MAPPING QTLs FOR LEAF RUST RESISTANCE IN THE MODEL PLANT BRACHYPODIUM DISTACHYON

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Brachypodium distachyon has been proposed as a model system for functional genomics in Triticeae, and thus in wheats and barley, because of its biological features and compact genome size. This new model plant has been employed to build a linkage map as a genetic resource for the scientific community, and to study the genetics of resistance to leaf rust fungi caused by *Puccinia* spp., that are important diseases in cereals in many regions of the world, causing severe yield losses.

Five *Brachypodium distachyon* inbred lines were challenged with different *Puccinia* spp. in order to identify leaf rusts able to elicit disease symptoms. An interesting variation in responses was observed following challenge of *B. distachyon* lines with a *Puccinia brachypodii* isolate. In all *Brachypodium* lines the fungus developed sporulating lesions. Different levels of partial resistance, defined as a resistance that results in reduced epidemic development despite a compatible infection type, were observed between the five lines. In some lines, however, the pustules were associated with rather extensive necrosis of plant tissue.

A genetic linkage map of *B. distachyon* covering 1139 cM, with 171 AFLP loci, was constructed by using an F2 population of *B. distachyon* derived from a cross between the leaf rust susceptible line Bd1-1 and the partially resistant line Bd3-1. The F2 plants were quantitatively phenotyped for resistance to *P. brachypodii* at seedling and adult plant stages in the greenhouse. QTL analysis via MQM mapping method detected 3 QTLs for resistance at seedling stage and 1 QTL at adult plant stage. The QTL picture of partial resistance to leaf rust in *B. distachyon* could allow to compare the genetic architecture of quantitative leaf rust resistance in *Brachypodium* and that in major cereals like barley and wheat.