

## **META-QTL ANALYSIS OF THE GENETIC CONTROL OF POWDERY MILDEW RESISTANCE IN WHEAT**

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*wheat, powdery mildew resistance, quantitative trait loci (QTL), meta-QTL analysis*

Powdery mildew (*Blumeria graminis* f. sp. *tritici*) is one of the most damaging diseases of wheat (*Triticum aestivum*). The objective of this study was to identify genomic regions involved in the control of powdery mildew resistance applying a QTL meta-analysis approach. The Meta-QTL (MQTL) analysis permits to collect QTL data from different published studies in order to obtain consensus QTL across different genetic backgrounds and provides a better definition of the regions responsible for the trait and the possibility to obtain molecular markers suitable for Marker-Assisted Selection (MAS). More than 80 independent QTL and 51 resistance genes from 62 different mapping populations were projected onto a consensus map, by means of the statistical “Biomercator” software. We obtained twenty-four MQTL, comprising each 2-6 initial QTL with widely varying confidence intervals, distributed on 15 chromosomes. The co-location of resistance QTL and genes was investigated. Moreover, from the analysis of the sequence of DArT markers, 28 DArT clones mapped on wheat chromosomes have been found to be associated to NBS-LRR genes and positioned in the same regions of MQTL for powdery mildew resistance, providing a very useful tool for the identification of candidate genes for the investigated trait.