Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 8.08

EVOLUTION OF THE GENETIC STRUCTURE IN *TRITICUM DURUM* DESF. GERMPLASM FROM SOUTHERN ITALY

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Triticum durum, genetic resources, morphological traits, SSR, conservation measure

Among the Mediterranean countries, Italy has the longest tradition in durum wheat (Triticum durum Desf.) breeding and its germplasm can be considered as one of the richest and most valuable. There are indications that in the past decades the genetic bases of this crop may have been eroded coupled with the diffusion of a relatively small number of outstanding genotypes with proven adaptability and yield potential. Over time large germplasm collections have been established and now "old type" germplasm can be recovered from genebanks. In southern Italy durum wheat germplasm has been collected starting from the 1947 up to year 2000 and the changes of the genetic structure of this precious wheat germplasm that occurred over time have been studied on the basis of morphological traits and molecular markers, particularly SSR.

A sample of 107 durum wheat accessions collected since 1947 in Southern Italy was analyzed at the University of Basilicata by 22 quanti-qualitative morphological traits and 30 microsatellite loci. The accessions were grouped into two groups on the basis of their collection date.

A great variability was observed for morphological traits, particularly for quantitative ones. These characters showed a significative differentiation among the two groups.

Molecular markers revealed high polymorphism and identified 115 alleles, with an average of 3,83 alleles per locus. Nine private alleles were found in the first group, while in the second one they were five; it was also possible to identify accessions with rare alleles, mostly of the first group. Molecular analysis revealed a decrease of the genetic diversity over time.

The use of morphological and molecular markers revealed of great utility in assessing temporal trends in the diversity of Southern Italy wheat germplasm. The evidence of both genetic diversity and genetic erosion of durum wheat genepool further strengthens the strategic relevance of undertaking appropriate genetic conservation measure either at local or global scale.