Pharmacopsychiatry* 2016;49:186-190 en persoonlijke communicatie (correctie: totaal aantal patiënten met sub- en supra-therapeutische plasmaconcentraties na 3 weken waren omgewisseld in tabel 3, en het totale aantal patiënten met TDM na 3 weken was 37).
9. Jiang F et al. The influences of CYP2D6 genotypes and drug interactions on the pharmacokinetics of venlafaxine: exploring predictive biomarkers for treatment outcomes. *Psychopharmacology (Berl)* 2015;232:1899-909.
10. Waade RB et al. Impact of age on serum concentrations of venlafaxine and escitalopram in different CYP2D6 and CYP2C19 genotype subgroups. *Eur J Clin Pharmacol* 2014;70:933-40.
11. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
12. Ng C et al. Pharmacogenetic polymorphisms and response to escitalopram and venlafaxine over 8 weeks in major depression. *Hum Psychopharmacol* 2013;28:516-22.
13. Van Nieuwerburgh FC et al. Response to serotonin reuptake inhibitors in OCD is not influenced by common CYP2D6 polymorphisms. *Int J Psychiatry Clin Pract* 2009;13:345-8.
14. Hermann M et al. Serum concentrations of venlafaxine and its metabolites O-desmethylvenlafaxine and N-desmethylvenlafaxine in heterozygous carriers of the CYP2D6*3, *4 or *5 allele. *Eur J Clin Pharmacol* 2008;64:483-7.
15. McAlpine DE et al. Cytochrome P450 2D6 genotype variation and venlafaxine dosage. *Mayo Clin Proc* 2007;82:1065-8.
16. Shams ME et al. CYP2D6 polymorphism and clinical effect of the antidepressant venlafaxine. *J Clin Pharm Ther* 2006;31:493-502.
17. Whyte EM et al. CYP2D6 genotype and venlafaxine-XR concentrations in depressed elderly. *Int J Geriatr Psychiatry* 2006;21:542-9.
18. Fukuda T et al. The impact of the CYP2D6 and CYP2C19 genotypes on venlafaxine pharmacokinetics in a Japanese population. *Eur J Clin Pharmacol* 2000;56:175-80.
19. Veeffkind AH et al. Venlafaxine serum levels and CYP2D6 genotype. *Ther Drug Monit* 2000;22:202-8.
20. Fukuda T et al. Effect of the CYP2D6*10 genotype on venlafaxine pharmacokinetics in healthy adult volunteers. *Br J Clin Pharmacol* 1999;47:450-3.

Date 14-11-2022

CYP2D6 PM: venlafaxine

[2385](#)

There are indications of an increased risk of side effects and a reduced chance of efficacy. The gene variation reduces the conversion of venlafaxine to the active metabolite O-desmethylvenlafaxine, whilst an association between high O-desmethylvenlafaxine/venlafaxine ratios and response without side effects was found.

It is not possible to offer adequately substantiated advice for dose reduction based on the literature.

- avoid venlafaxine

Antidepressants that are not metabolised by CYP2D6 - or to a lesser extent - include, for example, duloxetine, mirtazapine, (es)citalopram and sertraline.

- If it is not possible to avoid venlafaxine and side effects occur:

- reduce the dose

- monitor the effect and side effects or check the plasma concentrations of venlafaxine and O-desmethylvenlafaxine

It is not known whether it is possible to reduce the dose to such an extent that the side effects disappear, while the effectiveness is maintained. In general, it is assumed that the effectiveness is determined by the sum of the plasma concentrations of venlafaxine and O-desmethylvenlafaxine. However, the side effects do not appear to be related to this sum.

Furthermore, a reduced effectiveness of venlafaxine has been observed in depression patients with this gene variation.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022 Jul 15. Online ahead of print.
2. Austin-Zimmerman I et al. The influence of CYP2D6 and CYP2C19 genetic variation on diabetes mellitus risk in people taking antidepressants and antipsychotics. *Genes (Basel)* 2021;12:1758.
3. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor metabolizer phenotype. *Ther Drug Monit* 2021;43:672-80.
4. Kringen MK et al. The influence of combined CYP2D6 and CYP2C19 genotypes on venlafaxine and O-desmethylvenlafaxine concentrations in a large patient cohort. *J Clin Psychopharmacol* 2020;40:137-44.
5. Lin XQ et al. The associations between CYP2D6 metabolizer status and pharmacokinetics and clinical outcomes of venlafaxine: a systematic review and meta-analysis. *Pharmacopsychiatry* 2019;52:222-31.
6. Ahmed AT et al. Pharmacokinetic-pharmacodynamic interaction associated with venlafaxine-XR remission in patients with major depressive disorder with history of citalopram / escitalopram treatment failure. *J Affect Disord* 2019;246:62-8.

7. Taranu A et al. Should a routine genotyping of CYP2D6 and CYP2C19 genetic polymorphisms be recommended to predict venlafaxine efficacy in depressed patients treated in psychiatric settings? *Pharmacogenomics* 2017;18:639-50.
8. Berm E et al. Relation between CYP2D6 genotype, phenotype and therapeutic drug concentrations among nortriptyline and venlafaxine users in old age psychiatry. *Pharmacopsychiatry* 2016;49:186-190
en persoonlijke communicatie (correctie: totaal aantal patiënten met sub- en supra-therapeutische plasmaconcentraties na 3 weken waren omgewisseld in tabel 3, en het totale aantal patiënten met TDM na 3 weken was 37).
9. Waade RB et al. Impact of age on serum concentrations of venlafaxine and escitalopram in different CYP2D6 and CYP2C19 genotype subgroups. *Eur J Clin Pharmacol* 2014;70:933-40.
10. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
11. Ng C et al. Pharmacogenetic polymorphisms and response to escitalopram and venlafaxine over 8 weeks in major depression. *Hum Psychopharmacol* 2013;28:516-22.
12. Lobello KW et al. Cytochrome P450 2D6 phenotype predicts antidepressant efficacy of venlafaxine: a secondary analysis of 4 studies in major depressive disorder. *J Clin Psychiatry* 2010;71:1482-7.
13. Van Nieuwerburgh FC et al. Response to serotonin reuptake inhibitors in OCD is not influenced by common CYP2D6 polymorphisms. *Int J Psychiatry Clin Pract* 2009;13:345-8.
14. Preskorn S et al. Comparison of the pharmacokinetics of venlafaxine extended release and desvenlafaxine in extensive and poor cytochrome P450 2D6 metabolizers. *J Clin Psychopharmacol* 2009;29:39-43.
15. Hermann M et al. Serum concentrations of venlafaxine and its metabolites O-desmethylvenlafaxine and N-desmethylvenlafaxine in heterozygous carriers of the CYP2D6*3, *4 or *5 allele. *Eur J Clin Pharmacol* 2008;64:483-7.
16. Shams ME et al. CYP2D6 polymorphism and clinical effect of the antidepressant venlafaxine. *J Clin Pharm Ther* 2006;31:493-502.
17. Whyte EM et al. CYP2D6 genotype and venlafaxine-XR concentrations in depressed elderly. *Int J Geriatr Psychiatry* 2006;21:542-9.
18. Eap CB et al. Role of CYP2D6 in the stereoselective disposition of venlafaxine in humans. *Pharmacogenetics* 2003;13:39-47.
19. Lessard E et al. Influence of CYP2D6 activity on the disposition and cardiovascular toxicity of the antidepressant agent venlafaxine in humans. *Pharmacogenetics* 1999;9:435-43.
20. Veefkind AH et al. Venlafaxine serum levels and CYP2D6 genotype. *Ther Drug Monit* 2000;22:202-8.

Date 14-11-2022

CYP2D6 UM: venlafaxine

[2387](#)

NO action is required for this gene-drug interaction.

The effect on the plasma concentration of venlafaxine + O-desmethylvenlafaxine is small. No reduction of effectiveness or influence on side effects has been demonstrated.

Literature:

1. Scherf-Clavel M et al. Effects of pharmacokinetic gene variation on therapeutic drug levels and antidepressant treatment response. *Pharmacopsychiatry* 2022 Jul 15. Online ahead of print.
2. Ganesh SV et al. Therapeutic drug monitoring of psychotropics as a diagnostic tool for CYP2D6 poor metabolizer phenotype. *Ther Drug Monit* 2021;43:672-80.
3. Kringen MK et al. The influence of combined CYP2D6 and CYP2C19 genotypes on venlafaxine and O-desmethylvenlafaxine concentrations in a large patient cohort. *J Clin Psychopharmacol* 2020;40:137-44.
4. Ahmed AT et al. Pharmacokinetic-pharmacodynamic interaction associated with venlafaxine-XR remission in patients with major depressive disorder with history of citalopram / escitalopram treatment failure. *J Affect Disord* 2019;246:62-8.
5. Taranu A et al. Should a routine genotyping of CYP2D6 and CYP2C19 genetic polymorphisms be recommended to predict venlafaxine efficacy in depressed patients treated in psychiatric settings? *Pharmacogenomics* 2017;18:639-50.
6. Jiang F et al. The influences of CYP2D6 genotypes and drug interactions on the pharmacokinetics of venlafaxine: exploring predictive biomarkers for treatment outcomes. *Psychopharmacology (Berl)* 2015;232:1899-909.
7. Brandl EJ et al. Influence of CYP2D6 and CYP2C19 gene variants on antidepressant response in obsessive-compulsive disorder. *Pharmacogenomics J* 2014;14:176-81.
8. Shams ME et al. CYP2D6 polymorphism and clinical effect of the antidepressant venlafaxine. *J Clin Pharm Ther* 2006;31:493-502.
9. Veefkind AH et al. Venlafaxine serum levels and CYP2D6 genotype. *Ther Drug Monit* 2000;22:202-8.

Date 14-11-2022

The gene variation can reduce the conversion of voriconazole and consequently increase the plasma concentration. This could result in improved efficacy or an increase in the risk of side effects.

- monitor the plasma concentration

Literature:

1. Tian X et al. Impact of CYP2C19 phenotype and drug-drug interactions on voriconazole concentration in pediatric patients. *Antimicrob Agents Chemother* 2021;65:e0020721.
2. Zhao YC et al. Predictors of adverse events and determinants of the voriconazole trough concentration in kidney transplantation recipients. *Clin Transl Sci* 2021;14:702- 11.
3. Shang S et al. Effect of CYP2C19 polymorphism on the plasma voriconazole concentration and voriconazole-to-voriconazole-N-oxide concentration ratio in elderly patients. *Mycoses* 2020 May 16 (online ahead of print).
4. Hicks JK et al. Prospective CYP2C19-guided voriconazole prophylaxis in patients with neutropenic acute myeloid leukemia reduces the incidence of subtherapeutic antifungal plasma concentrations. *Clin Pharmacol Ther* 2020;107:563-70.
5. Patel JN et al. Evaluation of CYP2C19 genotype-guided voriconazole prophylaxis after allogeneic hematopoietic cell transplant. *Clin Pharmacol Ther* 2020;107:571-9.
6. Song Y et al. Association of CYP2C19 and UGT1A4 polymorphisms with voriconazole-induced liver injury. *Per Med* 2020;17:15-22.
7. Blanco-Dorado S et al. Impact of CYP2C19 genotype and drug interactions on voriconazole plasma concentrations: a Spain pharmacogenetic-pharmacokinetic prospective multicenter study. *Pharmacotherapy* 2020;40:17-25.
8. Yamada T et al. Impact of flavin-containing monooxygenase 3 and CYP2C19 genotypes on plasma disposition and adverse effects of voriconazole administered orally in immunocompromised patients. *J Infect Chemother* 2019;25:1019-25.
9. Mafuru M et al. The influence of proinflammatory cytokines on voriconazole trough concentration in patients with different forms of hematologic disorders. *J Clin Pharmacol* 2019;59:1340-50.
10. Miao Q et al. Correlation of CYP2C19 genotype with plasma voriconazole exposure in South-western Chinese Han patients with invasive fungal infections. *Medicine (Baltimore)* 2019;98:e14137.
11. Sienkiewicz B et al. Influence of CYP2C19 genotypes on the occurrence of adverse drug reactions of voriconazole among hematological patients after allo-HSCT. *Pathol Oncol Res* 2018;24:541-5.
12. Hamadeh IS et al. Impact of the CYP2C19 genotype on voriconazole exposure in adults with invasive fungal infections. *Pharmacogenet Genomics* 2017;27:190-6.
13. Li X et al. Effect of cytochrome P450 2C19 polymorphisms on the clinical outcomes of voriconazole: a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2016;72:1185-93.
14. Wang Y et al. Risk factors for voriconazole-associated hepatotoxicity in patients in the intensive care unit. *Pharmacotherapy* 2016;36:757-65.
15. Chuwongwattana S et al. A prospective observational study of CYP2C19 polymorphisms and voriconazole plasma level in adult Thai patients with invasive aspergillosis. *Drug Metab Pharmacokinet* 2016;31:117-22.
16. Teusink A et al. Genotype-directed dosing leads to optimized voriconazole levels in pediatric patients receiving hematopoietic stem cell transplantation. *Biol Blood Marrow Transplant* 2016;22:482-6.
17. Lamoureux F et al. Impact of CYP2C19 genetic polymorphisms on voriconazole dosing and exposure in adult patients with invasive fungal infections. *Int J Antimicrob Agents* 2016;47:124-31.
18. Chawla PK et al. Correlation of CYP2C19 genotype with plasma voriconazole levels: a preliminary retrospective study in Indians. *Int J Clin Pharm* 2015;37:925-30.
19. Yamada T et al. Saturated metabolism of voriconazole N-oxidation resulting in nonlinearity of pharmacokinetics of voriconazole at clinical doses. *Biol Pharm Bull* 2015;38:1496-503.
20. Mori M et al. Pharmacokinetics and safety of voriconazole intravenous-to-oral switch regimens in immunocompromised Japanese pediatric patients. *Antimicrob Agents Chemother* 2015;59:1004-13.
21. Wang T et al. Efficacy and safety of voriconazole and CYP2C19 polymorphism for optimised dosage regimens in patients with invasive fungal infections. *Int J Antimicrob Agents* 2014;44:436-42.
22. Liu P et al. Population pharmacokinetic-pharmacodynamic analysis of voriconazole and anidulafungin in adult patients with invasive aspergillosis. *Antimicrob Agents Chemother* 2014;58:4727-36.
23. Zonios D et al. Voriconazole metabolism, toxicity, and the effect of cytochrome P450 2C19 genotype. *J Infect Dis* 2014;209:1941-8.
24. Hicks JK et al. Voriconazole plasma concentrations in immunocompromised pediatric patients vary by CYP2C19 diplotypes. *Pharmacogenomics* 2014;15:1065-78.
25. Kim SH et al. Clinical impact of cytochrome P450 2C19 genotype on the treatment of invasive aspergillosis under routine therapeutic drug monitoring of voriconazole in a Korean population. *Infect Chemother* 2013;45:406-14.
26. Racil Z et al. Monitoring trough voriconazole plasma concentrations in haematological patients: real life multicentre experience. *Mycoses* 2012;55:483-92.
27. Kim SH et al. Voriconazole-related severe adverse events: clinical application of therapeutic drug monitoring in Korean patients. *Int J Infect Dis* 2011;15:e753-8.
28. Berge M et al. Effect of cytochrome P450 2C19 genotype on voriconazole exposure in cystic fibrosis

- lung transplant patients. *Eur J Clin Pharmacol* 2011;67:253-60.
29. Brüggemann RJ et al. Pharmacokinetics and safety of 14 days intravenous voriconazole in allogeneic haematopoietic stem cell transplant recipients. *J Antimicrob Chemother* 2010;65:107-13.
 30. Matsumoto K et al. Correlation between voriconazole trough plasma concentration and hepatotoxicity in patients with different CYP2C19 genotypes. *Int J Antimicrob Agents* 2009;34:91-4.
 31. Karlsson MO et al. Population pharmacokinetic analysis of voriconazole plasma concentration data from pediatric studies. *Antimicrob Agents Chemother* 2009;53:935-44.
 32. Weiss J et al. CYP2C19 genotype is a major factor contributing to the highly variable pharmacokinetics of voriconazole. *J Clin Pharmacol* 2009;49:196-204.
 33. Levin MD et al. Hepatotoxicity of oral and intravenous voriconazole in relation to cytochrome P450 polymorphisms. *J Antimicrob Chemother* 2007;60:1104-7.
 34. Mikus G et al. Potent cytochrome P450 2C19 genotype-related interaction between voriconazole and the cytochrome P450 3A4 inhibitor ritonavir. *Clin Pharmacol Ther* 2006;80:126-35.
 35. Rengelshausen J et al. Opposite effects of short-term and long-term St John's wort intake on voriconazole pharmacokinetics. *Clin Pharmacol Ther* 2005;78:25-33.
 36. Ikeda Y et al. Pharmacokinetics of voriconazole and cytochrome P450 2C19 genetic status. *Clin Pharmacol Ther* 2004;75:587-8.
 37. SPC Vfend (NL en VS).

Date 15-11-2021

CYP2C19 PM: voriconazol

[2446](#)

The gene variation can reduce the conversion of voriconazole and consequently increase the plasma concentration. This could result in improved efficacy or an increase in the risk of side effects. Initially, the risk of side effects is of particular interest.

- use 50% of the standard dose and monitor the plasma concentration

Literature:

1. Tian X et al. Impact of CYP2C19 phenotype and drug-drug interactions on voriconazole concentration in pediatric patients. *Antimicrob Agents Chemother* 2021;65:e0020721.
2. Zhao YC et al. Predictors of adverse events and determinants of the voriconazole trough concentration in kidney transplantation recipients. *Clin Transl Sci* 2021;14:702- 11.
3. Shang S et al. Effect of CYP2C19 polymorphism on the plasma voriconazole concentration and voriconazole-to-voriconazole-N-oxide concentration ratio in elderly patients. *Mycoses* 2020 May 16 (online ahead of print).
4. Yuan ZQ et al. The impact of plasma protein binding characteristics and unbound concentration of voriconazole on its adverse drug reactions. *Front Pharmacol* 2020;11:505.
5. Hicks JK et al. Prospective CYP2C19-guided voriconazole prophylaxis in patients with neutropenic acute myeloid leukemia reduces the incidence of subtherapeutic antifungal plasma concentrations. *Clin Pharmacol Ther* 2020;107:563-70.
6. Patel JN et al. Evaluation of CYP2C19 genotype-guided voriconazole prophylaxis after allogeneic hematopoietic cell transplant. *Clin Pharmacol Ther* 2020;107:571-9.
7. Song Y et al. Association of CYP2C19 and UGT1A4 polymorphisms with voriconazole-induced liver injury. *Per Med* 2020;17:15-22.
8. Blanco-Dorado S et al. Impact of CYP2C19 genotype and drug interactions on voriconazole plasma concentrations: a Spain pharmacogenetic-pharmacokinetic prospective multicenter study. *Pharmacotherapy* 2020;40:17-25.
9. Yamada T et al. Impact of flavin-containing monooxygenase 3 and CYP2C19 genotypes on plasma disposition and adverse effects of voriconazole administered orally in immunocompromised patients. *J Infect Chemother* 2019;25:1019-25.
10. Mafuru M et al. The influence of proinflammatory cytokines on voriconazole trough concentration in patients with different forms of hematologic disorders. *J Clin Pharmacol* 2019;59:1340-50.
11. Miao Q et al. Correlation of CYP2C19 genotype with plasma voriconazole exposure in South-western Chinese Han patients with invasive fungal infections. *Medicine (Baltimore)* 2019;98:e14137.
12. Hamadeh IS et al. Impact of the CYP2C19 genotype on voriconazole exposure in adults with invasive fungal infections. *Pharmacogenet Genomics* 2017;27:190-6.
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20. Mori M et al. Pharmacokinetics and safety of voriconazole intravenous-to-oral switch regimens in immunocompromised Japanese pediatric patients. *Antimicrob Agents Chemother* 2015;59:1004-13.
21. Wang T et al. Efficacy and safety of voriconazole and CYP2C19 polymorphism for optimised dosage regimens in patients with invasive fungal infections. *Int J Antimicrob Agents* 2014;44:436-42.
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23. Zonios D et al. Voriconazole metabolism, toxicity, and the effect of cytochrome P450 2C19 genotype. *J Infect Dis* 2014;209:1941-8.
24. Hicks JK et al. Voriconazole plasma concentrations in immunocompromised pediatric patients vary by CYP2C19 diplotypes. *Pharmacogenomics* 2014;15:1065-78.
25. Kim SH et al. Clinical impact of cytochrome P450 2C19 genotype on the treatment of invasive aspergillosis under routine therapeutic drug monitoring of voriconazole in a Korean population. *Infect Chemother* 2013;45:406-14.
26. Driscoll TA et al. Comparison of pharmacokinetics and safety of voriconazole intravenous-to-oral switch in immunocompromised adolescents and healthy adults. *Antimicrob Agents Chemother* 2011;55:5780-9.
27. Kim SH et al. Voriconazole-related severe adverse events: clinical application of therapeutic drug monitoring in Korean patients. *Int J Infect Dis* 2011;15:e753-8.
28. Lei HP et al. Lack of effect of Ginkgo biloba on voriconazole pharmacokinetics in Chinese volunteers identified as CYP2C19 poor and extensive metabolizers. *Ann Pharmacother* 2009;43:726-31.
29. Wang G et al. The CYP2C19 ultra-rapid metabolizer genotype influences the pharmacokinetics of voriconazole in healthy male volunteers. *Eur J Clin Pharmacol* 2009;65:281-5.
30. Weiss J et al. CYP2C19 genotype is a major factor contributing to the highly variable pharmacokinetics of voriconazole. *J Clin Pharmacol* 2009;49:196-204.
31. Mikus G et al. Potent cytochrome P450 2C19 genotype-related interaction between voriconazole and the cytochrome P450 3A4 inhibitor ritonavir. *Clin Pharmacol Ther* 2006;80:126-35.
32. Rengelshausen J et al. Opposite effects of short-term and long-term St John's wort intake on voriconazole pharmacokinetics. *Clin Pharmacol Ther* 2005;78:25-33.
33. Ikeda Y et al. Pharmacokinetics of voriconazole and cytochrome P450 2C19 genetic status. *Clin Pharmacol Ther* 2004;75:587-8.
34. SPC Vfend (NL en VS).

Date 15-11-2021

CYP2C19 UM: voriconazol

[2447](#)

The gene variation increases the conversion of voriconazole, which increases the risk of ineffectiveness.

- use an initial dose that is 1.5x higher and monitor the plasma concentration

Literature:

1. Patel JN et al. Evaluation of CYP2C19 genotype-guided voriconazole prophylaxis after allogeneic hematopoietic cell transplant. *Clin Pharmacol Ther* 2020;107:571-9.
2. Blanco-Dorado S et al. Impact of CYP2C19 genotype and drug interactions on voriconazole plasma concentrations: a Spain pharmacogenetic-pharmacokinetic prospective multicenter study. *Pharmacotherapy* 2020;40:17-25.
3. Sienkiewicz B et al. Influence of CYP2C19 genotypes on the occurrence of adverse drug reactions of voriconazole among hematological patients after allo-HSCT. *Pathol Oncol Res* 2018;24:541-5.
4. Hamadeh IS et al. Impact of the CYP2C19 genotype on voriconazole exposure in adults with invasive fungal infections. *Pharmacogenet Genomics* 2017;27:190-6.
5. Williams K et al. Association of CYP2C19 *17/*17 genotype with the risk of voriconazole-associated squamous cell carcinoma. *JAMA Dermatol* 2016;152:719-20.
6. Lamoureux F et al. Impact of CYP2C19 genetic polymorphisms on voriconazole dosing and exposure in adult patients with invasive fungal infections. *Int J Antimicrob Agents* 2016;47:124-31.
7. Chawla PK et al. Correlation of CYP2C19 genotype with plasma voriconazole levels: a preliminary retrospective study in Indians. *Int J Clin Pharm* 2015;37:925-30.
8. Zonios D et al. Voriconazole metabolism, toxicity, and the effect of cytochrome P450 2C19 genotype. *J Infect Dis* 2014;209:1941-8.
9. Hicks JK et al. Voriconazole plasma concentrations in immunocompromised pediatric patients vary by CYP2C19 diplotypes. *Pharmacogenomics* 2014;15:1065-78.
10. Driscoll TA et al. Comparison of pharmacokinetics and safety of voriconazole intravenous-to-oral switch in immunocompromised children and healthy adults. *Antimicrob Agents Chemother* 2011;55:5770-9.
11. Driscoll TA et al. Comparison of pharmacokinetics and safety of voriconazole intravenous-to-oral switch in immunocompromised adolescents and healthy adults. *Antimicrob Agents Chemother* 2011;55:5780-9.

12. Berge M et al. Effect of cytochrome P450 2C19 genotype on voriconazole exposure in cystic fibrosis lung transplant patients. *Eur J Clin Pharmacol* 2011;67:253-60.
13. Wang G et al. The CYP2C19 ultra-rapid metabolizer genotype influences the pharmacokinetics of voriconazole in healthy male volunteers. *Eur J Clin Pharmacol* 2009;65:281-5.
14. Weiss J et al. CYP2C19 genotype is a major factor contributing to the highly variable pharmacokinetics of voriconazole. *J Clin Pharmacol* 2009;49:196-204.
15. Li X et al. Effect of cytochrome P450 2C19 polymorphisms on the clinical outcomes of voriconazole: a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2016;72:1185-93.

Date 15-11-2021

CYP2C9 IM ANDERS: warfarine

[5776](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 65% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm. Algorithms for Caucasian patients usually contain only the *2 and *3 allele. If the activity of the reduced-activity alleles is comparable to the activity of *2 or *3, then the algorithm can be completed as if *1/*2 or *1/*3 is present. See <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics> for Excel files containing calculation modules for oral and equivalent intravenous doses. From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Modified dose algorithms have been developed for patients of African or (East) Asian heritage.

Literature:

1. Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
2. Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
3. Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
4. Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
5. Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
6. Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
7. Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
8. Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGENet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
9. SPC Coumadin (VS).

Date 24-08-2016

CYP2C9 PM ANDERS: warfarine

[5777](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 20% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm. Algorithms for Caucasian patients usually contain only the *2 and *3 allele. If the activity of the reduced-activity alleles is comparable to the activity of *2 or *3, then the algorithm can be completed as if *2 or *3 is present. See <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics> for Excel files containing calculation modules for oral and equivalent intravenous doses. From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Modified dose algorithms have been developed for patients of African or (East) Asian heritage.

Literature:

1. Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
2. Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
3. Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
4. Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
5. Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
6. Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
7. Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
8. Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGENet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
9. SPC Coumadin (VS).

Date 24-08-2016

CYP2C9*1/*2: warfarine

[5771](#)

NO action is required for this gene-drug interaction.

Genetic variation may lead to a decrease in the required maintenance dose. However, there is insufficient evidence that this causes problems when therapy is initiated as usual.

Literature:

1. Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
2. Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
3. Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
4. Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
5. Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
6. Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
7. Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
8. Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGENet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
9. SPC Coumadin (VS).

Date 24-08-2016

CYP2C9*1/*3: warfarine

[5772](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 65% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm, as used in EU-PACT: see <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics>.

From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Literature:

1. Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
2. Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.

- Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
- Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
- Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
- Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
- Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
- Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGenet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
- SPC Coumadin (VS).

Date 24-08-2016

CYP2C9*2/*2: warfarine

[5773](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 65% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm, as used in EU-PACT: see <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics>.

From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Literature:

- Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
- Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
- Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
- Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
- Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
- Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
- Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
- Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGenet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
- SPC Coumadin (VS).

Date 24-08-2016

CYP2C9*2/*3: warfarine

[5774](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 45% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm, as used in EU-PACT: see <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics>. From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Literature:

- Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.

- Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
- Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
- Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
- Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
- Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
- Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
- Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGenet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
- SPC Coumadin (VS).

Date 24-08-2016

CYP2C9*3/*3: warfarine

[5775](#)

This gene variation reduces the conversion of warfarin to inactive metabolites. This can increase the risk of bleeding.

Recommendation:

- use 20% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm, as used in EU-PACT: see <https://www.knmp.nl/producten-en-diensten/gebruiksrecht-g-standaard/medicatiebewaking-g-standaard/background-information-pharmacogenetics>.

From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Literature:

- Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015; 39:228-34.
- Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014; 177:654-7.
- Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014; 12:1480-7.
- Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014; 174:1330-8.
- Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013; 168:4234-43.
- Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012; 7:e44064.
- Lindh JD et al. Influence of CYP2C9 genotype on warfarin dose requirements--a systematic review and meta-analysis. *Eur J Clin Pharmacol* 2009; 65:365-75.
- Sanderson S et al. CYP2C9 gene variants, drug dose, and bleeding risk in warfarin-treated patients: a HuGenet systematic review and meta-analysis. *Genet Med* 2005; 7:97-104.
- SPC Coumadin (VS).

Date 24-08-2016

VKORC1 -1639 AA: warfarine

[5779](#)

The genetic variation results in increased sensitivity to warfarin. This results in an increase in the risk of excessively severe inhibition of blood clotting (INR > 4) during the first month of the treatment.

Recommendation:

- use 60% of the standard initial dose

The genotype-specific initial dose and maintenance dose can be calculated using an algorithm, as used in EU-PACT: see <https://www.knmp.nl/patientenzorg/medicatiebewaking/farmacogenetica>.

From day 6 on the standard algorithm without genotype information can be used to calculate the dose.

Literature:

- Zhang J et al. The influence of VKORC1 gene polymorphism on warfarin maintenance dosage in

- pediatric patients: A systematic review and meta-analysis. *Thromb Res* 2015;136:955-61.
- Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015;39:228-34.
 - Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014;177:654-7.
 - Franchini M et al. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost* 2014;12:1480-7.
 - Stergiopoulos K et al. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med* 2014;174:1330-8.
 - Jin B et al. The impact of VKORC1-1639G > A genetic polymorphism upon warfarin dose requirement in different ethnic populations. *Curr Med Res Opin* 2014;30:1505-11.
 - Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013;168:4234-43.
 - Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012;7:e44064.
 - Yang L et al. Impact of VKORC1 gene polymorphism on interindividual and interethnic warfarin dosage requirement--a systematic review and meta analysis. *Thromb Res* 2010;125:e159-66.
 - SPC Coumadin (VS).

Date 24-08-2016

VKORC1 -1639 GA: warfarine

[5778](#)

NO action is required for this gene-drug interaction.

The genetic variation results in a reduction in the required dose and an increase in the risk of excessively severe inhibition of blood clotting during the first month of the treatment. However, the effect is small and GA is also the most common genotype, meaning that the standard treatment will primarily be based on patients with this genotype.

Literature:

- Zhang J et al. The influence of VKORC1 gene polymorphism on warfarin maintenance dosage in pediatric patients: A systematic review and meta-analysis. *Thromb Res* 2015;136:955-61.
- Liao Z et al. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis* 2015;39:228-34.
- Xu H et al. Meta-analysis of efficacy and safety of genotype-guided pharmacogenetic dosing of warfarin. *Int J Cardiol* 2014;177:654-7.
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- Jin B et al. The impact of VKORC1-1639G > A genetic polymorphism upon warfarin dose requirement in different ethnic populations. *Curr Med Res Opin* 2014;30:1505-11.
- Yang J et al. Influence of CYP2C9 and VKORC1 genotypes on the risk of hemorrhagic complications in warfarin-treated patients: a systematic review and meta-analysis. *Int J Cardiol* 2013;168:4234-43.
- Jorgensen AL et al. Influence of CYP2C9 and VKORC1 on patient response to warfarin: a systematic review and meta-analysis. *PLoS One* 2012;7:e44064.
- SPC Coumadin (VS).

Date 24-08-2016

CYP2D6 IM: zuclopentixol

[2395](#)

The risk of side effects may be elevated. The genetic variation leads to decreased conversion of zuclopentixol, which causes the plasma concentration to be approximately 1.35-fold higher.

- use 75% of the standard dose

Literature:

- Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopentixol. *Br J Clin Pharmacol* 2021;87:2228-35.
- Tveito M et al. Impact of age and CYP2D6 genotype on exposure of zuclopentixol in patients using long-acting injectable versus oral formulation-an observational study including 2044 patients. *Eur J Clin Pharmacol* 2021;77:215-21.
- Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopentixol. *Eur J Clin Pharmacol* 2016;72:175-84.

4. Van Berlo-van de Laar et al. Dosering aanpassen aan eliminatiesnelheid. Pharm Weekblad 2004; 139:740-43.
5. Jaanson P et al. Maintenance therapy with zuclopentixol decanoate: associations between plasma concentrations, neurological side effects and CYP2D6 genotype. Psychopharmacology 2002;162:67-73.
6. Jerling M et al. The CYP2D6 genotype predicts the oral clearance of the neuroleptic agents perphenazine and zuclopentixol. Clin Pharmacol Ther 1996;59:423-8.
7. SmPC's Cisordinol en Cisordinol Depot.

Date 13-09-2021

CYP2D6 PM: zuclopentixol

[2394](#)

The risk of side effects may be elevated. The genetic variation results in a decreased conversion of zuclopentixol, which causes the plasma concentration to be approximately 1.6-fold higher.

- use 50% of the standard dose

Literature:

1. Waade RB et al. Impact of CYP2D6 on serum concentrations of flupentixol, haloperidol, perphenazine and zuclopentixol. Br J Clin Pharmacol 2021;87:2228-35.
2. Tveito M et al. Impact of age and CYP2D6 genotype on exposure of zuclopentixol in patients using long-acting injectable versus oral formulation-an observational study including 2044 patients. Eur J Clin Pharmacol 2021;77:215-21.
3. Van Berlo-van de Laar et al. Dosering aanpassen aan eliminatiesnelheid. Pharm Weekblad 2004; 139:740-43.
4. Jaanson P et al. Maintenance therapy with zuclopentixol decanoate: associations between plasma concentrations, neurological side effects and CYP2D6 genotype. Psychopharmacology 2002;162:67-73.
5. Linnet K et al. Influence of Cyp2D6 genetic polymorphism on ratios of steady-state serum concentration to dose of the neuroleptic zuclopentixol. Ther Drug Monit 1996;18:629-34.
6. Jerling M et al. The CYP2D6 genotype predicts the oral clearance of the neuroleptic agents perphenazine and zuclopentixol. Clin Pharmacol Ther 1996;59:423-8.
7. Dahl ML et al. Disposition of the neuroleptic zuclopentixol cosegregates with the polymorphic hydroxylation of debrisoquine in humans. Acta Psychiatr Scand 1991;84:99- 102.
8. SmPC's Cisordinol en Cisordinol Depot.

Date 13-09-2021

CYP2D6 UM: zuclopentixol

[2396](#)

The risk of ineffectiveness may be elevated. The genetic variation leads to an increased conversion of zuclopentixol, which can result in a reduction of the plasma concentration.

There is insufficient information available to make a dosage recommendation.

- if the effectiveness is insufficient: try a dose increase
Do not exceed 1.5 times the standard dose

Literature:

1. Tveito M et al. Impact of age and CYP2D6 genotype on exposure of zuclopentixol in patients using long-acting injectable versus oral formulation-an observational study including 2044 patients. Eur J Clin Pharmacol 2021;77:215-21.
2. Patteet L et al. Genotype and co-medication dependent CYP2D6 metabolic activity: effects on serum concentrations of aripiprazole, haloperidol, risperidone, paliperidone and zuclopentixol. Eur J Clin Pharmacol 2016;72:175-84.
3. SmPC's Cisordinol en Cisordinol Depot.

Date 13-09-2021
