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MICROSATELLITE MARKERS ARE POWERFUL TOOL FOR DISCRIMINATING AMONG OLIVE CULTIVARS AND ASSIGNING THEM TO GEOGRAPHICALLY DEFINED POPULATIONS

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More than 1,275 olive cultivars have been described. Their uncertain origin, the simultaneous presence, in a given area, of local, cosmopolitan and patchy distributed varieties, the clonal variation found in some of them, their denominations related to fruit shape or color, oil taste and tree structure, or associated to the toponym of the cultivation site, seriously affect the identification of the cultivars, making the management of olive as a resource extremely complex. Furthermore, the spread of olive from few centers of origin and a further multilocal selection, joined with the continuous interchange of plant material within different regions, have contributed to the confused pattern of cultivar geographical distribution. However, the possibility of discriminating with certainty and relative ease between olive cultivars would be of great interest, e.g., in order to certificate the origin and quality of oils. Moreover, it would be of interest to be able to distinguish between local and allochthonous germplasm, in order to recognize the regional resources, evaluate the adaptation capacity of each variety and support the initiatives to identify and promote typical olive oils.

Simple sequence repeats (SSRs) in the nuclear DNA have been suggested to be reliable and easy-to-use markers for genotype identification. In an attempt to establish their effectiveness in discriminating among olive cultivars and assessing their ability in assigning individuals to varietal populations according to geographic criteria, twelve SSR loci were selected and used to analyze the genetic structure of olive cultivar gene pools and differentiate among one hundred and eighteen cultivars sampled in several countries of the Mediterranean Basin. The markers were found to have a high discrimination power. On average, with a single assay was possible to discriminate 96% of the pairwise comparisons and, with a combination of three loci, virtually all cultivars were distinguished. The markers were also tested for their utility to assign cultivars to their geographic population of origin. A selection of six markers was found to maximize assignment accuracy, correctly reallocating up to 75.4% of cultivars to their aboriginal population.