# OLIVE TREE GALEGA CULTIVAR ACESSIONS' IDENTIFICATION BASED ON RAPD MARKERS

**Elisa Figueiredo[1], Jorge M. Canhoto[1], Maria Margarida Ribeiro[2]**

[1] Centre of Functional Ecology, Department of Life Sciences, University of Coimbra, Ap. 3046, 3001-401 Coimbra, Portugal. Email: efigueiredo@ci.uc.pt; jorgecan@bot.uc.pt

[2] Department of Natural Resources and Sustainable Development, Escola Superior Agrária, 6001-909 Castelo Branco. Portugal. Email: mataide@ipcb.pt

## Abstract

*Olea europaea* ssp. *europaea* (Oleaceae) grows in the Mediterranean region. The fruits are used for olive oil and for fruit canning, besides the species is drought and salt tolerant. The Galega cultivar represents 80% of the Portuguese olive area, and it is used in four out of the five Protected Origin Denomination (POD) regions. Despite the large distribution area in the country, cultivar certification is done through phenotypic characteristics, but environmental influence might blur informativeness, and molecular markers could help in clarifying cultivar accessions certification.

The 79 putative Galega accessions studied are from a clonal bank, three of them previously identified as Galega, but with different denominations, GGN (Galega Grada Normal), GGS (Galega Grada de Serpa), GGE (Galega Grada de Évora), and one as NG (non-Galega). The remaining accessions were propagated from trees considered as belonging to the Galega cultivar, but situated in different parts of the country. We have screened all the accessions with 20 RAPD primers, that amplified 144 bands and 29.2% were polymorphic. The expected heterozygosity was low, as expected in clonal propagated plants (0.10±0.01).

A Principal Component Analysis (PCA) using the Dice coefficient matrix had 81% and 7% of the variance explained by the first and the second component, respectively. The PCA identified two groups. Group A included all the accessions including GGN, but not #502. Group B included NG, GGE, GGS and #502. The AMOVA (analysis of molecular variance) confirmed a very high differentiation between groups ($F_{ST}$=0.88) and a relative higher homogeneity within groups (12%). Assuming that the GGN individual represents a Galega cultivar pattern, we might assume that all the A group trees are Galega cultivar accessions. Nevertheless, some variability exists within groups, may be due to the accumulation of somatic mutations and/or a putative origin from different but closely related genotypes. Finally, GGS and GGE, together with #502 plot together with the individual identified as not belonging to the Galega cultivar (NG). Group B trees had certainly a very different genetic origin compared to group A genotypes, already reflected in the difference of the names. A future study using a broader sampling and higher discriminant molecular markers, such as microsatellites, would help to unambiguously fingerprinting the Galega cultivar genotypes.

Key words: Fingerprinting, molecular markers, multivariate analysis, *Olea europaea*