

METAPOP: When Genomics meets MARS



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Metapop is a tool built to detect, validate and use QTL in wheat.

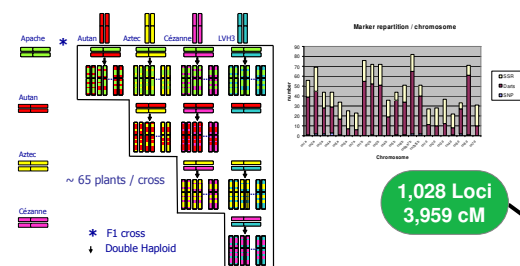
Metapop relies on a **detection population** composed of 614 double haploids (DH) obtained by crossing 5 elite French lines following a incomplete semi-diallel design, and on a **validation population** that allows to build Near Isogenic Lines (NIL) for any detected Quantitative Trait Loci (QTL) in only one generation. As all this material was derived from elite germplasm, QTL may be used easily in modern breeding programs by **MARS (Marker-Assisted Recurrent Selection)**. Also the best RIL could be crossed with eachother to accumulate favourable alleles in an "ideal" new genotype and therefore enrich breeding programs.

Metapop is used to study different traits such as **Yield, Yield Components and Nitrogen Use Efficiency** in several Genoplante collaborative projects: "WheatGrowth, WheatPerformance and ProtNblé" supported by the competitiveness cluster "Céréales vallée".

Strategy:

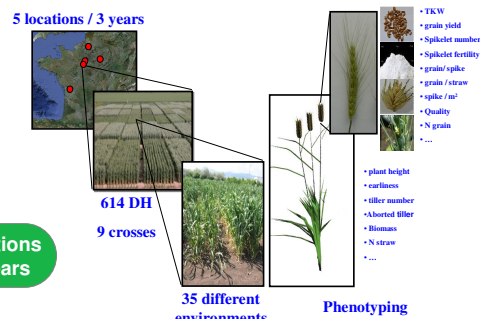
Detection population

The population has been built by **intercrossing 5 elite French varieties** in an **incomplete semi diallel design**. The parental lines display a large range of phenotypic diversity for traits related to our interest, and particularly for tillering and for yield elaboration. All those lines belong to Limagrain and represent more than **25% of the French market**. From those 9 crosses, a population of **614 plants** was derived by a **doubled haploid** method. **366 SSR markers** chosen for their polymorphism and their good coverage of the whole genome, **642 DaRT Markers** (<http://www.diversityarrays.com/>) and **20 SNP** were used to genotype DH lines.



Field Evaluation

The **614 DH** lines were evaluated under field conditions during **3 years** (2005-2006-2007), in **5 locations** and **different conditions** (sowing date, fertilisation, density ...). The field experimentation design represents a total of **35 different environments**. The phenotypic scorings conducted by our partners (Limagrain, Arvalis institut du végétal, INRA) were focused on **yield, yield components and nitrogen**.

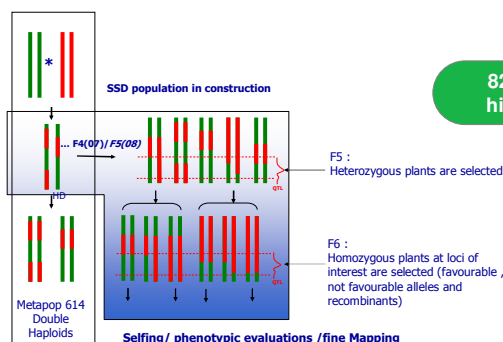
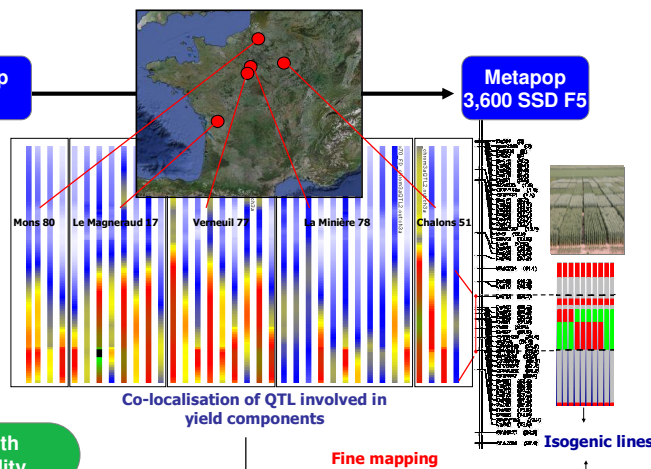


QTL detection

The specific population design (diallel cross) required the use of a specific software: **MCQTL** (Jourjon *et al.* 2005). After detection, we analysed the **QTL co-localisation** (for the same trait) between years, locations and different conditions to select regions of interest with **high stability and reproducibility**. Also, we compared these loci with candidate genes and known QTLs identified in other crosses, by Meta-analysis of QTL (INRA collaboration).

1,802 QTL

82 Loci with high stability



Validation population

From the 9 initial crosses, 400 lines per cross were produced using **Single Seed Descent (SSD)**. Those **3,600 Heterogeneous Inbred Families (HIF)** were selfed until F5. At this stage each line is homozygous for 93.75% of its genome and so heterozygous for the remaining 6.25%. As far as a QTL is detected, lines still heterozygous in the QTL zone are identified using molecular markers. After only one selfing **NIL with different alleles at the QTL can be obtained**. As it is possible to get some recombinants in the QTL zone it is possible to **shorten QTL confidence interval** and carry on with the **fine mapping**.

6 NIL in production
10 more under consideration

Results :

The use of Metapop in several collaborative projects has allowed us to build a powerful **genetic map** with more than **1,000 mapped loci** and collect **many phenotypic data**. To date, several hundreds of QTL **have been detected** in different themes. For Yield, Yield Components and Nitrogen the analysis of **QTL co-localisation**, on the **1,802 QTL** detected, allowed us to identify **82 loci of interest with high stability**, represented by 834 QTL. In the same time, a Meta-analysis of QTL between the Metapop data and all the other published QTL data is under process (INRA collaboration), to increase interest on these 82 loci. The most promising QTL are in validation phase, **couple of NIL are already in production** and a second set is under consideration. We plan to validate the QTL effect on the first NIL and start the fine mapping at the end of the year. Also for those interesting QTL, the best RIL will be chosen to be re-crossed to build **superior genotypes pyramiding many favourable alleles**. The Metapop design with the **detection population** and the **validation population** is a good way to fine-map QTL and find candidate genes in a short time. A part of this QTL fine-mapping are under way and some of them are already used by **MARS** in Limagrain's breeding programs.

Our target is to improve our knowledge and enrich the germplasm of our breeding program with favourable alleles to hopefully deliver to the market new successful varieties.