

Molecular mapping of resistance to Fusarium head blight derived from three *Triticum* species

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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 wheat relatives, and from tetraploid wheats so far. In this contribution we report about genetic analysis of FHB resistance derived from three *Triticum* sources:

- 1) *Triticum macha* (Georgian spelt wheat),
- 2) *Triticum dicoccum* (cultivated emmer) and
- 3) *Triticum dicoccoides* (wild emmer).

Back-cross derived recombinant inbred line populations were developed from crosses of the resistance donors with adapted cultivars. The populations were evaluated for Fusarium response in well replicated experiments with artificial inoculation. The same lines were genetically analysed using SSR and AFLP markers. Map

construction based in the backcross derived RIL populations was done with Carthagene and QTL mapping in Qgene. Several novel QTL were identified. In *T. macha* five new QTL were found on four chromosomes (2A, 2B, 5A, 5B), the largest effect QTL overlapped with the *Q* locus (spelt type) on 5A. In *T. dicoccum* the largest QTL mapped to chromosome 4B (overlapping with *RhtB1*). In wild emmer (*T. dicoccoides*) significant QTL were detected on chromosomes 3A and 6B.

Keywords

Emmer, genetic resources, QTL, resistance, spelt, wheat

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