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Genome-wide association study for resistance to stripe rust in Central European winter wheat

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'*WheatSustain*'

Stripe rust disease in wheat

- Stripe rust or yellow rust (Yr) is a fungal and one of the most destructive diseases of wheat (*Triticum aestivum* L.)

- *Puccinia striiformis* (*Pst*) is causing stripe rust in wheat

- It leads to a significant economic damage to the production of wheat, with losses up to 70-80% of total yields in epidemic conditions; annual estimated losses are 5.47 million tonnes of wheat worth US$979 million

- Sustainable management of wheat stripe rust is only possible by identifying and introducing rust resistant genes into the wheat elite cultivars


https://striperust.wsu.edu/

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Genetics of resistance to rust diseases

- Resistance to rust diseases is classified into two main groups:

    i. all stage resistance (ASR); resistance genes are effective against avirulent pathotypes throughout all growth stages of the plant (race specific, qualitatively inherited, and can be overcome by new races)

    ii. adult plant resistance (APR); whereas APR genes express resistance only at the post-seedling stages (race non-specific, quantitatively inherited, and more likely durable)

➢ A single effective ASR gene can protect a wheat variety from stripe rust; however, it places selection pressure on the pathogen to acquire virulence for the singly deployed gene

➢ Therefore, the deployment of known APR genes in combination with effective ASR genes present in modern wheat cultivars are needed to deliver commercially acceptable levels of resistance

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- Chromosomal locations of several stripe rust resistance genes were determined using:

  i. monosomic analysis

  ii. bulked segregant analysis (BSA)

  iii. selective genotyping (SG)

  iv. whole genome scanning using the high throughput molecular technologies (such as the Illumina iSelect 90 K Infinium SNP-genotyping array and DArTseq technology)

- The 2013 Catalogue of Gene Symbols for Wheat includes 67 officially named Yr genes (Yr1-Yr67) and 42 with temporary Yr designations
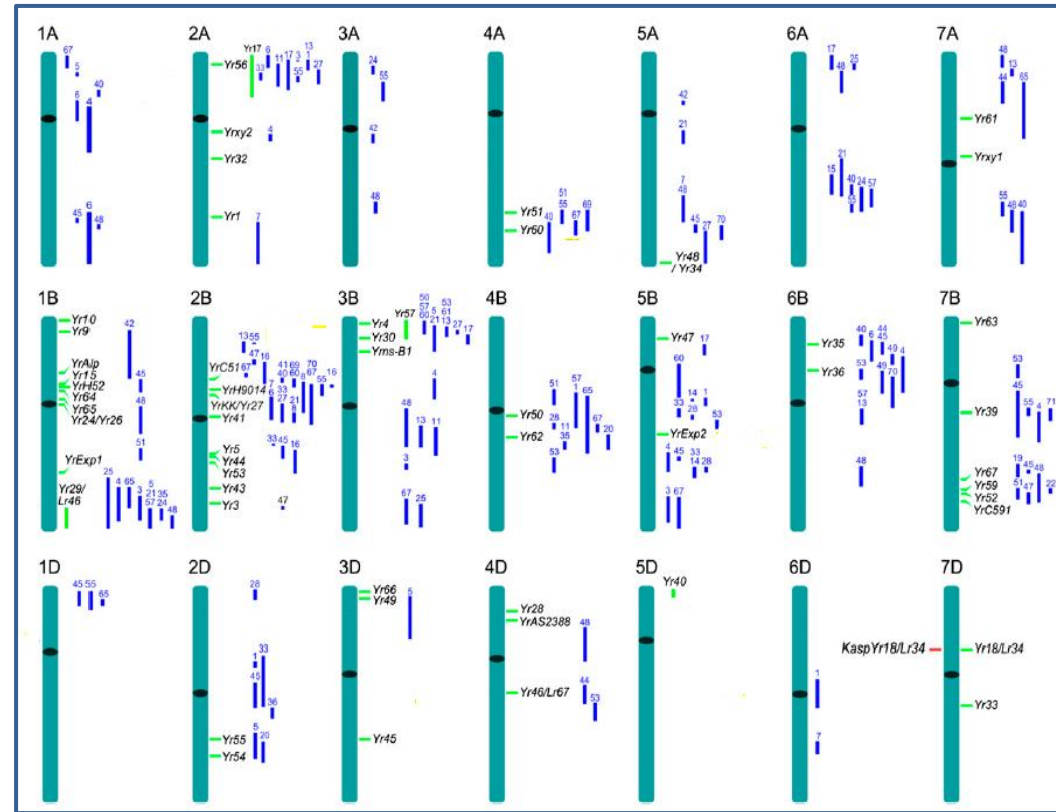
Maccaferri et al., 2015

Objectives

- To evaluate the diversity for seedling and adult-plant resistance to Warrior Pst pathotypes in bread wheat cultivars and breeding lines

- To conduct GWAS analysis for identifying the sources of effective resistance genes and associated QTL for utilization in future breeding programs

- To compare the Pst resistance loci identified in this study with previously identified Yr genes and QTL

- To apply significant associated markers in genomic prediction of resistance to stripe rust in breeding programs

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Training and Validation Population

- **Training Population:**

  A collection of 230 wheat cultivars and breeding lines from the Central Europian countries (Norway, Sweden, Austria, Germany, Poland, Denmark and Switzerland), evaluated in five environments (2020-2021)

- **Validation population:**

  - Two different sets of nearly 1000 breeding lines belonging to German breeding companies (WheatSustain), evaluated in Lemgo, Germany

   -175 breeding lines belonging to LfL, evaluated in Lenglern, Germany

- **Genotyping platform:**

  Wheat Illumina 25K Infinium SNP array

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Population structure analysis

- Training set (No. of loci: 8900 ; No. of ind.: 230)

■ Subpopulation 1 (N=92, Austrian lines)

■ Subpopulation 2 (N=138, German & other lines)
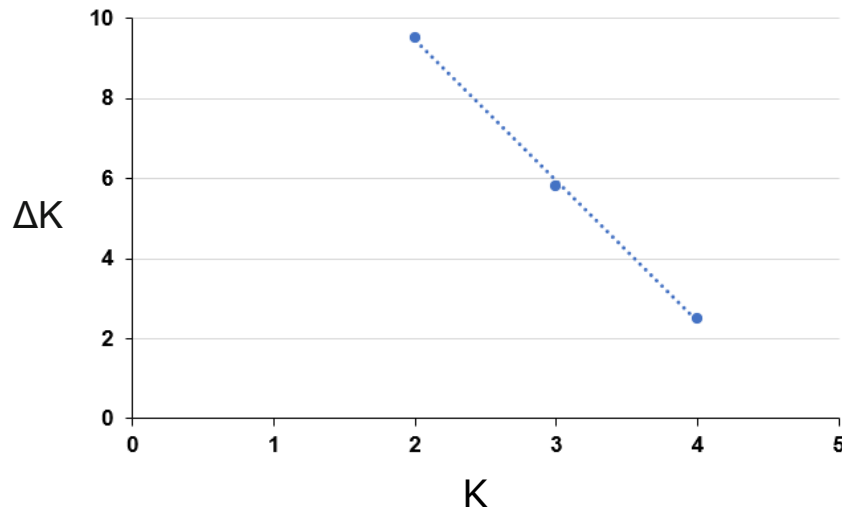
Determination of the number of subpopulations via the ad hoc statistic ΔK
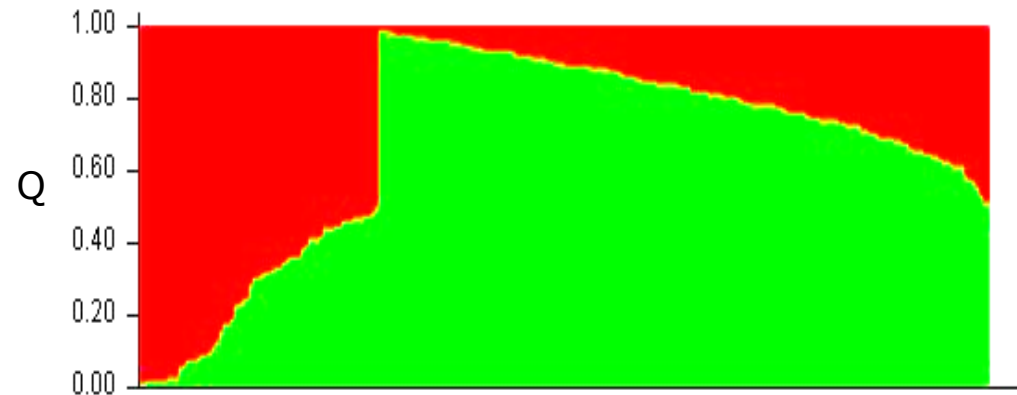
Fast structure analysis showing 2 subpopulations at K=2
y axis: membership coefficient (Q) of individuals

Population structure analysis

- Training set (No. of loci: 8900 ; No. of ind.: 230)

Principal component analysis of distance matrix using SNP genotyping data

PC1 vs. PC2
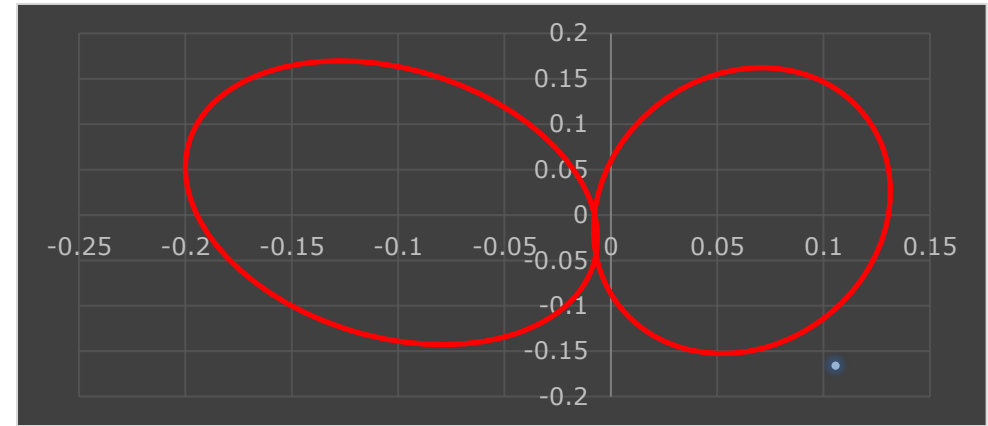
Minor Allele Frequency Distribution

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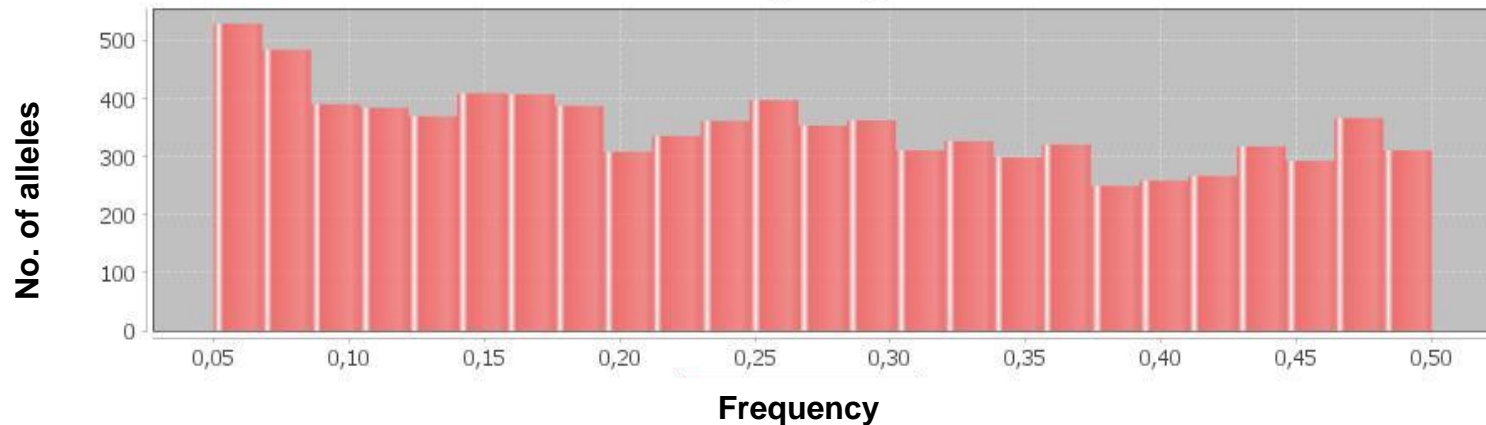
Frequency distribution of disease severity (%)

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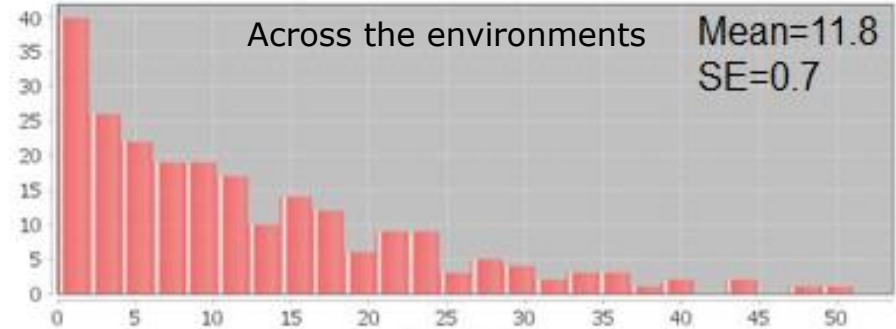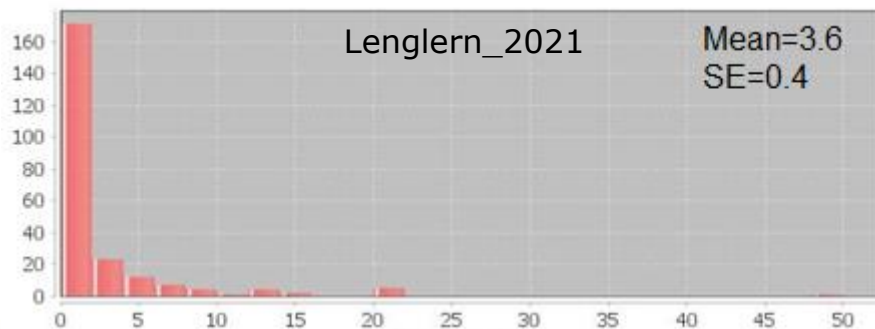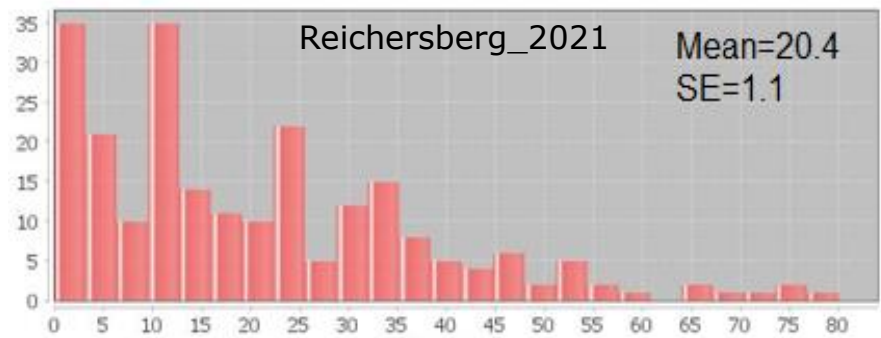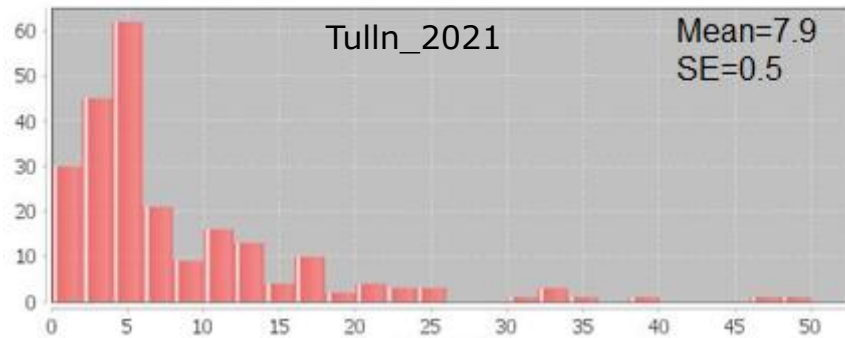
ArcSinSQRT transformed disease severity of stripe rust- Residual Distribution

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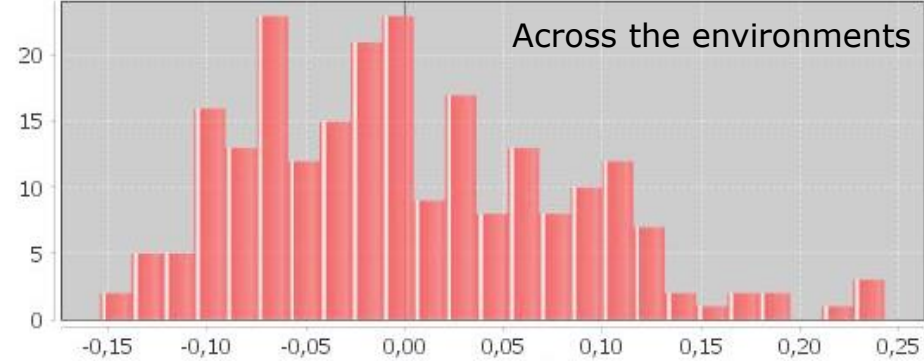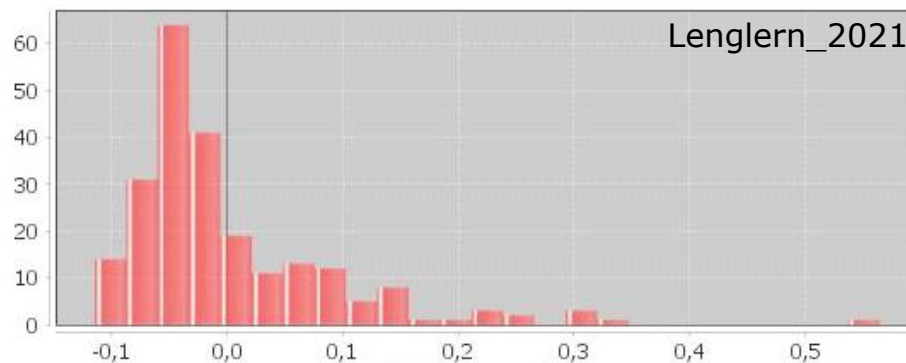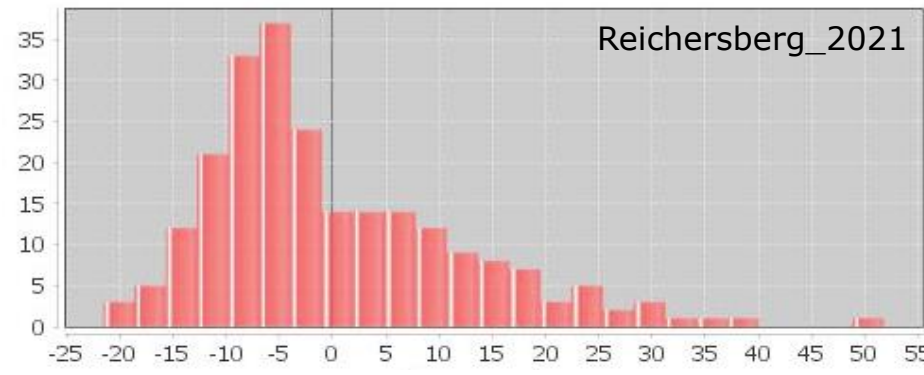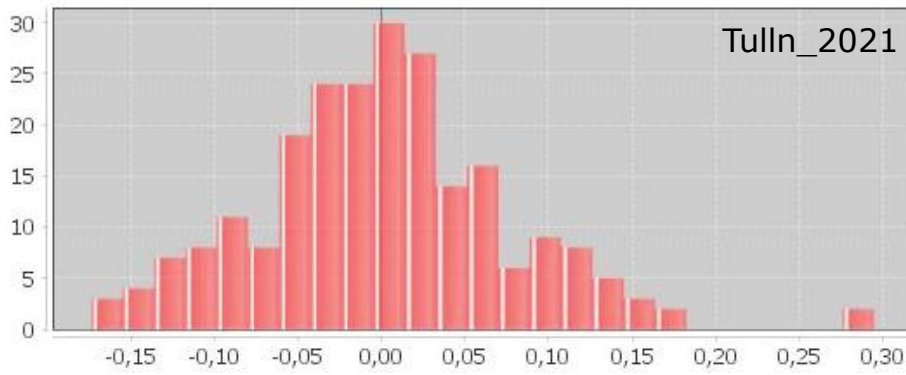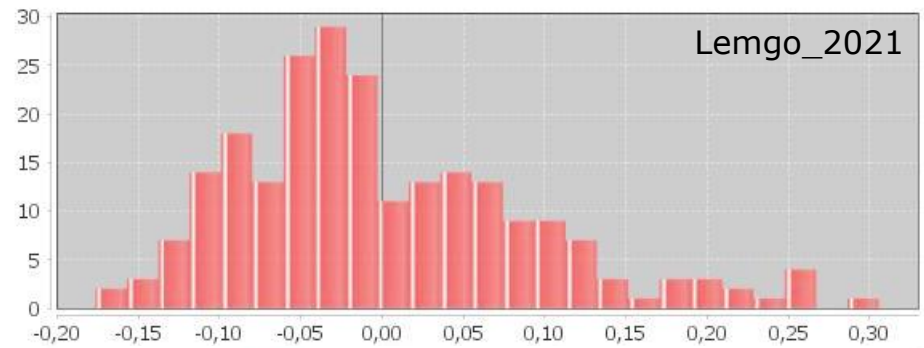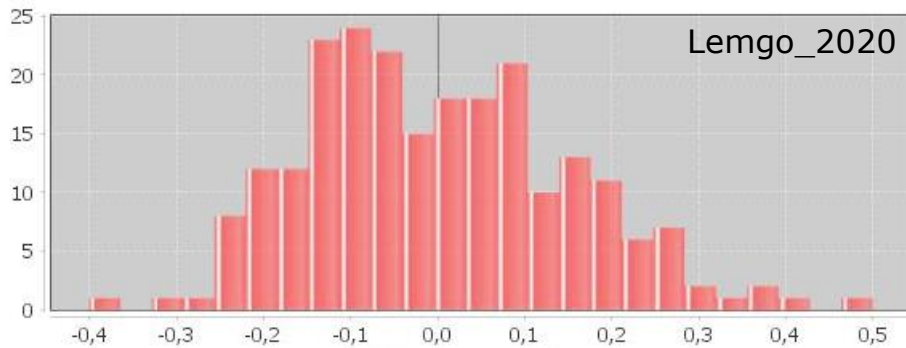
SNPs significantly associated with disease severity

GWAS was performed using the pairwise kinship matrix and mixed linear model (MLM)

Environment	No. SNPs	Chromosome	R2 (%)
Lemgo_Germany 2020	14	1A, 2B, 3A, 3B, 4B, 6A	5-7
Lemgo_Germany 2021	13	2B, 6A, 7A	6-11
Lenglern_Germany 2021	23	2A, 2B, 7A, 7B, 7D	6-7
Tulln_Austria_2021	10	1A, 4B, 5B, 5D, 7A, 7B	5-6
Reichersberg_Austria_2021	6	2B, 4B, 5A, 7A	5-7
Across the environments	12	2B, 4B, 6A, 7A, 7B, 7D	5-7

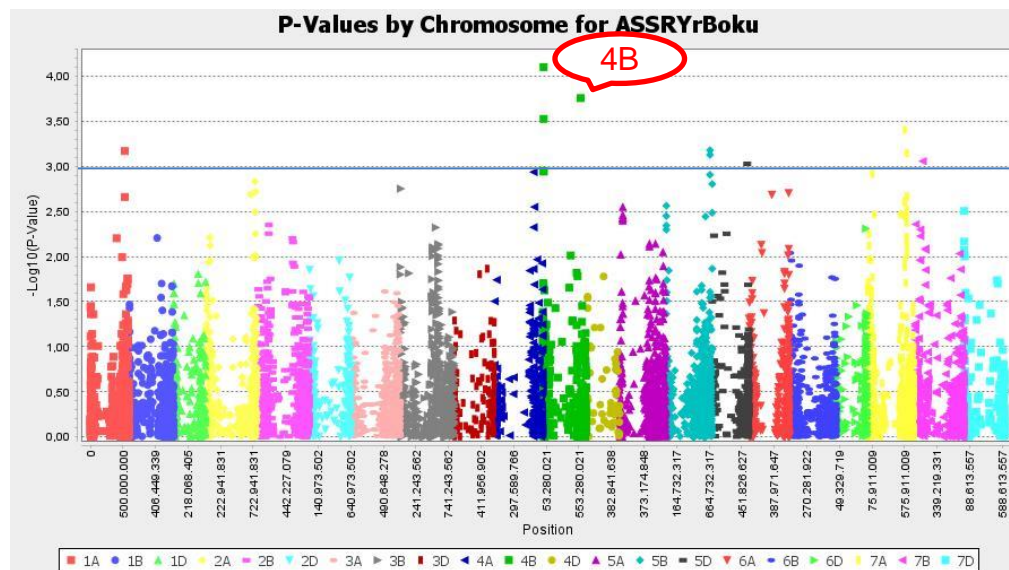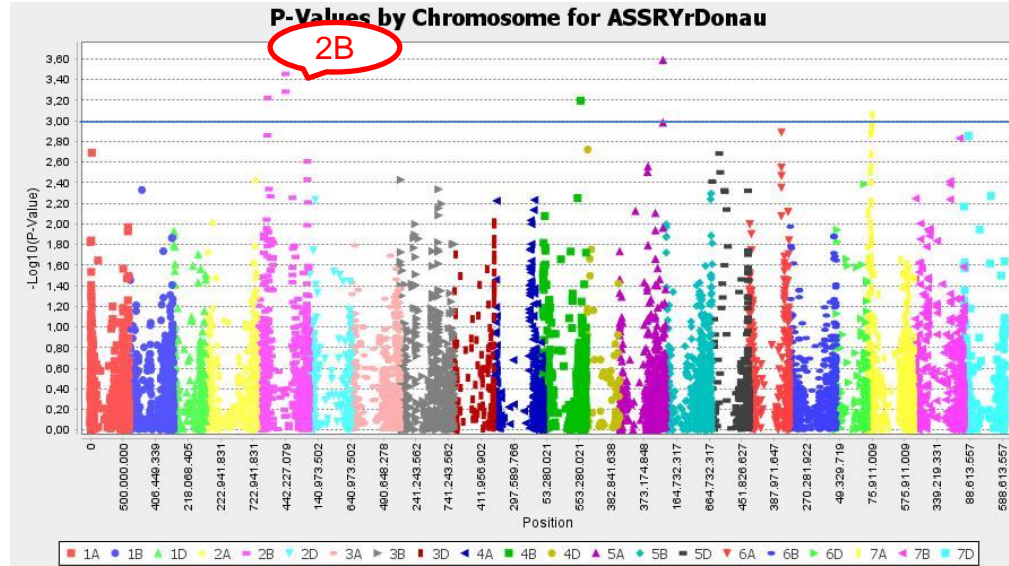# SNPs significantly associated with disease severity in Germany

Lemgo_2020

Lemgo_2021

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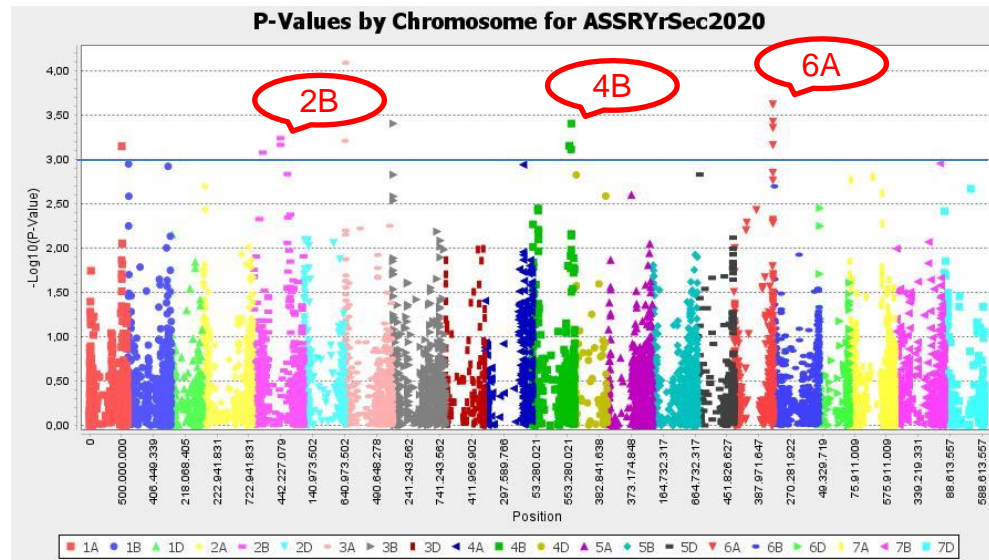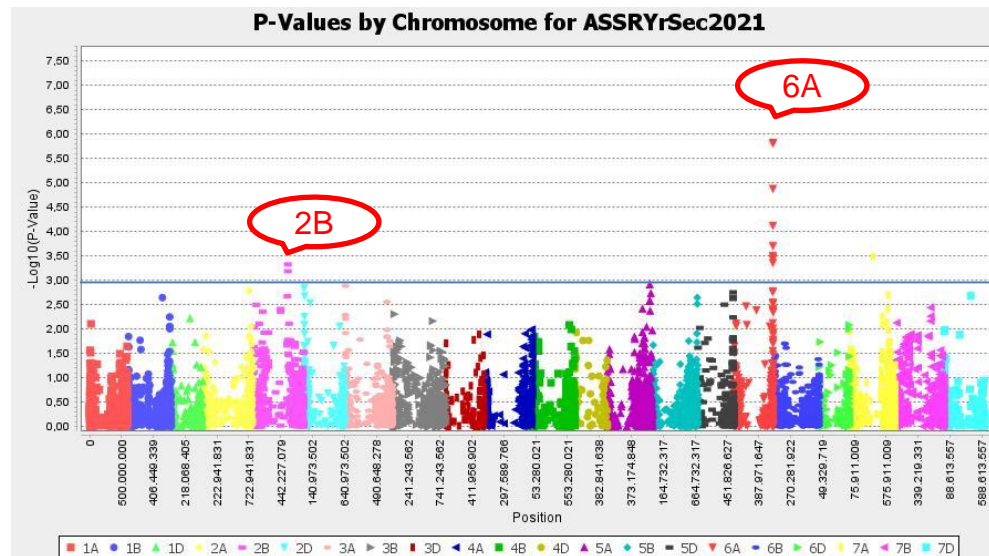
SNPs significantly associated with disease severity in Austria

Reichersberg_2021

Tulln_2021

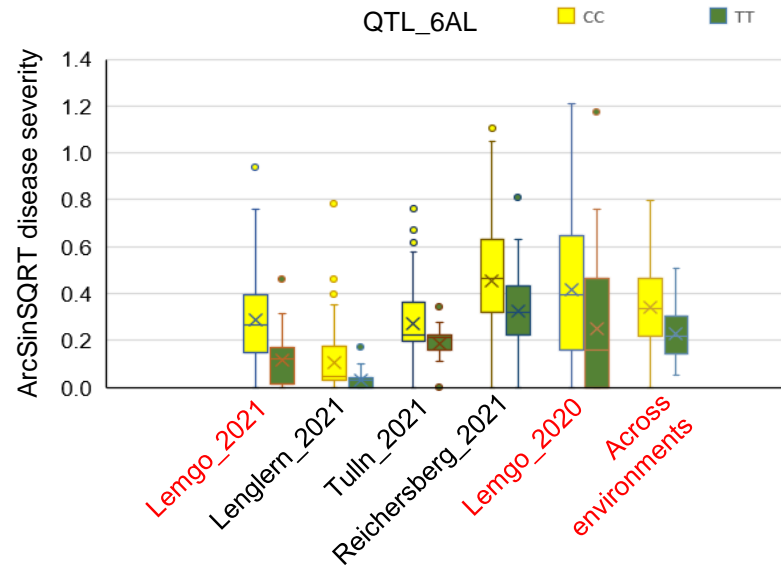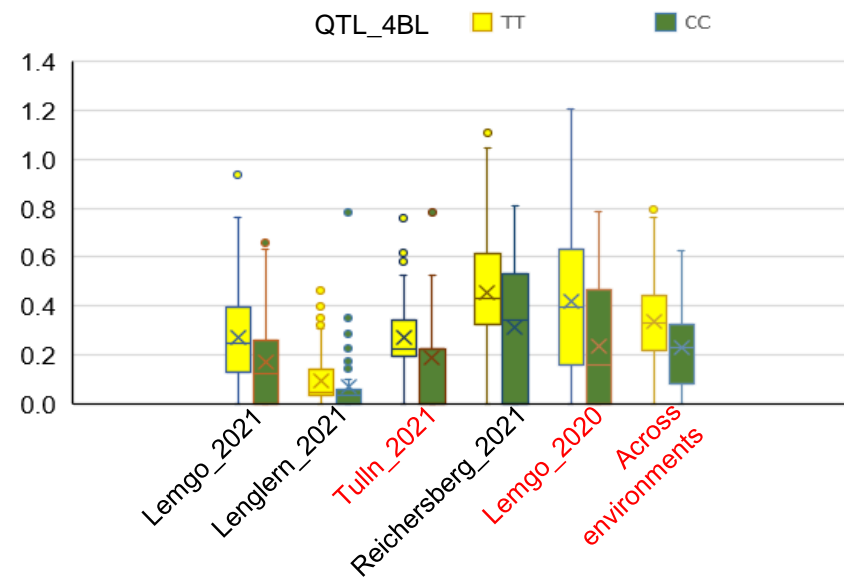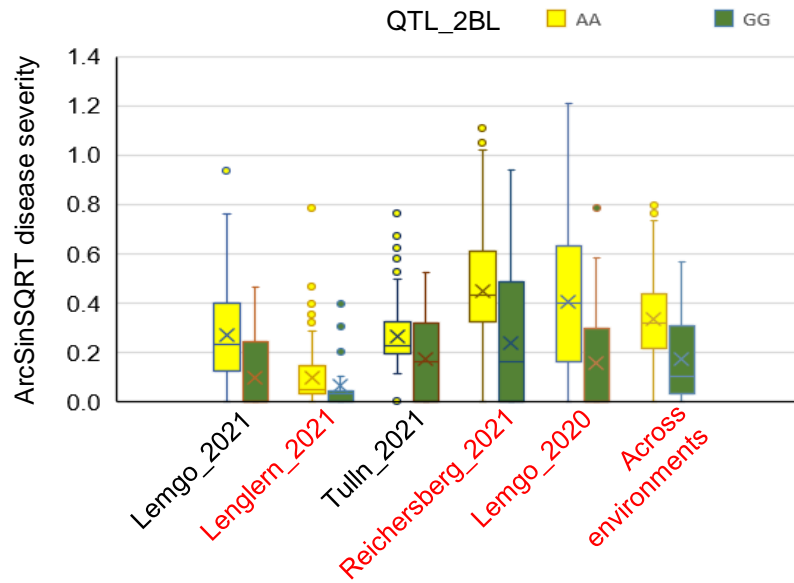Institute for Crop Science and Plant Breeding

SNPs significantly associated with disease severity across the environments
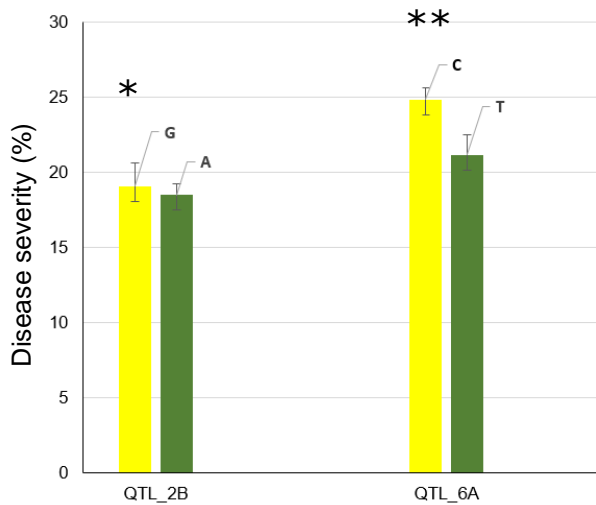
Lenglern_2021

Across the environments

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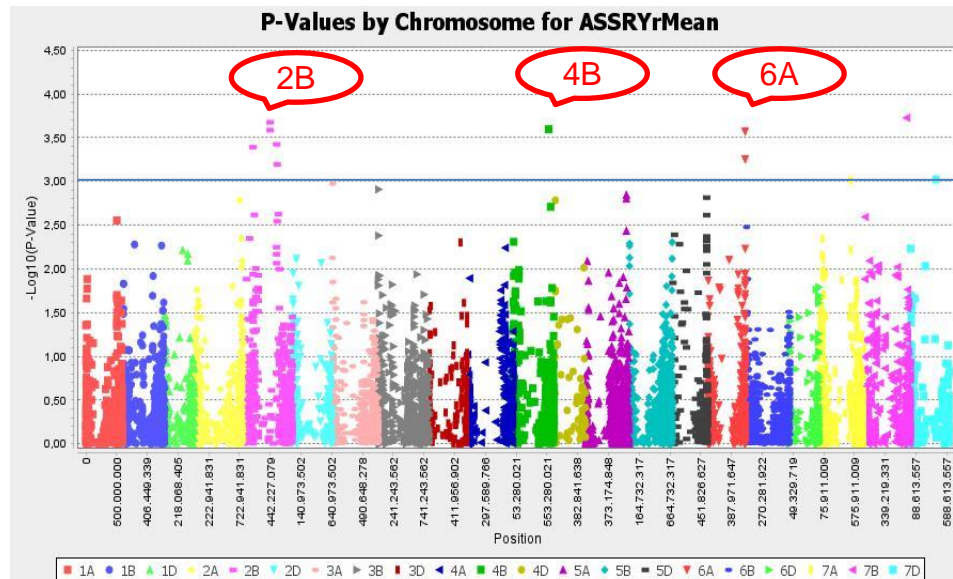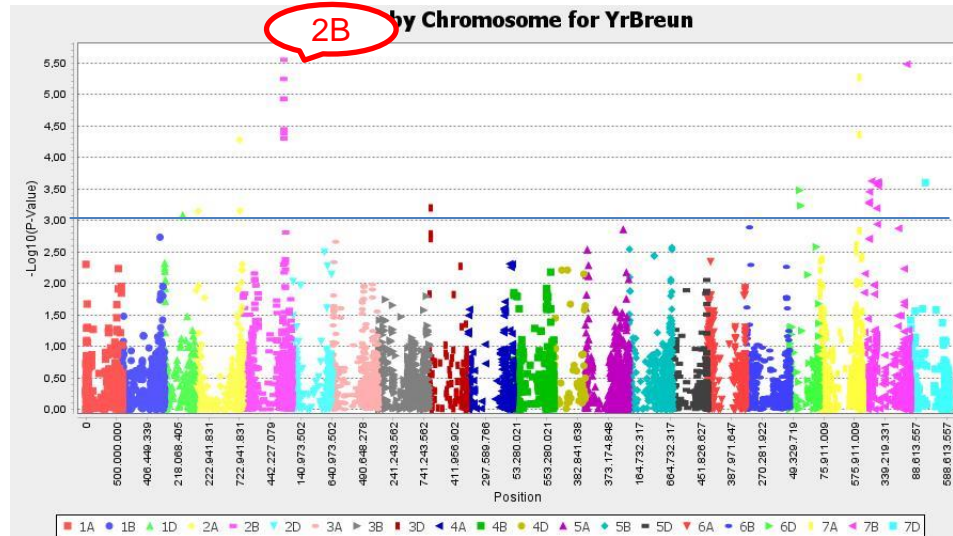
Allelic effect of common loci for stripe rust

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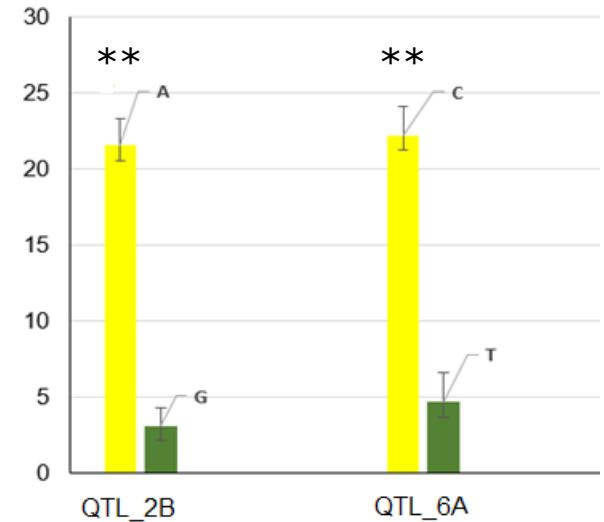
Validation of common loci in breeding materials

813 WheatSustain V.S., evaluated in Lemgo_Germany (year 2020)
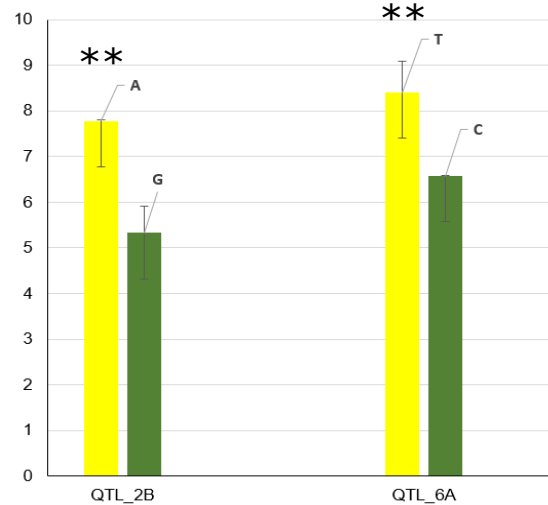
1230 WheatSustain V.S., evaluated in Lemgo_Germany (year 2021)

175 independent breeding lines, evaluated in Lenglern_Germany (year 2021)

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Comparison with previously mapped resistance loci

QTL	Physical interval (bp)	Known genes or QTL *
QTL_2BL	439225308-665669936	*QYr.inra-2B.2_CampRemy*
		QYr.caas-2BL_Naxos
		QYraq.cau-2AL_Aquileja
		QRYr2B.2_ICARDA
		Yr5
		Yr44
QTL_4BL	581078314-612253980	*QYr.hbaas-4BL.1*
		QYr.hbaas-4BL.2
		Qyr.wpg-4B.1
		Yr62
QTL_6AL	609380034-611661202	present study

* https://wheat.pw.usda.gov/cgi-bin/GG3/browse.cgi

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