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Edited by Gabriella De Lorenzis, Laura Rustioni and Osvaldo Failla

# GRAPEVINE GERMPLASM FROM CENTRAL ASIA: ASSESSMENT OF GENETIC DIVERSITY AND RELATIONSHIPS WITH 22 SSR MARKERS

Annarita MARRANO<sup>1</sup>, Lukasz GRZESKOWIAK<sup>1</sup>, Paula MORENO SANZ<sup>1</sup>, Silvia LORENZI<sup>1</sup>,  
Maria Lucia PRAZZOLI<sup>1</sup>, Arkadiy ARZUMANOV<sup>2</sup>, Mahfurat AMANOVA<sup>2</sup>, Osvaldo FAILLA<sup>3</sup>,  
David MAGHRADZE<sup>4</sup>, Maria Stella GRANDO<sup>1</sup>

<sup>1</sup> *Fondazione Edmund Mach, Research and Innovation Centre, San Michele all'Adige (Trento) Italy*

<sup>2</sup> *Uzbek Research Institute of Plant Industry, Tashkent, Uzbekistan*

<sup>3</sup> *Dipartimento di Scienze Agrarie e Ambientali, Università degli Studi di Milano, Italy*

<sup>4</sup> *Institute of Horticulture, Viticulture and Oenology, Agricultural University of Georgia, Georgia*

**INTRODUCTION** – The Eurasian grapevine (*Vitis vinifera* L.) is one of the most economically important crops worldwide. It includes two subspecies, the cultivated form *sativa* and the wild form *sylvestris*. They are different for several traits, such as flower sex, berry and bunch size, shapes of seed and leaf. How these changes occurred and if multiple domestication events also arose are still uncertain. The evaluation of genetic diversity in under-explored grapes collections from Central Asia may help to better understand the history of viticulture.

**AIMS AND SCOPE** – The present study aimed to investigate genetic diversity of grape germplasm collections from Central Asia and Georgia.

**MATERIALS AND METHODS** – Nine standard SSR loci were used to profile genotypes of 80 cultivated and 21 wild accessions from the region of Central Asia (Uzbekistan, Tajikistan and Kyrgyzstan) and 60 cultivars from Georgia. The resultant non-redundant set of unique profiles was further characterized using 13 additional microsatellites. The main indices of genetic diversity were calculated in the GenAlex program. The population structure was inferred using principal coordinate analysis (PCoA), and the Bayesian method implemented in the STRUCTURE software. Further, the genetic profiles were subjected to cluster analysis with the DARwin software package.

**RESULTS AND DISCUSSIONS** – A collection of 161 accessions from Central Asia and Georgia was characterized with 22 SSRs. After removing redundant genotypes and individuals with missing data, a final set of 119 unique profiles was obtained. It was composed by 66 cultivars and 13 wild genotypes from Central Asia and 40 varieties from Georgia. The analysis of genetic diversity revealed high and comparable levels of expected heterozygosity (0.77 for the Central Asian cultivars, 0.66 for the Central Asian wild accessions, and 0.73 for the Georgian varieties). The relationship between genotypes was plotted based on their first two principal coordinates (accounting for 8.94% and 5.57% of total variability, respectively). The accessions from Central Asia and Georgia were well distinguished along the first coordinate axis, while the second axis differentiated the wild and cultivated genotypes of Central Asia origin. The analysis in STRUCTURE highlighted two main groups: i) the group of Central Asia accessions and ii) the group of Georgian accessions. Further confirmation of the revealed population structure was obtained from a neighbor-joining dendrogram.

**CONCLUSIONS AND POSSIBLE APPLICATIONS** – The evidence of high heterozygosity in both Central Asian and Georgian groups confirms the genetic richness of accessions from these viticultural regions. Additional studies may help to understand how these varieties contribute to the domestication process and how they can contribute to future grape improvement through marker-assisted breeding or genetic engineering.