

Mapping of QTL for Fusarium head blight resistance in three backcross populations derived from *Triticum dicoccum* × *T. durum*

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Summary

Breeding for resistance to Fusarium head blight (FHB) in durum wheat continues to be hindered by the lack of effective resistance sources. Only limited information is available on resistance QTL for FHB in tetraploid wheat. Out of 52 QTL studies reviewed by BUERSTMAYR et al. (2009), only four concern resistance sources of tetraploid wheat. Although intensive screenings for FHB resistance in durum wheat were performed, only five lines - from a Tunisian source - with moderate resistance to FHB spread (ELIAS et al. 2005, HUHNS et al. 2012), were found. Therefore, further studies have been conducted to find resistance sources in cultivated or wild relatives of durum wheat (MILLER et al. 1998, BUERSTMAYR et al. 2003, CLARKE et al. 2004, KISHII et al. 2005, OLIVER et al. 2007, 2008). Moderately to good resistant material was found in *T. dicoccoides* (BUERSTMAYR et al. 2003, MILLER et al. 1998, OLIVER et al. 2007), cultivated emmer wheat, *T. dicoccum*, and Persian wheat, *T. carthlicum* (OLIVER et al. 2008).

In this study the resistance to FHB of a *T. dicoccum* line in the background of three Austrian *T. durum* cultivars was genetically characterized. Three populations of BC₁F₄-derived RILs were developed from crosses between the resistant donor line *T. dicoccum*-161 and the Austrian *T. durum* recipient varieties DS-131621, 'Floradur' and 'Helidur'. About 130 BC₁F₄-derived lines per population were evaluated for FHB response using artificial spray inoculation in four field experiments during two seasons. Lines were genetically fingerprinted using SSR and AFLP markers. Map construction was done with CarthaGene 1.2-LKH for Linux (DE GIVRY et al. 2005). For this the marker data of all three populations

were merged and maps were calculated in that way, that the linkage groups in the individual populations shared the same marker ordering, but the distances between the markers were separately estimated within each population. QTL calculations were carried out with R version 2.12.2 (R DEVELOPMENT CORE TEAM 2011). For FHB severity the mean temperature over four days after first inoculation was included as a covariable, and for the joint analysis of all experiments a multi-environment analysis was used.

Genomic regions on chromosomes 3B, 4B, 6A, 6B and 7B were significantly associated with FHB severity. FHB resistance QTL on 6B and 7B were identified in two populations and a resistance QTL on 4B appeared in three populations. The alleles that enhanced FHB resistance were derived from the *T. dicoccum* parent, except for the QTL on chromosome 3B. All QTL except the QTL on 6A mapped to genomic regions where QTL for FHB have previously been reported in hexaploid wheat. QTL on 3B and 6B coincided with *Fhb1* and *Fhb2*, respectively. This implies that tetraploid and hexaploid wheat share common genomic regions associated with FHB resistance. QTL for FHB resistance on 4B co-located with a major QTL for plant height and mapped at the position of the *Rht-B1* gene, while QTL on 7B overlapped with QTL for flowering time. Selected moderately FHB-resistant experimental lines from this project are used for further crossing and pyramiding FHB resistance into adapted durum wheat germplasm. For more details please refer to BUERSTMAYR et al. (2012).

Keywords

Durum wheat, Fusarium head blight, QTL mapping, *Triticum dicoccum*

Acknowledgments

We acknowledge funding of this work by FWF (Austrian Science Fund), project number: 17310-B05.

We also thank Peter Jack and James Christopher (RAGT, Cambridge, UK) for their assistance in SSR marker genotyping.

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