Proceedings of the 50th Italian Society of Agricultural Genetics Annual Congress
Ischia, Italy – 10/14 September, 2006
ISBN **88-900622-7-4**

Poster Abstract – A.60

IDENTIFICATION AND MOLECULAR TAGGING OF A POWDERY MILDEW RESISTANCE GENE IN TETRAPLOID WHEAT

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Triticum turgidum, powdery mildew, resistance gene, molecular markers

Powdery mildew caused by the pathogen *Blumeria graminis f.sp. tritici* is a destructive foliar disease in regions with a maritime climate. Breeding for varieties with resistant alleles is the most economical and effective way for controlling the disease. *Triticum turgidum* L. *var. dicoccoides* (2n=4x,AABB) the progenitor of cultivated wheats, is crossable with both durum and common wheat and simply breeding procedures enable an efficient transfer of desirable alleles from each wild chromosome into its cultivated homoeologue. In a previous screening of emmer wheat collection, the accession MG29896 resulted particularly interesting for high seed protein content and resistance to powdery mildew. It was crossed to susceptible durum wheat cultivar Latino and a set of backcross inbred lines (BILs) was produced. These lines were essayed for powdery mildew resistance in field condition: one BC_5F_5 line (5BIL-42) resulted highly resistant and was crossed to Latino. Segregation analysis of F_2 plants showed that the resistance was inherited as a single and dominant locus. One hundred and twenty F_3 progenies were also essayed in field condition to confirm F_2 phenotype and to distinguish resistant and susceptible homozygous from segregant progenies.

Ten homozygous resistant and ten homozygous susceptible F_3 progenies were used in the bulked segregant analysis (BSA). Molecular markers (SSR and EST-SSR) were used to identify genetic markers associated to the resistance gene. Fifty hundred and twenty eight SSRs and 409 EST-SSRs have been tested, 194 and 76 were polymorphic between Latino and MG29896 respectively. Among them 9 SSRs and 8 EST-SSRs were polymorphic between Latino and 5BIL-42 and one marker, EST-SSR BJ261635(AC*),* was polymorphic also between the resistant and susceptible bulks. Such marker was screened on the complete F_3 progeny and from the regression analysis resulted completely linked to the resistance gene. The marker was mapped on chromosome arm 5BL using nulli-tetrasomic and ditelosomic lines of Chinese Spring.

In order to saturate the chromosome region with the resistance gene, analysis by new PCR-based markers (Target Region Amplification Polymorphism) is in progress.

The molecular marker identified in this study has potential use in marker-assisted selection and pyramiding of genes for resistance to powdery mildew in wheat.