RELATIONSHIPS AND GENETIC DIVERSITY OF GRAPEVINE (*VITIS VINIFERA* L.) GROWN IN ALGERIA AND IN MEDITERRANEAN BASIN

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Summary
Algeria represents a great resource of almost unknown genetic diversity for all the Mediterranean species, in particular for grapevine (*Vitis vinifera* L). Often, different local names were given to plant material that resulted identical from the genetic point of view. In this work 12 SSR markers were used to study the relationships and the genetic diversity among 60 autochtonous and cultivated grape varieties coming from the Mediterranean Basin.

Keywords: genetic characterization, DNA, microsatellite markers, SSR, synonymy

Introduction

Algeria has a long viticulture history and a rich tradition due to the settlement of many populations and civilizations. For many centuries, this situation made of Algeria the place of choice for the production and exchange of plant material [1]. This inheritance has led to the existence of a quite large grapevine germplasm, but also to the occurrence of cases of homonymy and synonymy.

At present, it is widely acknowledged that DNA markers represent a significant resource for creating genetic and physical maps, distinguishing individuals and investigating genetic relatedness. Since the first application of SSR (Simple Sequence Repeat) markers in the grapevine identification, microsatellites have increasingly become quite the ideal tool for genetic studies due to their high polymorphism and the ease with which they can be detected.

In this context, for the first time SSR markers were used to study the relationships and genetic diversity among wild and cultivated grapevine cultivars coming from Algeria and the Mediterranean Basin.

Material and Methods

Grapevine accessions from the two Algerian collections of Benchicao (Medea) and Mascara, and from the French collection of Montpellier (INRA) were analysed. Total genomic DNA was extracted from young leaves using the procedure described by [2] and sixty DNA samples were analysed at 12 SSR loci (Table 1) characterized by [3], [4] and [5]. The PCR was performed on 20 µl of a mixture containing: 50 ng DNA, 0.5 U AmpliTaq Gold polymerase (Applied Biosystems, USA), 2 µL GeneAmp 10x PCR buffer (Applied Biosystems), 1.6 mM $MgCl_2$, 200 µM dNTP and 0.5 µM of each primer, using a MJ Research PTC 100 thermal cycler. Amplification cycles consisted of an initial step at 95°C for 9 min, followed by 26 cycles of denaturation (50 sec at 95°C), annealing (45 sec at 50°C) and extension (90 sec at 72°C); a final elongation step was done at 72°C for 45 min. PCR-amplicons were analysed on a sequencing gel using an ABI-PRISM 377 DNA sequencer (Applied Biosystems). Data were analysed with the GENESCAN software (Applied Biosystems) and alleles were defined by their size, determined in base pairs by comparison

with the size standard. Statistical analyses were performed using the software POWER MARKER v 3.22 (http://www.powermarker.net).

Results and Discussion

The microsatellite loci chosen for this study, discriminated 34 different genotypes in 60 analysed cultivars. The genetic variability of this germplasm (Table 1) was evaluated on the basis of the number of alleles (mean: 9.1), gene diversity (GD: 0.79), observed heterozigosity (Ho: 0.80), and polymorphism information content (PIC: 0.77). These data indicated the presence of a high genetic variability in the local germplasm, comparable to the variability found in the Spanish grape germplasm [6]. Total probability of identity for the 12 loci was 6.67×10^{-15}, thus, cultivars with identical genotypes were considered synonyms. Among the investigated cultivars, DNA profiles showed the following synonymies: Ahmeur bou ahmeur, H. de Mascara, and Bordji; Chaouch rose and Chaouch; Amokrane and Amelal; Regina dei Vigneti and Dattier de Beyrout.

Locus	N° of genotype	N° of alleles	GD	Ho	PIC
VvS2	20	11	0.864	0.967	0.849
VvS5	18	11	0.828	0.655	0.807
VvMD5	24	8	0.837	0.900	0.816
VvMD7	16	9	0.774	0.883	0.745
VvMD24	13	7	0.659	0.483	0.620
VvMD27	15	7	0.764	0.767	0.735
VvMD31	18	8	0.821	0.800	0.797
VvMD36	17	12	0.814	0.767	0.792
VrZAG21	16	7	0.785	0.800	0.755
VrZAG62	19	9	0.783	0.850	0.755
VrZAG67	20	10	0.798	0.967	0.775
VrZAG 79	22	10	0.795	0.783	0.770
Mean	18.2	9.1	0.794	0.802	0.768

Table 1 - Number of genotypes, number of alleles, gene diversity (GD), observed heterozygosity (Ho), polymorphism information content (PIC) of 12 SSR loci studied in 60 *V. vinifera* cultivars.

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