

#ret #incomplete

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1 | SNP. Project. Write-up.

Resources: [\[\[KBxSNPPCR\]\]](#) Instructions

1.0.1 | Init Planning

Outline

- basics
- function and regulation
- SNP effect

Writing!%%

1.0.2 | Part One!

The *COMT* gene, or catechol-O-methyltransferase, encodes the *COMT* enzyme which is responsible for breaking down neurotransmitters in the brain's prefrontal cortex. More specifically, it acts as a catalyst for the transfer of a methyl group from S-adenosylmethionine to dopamine, epinephrine, and norepinephrine. This process, called O-methylation, leads to the degradation of the aforementioned neurotransmitters. The *COMT* enzyme also affects the metabolism of exogenous substances, but that is irrelevant for the mutation at hand citation. The *COMT* gene itself is 27.22kb long and located on chromosome 22q11.2 citation. It has ubiquitous expression in 27 tissues, including the placenta, the adrenal, and the lung citation. Val158Met, also known as rs4680, is a common missense mutation swapping a guanine for an adenine. It has the frequency G=0.510915, and thus, A=0.489085. Val158Met causes the *COMT* enzyme to be roughly 25% as effective compared to the wild type. Expression levels in mRNA, despite its reduced protein abundance, are not affected by Val158Met citation & citation. Thus, Val158Met must be located in a protein-coding region causing the *COMT* enzyme to have lower protein integrity, explaining the discrepancy between mRNA expression and protein expression. This lower protein integrity is most likely manifested as diminished thermostability of the enzyme citation. The higher level effect of this reduced enzyme efficacy is greatly debated, and linked to many different phenotypes. At a broad level, lower *COMT* activity leads to higher levels of catecholamines in the prefrontal cortex. The actual effect of these increased levels are not well understood. One proposed theory is the Warrior versus Worrier hypothesis, which outlines two groups of personality traits based upon the Val158Met mutation citation. The "Warrior" group, defined as the wild type group with lower levels of catecholamines like dopamine, are said to have an advantage in processing aversive stimuli. They are also said to have higher pain tolerance, be less prone to stress, less exploratory, and ect. However, many of these claims are not well defined and bordering on pseudoscience citation. The "Worrier" group, those with the mutation, are said to have an advantage in memory and attention tasks citation. The Val158Met mutation has also been linked to schizophrenia, but this claim is debated citation.

Citations: (order of appearance)

- NCBI COMT catechol-O-methyltransferase *Homo sapiens* (human)
- Chromosomal mapping of the human catechol-O-methyltransferase gene to 22q11.1—q11.2
- Gene Expression – NCBI COMT catechol-O-methyltransferase *Homo sapiens* (human)
- Lack of Association between rs4680 Polymorphism in Catechol-O-Methyltransferase Gene and Alcohol Use Disorder: A Meta-Analysis
- Functional Analysis of Genetic Variation in Catechol-O-Methyltransferase (COMT): Effects on mRNA, Protein, and Enzyme Activity in Postmortem Human Brain
- Kinetics of human soluble and membrane-bound catechol O-methyltransferase: a revised mechanism and description of the thermolabile variant of the enzyme
- Warriors versus worriers: the role of COMT gene variants
- Self Decode rs4680
- The effect of rs1076560 (DRD2) and rs4680 (COMT) on tardive dyskinesia and cognition in schizophrenia subjects

1.0.3 | Feedback and revisions

This is looking good so far. It is based in solid research and you're clear about what's still unknown.

The *COMT* gene, or catechol-O-methyltransferase, encodes the *COMT* enzyme which is responsible for breaking down neurotransmitters in the brain's prefrontal cortex. More specifically, it acts as a catalyst for the transfer of a methyl group from S-adenosylmethionine to dopamine, epinephrine, and norepinephrine. This process, called O-methylation, leads to the degradation of the aforementioned neurotransmitters. The *COMT* enzyme also affects the metabolism of exogenous substances, but that is irrelevant for the mutation at hand citation. The *COMT* gene itself is 27.22kb long and located on chromosome 22q11.2 citation. It has ubiquitous expression in 27 tissues, including the placenta, the adrenal, and the lung citation. This expression is dynamically regulated during brain development and due to environmental stimuli. Despite much research into COMT regulation, the actual processes are still mostly unknown citation. COMT has two promoters — P2 functions constitutively, whereas P1 has tissue dependent regulation. This tissue specific regulation is most likely done by C/EBPalpha. citation. Val158Met, also known as rs4680, is a common missense mutation swapping a guanine for an adenine. It has the frequency G=0.510915, and thus, A=0.489085. Val158Met causes the *COMT* enzyme to be roughly 25% as effective compared to the wild type. Expression levels in mRNA, despite its reduced protein abundance, are not effected by Val158Met citation & citation. Thus, Val158Met must be located in a protein-coding region causing the *COMT* enzyme to have lower protein integrity, explaining the discrepancy between mRNA expression and protein expression. This lower protein integrity is most likely manifested as diminished thermostability of the enzyme, in turn leading to its reduced effectiveness citation. The higher level effect of this reduced enzyme efficacy is greatly debated, and linked to many different phenotypes. At a broad level, lower *COMT* activity leads to higher levels of catecholamines in the prefrontal cortex. The actual effect of these increased levels are not well understood. One proposed theory is the Warrior versus Worrier hypothesis, which outlines two groups of personality traits based upon the Val158Met mutation citation. The “Warrior” group, defined as the wild type group with lower levels of catecholamines like dopamine, are said to have an advantage in processing aversive stimuli. They are also said to have higher pain tolerance, be less prone to stress, less exploratory, and ect. However, many of these claims are not well defined and bordering on pseudoscience citation. The “Worrier” group, those with the mutation, are said to have an advantage in memory and attention tasks citation. The Val158Met mutation has also been linked to schizophrenia, but this claim is debated citation.

<https://pubmed.ncbi.nlm.nih.gov/21095457/>

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- Chromosomal mapping of the human catechol-O-methyltransferase gene to 22q11.1—q11.2
- Gene Expression – NCBI COMT catechol-O-methyltransferase *Homo sapiens* (human)
- The Catechol-O-Methyltransferase Gene: Its Regulation and Polymorphisms
- Characterization of the rat catechol-O-methyltransferase gene proximal promoter: identification of a nuclear protein-DNA interaction that contributes to the tissue-specific regulation (<https://pubmed.ncbi.nlm.nih.gov/8672242/>)
- Lack of Association between rs4680 Polymorphism in Catechol-O-Methyltransferase Gene and Alcohol Use Disorder: A Meta-Analysis
- Functional Analysis of Genetic Variation in Catechol-O-Methyltransferase (COMT): Effects on mRNA, Protein, and Enzyme Activity in Postmortem Human Brain
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1.0.4 | Part Two!

infographic time.

- **Create an infographic that diagrams the various connections between the gene/SNP genotypic variants and the known phenotypic associations. This graphic should visually show the biological effects of the gene/protein and studied genotypes on human traits/phenotypes. It is also important to highlight the ways in which the environment affects gene expression, protein function and/or phenotype (see the example infographic for APOE below, which makes connections to diet and traumatic brain injury). You can choose to visually organize and/or lay out your graphic in a variety of formats, but make sure that the following information is included:**
- info to include
 - **gene basics**
 - yeah
 - yeah
 - reg
 - estrogen?
 - brain development
 - environmental
 - P2:
 - constitutively
 - P1:
 - tissue dependent, C/EBPalpha, ect.
 - **SNP variants to human phenotype relationships**
 - **Gene-environment Interactions**