Proceedings of the XLVIII Italian Society of Agricultural Genetics – SIFV-SIGA Joint Meeting
Lecce, Italy – 15/18 September, 2004
ISBN **88-900622-5-8**

Poster Abstract - F.63

SNP DEVELOPMENT IN OLIVE AND THEIR APPLICATION ON VARIETAL DETERMINATION IN OLIVE OIL

L. PALMIERI*, M. VIETINA*, C. BOTTURA*, P. DONINI**, N. MARMIROLI *

*) Dept of Environmental Science University of Parma, Parco Area delle Scienze 11/a, 43100 Parma, Italy
luisa.palmieri@libero.it
**) NIAB, Huntingdon Road, Cambridge CB3 0LE, U.K.

Olea europaea, olive oil, SNP, RealTime PCR, variety composition

Single-nucleotide polymorphisms (SNPs) represent the most common class of genetic markers in different plants species. Technological improvements make the use of SNP attractive for high-throughput use in marker-assisted breeding, for populations studies and to obtain high-density maps. Moreover SNPs are usefully applied in Real-Time PCR to obtain a quantitative analysis for disease association studies in human and for food adulteration discovery.

This research work has been conducted in the frame of European Union funded project OLIV-TRACK, and was aimed at the application of pre-existing molecular techniques and development of new set of SNP markers and new technologies to be used in the variety identification of olive and to qualitative and quantitative determination of olive oil variety composition.

Five SNPs were detected on two candidates genes involved in fatty acid biosynthesis pathways and screened on 74 European and 5 non-European olive varieties in a genetic diversity study with different aims. The SNPs individuated were then checked on olive oils derived from the varieties previously screened. To perform this analysis on olive oil a new DNA extraction method from this food matrix was developed.

Following the identification of SNPs and their testing on the set of varieties, a SNPs selection was performed aimed at the development a quantitative Real-Time PCR analysis, using NFQ-MGB TaqMan probes, to determine the relative contribution of different varieties entering the composition of olive oils.

The results and findings of this research work could be of extreme value in the development of new diagnostic protocols and to produce a larger set of SNP markers, offering great potential for basic genetic diversity studies in olive, for investigating functional diversity of important genes in this crop and for developing new tools for authenticity and traceability testing of food matrices from plant species and olive oil in particular.