Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – F.03

MOLECULAR CHARACTERIZATION OF CURRANT (*RIBES SPP.*) ACCESSIONS USING SNP AND SSR MARKERS

SORDO M., PALMIERI L., GIONGO L., GRANDO M.S.

Fondazione Edmund Mach, IASMA Research Center, Via Mach 1, 38010 San Michele all'Adige (TN) (Italy)

molecular markers, genotyping, Single Nucleotide Polymorphism, Ribes

Ribes species belong to the Saxifragaceae genus, which is taxonomically fairly isolated, and the most commercially important species, especially in Northern European countries, are the red currant (*R. rubrum* L.) mainly used for fresh consumption and blackcurrant (*R. nigrum* L.), used for processing. Currants have known a slight production increase in the last years for their health biocomponents, highly concentrated both in fresh and in processed products.

In Italy, a small germplasm collection is present at IASMA, and the plant material includes contributions from *R. rubrum* L., *R. sativum* Syme, *R. petraeum* Wulf., *R. multiflorum*, *R. longeracemosum* L., *R. grossularia* L., *R. sanguineum* Pursh., *R. nigrum* L. and *R. dikuscha* Blue.

Single Nucleotide Polymorphisms (SNPs) are the most abundant type of DNA sequence polymorphism and can be theoretically found within every genomic sequence. Thanks to their high availability and stability, also compared to Simple Sequence Repeats (SSRs), they can be used as molecular markers for many purposes, such as cultivar identification and evaluation of genetic diversity.

The aim of this work is represented by the development of informative molecular markers for characterizing the germplasm collection of these *Ribes* species, that have been phenotyped for six consecutive production season in order to obtain a large informative picture of the cultivars and selections, concerning flowering, fruiting, horticultural traits, biotic and abiotic resistances, and health compounds.

New SNP markers were detected by re-sequencing several loci amplified from a selection of *Ribes* accessions. Primers based on Expressed Sequence Tags having homology to known genes involved in fruit development were applied and a SNaPshot assays is now being developed for the SNP genotyping.

In order to investigate the genetic relationships among *Ribes* varieties a set of genomic and ESTs derived SSR marker was also tested.