## Genetic Diversity in Local Spanish Olive Cultivars Assessed by Molecular Characterization with SSRs

## Angel Fernández i Martí<sup>1</sup>, Carolina Font i Forcada<sup>2</sup> and María J. Rubio-Cabetas<sup>2</sup>

<sup>1</sup> Plant Breeding & Genomics Division, Parque Científico Aula Dei (PCTAD. Av. Montañana 930, 50059, Zaragoza, Spain

<sup>2</sup> Fruit Tree Department, Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Av. Montañana 930, 50059, Zaragoza, Spain

Olive [Olea europaea] is an old traditional crop and one of the most economically important evergreen fruit crops in Spain. The olive has been domesticated from the wild at various locations resulting in a vast number of cultivars worldwide in the Mediterranean basin. In the northeast area of Spain (Aragon) an environment characterized by semi-arid climatic conditions at different altitudes, olive cultivars colonizes different environments. Around 100 genotypes were prospected and characterized in abandoned sites. Some cultivars are common from those in other region of Spain, but the majority (90%) seems to be autochthones. In this study, 11 nuclear SSRs were used to discriminate among the cultivars to establish the genetic relationship All primers produced a successful amplification giving a total of 177 fragments in the genotypes studied, with an average of 16 alleles per SSR, ranging from 6 (DCA15) to 24 (DCA9 and DCA11). Allele size ranged from 120 bp at locus UDO99 to 244 bp at locus DCA59. The dendrogram generated using the variability observed classified most of the genotypes according to their geographical origin, confirming the particular evolution of different olive ecotypes. In addition, the olive cultivars were evaluated for stratification or admixture using STRUCTURE. SSRs markers have consequently shown their usefulness for cultivar identification in olive, for establishing geographical relationships.