



THE PRESENCE OF GENETIC VARIABILITY IN GRAPE VARIETIES

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ABSTRACT: - 222 cultivated (*Vitis vinifera*) and 22 wild (*V. vinifera* ssp. *sylvestris*) grape accessions were analysed for genetic diversity and differentiation at eight microsatellite loci. A total of 94 alleles were detected, with extensive polymorphism among the accessions. Multivariate relationships among accessions revealed 16 genetic groups structured into three clusters, supporting the classical eco-geographic grouping of grape cultivars: *occidentalis*, *pontica* and *orientalis*.

KEYWORDS: Genetic, grape, cultivate, wild, allele, *occidentalis*, *pontica*, *orientalis*.

INTRODUCTION

Cultivated grape, *Vitis vinifera* L., is the sole European representative of the genus *Vitis* L., a large member of Vitaceae with y60 species. Two-thirds of these species are native to North America and onethird is distributed over central and east Asia. The cultivated grape is believed to have been domesticated around 4000 BC from a perennial wild grape

originally classified as *V. sylvestris* C.C. Gmelin occurring from north-eastern Afghanistan to the southern borders of the Black Sea and the Caspian Sea. However, based on a recent archaeological finding in the Zagros mountains of Iran, McGovern et al. suggested 5400–5000 BC as the probable period of domestication of the grape. Currently, most botanists regard the wild ancestral grape *V.*

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sylvestris as the primitive form of the cultivated grape because of the close morphological resemblance and free gene flow between them (Heywood & Zohary, 1991) and consequently have reduced its taxonomic status to subspecies level within the *V. vinifera* crop complex. The wild grapes are predominantly forest climbers and occur in disjunct populations from the Atlantic coast to Tadzhikistan and the western Himalayas. They occasionally come into contact with cultivated forms in nearby vineyards, forming complex introgressive hybrid swarms in transition zones. Domestication of grape involved a shift in the mode of reproduction from dioecious to hermaphroditic, ensuring self-pollination without the need for external pollen donors. The earliest signs of grape cultivation come from Chalcolithic and Early Bronze Age (3500–2300 BC) sites in the Jordan Valley, where wild and cultivated grapes provided fresh fruits, easily stored raisins and juice for fresh consumption and fermentation into wine. Over the next 2000 years, grape cultivation spread to the eastern, northern and western parts of Eurasia and to northern Africa, following the trade routes and migration of ancient tribes. Traditional viticulture was based on thousands of distinct cultivars exhibiting a wide range of adaptations, growth habits and fruit characteristics. Currently, over 6000 cultivars are documented, including wine, table and raisin types. Nevertheless, cultivar names are often ambiguous owing to transliteration, the substitution of local or regional names for the original cultivar names, the presence of variants within cultivars (clones) and poor documentation of passport data, which includes ecogeographical, climatological and ethnographic information associated with germplasm accessions. Moreover, the wide distribution and long cultivation history of the grape have led to the development of numerous cultivars that have many

synonyms, a problem that plagues germplasm collections. Traditional methods of describing grape vine varieties based on the plant's vegetative and reproductive traits (ampligraphy) have contributed greatly to establishing the identity and relationships among *V. vinifera* cultivars. Nevertheless, ampelographic traits are often plastic, with a large genotype–environment interaction component rendering them less useful in classifying closely related cultivars. Early efforts to classify the eco-geographic variation within the cultivated grape resulted in the classification of cultivars into groups: *occidentalis*, the small-berried wine grapes of western Europe; *orientalis*, the large-berried table grapes of West Asia; and *pontica*, the intermediate type from the basin of the Black Sea and eastern Europe. Levadoux summarized the eco-geographic differentiation of wild and cultivated *V. vinifera* populations from western Europe and the Mediterranean region, and discussed the consequences of isolation of eastern and western populations during the glacial period and post-glacial proliferation for population differentiation, climatic adaptations and early selection and cultivation by man. More recently, Bisson proposed the eco-regional classification for French cultivars and discussed the implications for grape breeding. A wide range of biochemical and molecular markers are being used to characterize and classify grape germplasm collections. However, the use of molecular markers to study genetic structure and differentiation in *V. vinifera* is limited to a few investigations. Microsatellite markers, being abundant, multiallelic and highly polymorphic, provide an efficient and accurate means of detecting genetic polymorphism. Most importantly, their co-dominant nature makes them the markers of choice for population genetic analysis to assess genetic structure and differentiation in germplasm collections and

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natural populations. The knowledge of the amount and pattern of distribution of genetic variation is central to the development of effective conservation strategies and efficient use of *Vitis* germplasm. The present study evaluated the genetic diversity, structure and differentiation in a grape germplasm collection using polymorphisms at eight microsatellite loci. In addition, we examined the genetic relationship between cultivated and wild grapes to draw inferences about the history of domestication. Further, we elucidated the possible relationships between geographic origin of cultivars and the pattern of microsatellite polymorphism.

In summary, the gene pool of cultivated grapes surveyed has significant amounts of genetic variation and exhibits narrow differentiation. The French wine grapes appear to be distinct and show close affinity to the *ssp. sylvestris* included in the study. The overall organization of genetic diversity suggests that the germplasm of cultivated grapes represents a single complex gene pool and its genetic structure has been influenced by strong artificial selection. In regard to germplasm management, our results show that the germplasm collection is highly variable and most variation (85%) is common to all the genetic groups identified. Second, only minimal gains in the variability are possible through extensive collection from diverse eco-geographic sources. Third, unique cultivated genotypes, wild (*ssp. sylvestris*) and spontaneous introgressive hybrids are major sources of new alleles, in addition to the slow process of bud mutation. Finally, diverse wild grape germplasm is a potential source of unique alleles and is important for the improvement of both wine and table grapes.

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