Genetic Architecture of Powdery Mildew Resistance in Southeastern Soft Red Winter Wheat

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BACKGROUND

- Powdery mildew (*Blumeria graminis* f.sp. *Tritici*; hereafter PM) is a significant reducer of wheat grain yields in Southeastern U.S. growing conditions.
- Resistant germplasm is the most economical method of fungal control.
- Wheat resistance is driven by a combination of quantitative and qualitative resistance genes.

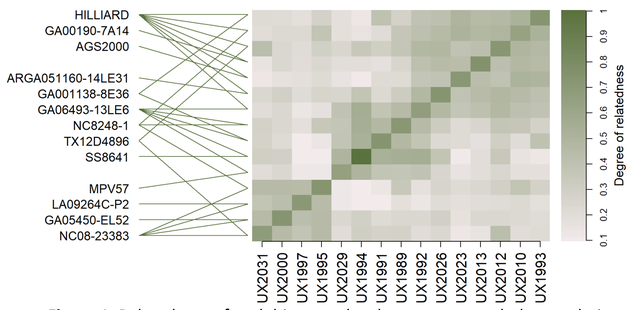

Figure 1: Relatedness of each biparental; color represents whole-population averages. Right column and lines shows parentage of biparental.

POPULATION

- Created 15 biparental RIL populations.
- These were divided into 3 nested association map (NAM) groups.
- Planted ~132 individuals from each biparental in three environments.

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Figure 3: PM infested wheat flagleaf: rating 4

GENOTYPING

- Sequenced all lines with GBS.
  - Filtered raw data and created biparental linkage maps and a whole-population imputed dataset.
- Ran KASP assays for major known PM genes on parents.

Figure 4: Plot of imputed marker density along all chromosomes. There are small gaps in coverage in most centromeric regions shown by gray segments, with increased coverage density towards the distal ends.

Line name	Pedigree	1RS	Known PM genes
AGS2000	PIONEER-2555/PF-84301//FL-302	1RS:1BL	*Pm3a*
ARGA051160-14LE31	SC996284/SS8641//SS8641	no	*Pm3a, Pm4b/d*
G001138-8E36	GA961581/PIONEER26R61	1RS:1BL	*Pm3a*
GA00190-7A14	931298/GA92601	1RS:1BL	*Pm3e*
GA05450-EL52	GA96229-3E39/C9553	no	*Pm3a, Pm4b/d*
GA06493-13LE6	981394-16-2-1/981622-10-2-3	no	*Pm1a, Pm3a, Pm4b/d*
HILLIARD	PIONEER25R47/JAMESTOWN	no	*Pm4a*
LA09264C-P2	LA841/VA02W-713//LA01139D-56-1	no	*Pm3e, Pm4a*
MPV57	FFR555W/3/Lovrin29/Tyler//Redcoat*2/Gaines	1RS:1BL	*Pm3a/e, Pm4b/d*
NC08-23383	PATTON/NC96-13374//MCCORMICK	1RS:1AL	
NC8248-1	Neuse/Bess	no	
SS8641	GA881130/GA881582//GA881582	no	*Pm1a, Pm3a, Pm4b/d*
TX12D4896	PIONEER26R61/SS8641	no	*Pm3a/e, Pm4b/d*

Table 1: KASP assay results for population parents. NAM founder parents are bold. 1RS refers to rye (*Secale cereal L.*) introgressions containing PM genes. Known PM genes has list of resistance alleles in major PM genes.

PHENOTYPE

- PM infection rated from 0 (no infection) to 4 (flagleaf infested).
- Calculated BLUEs using a discrete ordered categorized response variable through a cumulative logit link function:

$$y = Xb_{Genotype} + Zu_{Location:Year:Block} + \varepsilon$$

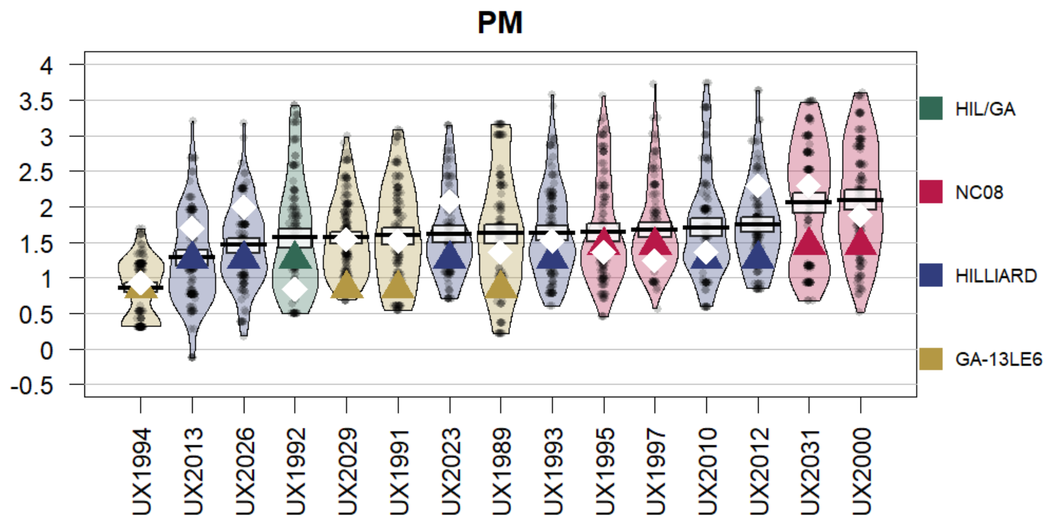

Figure 2: BLUEs for all lines plotted in black dots by biparental. Violin shows distribution of BLUE and color designates NAM founder, with colored triangle designating NAM founder BLUE. White diamond shows diversity parent BLUE, black line shows population mean.

QTL ID

- Performed linkage analysis on each biparental separately using r/qtl2.
- Performed GWAS on whole population using r/ASReml, rrBLUP, and GAPIT. Highest significance marker from each cluster, regardless of test, is presented.

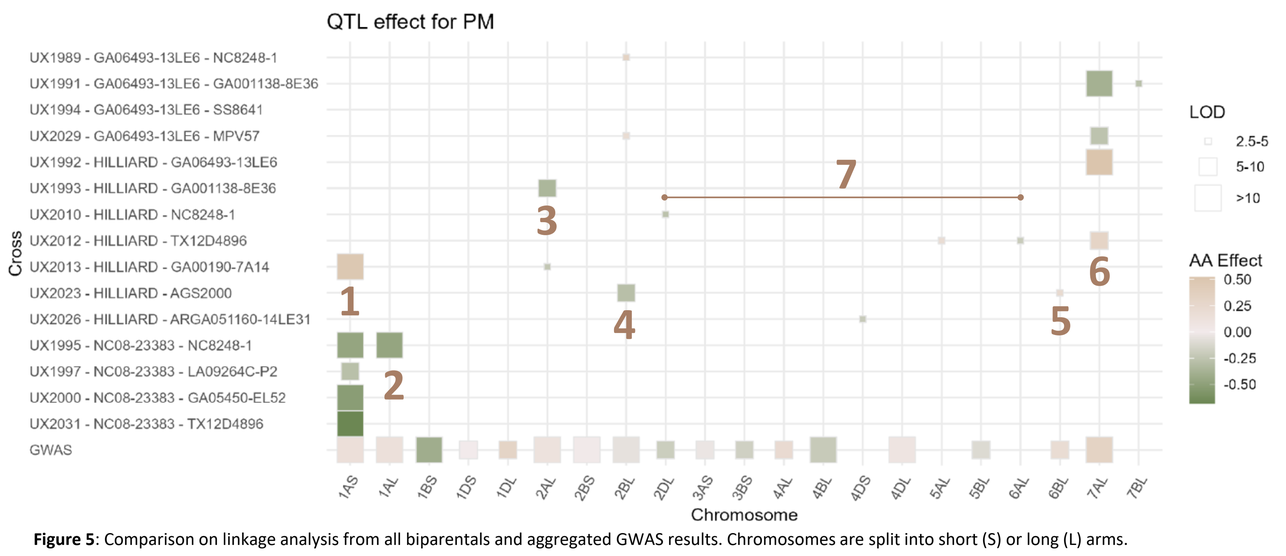

Figure 5: Comparison on linkage analysis from all biparentals and aggregated GWAS results. Chromosomes are split into short (S) or long (L) arms.

Figure 6: Pictogram showing linkage analysis and GWAS results in chromosomal position, with identified genes (black); putative genes (gray); and proximal but rejected genes from literature (red) for each QTL peak.

RESULTS

1. Corresponds to *Pm3e* resistance from GA00190-7A14
2. NC08-23383 has *Pm17* on the 1RS:1AL introgression. *Pm17* should not confer field resistance in NC, but may contribute to effective resistance in gene combinations.
3. Corresponds to location of *Pm4* that is common in this germplasm.
4. Probable novel QTL.
5. Corresponds to *Pm54* resistance from AGS2000.
6. Major resistance comes from *Pm1a* in GA06493-13LE6 crosses; UX2012 does not segregate for this gene and thus that peak on 7AL represents a new gene.
7. There are many small-effect loci identified by only 1-2 tests from 2D-5B. None have likely known genes associated with them.

CONCLUSIONS

- In this germplasm, PM resistance is due to the aggregate effect of many genes. Some well-characterized genes such as *Pm1* and *Pm4* play a large effect, but there are many novel QTL contributing to resistance.
- Linkage analysis and GWAS act in tandem to improve mapping resolution and to leverage diverse strengths for better identification.
- There is significant potential for follow-up investigations to describe these novel QTL regions.

Small Grains Genotyping

USDA

Wheat CAP Coordinated Agricultural Project

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