

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

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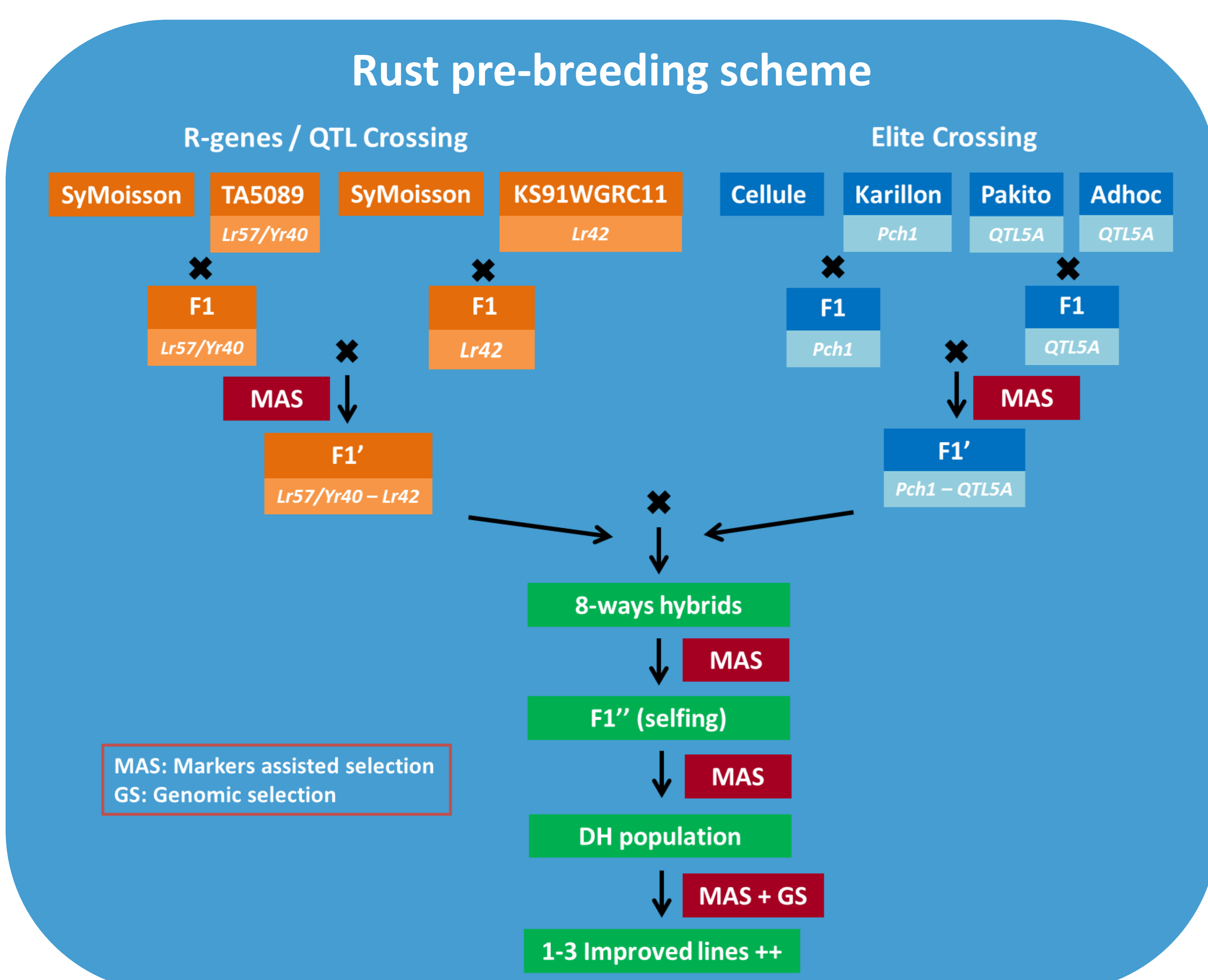
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**Abstract:** We proposed a pre-breeding strategy which combines marker-assisted selection (MAS) for major genes coming from exotic materials, and genomic selection (GS) to optimize the genetic elite background. Two real and separate pre-breeding schemes 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.

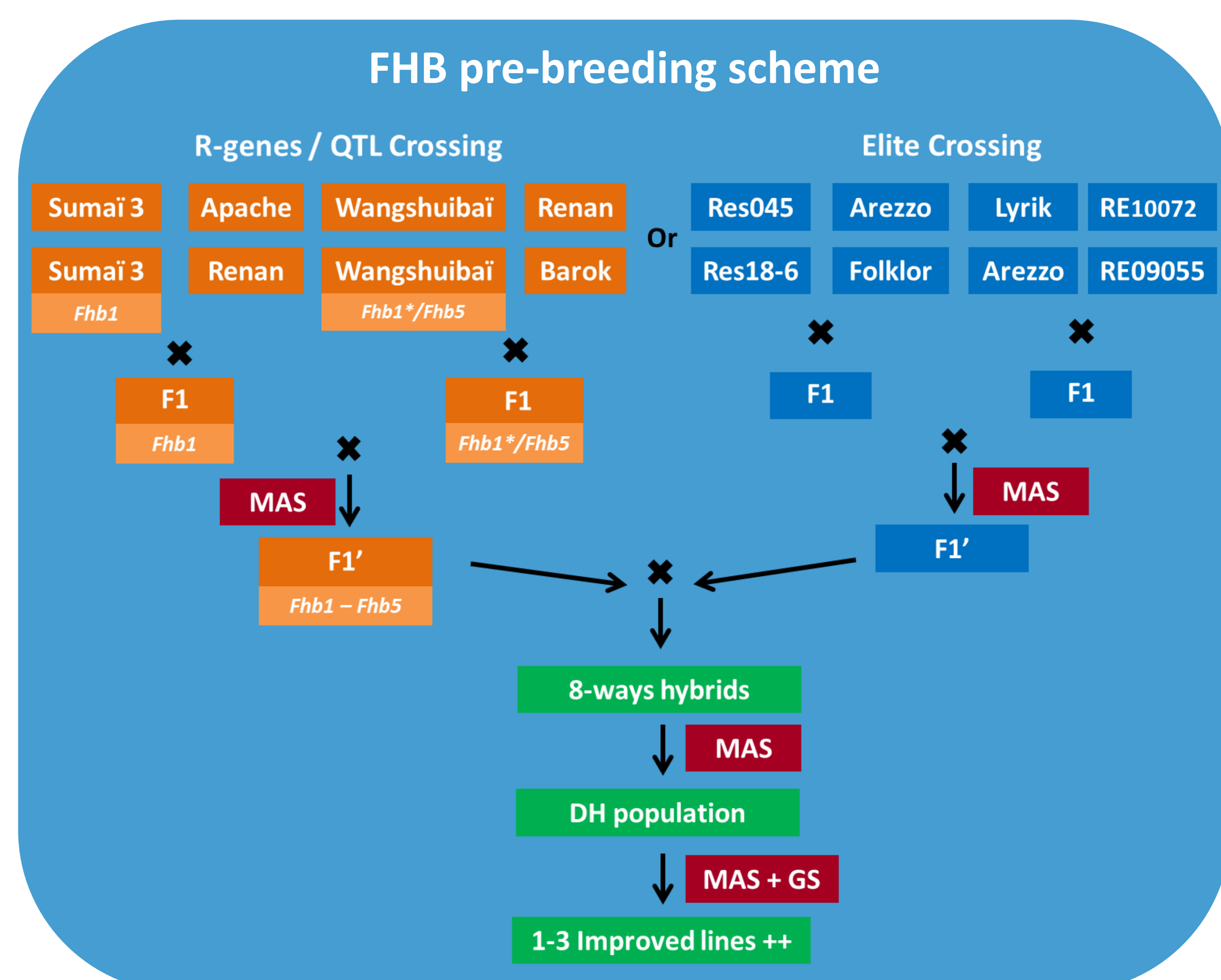
**Introduction:** GS is a valuable approach for plant breeding, primarily designed for complex traits controlled by many loci. To achieve high GS accuracy, the relationship between the training population and the test population is essential as genome-wide markers needs to be in the same linkage disequilibrium 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



MAS: Markers assisted selection  
GS: Genomic selection

## FHB pre-breeding scheme



## Plant material

Line	Gene/QTL	Markers	Ref
KS91WGRC11	Lr42	Xwmc432 and Xgdm33	Martin et al., 2003
TA5089	Lr57/Yr40	XLr57/Yr40-MAS-CAPS16	Kuraparthy et al., 2009

Variety	Registration	Breeder	Important features
CELLULE	2012	FD	Rht1, breadmaking quality, STB resistant
KARILLON	2010	AO	Rht1, breadmaking quality, Pch1
PAKITO	2011	RAGT	Rht1, breadmaking quality, QTL5A
ADHOC	2011	Momont	Rht1, breadmaking quality, QTL5A, cold resistant
SY MOISSON	2011	Syngenta	Rht1, breadmaking quality, powdery mildew resistant

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 (*QTL5A*). 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-QTL5A*), 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. These new selected progenitors will allow the broadening of the genetic base of plant material in breeding.

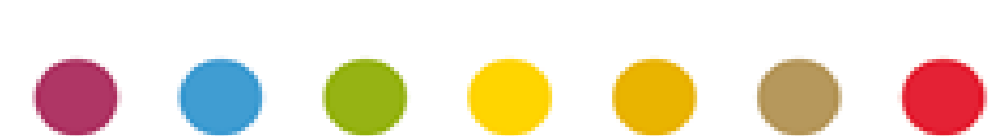
**References:** Martin et al (2003) Contributions of leaf rust resistance and awns to agronomic and grain quality performance in winter wheat. *Crop Science* 43:1712-1717  
Kuraparthy et al. (2009) Development of a PCR Assay and Marker-Assisted Transfer of Leaf Rust and Stripe Rust Resistance Genes *Lr57* and *Yr40* into Hard Red Winter Wheats. *Crop Science* 49:120-126  
Bernardo et al. (2012) Single nucleotide polymorphism in wheat chromosome region harboring *Fhb1* for Fusarium head blight resistance. *Molecular Breeding* 29:477-488  
Lin et al. (2006) Mapping QTL associated with resistance to Fusarium head blight in the Nanda2419 × Wangshuibai population. II: Type I resistance. *Theor Appl Genet*,112:528-535

## Plant material

Line	Genes /QTLs	Markers	Ref
SUMAÏ 3	<i>Fhb1</i>	8 SNPs in Umn10	Bernardo et al., 2012
WANGSHUIBAÏ	<i>Fhb1*</i> / <i>Fhb5</i>	<i>Xwmc96</i> and <i>Xgwm304</i>	Lin et al., 2006

Variety	Registration	Breeder	Important features
AREZZO	2007	RAGT	Breadmaking quality
BAROK	2009	AO	FHB resistant
FOLKLOR	2011	AO	Breadmaking quality, YR resistant
LYRIK	2012	AO	Breadmaking quality
RESY18-6	-	INRA	STB resistant
RESY045	-	INRA	STB resistant
APACHE	1998	LG	Breadmaking quality, FHB resistant
RENAN	1990	AO	FHB resistant

Two different FHB pre-breeding schemes were carried out in parallel. FHB resistant lines were Sumaï 3 (*Fhb1*) and Wangshuibai (*Fhb1\*/Fhb5*), for which the resistances were selected by markers, as well as Apache, Barok and Renan, carrying minor resistance QTLs. *Fhb1* alleles were different between Sumaï 3 and Wangshuibai. The genetic background will also be selected with prediction algorithms based on the Axiom® Wheat Breeder's Genotyping array in the last step, trained on a large breeding population.



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