Development of a new pre-breeding scheme combining marker-assisted selection and genomic selection, for improving wheat disease resistance

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Abstract: We proposed a pre-breeding strategy which combines marker-assisted selection (MAS) for major genes coming from exotic materials, and genomic selection (GS) to optimize the genetic elite background. Two real and separate pre-breeding schemes are described in bread wheat (Triticum aestivum L.) for the introgression of disease resistance genes into optimized elite backgrounds. The first one focused on the construction of genitors with improved yellow rust (YR) and leaf rust (LR) resistances, whereas the other one was based on the creation of fusarium head blight (FHB) resistant genitors with improved genetic background.

Introduction: GS is a valuable approach for plant breeding, primarily designed for complex traits controlled by many loci. To achieve high GS accuracy, the relationship between the training population and the test population is essential as genome-wide markers needs to be in the same linkage disequilibrium with the true QTLs in both populations to be good predictors. In pre-breeding programs, exotic plant materials are often introduced for their notable behaviour for a specific trait, for example disease resistances, but are not well-characterized for complex traits. Applying GS directly on this exotic material would not be powerful because of the poor relationship between this exotic material and training populations, most commonly composed of breeding elite material. We developed a pre-breeding strategy in two main steps combining marker-assisted selection (MAS) for pyramiding major genes coming from exotic materials, and genomic selection (GS) to optimize the genetic elite background of the receiving lines. The first step was based on several crosses, controlled by MAS, in order to combine all the desirable alleles coming from exotic lines into the same genotypes with a significant elite genetic background. Hybrids cumulating these major genes were then used to produce a large doubled haploid population. Finally, the DH individuals were selected by genome-wide predictions to optimize their elite background.

Rust pre-breeding scheme

FHB pre-breeding scheme

Plant material

In the rust pre-breeding scheme, two major genes of rust resistance were followed (Lr57/Yr40 and Lr42), as well as one gene of eyespot resistance (Pch1) and one QTL of FHB resistance (QTLSA). The improvement of the genetic background will be controlled with the Axiom® Wheat Breeder’s Genotyping array, containing around 35K SNP markers, in the last step of the scheme.

Results / Discussion

These different pyramiding schemes have allowed, on one hand the production of 695 doubled haploids (DH) accumulating two rust resistance genes (Lr57/Yr40, Lr42) and two genes/ QTL of resistance to other important diseases (Pch1, FHB-QTLSA), and on the other hand the production of 236 DH lines accumulating at least two major FHB resistant genes (Fhb1/Fhb5) and probably a few minor QTLs of FHB resistance. These DH lines were composed of a large part of elite genetic background thanks to the use of elite parents in the initial crosses but the genetic background still need to be optimized. In 2017, DH lines will be selected using genomic estimated breeding values. The improved lines, that will be selected, will be validated in the field for their disease resistance and yield. Theses new selected progenitors will allow the broadening of the genetic base of plant material in breeding.


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