Population genetic analysis in old Montenegrin vineyards reveals ancient ways currently active to generate diversity in *Vitis vinifera*

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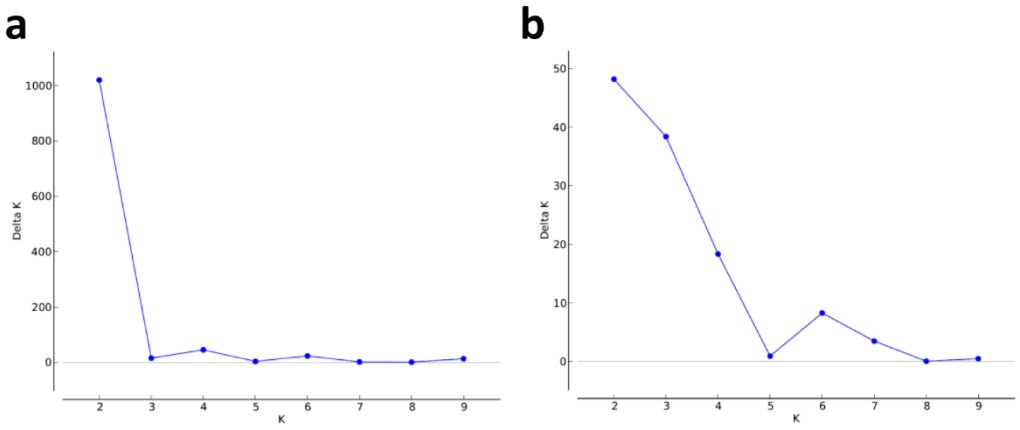
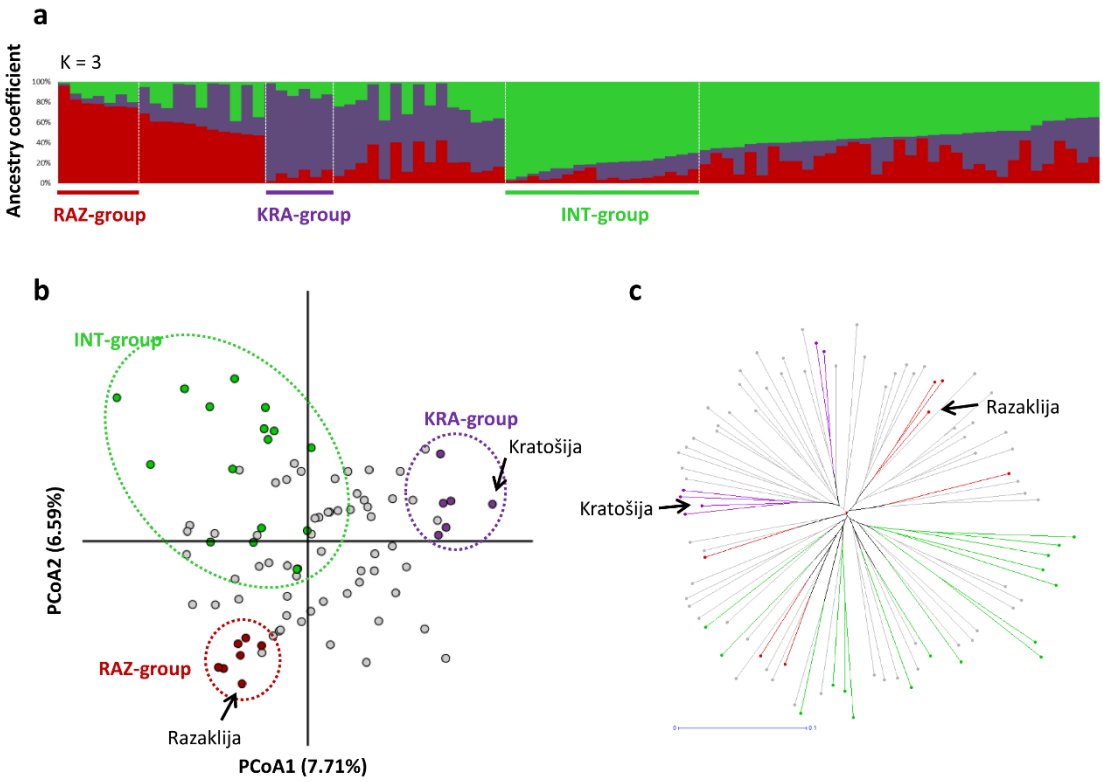
List of Supplementary Figures



Supplementary Figure S1. Delta K plots obtained from STRUCTURE HARVESTER to set the most likely number of genetic groups present within 131 (A) or 91 (B) non-redundant grapevine genotypes identified in this study.



Supplementary Figure S2. Population structure analysis of 91 non-redundant cultivated varieties found in Montenegro**.** In A, STRUCTURE analysis also suggested the existence of three major genetic groups (RAZ-group, KRA-group and INT-group). Every non-redundant genotype is shown as a vertical line, with color segment lengths proportional to their inferred ancestry to the RAZ-group, KRA-group and INT-group (in red, purple and green, respectively). The number of genetic groups (K=3) was set considering the *ΔK* criterion[65]. Considering a critical ancestry coefficient of $q \geq 0.70$, 7, 6 and 17 genotypes were assigned to RAZ-group, KRA-group and INT-group, respectively (61 genotypes were considered as admixed). In B, a principal coordinate analysis (PCoA) obtained from a dissimilarity matrix calculated in DARwin from genetic data (194 SNPs) from the non-redundant cultivated genotypes is shown. The variance explained by the PCoA1 and PCoA2 is indicated as %. In C, the unweighted neighbor-joining (UwNJ) radiation tree obtained for the same dataset by means of DARwin is shown. In B and C, genotypes assigned to RAZ-group, KRA-group and INT-group are shown as red, purple and green dots, respectively (admixed genotypes are shown in grey).