

Figure Captions

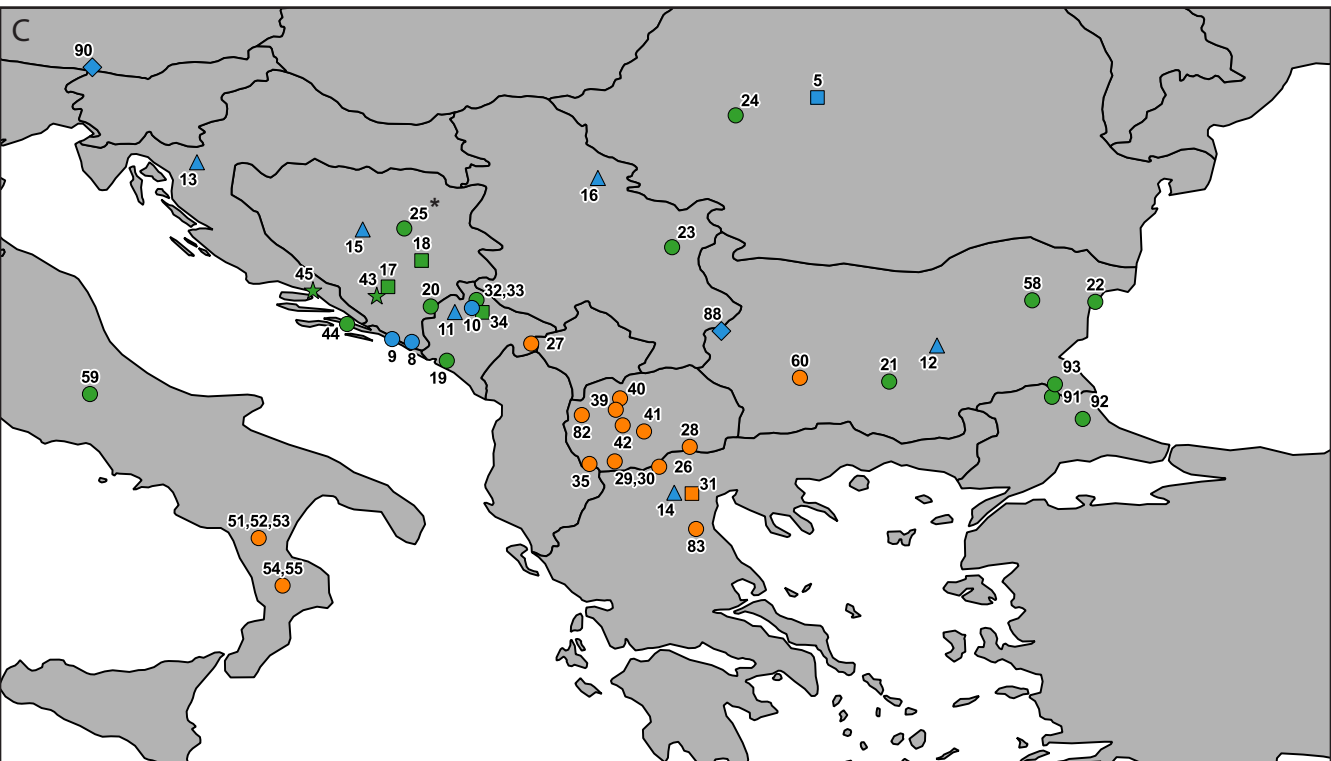
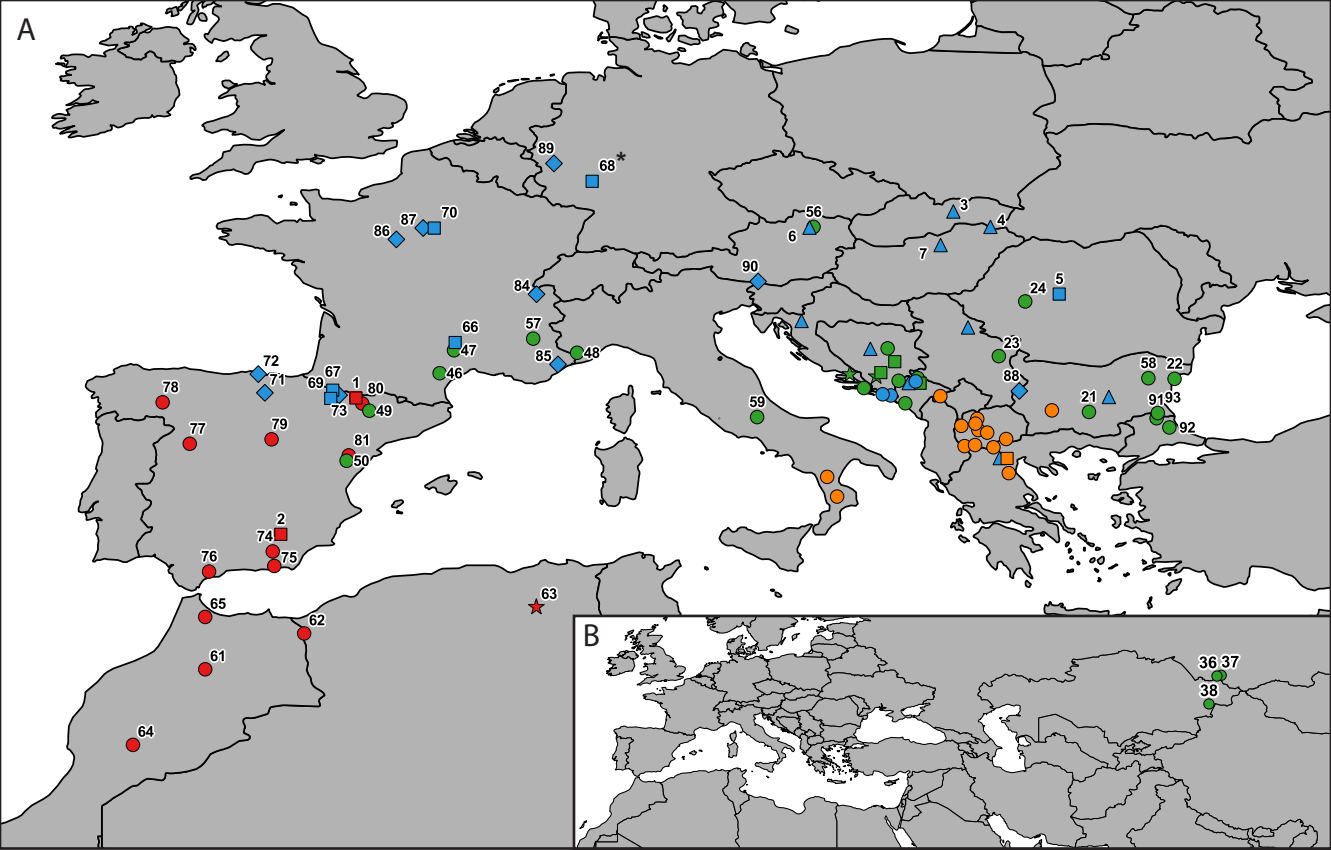
Fig. 1. Maps of sampling sites. Population codes follow Table S1, symbol shapes represent ploidy level (○ 2x; □ 4x; △ 6x; ◇ 8x; ☆ mixed-ploidy populations), and colours indicate cluster affiliation. An asterisk (*) indicates missing data for DNA-ploidy level. **A, B,** Locations of the 93 populations of *Veronica* subsect. *Pentasepalae* analyzed in this study. **C,** Detailed distribution map of studied populations from the Balkan Peninsula.

Fig. 2. A, Neighbor-Net based on 1127 AFLP scored fragments of 241 individuals of *Veronica* subsect. *Pentasepalae* using Jaccard's genetic distances. Individual codes are shown following Table S1. Archs delimit taxa whose initial taxonomic determination and ploidy are shown. Range of colours of the archs differentiates the four clusters identified by the Structure analyses. Bootstrap values (BS) > 50% are shown. **B,** Bayesian clustering analyses based on the entire AFLP dataset. Four main clusters are represented by different colors. Black lines separate different populations which are indicated below the graph (population codes follow Table S1).

Fig. 3. Principal Coordinate Analysis (PCoA) of the AFLP dataset of 241 individuals based on Jaccard's distances and DCENTER module. Axis 1 and Axis 2 explains 8.36 and 6.20% of the variation, respectively. **A,** The two clusters supported by genetic structure analyses using K-means clustering algorithm are represented by colours. **B,** Colours indicate the four genetic clusters estimated by Bayesian clustering analyses using Structure.

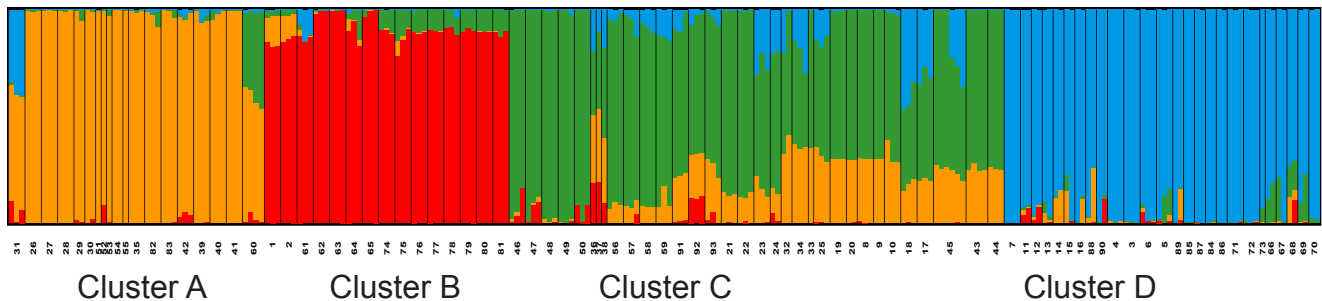
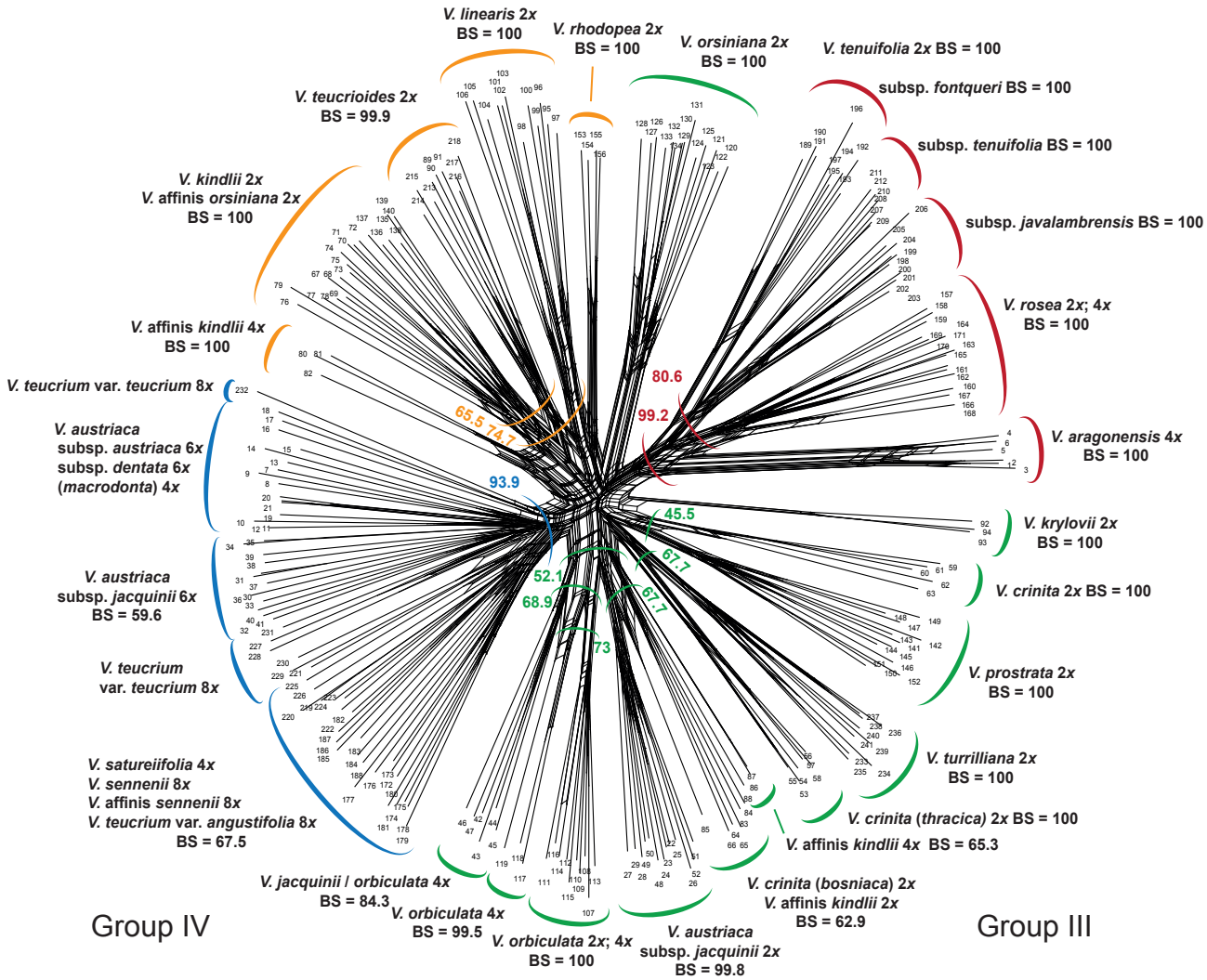
Fig. 4. Genetic structure analysis based on AFLP data of 58 individuals from 26 populations (corresponding with group IV/cluster D, which comprises most polyploidy taxa from Central Europe and North of Spain). **A,** Bayesian model-based clustering at K = 2 using Structure.

Colours represent different clusters (dark blue vs. light blue) and black lines separate individuals of different populations, which are indicated below the graph (codes follow Table S1). Taxonomic names from each population are shown above the graph. **B**, Part of the Neighbor-Net (presented in Fig. 2) representing the 58 analyzed individuals. **C**, Distribution map of populations included in genetic structure analysis of cluster D.

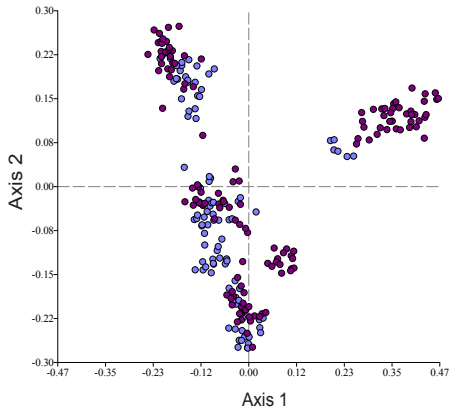


Group I

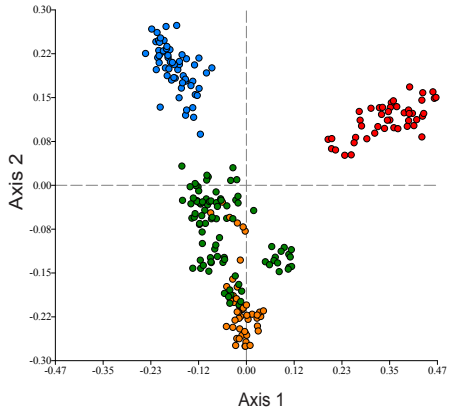
Group II



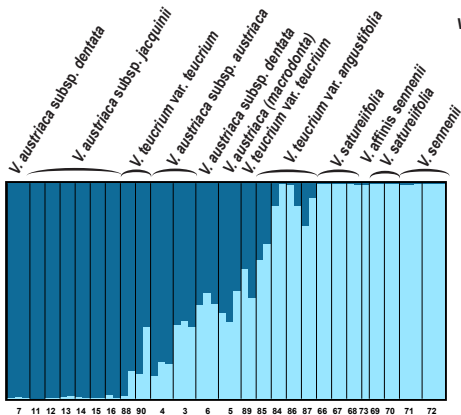
A



B



A



B

