

# Genetic Characterization of Tunisian Olive Table Cultivars (*Olea europaea* L.): Inventory Based on Microsatellite Analysis

Sofiane Abdelhamid<sup>1\*</sup> • Naziha Grati-Kamoun<sup>1</sup> • Francesco P. Marra<sup>2</sup> • Tiziano Caruso<sup>2</sup>

<sup>1</sup> Olive Tree Institute, Rue de l'Aéroport, B.P 1087, 3000-Sfax, Tunisia

<sup>2</sup> Dipartimento Culture Arboree, Università Degli Studi Di Palermo, 90128-Palermo, Italy

Corresponding author: \* sofiane.abdelhamid@gmail.com

## ABSTRACT

Olive (*Olea europaea* L.) is an ancient crop which spread from the Middle East towards the western Mediterranean region. In addition to its agronomical and economical importance, the olive industry has a great social and cultural interest as part of our heritage. In order to characterize and to study the genetic relationship among cultivars, five polymorphic microsatellite loci were used in this study and were generated a total of 56 polymorphic alleles with an average of 11 alleles by locus. For all genotypes, the highest number of polymorphic alleles was obtained by the locus UDO043 and GAPI 103. The polymorphism index content ranged from 0.836 for the locus ssrOeUADCA-04 and 0.919 for the locus GAPI-103. The analysis of the dendrogram and the principal coordinates analysis produced by SSR markers grouped studied cultivars into four distinct clusters by cutting the dendrogram at genetic similarity value of 0.1. Accessions of 'Marsaline', 'Fouji' and 'Fokhari' are grouped in one clear cluster. 'Zarrazi' and 'Meski' varieties are grouped in separated clear class. The last group was formed by 'Picholine' and 'Chemcheli' varieties.

**Keywords:** genetic diversity, genetic relationships, polymorphism, molecular markers, simple sequence repeats

## INTRODUCTION

Since the Romans and through all the civilizations that have marked the history of Tunisia, the olive tree (*Olea europaea* L.) occupies a large place in the Tunisian landscape and plays a vital role in its social and economic life. This species is extended throughout the country, under various biotopes and climates showing its spatial and temporal geographical distribution. Tunisia accounts approximately 24,500 ha of olive table which was widespread in the north (70-80%) (GICA 2008).

According to statistical data (IOOC 2003), Tunisian table olive annual production is about 23,000 tons, this production is steadily increasing due to the appreciation of olive fruit (good taste), as well its nutritional properties. Olive table is gaining the favor of consumers due to the beneficial effect that is attributed to a favorable fatty acid profile and to the presence of some minor components (Sakouhi *et al.* 2008; Yamada *et al.* 2008).

A total of 20 native olive table varieties are known in Tunisia and 4 indigenous varieties, 'Lucques' and 'Picholine' (French), 'Ascolana' (Italy) and 'Manzanille' (Spain). Currently, the most used cultivar for processing is 'Meski'. This cultivar is one of the most important and widely planted covering more than two thirds of the area for table olives (15,043 ha) and especially in the irrigated system.

'Meski' is known and appreciated for its taste and its technological interest in the local market and for export. It is characterized by a spherical fruit with an excellent external appearance, very fleshy and tastes good. The mean weight of the fruit is around 4 g. The pulp/stone ratio is very important (4: 6) and the core is easily removable (Mehri and Hellali 1995). Diagnosis of the sector's current situation shows that production levels are still modest and have not achieved the large genetic potential of existing varieties, which can be explained by the heterogeneity and the alternation of production (Mehri *et al.* 1990; Msallem and Hillali 2000; Mehri *et al.* 2003). However, some gene-

tic improvement programs that were established 20 years ago have led to new descendants that take into account the productivity and quality of fruits (Trigui 1996; Ben Amar *et al.* 2006).

Despite the wide genetic patrimony and the large number of synonyms and homonyms in olive table require powerful and precise methods of discrimination for cultivar identification and classification (Bracci *et al.* 2009).

Morphological characterization of Tunisian olive cultivars is carried out based on methodology adapted by the International Olive Oil Council (IOOC) (Mehri and Hellali 1995; Trigui and Msallem 2002). Morphological characters which are considered very heritable were used for describing olive cultivars held in the germplasm collection and in the field. The morpho-pomological characterization is based on a set of distinctive descriptors for qualitative and quantitative characters related to the tree (vigour, growth habit, canopy density and length of internodes), to the leaf (length, shape, width and longitudinal curvature of the blade), to the inflorescence (length, number of flowers/inflorescence), to the fruit (weight, shape, symmetry, colour presence of lenticels, etc.) and to the characters of the endocarp (stone) (weight, shape, symmetry, position of maximum transverse diameter, surface, number of grooves, distribution of the grooves, etc.) (Hannachi *et al.* 2006). Moreover, this approach yielded a considerably redundant number of different olive table cultivars. However, because of most discriminating characters related to fruit and flower, morphological identification has to be completed by a molecular approach.

Some authors applied isozymes techniques to identify and to study the genetic variability of olive (Trujillo *et al.* 1995). The use of isozyme markers to characterize and to study the genetic variation between and within cultivars, depend on several factors (environmental, limited in number) that limit the wider adoption of this technique (Grati-Kamoun *et al.* 2006).

Recently, molecular markers were used to identify olive

**Table 1** Studied accessions of olive table genotypes and their origin.

| Genotype   | End use             | Collection  | Geographic origin | Mean weight of fruit (g) |
|------------|---------------------|-------------|-------------------|--------------------------|
| Zarrazi    | Oil and olive table | -           | Zarzis            | 3.9                      |
| Picholine1 | Oil and olive table | Ksar Ghriss | Sidi BouZid       | 5.0                      |
| Picholine2 | Oil and olive table | Ksar Ghriss | Sidi BouZid       | 5.0                      |
| Marsaline1 | Oil and olive table | Ksar Ghriss | Sidi BouZid       | 7.0                      |
| Marsaline2 | Oil and olive table | Ksar Ghriss | Sidi BouZid       | 7.0                      |
| Chemcheli  | Oil and olive table | Boughrara   | Sfax              | 2.3                      |
| Fouji      | Oil and olive table | Boughrara   | Sfax              | 1.3                      |
| Fakhari    | Oil and olive table | Boughrara   | Sfax              | 2.0 -2.5                 |
| Meski1     | Olive table         | Boughrara   | Sfax              | >6.0                     |
| Meski2     | Olive table         | Boughrara   | Sfax              | >6.0                     |

**Table 2** Sequence of primers, temperature of hybridization (°C), product size range, allelic number, He, Ho, and PIC of the 5 SSR loci studied.

| Locus          | Repeat motif | Sequence of primers (5'-3')                              | Hybridization temperature (°C) | Size range (bp) | Number of alleles | Ho    | He    | PIC   |
|----------------|--------------|--|--------------------------------|-----------------|-------------------|-------|-------|-------|
| UDO099-043     | (GT)12       | TCGGCTTTACAACCCATTTC<br>TGCCAATTATGGGGCTAACT             | 52                             | 157-223         | 15                | 0.985 | 0.968 | 0.914 |
| GAPU-103       | (TC)26       | TGAATTAACTTTAAACCCACACA<br>GCATCGCTCGATTTTATCC           | 57                             | 127-199         | 15                | 0.996 | 0.973 | 0.919 |
| ssrOeUA DCA-04 | (GA)16       | CTTAACCTTTGTGCTTCTCCATATCC<br>AGTGACAAAAGCAAAAGACTAAAAGC | 55                             | 128-184         | 10                | 0.600 | 0.894 | 0.836 |
| ssrOeUA DCA-03 | (GA)19       | CCCAAGCGGAGGTGTATATTGTTAC<br>TGCTTTTGTGCTGTTTGTAGATGTTG  | 50                             | 122-252         | 11                | 0.900 | 0.921 | 0.863 |
| EMO-90         | (CA)10       | CATCCGGATTCTTGCTTTT<br>AGCGAATGTAGCTTTGCATGT             | 55                             | 123-200         | 14                | 0.987 | 0.952 | 0.897 |

cultivated and wild clones and cultivars (reviewed by Muzalupo and Perri 2008). DNA molecular markers techniques based on *in-vitro* enzymatic amplification of specific fragments of DNA via PCR (polymerase chain reaction) are of greater suitability in genetic diversity estimations and identification of olive genotypes (Doveri *et al.* 2008). Previous studies have assessed the genetic variability of olive using random amplified polymorphic DNA (RAPDs) (Belaj *et al.* 2003), amplified fragment length polymorphism (AFLPs) (Sanz-Cortés *et al.* 2003), inter simple sequence repeats (ISSRs) (Terzopoulos *et al.* 2005) and simple sequence repeats (SSRs or microsatellites) (Charafi *et al.* 2008; Besnard *et al.* 2009).

The objectives of this study were i) to identify and to verify by SSR markers DNA fingerprints of studied accessions of olive trees and ii) to test the above-mentioned markers for their ability to discriminate between and among cultivars.

## MATERIALS AND METHODS

### Plant material

In the present study, plant material was collected from morphologically different varieties of different collections in Tunisia. The origin of studied accessions of Tunisian varieties and are listed in **Table 1**.

### DNA extraction

Total DNA was extracted from young leaves using hexadecyltrimethyl ammonium bromide (CTAB) according to the method described by Doyle and Doyle (1990). High salt concentrations (100 mM Tris-HCl [pH 8.0], 20 mM EDTA, 1.4 M NaCl, 1% CTAB) and polyvinylpyrrolidone (Sigma-Aldrich Chemie GmbH, Steinheim, Germany) were added separately to remove polysaccharides and polyphenol compounds. Extraction was performed by an extended RNase A digest (Promega) treatment and a phenol-chloroform method (Rekik *et al.* 2008). DNA was resuspended in TE (pH 8) solution and stored at -20°C.

### DNA amplification by SSRs

The five selected microsatellite loci were used in other work on the characterization of varieties of cultivated and wild olive trees are considered as reliable molecular markers and reproducible.

Amplification was performed among three sets of SSR primers pairs: DCA (Sefc *et al.* 2000), GAPU (Carriero *et al.* 2002) and UDO primer pairs (Cipriani *et al.* 2002) (**Table 2**).

Amplification reactions were carried out in final volumes of 10 µl. The reaction contained 1X PCR buffer, 0.75 mM MgCl<sub>2</sub>, 2.5 mM dNTP, 10 µM of each primer, 0.5 U/µl *Taq* polymerase (Gotaq, Promega) and 50 ng/µl template DNA. PCR reactions were performed at the following conditions: 3 min at 94°C for initial denaturation, 35 cycles of 1 min at 93°C (denaturation), 1 min at optimal temperature ranging from 50 to 57°C (annealing) and 90 sec at 72°C (extension). A final extension step at 72°C for 10 min followed. Polymerase chain reaction (PCR) was carried out using a thermocycler (PE Applied Biosystems). The forward primer was 5' labeled with one of two fluorophores (6FAM or HEX) (Sigma).

0.5 µl of PCR product was mixed with a 12 µl of deionised formamide and 0.5 µl Gene Scan 500 (LIZ) size standard marker. The resulting mixture was heated for 2 min at 95°C and then quickly cooled on ice. Each sample was loaded and run on an ABI-310 automated DNA sequencer (capillary electrophoresis). GeneMapper v.4 software (PE Applied Biosystems) was used to score the SSR profiles.

### Data scoring and analysis

For each individual and for each primer that yielded a clear pattern, polymorphic DNA pics for SSR markers were scored as present (1) or absent (0). For the data set, dendrograms was constructed by UPGMA (Unweighted Pair-Group Method with Arithmetic Averages) cluster analysis according to Jaccard's coefficient (Sneath and Sokal 1973) using NTSYS software analysis and grouping.

Polymorphism Index Content (PIC), observed and expected heterozygosity were calculated by the software CERVUS v.2 (Marshall *et al.* 1998).

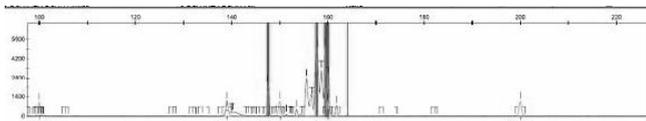
Principal Coordinates Analysis (PCoA) was performed by XLSTAT software.

Average fruit weight was determined according to the method indicated by IOOC (1997).

## RESULTS AND DISCUSSION

### Molecular markers

The results obtained by microsatellite DNA analysis revealed a clear separation of most Tunisian olive table cultivars and showed a significant degree of inter-varietal



**Fig. 1** Example of peaks revealed on automatic sequencer for *ssrOeUADCA-04* locus of 'Meski1' individual.

genetic diversity. The use of microsatellite techniques and their application in genetic diversity studies has allowed the discrimination between and among cultivated olive cultivars and with wild olive forms and the estimation of their genetic inter-relationships (Pollastri 2008).

The microsatellite method consists of short stretches of DNA tandemly repeated is becoming a powerful tool for genetic analysis and has a greater information content that can be helpful for organizing germplasm, for conservation of genetic resources, for the identification of cultivars and for selection of parents for breeding programs (Brito *et al.* 2008). The five microsatellite loci used in this study generated a total of 56 polymorphic alleles with an average of 11 alleles by locus (Table 2). For all genotypes, the highest number of polymorphic alleles was obtained by the locus UDO043 and GAPI 103.

The size of the alleles found for the five loci varies between 57 and 167 bp for *ssrOeUADCA-04* and UDO-43 respectively.

The PIC values were in a range from 0.836 for the locus *ssrOeUADCA-04* and 0.919 for the locus GAPI-103 and the five used loci as suitable for mapping ( $PIC > 0.7$ ) (Table 2), indicating a high discriminating power of the analysed microsatellite markers (Poljuha *et al.* 2008).

## Genetic diversity

Analysis of the dendrogram in Fig. 1 and PCoA in Fig. 2 depict the pattern of relationships between and among cultivars produced by SSR markers and grouped cultivars into four distinct clusters by cutting the dendrogram at a Genetic Similarity (GS) value of 0.1. There is no clear structure of the variability relative to the geographic origin and to the end use of olive table cultivars. Accessions of 'Marsaline', 'Fouji' and 'Fokhari' are grouped in one clear cluster. 'Zarrazi' and 'Meski' varieties are grouped in two clear clusters. The latest group was formed by 'Picholine' and 'Chem-

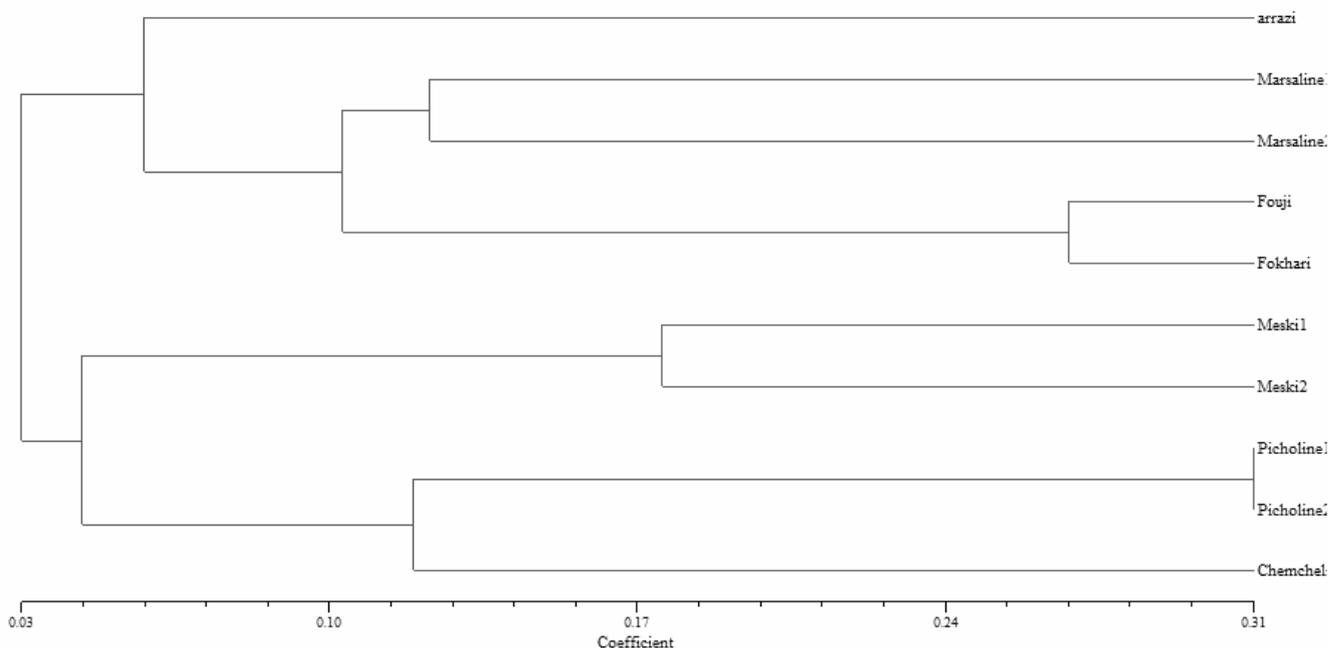
cheli' varieties.

In fact, 'Meski' (cultivated specially in the north of the country) and 'Zarrazi' cultivars (cultivated specially in the south: Zarzis) were grouped separately. The first variety is among the most important Tunisian table cultivars which is used for canning and have a high average fruit weight (6.0 g), whereas the letter is used for both oil and canning and have a high average fruit weight (3.9 g). Genetic differentiation based on fruit size and use has been observed in previous study (Grati-Kamoun *et al.* 2006). Taamalli *et al.* (2006), in their AFLP-SSR analysis of Tunisian olive varieties show that olive accessions inherent small fruit and medium fruit were clustered in separated groups. This result is consistent with previous findings indicating that Greek cultivars were clustered according to fruit size (Nikoloudakis *et al.* 2003).

Cluster 2 is composed of autochthon cultivars native to Tunisia: 'Marsaline' (Siliana and Zaghuan), 'Fouji' (Gafsa) and 'Fokhari' (Tataouine), whereas cluster 4 is composed by one foreign variety 'Picholine' from French and 'Chemcheli' from Gafsa. As indicated in Table 1, the geographic distribution of studied varieties was from the south to the north of the country and there is no clear clustering of the variability relative to the geographic origin of growing area or relative to the weight of fruit. This result may be explained by the fact that Tunisian olive germplasm is a rich assortment of polyclonal varieties, which are the results of a clonal selection process, generally done by farmers in terms of their needs or in terms of their aspiration to superior quality of olive fruit for oil or for canning (Rekik *et al.* 2008).

Lack of a clear clustering of olive cultivars according to their geographic origin was observed previously in several studies based on allozymes (Ouazzani *et al.* 1995) or based on molecular markers (Owen *et al.* 2005; Rekik *et al.* 2008). The agro-ecological adaptation area of cultivars (not wide geographical distribution), a possible exchange of plant material and seed among the different regions of Tunisia and the old cultural traditions may explain the clustering obtained by SSR's data among cultivars (Bartolini and Petruccioli 2002).

The presence of two varieties 'Picholine' and 'Chemcheli' in the same cluster could be explained by the common origin of olive trees. As reported by some previous studies (Hannachi *et al.* 2008), shown that Mediterranean olive was widely diffused in Mediterranean countries by human activities.



**Fig. 2** SSR dendrogram based on Jaccard's genetic distance.

## CONCLUSION

It may be concluded from this study that microsatellite markers provide consistent information for cultivar identification and are valuable tools for studying the genetic relationships between Tunisian olive cultivars which might allow us to make future germplasm collections.

It will be necessary to investigate the genetic diversity of much more Tunisian cultivars for future researches and to sample a large number of Mediterranean varieties in order to identify their genetic background in relation to Tunisian cultivars.

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