

Genetic structure and differentiation using only 13 SSRs (all free of any non-specific PCR-products)

1. Bayesian clustering analysis using the STRUCTURE method (Pritchard et al. 2000, Falush et al. 2003)

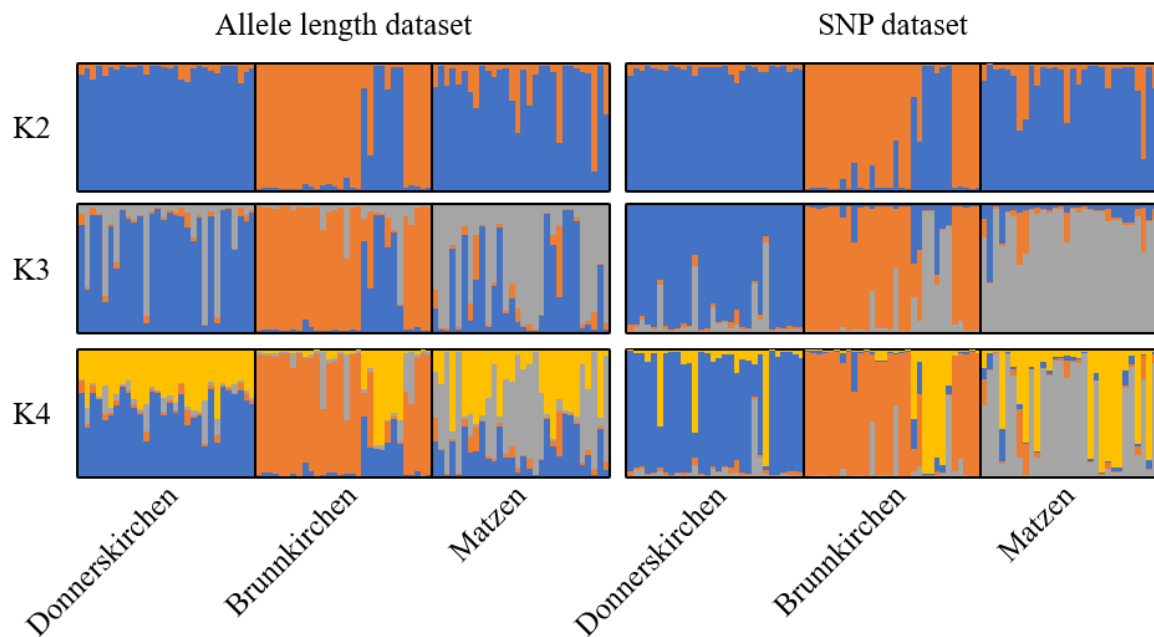


Figure S2.1 – STRUCTURE results (i) using the ‘allele length dataset’ and (ii) using the ‘SNP dataset’ for 2-4 assumed subpopulations (K). Each individual within a population (box) is represented with a vertical bar and each inferred cluster is marked with a different colour.

2. Results of Principal Coordinate Analysis (PCoA; Orloci 1978) based on pairwise F_{ST} -values (Weir and Cockerham 1984)

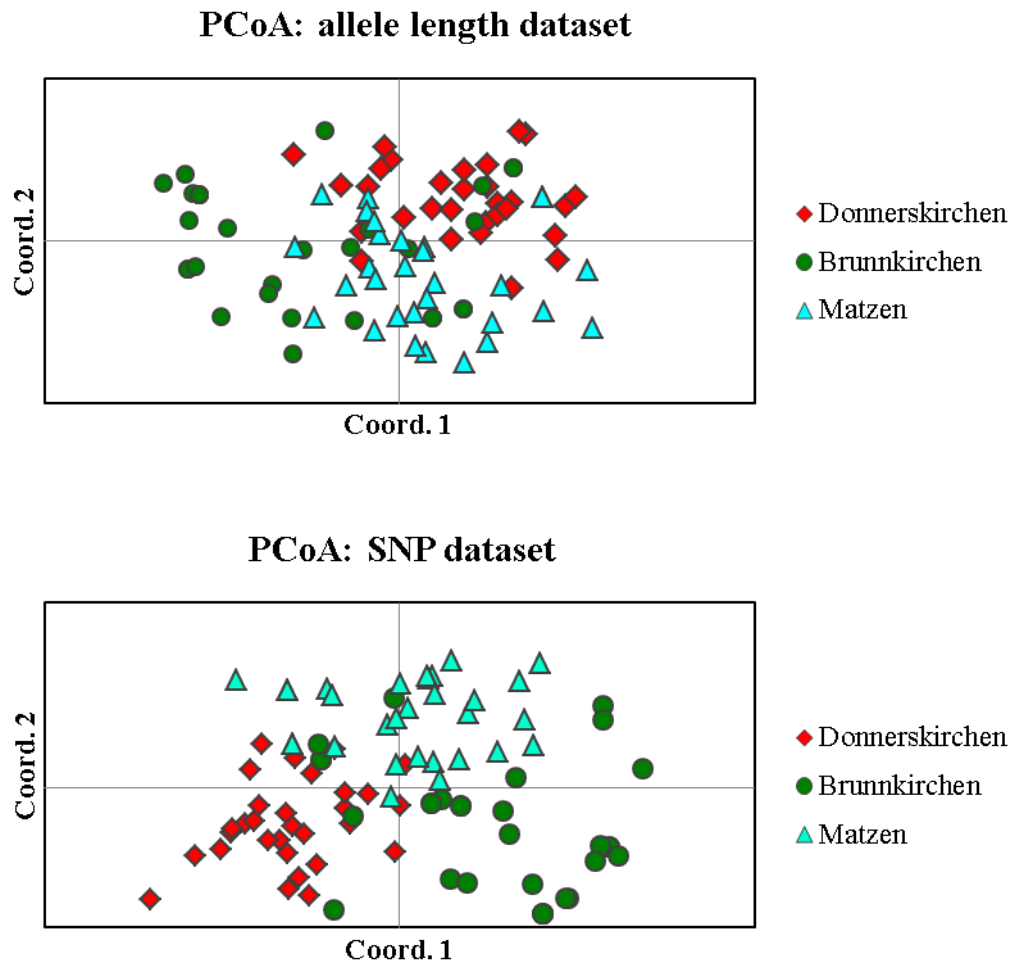


Figure S2.2 – Ordination along the first and second principal coordinates derived by a Principal Coordinate Analysis (PCoA) based on interindividual distances for the two different datasets used. Each point represents an individual. Populations are depicted with different shapes / colours. The percentage of explained variation of the two first Principal Coordinates was 20.2 and 20.3 % respectively.

Online Resource 2:

Supplementary material for: Neophytou et al. (2018) Analysis of microsatellite loci in tree of heaven (*Ailanthus altissima* (Mill.) Swingle) using SSR-GBS. Tree Genetics and Genomes

Reference list

Falush D, Stephens M, Pritchard JK (2003) Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164(4):1567-1587

Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics* 155(2):945-959

Orlóci L (1978) Multivariate analysis in vegetation research. Springer Netherlands, The Hague.

Weir BS, Cockerham CC (1984) Estimating F-statistics for the analysis of population structure. *Evolution* 38(6):1358-1370

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