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FINE MAPPING OF THE POWDERY MILDEW RESISTANCE LOCUS PM36 IN DURUM WHEAT

NIGRO D.*, BLANCO A.*, PIARULLI L.*, SIGNORILE M. A.*, COLASUONNO P.*, BLANCO E.**, SIMEONE R.*

*) Department of Soil, Plant and Food Sciences (DiSSPA), University of Bari Aldo Moro, Via Amendola 165/a, 70126, Bari, Italy
**) Institute of Biosciences and Bioresources, National Research Council, Via Amendola 165/A, 70126 Bari, Italy

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Powdery mildew (PM), caused by the fungus *Blumeria graminis*, is one of the most economically important foliar disease of cultivated cereals worldwide, spreading in areas with high rainfall and semi-continental climate as well as in hot and dry climate regions.

The prevention and control of wheat powdery mildew is based on different practices, such as fungicides and silicate application, biological control and, most importantly, the cultivation of resistant varieties. Indeed, the growing interest in practices with higher environmental, economic and social sustainability has led the integration of the different methods of disease control to reduce the massive deployment of phytosanitary products, which can have an impact on both the environment and human health. So far, the cultivation of disease-resistant varieties is considered the most efficient, sustainable and economical strategy to prevent and control fungal diseases in wheat and other crops generally protected by chemical treatments.

The objectives of the current study were to fine map the chromosomal region harboring the wild emmer PM resistance locus *Pm36* and to identify candidate genes by exploiting the improved tetraploid wheat genomic resources. A set of backcross inbred lines (BILs) of durum wheat were genotyped with the SNP 25K chip array and comparison of the PM-resistant and susceptible lines defined a 1.5 cM region (physical interval of 1.08 Mb) harboring *Pm36*. The

genetic map constructed with F2:3 progenies derived by crossing the PM resistant line 5BIL-42 and the durum parent Latino, restricted to 0.3 cM the genetic distance between *Pm36* and the SNP marker IWB22904 (physical distance 0.515 Mb). The distribution of the marker interval including *Pm36* in a tetraploid wheat collection indicated that the positive allele was largely present in the domesticated and wild emmer *Triticum turgidum* spp. *dicoccum* and ssp. *dicoccoides*. Ten high-confidence protein coding genes were identified in the *Pm36* region of the emmer, durum and bread wheat reference genomes, while three added genes showed no homologous in the emmer genome. The tightly linked markers can be used for marker-assisted selection in wheat breeding programs, and as starting point for the *Pm36* map-based cloning.