

Oral presentations

Grapevine genetic resources of Armenia: molecular fingerprinting and phylogenetic relationship among wild and cultivated grapevine

Margaryan, Kristine^{1, 2*}; Gasparyan, Boris³; Harutyunyan, Frunz¹; Töpfer, Reinhard⁴; Maul, Erika⁴

¹Research Group of Plant Genomics, Institute of Molecular Biology, National Academy of Sciences RA, Yerevan, Armenia

²Department of Genetics and Cytology, Yerevan State University, Yerevan, Armenia

³Institute of Archaeology and Ethnography, National Academy of Sciences RA, Yerevan, Armenia

⁴Julius Kühn Institute (JKI), Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany

*kristinamargaryan@ysu.am

Abstract

Armenia is characterized by high diversity of cultivated (*Vitis vinifera* L. subsp. *Vinifera*) and wild (*Vitis vinifera* L. subsp. *sylvestris*) grapes. The country has played a leading role in the centuries-lasting history of grapevine cultivation in Southern Caucasus. Varying climatic conditions and the existence of wild grapes lead to the formation and promotion of viticulture and winemaking, as evidenced by nearly 450 autochthonous varieties. Hundreds of unique indigenous cultivars are still preserved in old vineyards and abandoned gardens, though most of them are threatened by extinction. Wild grapes, thriving along riverbanks, climbing the rocks and embracing the trees can be found in Vayots Dzor, Tavush, Syunik regions and in Artsakh.

With the main goal to estimate the phylogenetic relationships among Armenian wild grapes and indigenous cultivars, and to estimate the possible contribution of wild grapes to the genetic makeup of indigenous cultivars, we analyzed 79 unique cultivars and 111 putative wild plants, collected from different viticultural regions, with 25 nSSR markers.

The genetic diversity analysis conducted for wild grapes and indigenous cultivars unfolded the allelic richness of wild and cultivated gene pools and surprisingly for us revealed the absence of significant differences for all genetic parameters between the two subspecies. Moreover, the results registered for the number of different alleles (Na), effective number of alleles (Ne), Shannon's information index (I) have shown comparatively high values for wild grapes, while the observed negative value of Fixation index (F) for indigenous cultivars mirrored an abundance of heterozygote genotypes presuming random mating. The neighbour-joining (NJ) cluster analysis indicated clear separation between the two subspecies *vinifera* and *sylvestris* and formed two main clusters. Applied non-hierarchical horizontal clustering using Structure software assigned the 190 genotypes into two clusters. The delta K criterion (ΔK) suggested K = 2 as the optimal uppermost hierarchical level of structure. Obtained results were absolutely comparable with the NJ cluster analysis and confirmed the divergence of *sylvestris* from *vinifera*, indicating a clear separation between two subspecies. Meanwhile, results highlighted the role of gene flow between wild grapes and cultivars through observed overlaps and admixed ancestry values. Grapevine genetic resources of Armenia can contribute overcoming biotic and abiotic stresses and better adaptation to climate change

Keywords: wild grape, indigenous cultivar, genetic diversity, phylogeny, Armenia