

Molecular mapping of resistance to Fusarium head blight in tetraploid wheat

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Abstract

While many reports on genetic analysis of Fusarium head blight (FHB) resistance in bread wheat have been published during the past decade, only limited information is available on FHB resistance derived from tetraploid wheat so far. In this contribution we report about genetic analysis of FHB resistance derived from two tetraploid *Triticum* sources: (1) *Triticum dicoccum* (cultivated emmer), and (2) *T. dicoccoides* (wild emmer). Backcross derived recombinant inbred line populations were developed from crosses of the resistance donors with adapted *T. durum* cultivars. The populations were evaluated for FHB response in well replicated experiments with artificial inoculation in the greenhouse (*T. dicoccoides*) or field (*T. dicoccum*). The same lines were genetically

analysed using SSR and AFLP markers. Map construction based in the backcross derived RIL populations was done with CarthaGène (DE GIVRY et al. 2004) and QTL mapping in QGene (NELSON 1997). Several QTL were identified. In the *T. dicoccum* populations the largest QTL mapped to chromosome 4B, overlapping with the semi-dwarf gene Rht-B1. In the *T. dicoccoides* accession Mt. Gerizim #36 significant QTL for resistance to fungal spreading (type 2 resistance) were detected on chromosomes 3A and 6B. These resistance QTL should be useful especially in durum wheat improvement.

Keywords

Fusarium head blight, marker assisted resistance breeding, QTL mapping, tetraploid wheat

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References

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Note: A similar contribution was presented at the 11th European Fusarium Seminar, Radzikow, 20-24 Sep 2010, at the US Fusarium Head Blight Forum, Milwaukee, 7-9 Dec 2010.

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