

ADVANCED BACK-CROSS QTL MAPPING OF RESISTANCE TO *FUSARIUM* HEAD BLIGHT DERIVED FROM *TRITICUM DICOCCUM*

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Abstract: The aim of the project is the detection, genetic mapping and characterization of quantitative trait loci (QTL) that confer resistance against *Fusarium* head blight in a resistant line of *Triticum dicoccum*.

Keywords: *Fusarium* head blight, quantitative trait loci (QTL), *Triticum dicoccum*, emmer wheat, resistance breeding

Introduction

Triticum durum is highly susceptible to *Fusarium* head blight (FHB) which causes severe grain and quality losses. Control of FHB by fungicide application and other practises is neither practical nor sustainable. The cultivation of genetically resistant cultivars is the most effective method to control the disease. Only a few sources with quantitative resistance to FHB have been detected in wild tetraploid wheats (Wan et al. 1997, Gilbert 1998, Miller et al. 1998, Buerstmayr et al. 2003). *T. dicoccum* as a resistance source to FHB was used to identify QTL conferring quantitative resistance against FHB.

Materials and methods

Three populations of 120 BC₁F₄ lines each, from crosses of one FHB resistant *T. dicoccum* line and three Austrian durum lines (Helidur, Floradur, DS-131621), were evaluated for FHB resistance during 5 seasons in Tulln. For artificial spray inoculation *F. graminearum* or *F. culmorum* were used. Inoculations were performed individually on each plot when 50% of the plants reached anthesis, and repeated 2 days later. The percentage of visually infected spikelets was scored 10, 14, 18, 22, and 26 days after inoculation. The area under the disease progress curve (AUDPC) was calculated as an integrated measure for FHB severity. Two populations were genotyped with 80 SSR and 220 AFLP markers. Linkage mapping was conducted using *CarthaGène* (de Givry et al. 2004) and QTL analysis using *QGene* (Nelson 1997).

Preliminary Results and discussion

The populations showed continuous variation for percentage of diseased spikelets and AUDPC after spray inoculation. Inoculation with *F. culmorum* led on average to more severe infections than with *F. graminearum*. Despite that, the correlation coefficient between the two isolates (*F. graminearum* and *F. culmorum*) was $r=0.57$ ($p<0.0001$). The resistant *T. dicoccum* line exhibited an AUDPC mean of 62 (9% diseased spikelets 22 days after inoculation), whereas Helidur had an AUDPC mean of 254 (37% diseased

spikelets 22 days after inoculation) and Floradur displayed an AUDPC mean of 314 (57% diseased spikelets 22 days after inoculation).

Marker segregation data were used to construct a genetic map consisting of 300 markers for each population covering 1601 cM (Haldane) in 33 linkage groups for the Helidur population and 1864 cM in 32 linkage groups for the Floradur population. Preliminary QTL analysis revealed associations of several genomic regions with resistance to FHB. The major effects associated with FHB resistance mapped on chromosome 1B ($r^2 = 0.11$, LOD = 6.1) and 6A. In addition, smaller QTL effects for FHB resistance were identified on chromosomes 2B, 3A, 4A, 4B, 5A and 7B. The major QTL 1B and 6A could be interesting for marker assisted selection to enhance FHB resistance in durum wheat.

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