

GBS-BASED SNP MARKERS TO ELUCIDATE GENETIC RELATIONSHIPS AMONG OLIVE MEDITERRANEAN CULTIVARS

PROCINO S.*, D'AGOSTINO N.**, MIAZZI M. M.*, MORAGA R.***, ZELASCO S.****, GADALETA S.*****, MONTEMURRO C.*****, TARANTO F.*****

*) Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro, Via Amendola 165/A, 70126 Bari, Italy

**) Department of Agricultural Sciences, University of Naples Federico II, Via Università 100, 80055 Portici, Italy

***) Tea Break Bioinformatics Ltd, Palmerston North, New Zealand

****) CREA Research Centre for Olive, Citrus and Tree Fruit, Rende, Italy

*****) SINAGRI S.r.l., Spin Off of the University of Bari Aldo Moro, 70126 Bari, Italy

*****) Support Unit Bari, Institute for Sustainable Plant Protection, National Research Council of Italy (CNR), 70125 Bari, Italy

*****) Institute of Biosciences and Bioresources (CNR-IBBR), 70126 Bari, Italy

Olea europaea, GBS, SNP markers, genetic diversity, gene flow

The olive tree (*Olea europaea*, ssp. *europaea*, var. *europaea*) is the most iconic tree in the Mediterranean basin and one of the best-adapted species to the Mediterranean climate. The cultivated olive tree was domesticated in the Middle East about 6,000 years ago and traces its history back to the migrations of the most ancient civilizations across the Mediterranean Sea. Unravelling domestication processes is critical to understanding how olive trees have responded to artificial selection, with the aim of predicting responses to global challenges (i.e., adaptation to climate change and increasing consumption of extra virgin oils) and directing future breeding programs. In this context, it is essential to preserve the olive germplasm from erosion and recover beneficial alleles left behind by selective breeding.

We enlarged the Italian germplasm collection previously analysed, including about 40 cultivars representative of other Mediterranean countries such as

Spain, Greece, France, Algeria. Genotyping-by-sequencing (GBS) was used to perform a genome-wide diversity study with the aim of identifying patterns of genetic diversity and clarifying geographical relationships among cultivars.

The reference-based SNP calling pipeline generated 67803, of which approximately 7k were retained for downstream analysis. Pairwise identity-by-state (IBS) distance revealed few cases of synonymy. Non-parametric (i.e., DAPC) and parametric (i.e., Admixture) approaches were used to investigate population structure, detecting from three to seven populations, respectively. In addition, pairwise divergent loci ($F_{ST} > 0.25$) and gene flow were computed between the groups previously identified based on ancestry.

The preliminary results defined clusters including cultivars with miscellaneous origins, confirming the large admixture between olive cultivars with different origin, due to human migration. A cluster of cultivars from central Italy were confirmed as autochthonous, as it does not show any relationship with the cultivars of other Mediterranean countries. Knowledge acquired so far has allowed us to formulate hypotheses on the genetic/geographical relationships between olive cultivars, and to identify the genomic regions subjected to natural and artificial selection. Finally, genetic diversity will provide valuable information on the existence of different gene pools and will represent a source of unexplored alleles useful in current and future breeding programs.