Online Resource 4

Article title: “Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat”

Journal: Theoretical and Applied Genetics

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Figure S1

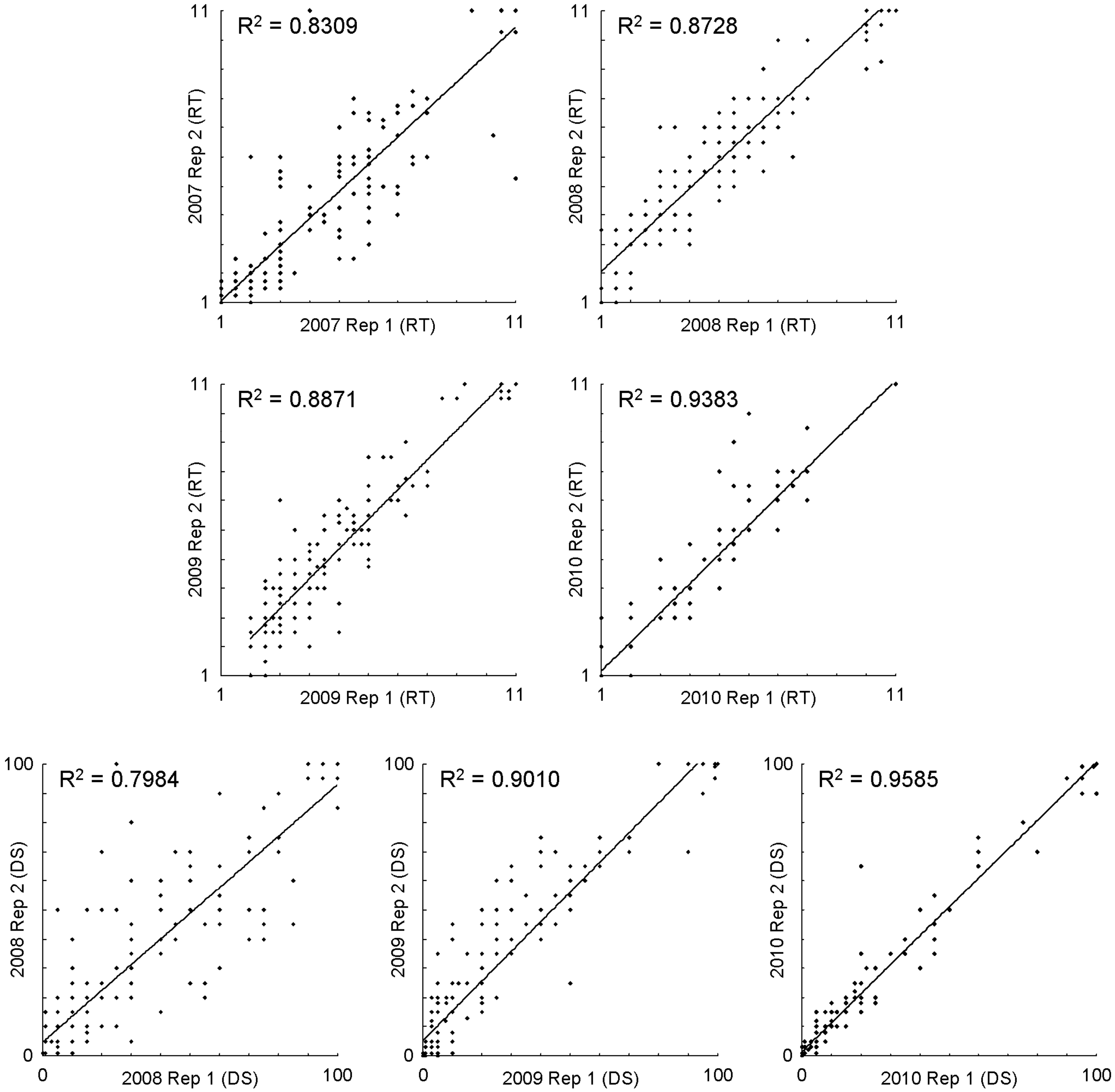

Figure S1. Scatterplots showing the correlations between population replications (Rep 1, Rep 2) within each season. Plots are shown for both phenotypic scales (RT = Reaction type, top four plots; DS = Disease Severity, bottom three plots)

Figure S2

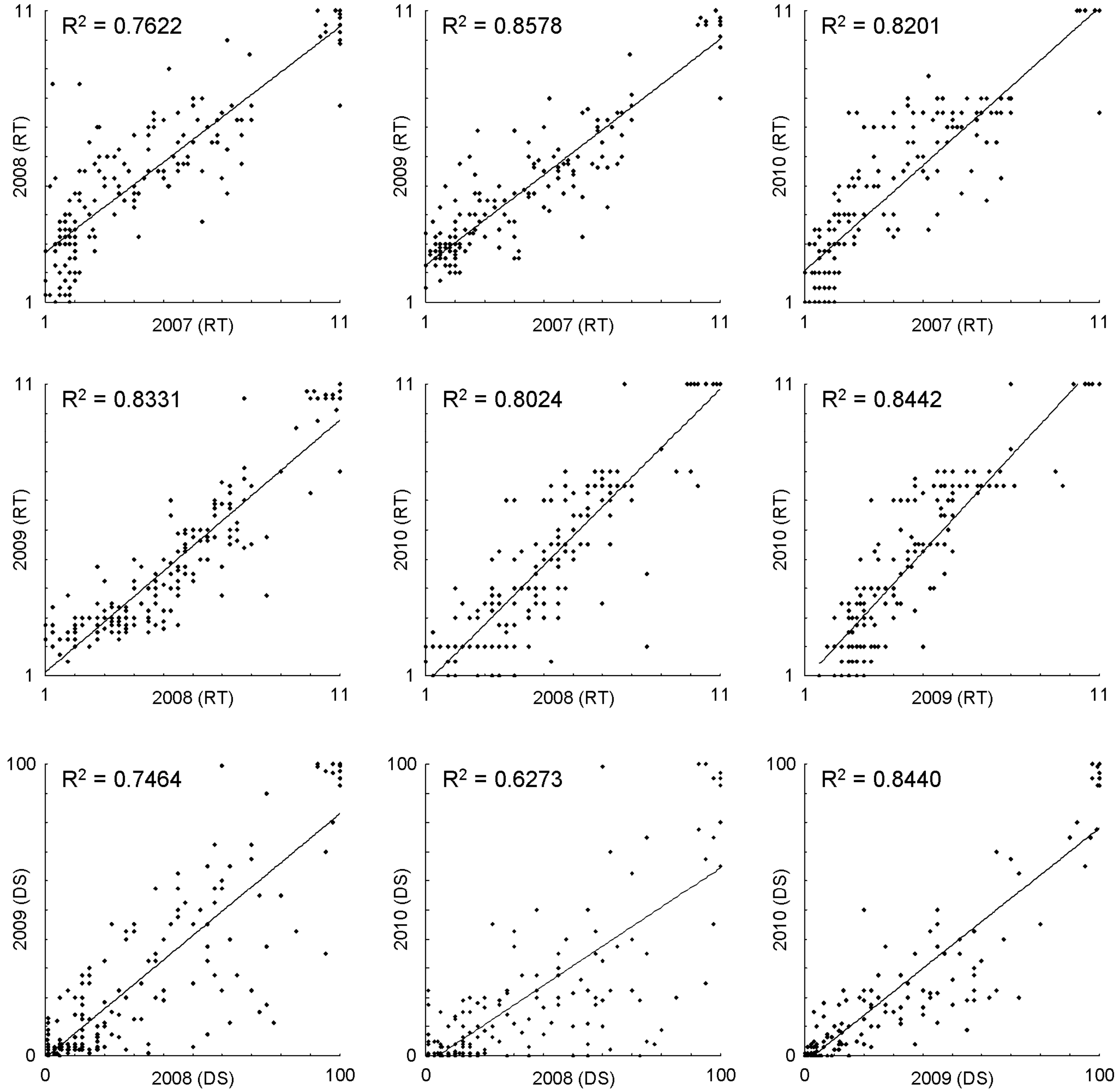

Figure S2. Scatterplots showing the correlations between seasons for all possible pairs of seasons in the study. For these plots, the phenotypic value of a RIL for each season is its average across the replications within that season. Plots are shown for both phenotypic scales (RT = Reaction type, top six plots; DS = Disease Severity, bottom three plots)

Figure S3

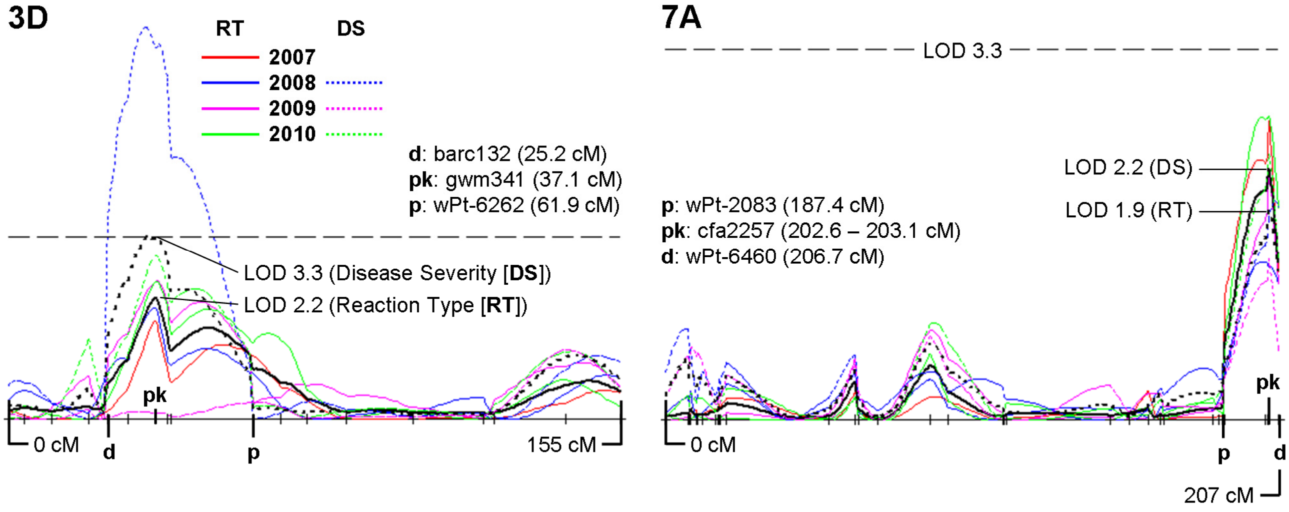

Figure S3. This figure shows LOD plots for two sub-threshold but consistent (2007-2010) stripe rust resistance QTL in the UC1110/PI610750 mapping population. The 3D resistance is contributed by UC1110, and the 7A resistance is contributed by PI610750. Both chromosomes are oriented with the telomere of the short arm to the left. As throughout this paper, distances are in Kosambi cM, with the telomere of the short arm positioned at 0 cM. Within each plot, solid color lines indicate the CIM results for reaction type for each season (2007-2010, see color key in figure); dashed color lines indicate the CIM results for disease severity for each season (2008-2010). The solid black line is the average LOD plot of the four seasons of 11-point reaction type data. The dashed black line is the average LOD plot of three seasons of % disease severity data. "pk" = QTL peak marker (i.e. the locus associated with the highest overall average LOD score); "d" = distal flanking marker; "p" = proximal flanking marker. Hatch marks along the x-axes indicate the positions of mapped loci (see complete genetic map in Online Resource 2), and the threshold LOD of 3.3 included in each plot for scale

Figure S4

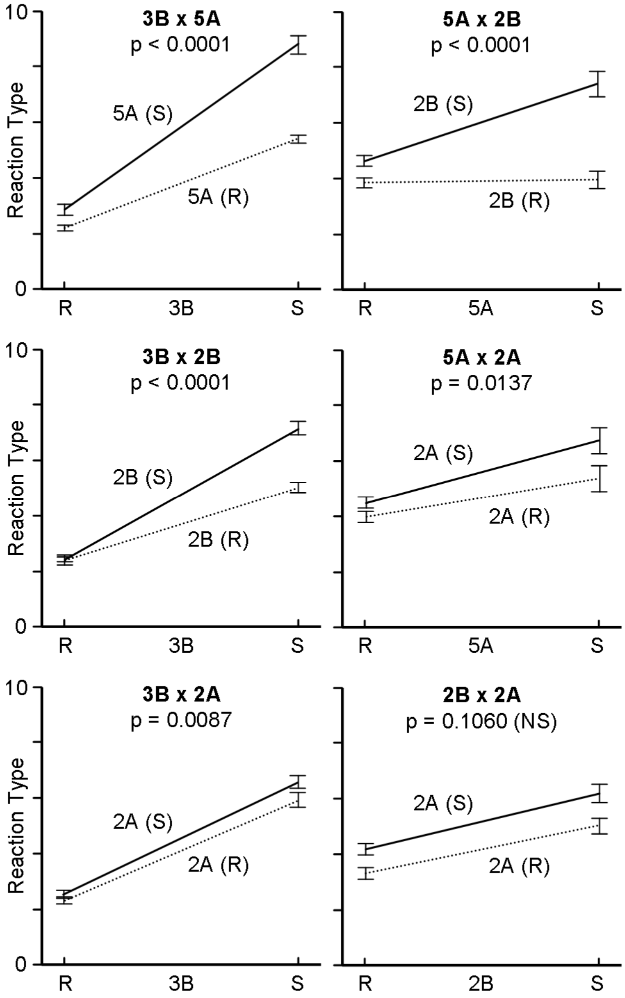

Figure S4. Two-way interaction plots (11-point reaction type) for the four detected QTL. In each plot, the QTL region of larger magnitude is shown on the x-axis ("R" = resistant; "S" = susceptible). The two phases of the smaller QTL are indicated by the two lines in each plot ("R" = dotted line; "S" = solid line). Error bars are ± 2 standard errors

Figure S5

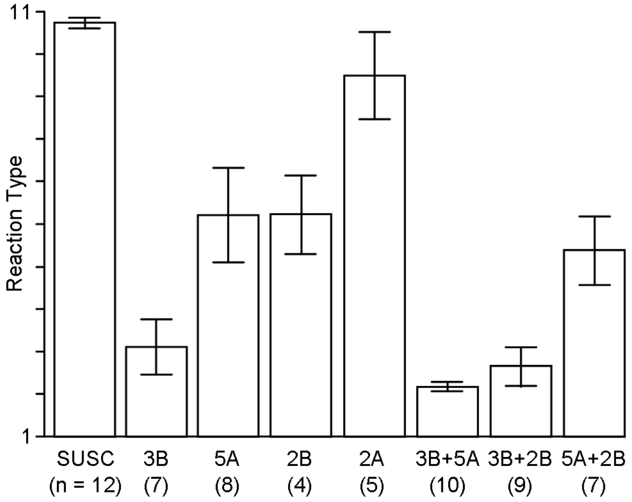

Figure S5. The effects of different QTL (and pairs of QTL) on reaction type in otherwise susceptible backgrounds. "SUSC" = The subset of fully susceptible RILs (i.e. lines with susceptible haplotypes at all four QTL regions); "3B" = The subset of RILs possessing only the 3B resistance in an otherwise susceptible background; "5A" = The subset of RILs possessing only the 5A resistance in an otherwise susceptible background; etc. "3B+5A" = The subset of RILs possessing 3B and 5A resistance only (i.e. no 2B or 2A resistance); etc. The numbers in parentheses under each label indicate the numbers of RILs in each class. Bar heights are averages over all seasons; error bars are ± 2 standard errors. Below is a detailed list of the RILs in each class:

SUSC: RILs 7,53,62,72,125,127,150,152,193,241,250,258
3B: RILs 13,47,107,111,139,140,233
5A: RILs 17,18,86,133,143,151,166,251
2B: RILs 6,130,175,194
2A: RILs 66,90,207,227,244
3B+5A: RILs 8,49,85,94,97,119,147,196,263,266
3B+2B: RILs 5,21,23,29,39,99,106,146,203
5A+2B: RILs 45,81,154,161,228,232,247

Figure S6

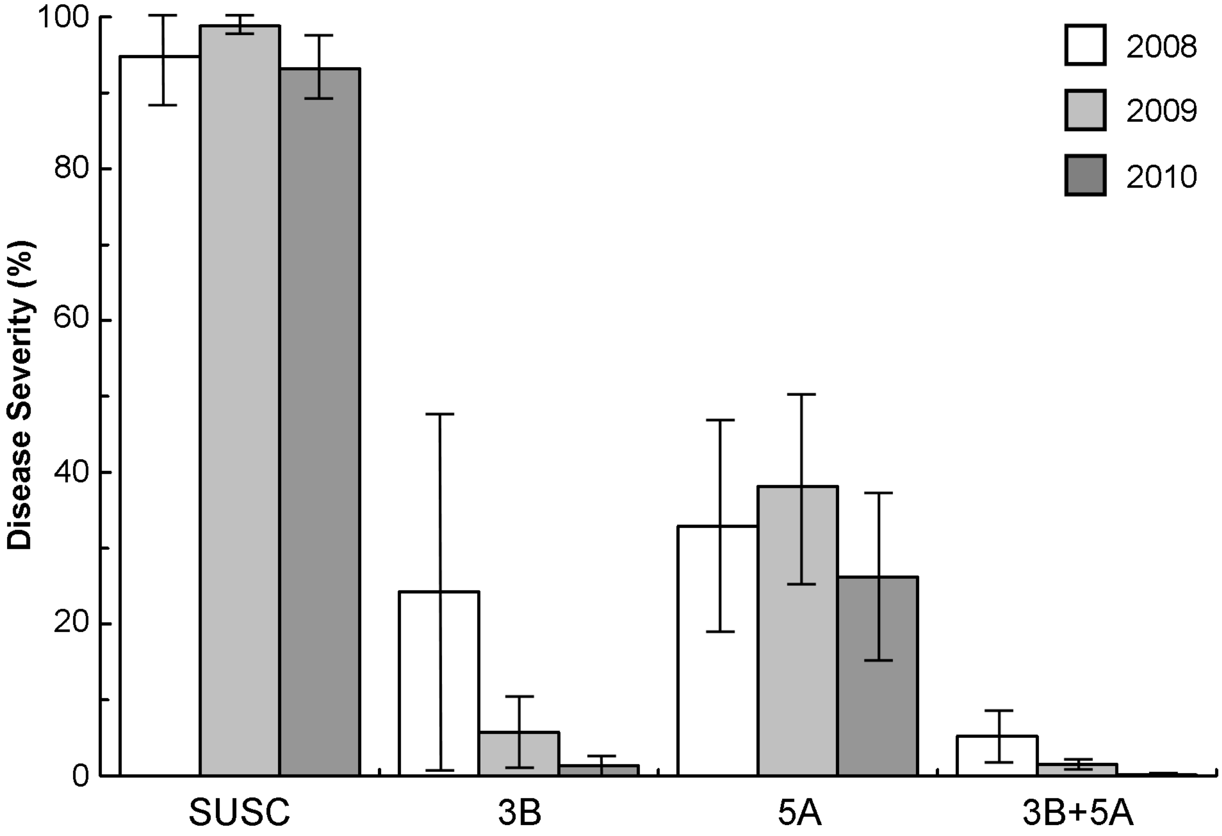

Figure S6. The effects of the 3B QTL, the 5A QTL, and the 3B+5A QTL combination on disease severity in otherwise susceptible backgrounds, by season. For a complete list of RILs in each class, see Figure S5. Bar heights are averages over all blocks within each season; error bars are ± 2 standard errors