Detection of QTLs Conditioning FHB Resistance in Two Wheat Germplasm. (C01-shen151050-Poster)

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Abstract:

The phenotypic evaluation for Fusarium head blight (FHB) resistance and bulked segregant analysis of SSR markers were conducted in two wheat RI populations, Ning 894037/Alondra and Patterson/F201R, to map QTLs for FHB resistance. Frequency distributions of disease severity indicate quantitative expression of the resistance. SSR marker analysis revealed three chromosome regions that associated with FHB resistance in Ning 894037/Alondra RILs, which are located on chromosomes 3B, 2D and 6B. The QTL in 3BS is likely the same as that of Sumai 3 and accounts for 42.5% of the phenotypic variation. SSR marker analysis also provides evidence that the 3BS QTL in Sumai 3 was derived from Taiwan Wheat instead of the Italian line Funo, which was supposed to be the donor of FHB resistance from previous pedigree analysis. Four QTLs were detected in the Patterson/F201R RILs. The QTLs on chromosomes 1B and 3A have relatively large effects and account for 18.7% and 13.0% of the phenotypic variation, respectively. The four QTLs jointly account for 32.7% of phenotypic variation. The mapping results showed the genetic diversity of resistance genes in Ning 894037 and F201R, which represent the Chinese and European resistance sources.

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