

QTLs FOR RESISTANCE TO THE LEAF RUST *Puccinia brachypodii* IN THE MODEL PLANT *Brachypodium distachyon*

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The wild grass *Brachypodium distachyon* (Brachypodium) was already proven as a useful model plant species for temperate cereals, but its potential to study the interactions with economically relevant pathogens remains underexploited. Leaf rust is one of the major fungal diseases affecting temperate cereals, and recently the interaction between Brachypodium and the leaf rust *Puccinia brachypodii* was proposed as a model plant pathosystem. The objective of our study was to identify genomic regions associated with quantitative resistance to leaf rust in Brachypodium. We selected two inbred lines Bd3-1 and Bd1-1 with quantitative differences in their level of susceptibility to *P. brachypodii*, that were crossed to develop an F₂ population. A set of 110 F₂ plants were evaluated for their reaction to a virulent isolate of *P. brachypodii* at both seedling and advanced growth stages. To validate the results obtained on the F₂ population, resistance levels were quantified in F₂-derived F₃ families in two independent experiments. Disease evaluations showed continuous, quantitative and transgressive segregation for leaf rust resistance. We applied the AFLP-based technology in Brachypodium, and provide a novel Brachypodium linkage map anchored to its genome sequence. The map, consisting of 203 loci and spanning 811.8 Kosambi cM, included AFLP, SSR, and SNP markers.

Three QTLs of leaf rust resistance were mapped on chromosomes 2, 3 and 4, repeatedly identified across experiments. This study is, to our knowledge, the first quantitative analysis of any trait in Brachypodium, in which we demonstrate that resistance to the *Puccinia brachypodii* isolate is governed by a few major loci with relatively large effects. The results obtained, coupled with the wide range of genomic resources available for Brachypodium, opens new avenues for exploring grass-rust interactions in this model grass.

Co-localization on physical/genetic maps of 10 candidate genes with the QTLs of resistance to leaf rust disease is being done. At the same time, the sequences of the CGs are being characterized in the two parents for further validation and selection. The research is coupled with the study of the organization of barley genes orthologous to the Brachypodium CGs in syntenic genomic regions. The two steps are a starting point towards QTL cloning, to understand mechanisms of quantitative resistance to leaf rust in the model grass, and to export this knowledge to the Triticeae species.