



MAGIC-RESIST

Identification and mapping of resistances against fungal diseases in the MAGIC-WHEAT population WM-800

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Introduction

Wheat (*Triticum aestivum* L.) takes almost one third of the world cereal production. However, its cultivation is threatened by a range of pathogens. Therefore, more sustainable crop protection strategies have to be pushed forward, including the efficient detection of new disease resistances. The MAGIC-RESIST project aims to combine an innovative crossing design with unmanned aerial vehicle (UAV)-based phenotyping in order to establish the basis for future large-scale resistance screening of breeding populations.

Materials and Methods

We phenotyped the WM-800 population (Sannemann et al. 2018, Fig. 1) for natural powdery mildew (*Blumeria graminis*) infestation in four environments in Germany (Figure 2). By combining the BLUEs with data for a total of 27,685 single nucleotide polymorphism (SNP) markers from Illumina wheat 15k SNP array and Affymetrix 135k array analysis, a genome-wide association study (GWAS) was performed with SAS 9.4 to identify powdery mildew resistance loci. After selection of co-factors with Proc GLMSELECT, a multiple linear regression model was fitted with Proc GLM for QTL detection (with $p \leq 0.0001$). The detected QTL were validated by five-fold cross validation with 20 replications. A detection rate of 35 % was considered as the threshold for significant marker-trait associations.

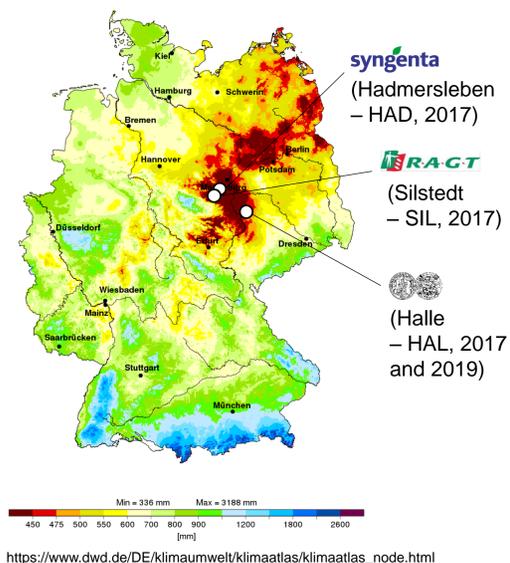


Figure 2. Geographical location of test environments in Germany with the annual precipitation.

Table 1. Descriptive statistics for powdery mildew infestation in W-800 across and within the four environments showing total number of observations (N), lowest and highest scoring (min and max), mean scoring and standard deviation (SD).

	Across	HAD2017	HAL2017	SIL2017	HAL2019
N	5,597	800	800	797	3,200
min	1.0	1.0	1.0	1.0	2.0
max	8.0	8.0	8.0	7.0	8.0
mean	3.7	1.8	2.1	2.6	4.8
SD	1.8	1.1	1.7	1.2	1.1

Results and Conclusion

The highest powdery mildew infestation scoring was obtained in HAL2019 with a mean score of 4.8, the lowest one in HAD2017 (1.8) (Table 1). The correlations between the environments were moderate ($r=0.32$ up to $r=0.61$, Figure 3), exhibiting a relatively high heritability of $h^2=79\%$. A total of 10 QTL for powdery mildew resistance could be consistently detected (Table 2). Out of these, six were located in the A genome, and two were detected in the B and D genome, respectively. The absolute effects ranged between 0.31 and 0.67 scoring units. Several described powdery mildew resistance genes can be considered as candidate genes according to the genetic chromosome location of Huang and Röder (2004). In addition, a number of NBS-LRR genes, a RPM1 gene and a peroxidase pathogen-related gene have been identified as candidate genes based on their physical genome positions (Alaux et al. 2018, RefSeq v 1.0).

Table 2. Significant QTL, founder allele distribution (Julius vs. non-Julius – J/NJ), chromosome (CHR), position in Mbp (POS), detection rate in % (DR), effect (EFF, defined as the mean difference between homozygous J and NJ genotypes), validated R^2 in % and candidate genes.

QTL name	J/NJ	CHR	POS	DR	EFF	R^2	Candidate genes
QPM.wm800-1A.a	3/5	1A	12.37	63	-0.57	10.6	Pm3 genes; several NBS-LRR genes at 12,2-12,6 Mbp
QPM.wm800-1A.b	2/6	1A	14.16	35	-0.59	8.0	Pm3 genes
QPM.wm800-2A.b	4/4	2A	524.15	35	0.41	3.7	Pm4a, Pm4b; a peroxidase gene is located at 525.62 Mbp
QPM.wm800-2A.a	7/1	2A	752.87	68	-0.57	2.7	Pm4a, Pm4b
QPM.wm800-3A	6/2	3A	7.3	60	0.48	5.6	
QPM.wm800-4A	5/3	4A	679.26	82	-0.31	2.5	leucine-rich repeat protein, putative, expressed (at 679.26 Mbp)
QPM.wm800-4D.b	1/7	4D	494.12	59	-0.58	0.7	
QPM.wm800-4D.a	2/6	4D	494.27	75	0.61	4.6	
QPM.wm800-6B	5/3	6B	32.01	52	-0.33	2.1	Pm12, Pm20
QPM.wm800-6B.a	7/1	6B	696.33	95	0.67	11.5	4 disease resistance loci (RPM1 protein) at 696.15-696.36 Mbp

Outlook

The WM-800 population is currently examined under inoculated conditions for resistances against stripe rust (*Puccinia striiformis*), leaf rust (*Puccinia tritici*) and Fusarium (*Fusarium culmorum*) with additional usage of UAV-based phenotyping.

References

- Alaux et al. (2018) Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. *Genome Biology* 19:111.
 Huang and Röder (2004) Molecular mapping of powdery mildew resistance genes in wheat: A review. *Euphytica* 137:203–223.
 Sannemann et al. (2018) Adaptive selection of founder segments and epistatic control of plant height in the MAGIC winter wheat population WM-800. *BMC Genomics* 19:559.

Acknowledgements

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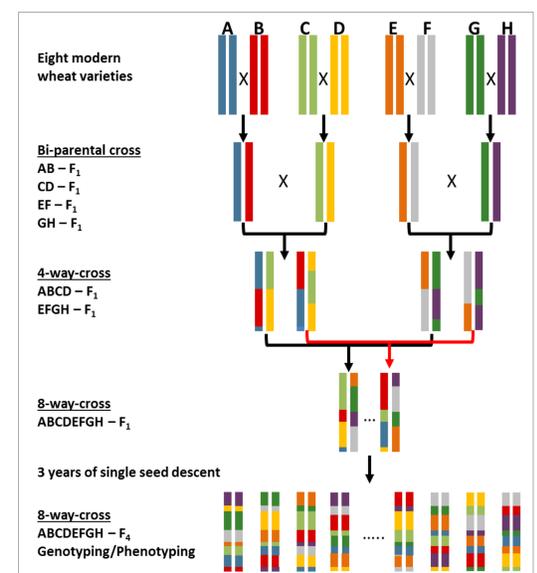


Figure 1. Eight-way crossing design of the WM-800 population (Sannemann 2016, unpublished).

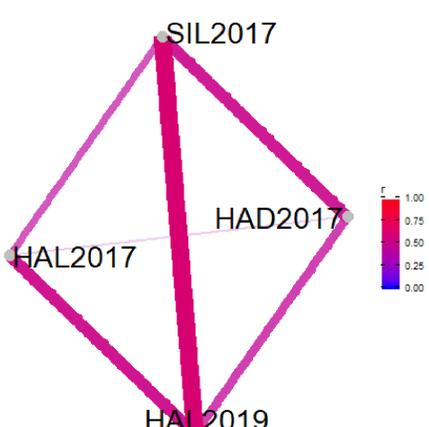


Figure 3. Graphical representation of the pairwise correlations (r) of the mean powdery mildew scores of WM lines between the four environments.

