GENOMIC SELECTION FOR LOW DON CONTENT IN WINTER WHEAT

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Introduction

Wheat contamination with mycotoxins caused by Fusarium is of great economic importance. The current routine method of disease evaluation (single-location trial based on visual symptoms) does not yield the comprehensive data needed to accelerate breeding for resistance to Fusarium. We intend to lay the foundation for more efficient resistance breeding against Fusarium, by targeting deoxynivalenol (DON), the most important mycotoxin, and improve resistance to DON accumulation by genomic selection (GS).
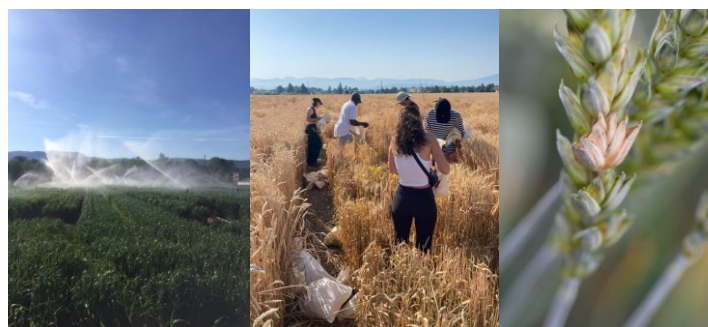
Material and Methods

A reference set (RS) of 300 cultivars and breeding lines was phenotyped in a three-location, artificially inoculated trial over two years. We evaluated resistance to Fusarium by visual scoring of symptoms, expressed as Area Under the Disease Progress Curve (AUDPC), and by measuring DON content of harvested grain by High-performance liquid chromatography (HPLC). We additionally scored plant height, heading date and anther extrusion. In the third year, a validation set (VS) of 225 new lines was integrated in the same experimental setting. The purpose of the VS was, on the one hand, to evaluate the potential of GS by comparing the observed phenotypes with corresponding genomic predictions obtained from models trained using the RS. On the other hand, the new lines would ultimately extend the number of genotypes available for GS model training to a total of 525. All lines and cultivars were genotyped using the 25K SNP chip by SGS - TraitGenetics GmbH, Germany.

Tabl. 1. Minimum, mean an maximum across 3 years (2021-2023) and 3 locations (n = 525 genotypes), and estimates of heritability (h^2)

|	Heading [days after 1.1]	Plant Height [cm]	Anther Extrusion [1 – 5]	Fusarium symptoms (AUDPC)	DON content [µg / kg]
Min.	130	66	1.4	916	1326
Mean	144	93	3.3	3829	9456
Max.	151	121	4.5	13494	29144
h^2	0.94	0.93	0.64	0.84	0.77

Results

We obtained satisfactory phenotypic results for all years and most locations, with generally high and homogeneous Fusarium pressure and subsequent DON accumulation, resulting in high heritability for both AUDPC and DON (Tabl. 1). The correlation between Fusarium symptoms and DON was moderate (r = 0.54), confirming that measurement of DON is a valuable asset for resistance breeding. Correlations with other traits were low to moderate, but significant, and confirmed that both height and earliness influence Fusarium infection and should be considered when implementing GS (Tabl. 2). For both Fusarium resistance traits, the first independent validation of GS through the VS yielded moderate prediction abilities (0.3 - 0.4), while prediction abilities from cross-validation schemes with the full set of available data (525 genotypes, 3 years) reached values of 0.5 to 0.6. Realistic estimates of prediction abilities for future GS-use should lie in the 0.4 – 0.5 range, and are sufficient for significant breeding progress (Fig. 1).

Tabl. 2. Pearson correlation coefficients (r) between traits (2021 - 2023, n = 525 genotypes)

	Heading	Plant Height	Anther Extrusion	Fusarium symptoms (AUDPC)
Plant Height	- 0.02 ns			
Anther Extrusion	- 0.33 ***	+ 0.22 ***		
Fusarium symptoms (AUDPC)	- 0.24 ***	- 0.36 ***	- 0.32 ***	
DON content	+ 0.39 ***	- 0.30 ***	- 0.55 ***	+ 0.54 ***

Fig.1 Genomic prediction accuracy using a Bayes-B model, «20 x 5 - fold cross validations»
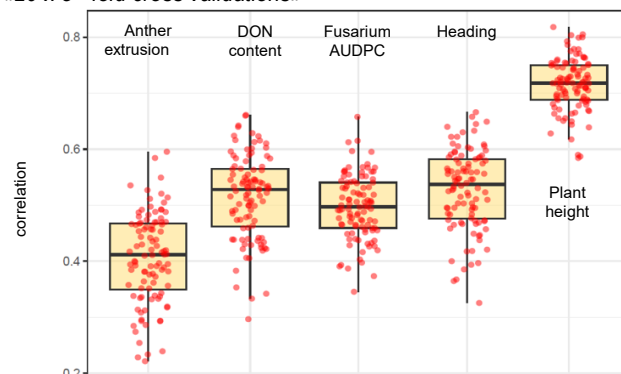
Conclusion

The GS model for DON content prediction can now join the other GS models developed for quality and agronomic traits. All the genomic predictions are used on ~5'000 already genotyped breeding lines to help selection across all stages of the breeding program.