## Poster Communication Abstract – 2A.79

## LINKAGE DISEQUILIBRIUM AND POPULATION STRUCTURE IN TETRAPLOID WHEAT

## LAIDÒ G.\*, TARANTO F.\*\*, MARONE D.\*, MANGINI G.\*\*, MASTRANGELO A.M.\*, CATTIVELLI L.\*\*\*, PAPA R.\*, BLANCO A.\*\*, DE VITA P.\*

\*) Cereal Research Centre, S.S. 16 km 675, 71100 Foggia (Italy)
\*\*) Department of Environmental and Agro-Forestry Biology and Chemistry, University Aldo Moro, Via Amendola 165/A, 70126 Bari (Italy)
\*\*\*) CRA-Genomic Research Centre, Fiorenzuola d'Arda, Piacenza (Italy)

## Linkage disequilibrium, population structure, association mapping, durum wheat

Together with knowledge on population structure, a critical step for the planning of association and population genomics studies is the level of linkage disequilibrium (LD) that characterizes the specie and the population employed for the analysis. We have analyzed the population structure and the LD in a large collection of tetraploid wheats (Triticum turgidum subsp.) made of 128 accessions of durum wheat and 104 wild and domesticated accessions. All of the accessions were analyzed with 26 SSR and 821 DArT markers, most of which were genetically mapped. Our results partially reflect previous knowledge on population structure of tetraploid wheats, and they clearly show a sharp separation of durum wheat accessions from the rest of the naked and hulled tetraploid wheats. The population structure of durum wheat cultivars were in agreement the knowledge on the breeding history. Indeed, a strong correlation was found between the genetic structure of modern varieties and vear of release. Landraces and wild accessions had a higher allelic diversity than modern durum wheat varieties for both genomes and all chromosomes in terms of total number of alleles and allelic richness. The wild accessions were characterized by very low levels of LD, while a higher LD value was observed for the subgroup containing the durum wheat genotypes (8.2, P<0.001). Wild and domesticated accessions represent a useful rich source of useful alleles for plant breeding and a powerful tool to detect and identify useful genes using association mapping and population genomics studies.