**The Genetic Map Comparator: a quick and easy way to visualize your genetic maps…**

### *Yan Holtz1\*, Jacques David1, Vincent Ranwez2\**

1 Montpellier SupAgro, UMR AGAP, F-34060 Montpellier (France)

2 INRA, UMR AGAP, F-34060 Montpellier (France)

\* Corresponding author

E-mail:

Yan.holtz@supagro.fr

Vincent.ranwez@supagro.fr

**ABSTRACT**

**Summary:** A www comparative genetic map graphical utility. Can compare up to 10 maps together. Give some basic statistics. PDF output.

**Availability:** The genetic map comparator is available online: <http://www.agap-sunshine.inra.fr/holtz-apps/GenMap-Comparator/>. Source code is freely available on GitHub for non-commercial use only. (<https://github.com/holtzy/GenMap-Comparator>)

**Contact:** [Yan.holtz@supagro.fr](mailto:Yan.holtz@supagro.fr) & [Vincent.ranwez@supagro.fr](mailto:Vincent.ranwez@supagro.fr)

**Introduction**

*Why comparing genetic maps?*

In this study, we investigated the genetic basis of WSSMV resistance in 2 RILs population of durum wheat. Two elite cultivars (Silur and Lloyd) were crossed with Dic2, a dicoccum that

*What tools are available yet?*

In this study, we investigated the genetic basis of WSSMV resistance in 2 RILs population of durum

*Why a new one was needed?*

- Permet de comparer des cartes plus denses (NGS). Exemple: map chart deviant illisible avec >100 marqueurs par chromosomes ( avérifier)

- Permet des comparaisons inter-chromosomiques.

- Utilisation sur le WEB -> 0 installation.

- Utilisation des outils de visualisation interactive actuels !

**User Interface**

It is a shiny application available online. No installation needed. Works on every device. An example dataset is available. Several sheet: Basic statistics / genetic map comparison with parallele representation / interchromosomal analyses / rough map. It is possible to export figures to pdf or other format with publication quality.

**Fig. 1: Parallele comparison of 4 genetic maps.**

A representation of the third sheet of the application. Each vertical black line illustrates the selected chromosome of the 4 populations, with a point for each marker. Numbers on the left side specifies positions in cM. Names of markers are available on hover. Common markers between 2 adjacent maps are represented by a purple line.

**Data and Formatting.**

**Linkage Data**

-The gene map comparator imports linkage data from map files, produced by software for linkage analysis.

-Most famous software for genetic map building are:

-Map files are thus in several format.

- The gene map comparator will automatically transform data from 2 formats..

- See Documentation page for more info.

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References

Avni, Raz et al. 2014. “Ultra-Dense Genetic Map of Durum Wheat × Wild Emmer Wheat Developed Using the 90K iSelect SNP Genotyping Assay.” *Molecular Breeding* 34(4): 1549–62. http://link.springer.com/10.1007/s11032-014-0176-2.

Barnett, O W. “Potyviridae, a Proposed Family of Plant Viruses.” *Archives of Virology* 118(1): 139–41. http://dx.doi.org/10.1007/BF01311310.

Bass, C et al. 2006. “The Sbm1 Locus Conferring Resistance to Soil-Borne Cereal Mosaic Virus Maps to a Gene-Rich Region on 5DL in Wheat.” *Genome / National Research Council Canada = Génome / Conseil national de recherches Canada* 49(9): 1140–48. http://www.ncbi.nlm.nih.gov/pubmed/17110994.

Cadle-Davidson, L, M E Sorrells, S M Gray, and G C Bergstrom. 2006. “Identification of Small Grains Genotypes Resistant to Soilborne Wheat Mosaic Virus.” *Plant Disease* 90(8): 1039–44. http://dx.doi.org/10.1094/PD-90-1039.

Carroll, J E, G C Bergstrom, and S M Gray. 1997. “Dynamics of Wheat Spindle Streak Mosaic Bymovirus in Winter Wheat.” *European Journal of Plant Pathology* 103(4): 313–21.

Cheng, R et al. 2010. “Genome-Wide Association Studies and the Problem of Relatedness among Advanced Intercross Lines and Other Highly Recombinant Populations.” *Genetics* 185. http://dx.doi.org/10.1534/genetics.110.116863.

Cheng, Riyan, Mark Abney, Abraham A Palmer, and Andrew D Skol. 2011. “QTLRel: An R Package for Genome-Wide Association Studies in Which Relatedness Is a Concern.” *BMC Genetics* 12(1): 1–3. http://dx.doi.org/10.1186/1471-2156-12-66.

Choulet, Frédéric et al. 2014. “Structural and Functional Partitioning of Bread Wheat Chromosome 3B.” *Science (New York, N.Y.)* 345(6194): 1249721. http://www.ncbi.nlm.nih.gov/pubmed/25035497.

Dilbirligi, Muharrem et al. 2004. “Identification of Wheat Chromosomal Regions Containing Expressed Resistance Genes.” *Genetics* 166(1): 461–81.

Driskel, Barbara a et al. 2004. “Soilborne Wheat Mosaic Virus Movement Protein and RNA and Wheat Spindle Streak Mosaic Virus Coat Protein Accumulate inside Resting Spores of Their Vector, Polymyxa Graminis.” *Molecular plant-microbe interactions : MPMI* 17(7): 739–48.

Esch, Elisabeth et al. 2007. “Using Crossover Breakpoints in Recombinant Inbred Lines to Identify Quantitative Trait Loci Controlling the Global Recombination Frequency.” *Genetics* 177(3): 1851–58.

de Givry, Simon et al. 2005. “CARTHAGENE: Multipopulation Integrated Genetic and Radiation Hybrid Mapping.” *Bioinformatics* 21(8): 1703–4.

Glaubitz, Jeffrey C. et al. 2014. “TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline.” *PLoS ONE* 9(2).

Gutiérrez, Andrés Gonzalo et al. 2010. “Identification of a Rice Stripe Necrosis Virus Resistance Locus and Yield Component QTLs Using Oryza Sativa X O. Glaberrima Introgression Lines.” *BMC plant biology* 10: 6. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=2824796&tool=pmcentrez&rendertype=abstract.

Hariri, D et al. 1996. “Comparison and Differentiation of Wheat Yellow Mosaic Virus (WYMV), Wheat Spindle Streak Mosaic Virus (WSSMV) and Barley Yellow Mosaic Virus (BaYMV) Isolates Using WYMV Monoclonal Antibodies.” *European Journal of Plant Pathology* 102(3): 283–92.

Heffner, Elliot L, Mark E Sorrells, and Jean-luc Jannink. 2009. “Genomic Selection for Crop Improvement.” *Crop Science* 49(February): 1–12.

HUNGERT, R. M., J. L. SHERWOOD, E. L. SMITH, and C. R. ARMITAGE. “Symptomatology and Enzyme-Linked Immunosorbent Assay Used to Facilitate Breeding for Resistance to Wheat Soilborne Mosaic.” *Crop science* 31(4): 900–905. http://cat.inist.fr/?aModele=afficheN&cpsidt=4380782 (March 9, 2016).

Kanyuka, Konstantin, Elaine Ward, and Michael J. Adams. 2003. “Polymyxa Graminis and the Cereal Viruses It Transmits: A Research Challenge.” *Molecular Plant Pathology* 4(5): 393–406.

Khan, a a, G C Bergstrom, J C Nelson, and M E Sorrells. 2000. “Identification of RFLP Markers for Resistance to Wheat Spindle Streak Mosaic Bymovirus (WSSMV) Disease.” *Genome / National Research Council Canada = Génome / Conseil national de recherches Canada* 43(3): 477–82. http://www.ncbi.nlm.nih.gov/pubmed/10902711.

Kojima, Hisayo et al. 2015. “Identification and Validation of a Quantitative Trait Locus Associated with Wheat Yellow Mosaic Virus Pathotype I Resistance in a Japanese Wheat Variety.” *Plant Breeding* 134(4): 373–78. http://dx.doi.org/10.1111/pbr.12279.

Leflon, Martine et al. 2010. “Crossovers Get a Boost in Brassica Allotriploid and Allotetraploid Hybrids.” *The Plant cell* 22(7): 2253–64.

Maccaferri, Marco, Rossella Francia, et al. 2011. “Genetic Analysis of Soil-Borne Cereal Mosaic Virus Response in Durum Wheat: Evidence for the Role of the Major Quantitative Trait Locus QSbm.ubo-2BS and of Minor Quantitative Trait Loci.” *Molecular Breeding* 29(4): 973–88. http://dx.doi.org/10.1007/s11032-011-9673-8.

Maccaferri, Marco, Claudio Ratti, et al. 2011. “Resistance to Soil-Borne Cereal Mosaic Virus in Durum Wheat Is Controlled by a Major QTL on Chromosome Arm 2BS and Minor Loci.” *Theoretical and Applied Genetics* 123(4): 527–44.

Maccaferri, Marco, Maria Cane’, et al. 2014. “A Consensus Framework Map of Durum Wheat (Triticum Durum Desf.) Suitable for Linkage Disequilibrium Analysis and Genome-Wide Association Mapping.” *BMC Genomics* 15(1): 873. http://www.biomedcentral.com/1471-2164/15/873.

Maccaferri, Marco, Andrea Ricci, et al. 2014. “A High-Density, SNP-Based Consensus Map of Tetraploid Wheat as a Bridge to Integrate Durum and Bread Wheat Genomics and Breeding.” *Plant biotechnology journal*: 1–16. http://www.ncbi.nlm.nih.gov/pubmed/25424506.

V. Marie-Jeanne A. Sohn, D.-E. Lesemann J Peyre B Alliot P A Signoret. 1999. “Characterization of an Antiserum Raised against Coat Protein of Wheat Spindle Streak Mosaic Virus Overexpressed in E. Coli / Charakterisierung Eines Antiserums Gegen in E. Coli überexprimiertes Hüllprotein von Wheat Spindle Streak Mosaic Virus.” *Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz / Journal of Plant Diseases and Protection* 106(6): 654–59. http://www.jstor.org/stable/43390126.

Nei, M. 1978. “Estimation of Average Heterozygosity and Genetic Distance from a Small Number of Individuals.” *Genetics* 89(3): 583–90.

Ordon, Frank et al. 2009. “Virus Resistance in Cereals: Sources of Resistance, Genetics and Breeding.” *Journal of Phytopathology* 157(9): 535–45. <Go to ISI>://WOS:000268707300002\nhttp://onlinelibrary.wiley.com/store/10.1111/j.1439-0434.2009.01540.x/asset/j.1439-0434.2009.01540.x.pdf?v=1&t=hbnssh9z&s=637dc18b9f29293229054bf89b6421cbf6ea640a.

Perovic, Dragan et al. 2009. “Mapping and Diagnostic Marker Development for Soil-Borne Cereal Mosaic Virus Resistance in Bread Wheat.” *Molecular Breeding* 23(4): 641–53. http://dx.doi.org/10.1007/s11032-009-9262-2.

Rohland, Nadin, and David Reich. 2012. “Cost-Effective, High-Throughput DNA Sequencing Libraries for Multiplexed Target Capture.” *Genome Research* 22(5): 939–46.

Sohn, a. et al. 1995. “Comparison of Wheat Spindle Streak Mosaic Virus (WSSMV) and Barley Yellow Mosaic Virus (BaYMV): 2 Closely Related Bymoviruses.” *Agronomie* 15(7-8): 427–31.

Taylor, Publisher et al. 2011. “A Major QTL for Resistance to Soil-Borne Cereal Mosaic Virus Derived from an Old Italian Durum Wheat Cultivar.” *Journal of plant Interactions* (November 2014): 37–41.

Vaïanopoulos, C et al. 2006. “Widespread Occurrence of Wheat Spindle Streak Mosaic Virus in Belgium.” *Plant Disease* 90(6): 723–28. http://www.scopus.com/inward/record.url?eid=2-s2.0-33646861657&partnerID=40&md5=6facec37d00d49cf6b947921179fe7f2.

Vaissayre, Laurence et al. 2012. “Elite Durum Wheat Genetic Map and Recombination Rate Variation in a Multiparental Connected Design.” *Euphytica* 185: 61–75. http://link.springer.com/10.1007/s10681-012-0627-y.

Vegetale, Patologia. 2003. “Reaction of Durum Wheat Cultivars to Mixed SBWMV and WSSMV Infection in Central Italy.” : 177–82.

Walker, Scott L, Steven Leath, J Paul Murphy, and Steven A Lommel. 1998. “Selection For Resistance and Tolerance to Oat Mosaic Virus and Oat Golden Stripe Virus in Hexaploid Oats.” *Plant Disease* 82(4): 423–27. http://dx.doi.org/10.1094/PDIS.1998.82.4.423.

Xiaoyun, Lu, Satoshi Kashiwazaki, Masaru Tamura, and Shigetou Namba. 1998. “The 3’ Terminal Sequence of RNA1 of Wheat Spindle Streak Mosaic Virus Canadian Isolate (WSSMV-C).” *European Journal of Plant Pathology* 104: 765–68. http://link.springer.com/article/10.1023/A:1008623326352.

Zhu, Xiaobiao et al. 2012. “Mapping and Validation of Quantitative Trait Loci Associated with Wheat Yellow Mosaic Bymovirus Resistance in Bread Wheat.” *Theoretical and Applied Genetics* 124(1): 177–88. http://www.ncbi.nlm.nih.gov/pubmed/21959905.

# Supporting Information

**S1 Fig: Comparison of the DS, DL and consensus genetic maps.**

For each chromosome, 3 parallel black lines represent the 3 genetic maps with lengths represented in cM. The consensus map is represented in the middle, with the DS map on its right and the DL map on its left. A black point represents each marker. A blue line links common markers between 2 adjacent maps.