

Pedigree based association analysis of FHB resistance derived from Tunisian wheat

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To expand the number of genes for FHB resistance in gene pyramiding programs, it is necessary to find genetically varied sources of resistance. In this study we used 184 BC₁F₆ and 189 BC₁F₇ lines derived from crossing of Tun7, Tun18, Tun34, Tun36 (all lines identified as sources of resistance from Tunisia) with durum cultivars 'Ben', 'Maier', 'Lebsock' and 'Mountrail' for association studies. As the pedigree of Tunisian lines show no relation to the popular Chinese sources of resistance, they could potentially carry different genes or alleles for resistance to FHB. We checked the parents and RILs in the greenhouse in two seasons for type II resistance to FHB by single floret injection inoculation method. The data showed that the Tunisian lines have different amount of resistance varying from 23% to 11% infection rate through the spikes as compared with D8750 (susceptible control) and Sumai3 (resistant control) with 41% and 9% of infection rate respectively.

We conducted the Diversity array (DArT) marker analysis to have a good coverage of the whole genome. DArT analysis used 2300 markers which showed 25% polymorphism between the parents. About 8% of the polymorphic markers were present in all the Tunisian lines but not the susceptible cultivars. The cluster analysis of the polymorphic markers revealed three distinct groups. Tun7 was in a separate group far from the other two and all the other Tunisian lines fell in a separate group from susceptible cultivars. As both Tun7 and Tun18 are more resistant to FHB than others and have different genetic backgrounds, they may be considered as potential candidates for new sources of resistance.

Linkage disequilibrium analysis on DArT markers revealed seven QTL associated to FHB resistance in Tun34 pedigree were located on Chromosomes 3B, 6B, 2A, 5B, 1B, 7A and 7B. Tun18 carries three QTL on 7B, 7A and 1B for FHB resistance. The 1B QTL were exactly in the same location as the one from Tun34 population. We have found three QTL on 3AS, 1BL and 2AL associated to FHB resistance in the Tun7 pedigree but the 2AL region associated with increased resistance was from the susceptible source parent. With this study we revealed some QTL in the same chromosome as had been reported in hexaploid wheat, which may change the belief of lacking the genes for FHB resistance in durum wheat as compared to hexaploid wheat. This may lead to future analysis identifying loci that may act as suppressors of resistance in the durum wheat making FHB resistance genes less effective compared to their action in hexaploid genetic background. Although we found several new potential QTL regions for FHB resistance in durum wheat, two regions located on 5B and 7B have not reported in the hexaploid wheat and may be valuable new sources for pyramiding once transferred into cultivated bread wheat background. This study also shows the power of pedigree based association mapping to find the minor QTL although we had problem with the pedigrees with less than 100 entries especially when there are selections in favor of the other agronomic traits beside FHB resistance.

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