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Assessment of genetic diversity among Algerian olive (*Olea europaea* L.) cultivars using SSR marker.

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ABSTRACT

In this study, molecular analyses of olive trees, sampled from different regions, were performed using nuclear microsatellites markers to assess genetic diversity in Algerian cultivated olive, *Oleaeuropaea* L. In total, 11 preselected polymorphic microsatellites markers were used on a set of 26 Algerian olive cultivars to study the genetic relationship among and within these cultivars. The number of alleles per locus ranged from 6 to 21, with a mean of 11 alleles. Sixty-one unique allelic patterns were observed. The observed heterozygosity ranged from 0.135 to 0.889, while the expected heterozygosity (He) varied from 0.07 to 0.51. For each studied marker, both high genetic variability and discrimination efficiency between genotypes were observed. The microsatellites genotyping allowed unambiguous identification of all the cultivars; a combination of 3 microsatellites markers was sufficient to discriminate 20 olive cultivars. In total, 129 reproducible bands were generated and the cultivars were clustered into nine groups. Homonyms were identified by allele differences between accessions of the same denomination. The information obtained from this study sheds some light on the origin of Algerian olive cultivars.

1. Introduction

Today's horticulture-based agricultural systems need a continuous supply of new cultivars and improved varieties, drawn from the available gene pool, in order to enhance food security and achieve balanced nutrition for rural and urban poor, adapted to drastic climate changes and sustain production systems on marginal lands. Genes for desirable traits are embedded in biodiversity and as such crop genetic diversity has a critical role to play in increasing and sustaining production levels and nutritional diversity throughout the full range of different agro ecological conditions (Lutaladio et al., 2010).

Olea europaea L. is considered as one of the most widely grown fruit crop in the countries of the Mediterranean basin. Many varieties with a significant phenotypic and genotypic diversity result from centuries of natural selection (Ouazzani et al., 1996).

The richness of the cultivated olive germplasm is an extraordinary case among horticultural crops, due to the tree's longevity and the lack of the turnover with new breeding genotypes (Belaja et al., 2011). The olive tree (*O. europaea* L.) exists in two forms: the cultivated form (*O. europaea* subsp. *europaea* var. *sativa*) and the wild form (*O. europaea* subsp. *europaea* var. *sylvestris*). Algeria is one of the olive growing countries. Olive tree occupies the first place representing one third, 33%, of the fruit trees in the dedicated growing areas (Algerian Ministry of Agriculture). However, the last publication on local olive cultivars collection goes back twenty years ago indicating that Algeria has about 150 cultivars (Hauville, 1953). This does not reflect the actual number of local cultivars listed by conservation institutions of the Ministry of Agriculture neither those, which are grown across the country and are not yet identified and characterized. According to recent prospections (data not shown), the real number of cultivars would be higher because of the lack of information on many local minor cultivars scattered throughout the country. The main areas of olive cultivation in Algeria are located in the north. Recently, Algerian Government supported a program of olive tree growing with the objectives to improve olive growing and olive oil production in different regions of the country and grants were given to agricultures. The huge variability of

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climates in Algeria permitted a selection of a high number of genotypes, well adapted to each particular local condition. Nevertheless, a large number of varietal synonyms and homonyms and the intensive material exchange hump correct varietal identification.

To manage the local genetic diversity using conservation programs, it is obvious that accessions should be characterized to eliminate all cases of redundancies (synonymy), disambiguation and identify multi polycolonal populations. In fact, some cultivars could have some denominations according to the region of growth. Moreover, knowledge of structure of genetic diversity is a key factor for the management of genetic resources in successful breeding programs, as reported by Manel et al. (2003) and Baldoni et al. (2006). The varietal structure of olives in a region, together with the olive oil extraction methods contribute greatly to the quality of the oil. Thus, evaluation and characterization of olive genetic resources are recognized as very important, since both productivity and oil quality are traits inherent to a variety (Bandelj et al., 2002).

The identification of local germoplasm is the first key step in the development of typical olive oil production. Moreover, the study of the less common cultivars is very important in preserving this biodiversity from the risk of genetic erosion due to the introduction of cultivars from foreign countries. Morphological descriptions of the International Olive Council (COI, 1997) are usually applied for description and identification of olive varieties. Nonetheless, molecular techniques are also used for precise genetic characterization. In fact, various types of molecular markers have been widely used to distinguish between olive varieties, determine cultivars origin and to study the genetic diversity (De Caraffa et al., 2002; Rao

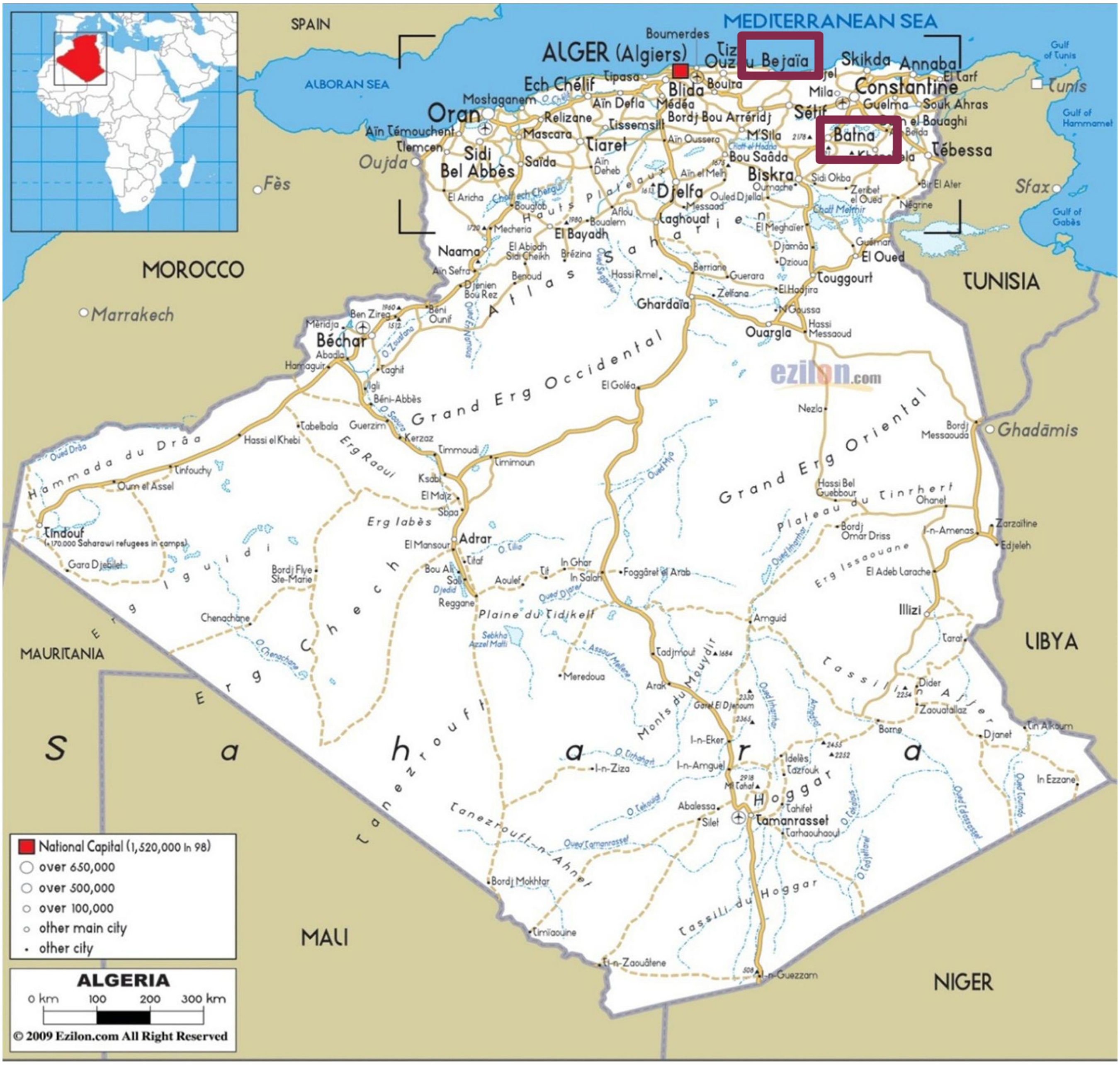

Fig. 1. Map of the sampled areas. The squares forms indicate the collection sites.