

P11 – Comparative genomics and phylogenetic analysis of *Vitis vinifera*: insides from the complete plastid genome sequences

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Abstract

Vitis L. belongs to one of the oldest Vitaceae family of flowering plants. The origins of the grapevine remain uncertain, this family possibly were originated on the boarder of Jurassic and Cretaceous periods and was widely distributed in the Old and New World. Its great age is testified by fossilised grape leaves and seeds in Palaeocene and Eocene deposits. Glacial period destroyed most of *Vitis* habitats and only in a certain area (refuges) they were survived. Such areas in Europe were located around Mediterranean basin and Southern part of Black and Caspian Seas. The current distribution of genus *Vitis* habitat includes three centres of diversity: East Asia, Northern south America, Central America and North America, Europe and Central Asia. Resent chemical analyses of ancient organic compounds absorbed into the pottery fabrics from sites in Georgia in the South Caucasus region, dating to the early Neolithic period (ca. 6,000–5,000 BC), provide the earliest biomolecular archaeological evidence for grape wine and viniculture from the Near East, at ca. 6,000–5,800 BC. The discovery of early sixth millennium BC grape wine in this region is crucial to the later history of wine in Europe and the rest of the world.

We present the analyses of plastid genome diversity of wild (*V. vinifera* ssp. *sylvestris*) and cultivated grapevines (*V. vinifera* ssp. *sylvestris*) from Georgia, Europe, Mediterranean basin and Asian and American species by the Next-generation Sequencing and Comparative Genomics. In particular, in the frame of our research: 1). Next-generation Illumina Sequencing of more than 40 genomes of *Vitis vinifera* from different geographic origins were conducted; 2). SNPs and indel regions were detected in each sequenced genome; 3). By using of comparative genomic approaches, the phylogenetic linkage study of the analyzed plastid genomes was performed. According to our results, it is shown that GTA haplotype dominates in wild grapevines of Europe (i.e., Germany and France), ATA and ATT haplotypes were found in the Mediterranean basin and Anatolia (i.e., Corsica, Greece, Turkey). Genetically unique AAA haplotype was found in Georgian wild and cultivated samples and ATA haplotype was detected in Asian and American species. The obtained results will help to understand the genetic relationships between wild and cultivated grapes from different geographical locations and explain the molecular bases of grape origin and evolution.

Keywords: *Vitis vinifera*, Plastid DNA, Next-generation sequencing, Comparative genomics,