

Supplementary Materials:

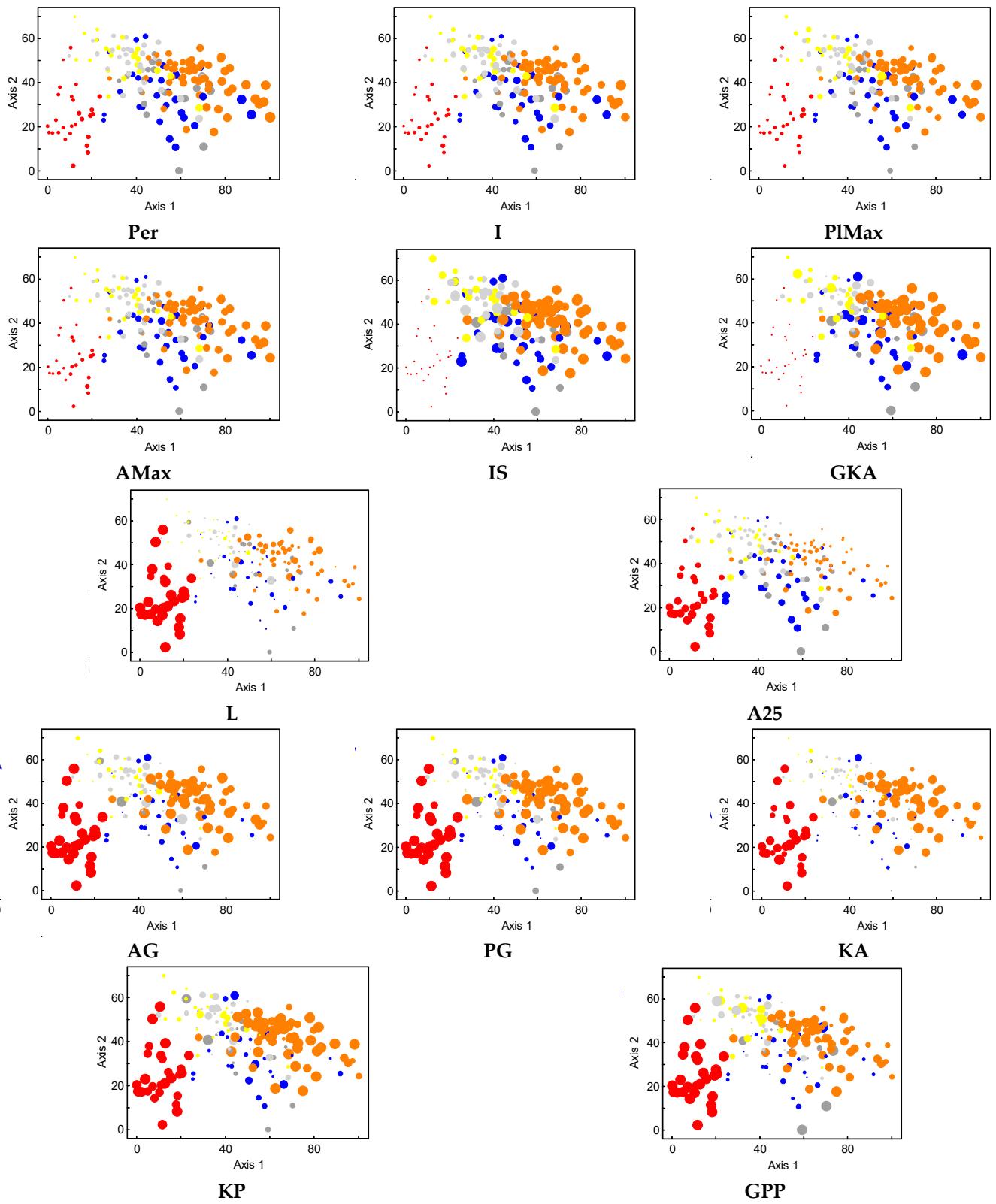


Figure S1. The PCA ordination plots of elm trees given separately for species-specific leaf morphology traits. The symbol size indicates the relative size of the morphology traits in the entity. The minimum value (zero) is shown on an overlay as the smallest size for that symbol. Abbreviations and color of the triangles are shown in Figure 3.

Table S1. List of nuclear microsatellite markers (nSSR's) used in our study.

Locus name (Gene Bank no.)	Primer sequences (5'-3')	Repeat motif of cloned allele	Size range (bp)	Annealing temp.°C
Ulm2 (AY300797)	F: GCGTCTCAGAACAAACAGCTTCA R: GGCTGCAAGATTGAACCTTGAT	(CAG)8	83-104	35
Ulm3 (AY300798)	R: GGCTGCAAGATTGAACCTTGAT R: GGACCACATCTCTCGCTGTTGT	(CAG)8 (CAG)10 (CAG)7+ (CT)10	166-169	35
Ulmi1-21 (AY520827)	F: GCGGTCTTACGTGAGCTTC R: AAAGAGGCAGACGAAGATGG		209-227	35
Ulmi1-98 (AY520829)	F: AAATGGCCGGAATGTGTTAC R: TGGGTGAGAGGACAAGTCAA	(CT)6 N14 (CT)7	156	35
Ulmi1-165 (AY520830)	F: CTCTTCCATTCTCGCCTCAC R: GAGGTGCCATAAGCCAAGAA	(CT)9	156-174	35
Ulm19 (AY300804)	F: ACAAGCATCCTTATACACAC R: TCTATCTCTCTCAATTCTG	(CA)13 (CA)3 (TG)4	254-276	29
Ulm6 (AY300799)	F: CCTTCATGATTGCAATCGGTA R: ACAATAATCGTAACCACCTT	(CA)13	148-160	29
UR158 (EF123158)	F: TTCTTCATAGGCGCTGAGGT R: TGCACCCCTGTCAAAGCTAAA	(TGTA)5	176-208	32

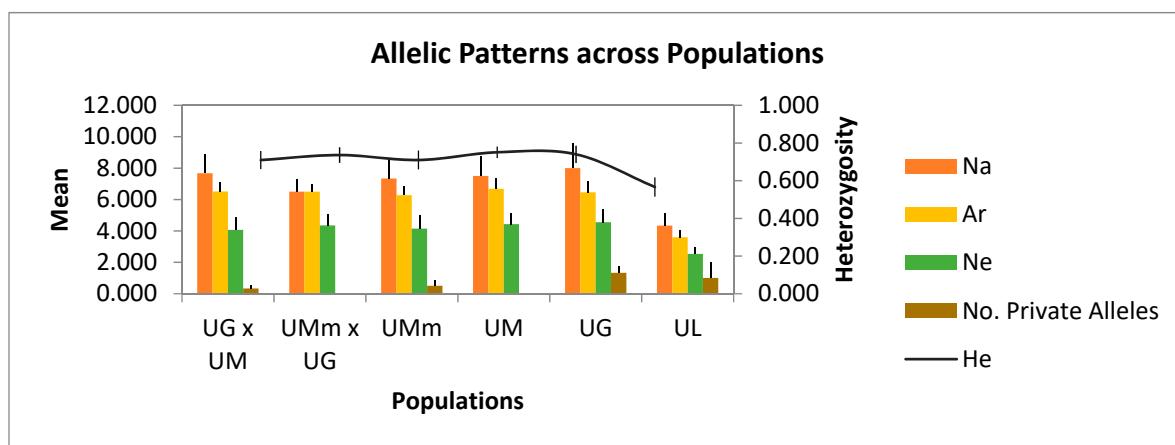


Figure S2. Distribution of genetic diversity among six sampled *Ulmus* spp. groups (Na – Mean no. of Different Alleles; Ne – Mean no. of Effective Alleles; Ar - Mean allelic richness (based on min. sample size of 12 diploid individuals.), Npriv - No. of Private Alleles; He - Expected Heterozygosity) (GenAIEx 6.5 [61]); Populations abbreviations in Table 4.

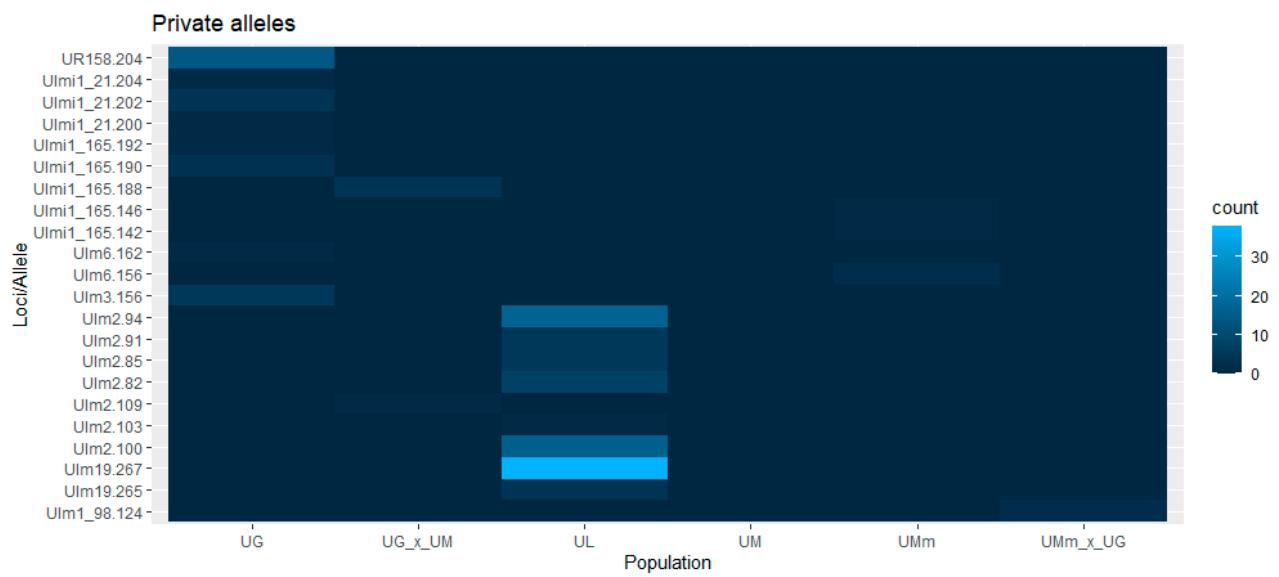


Figure S3. Private alleles distribution among the studied six *Ulmus* spp. groups (133 individuals) (R package *poppr* [62]).

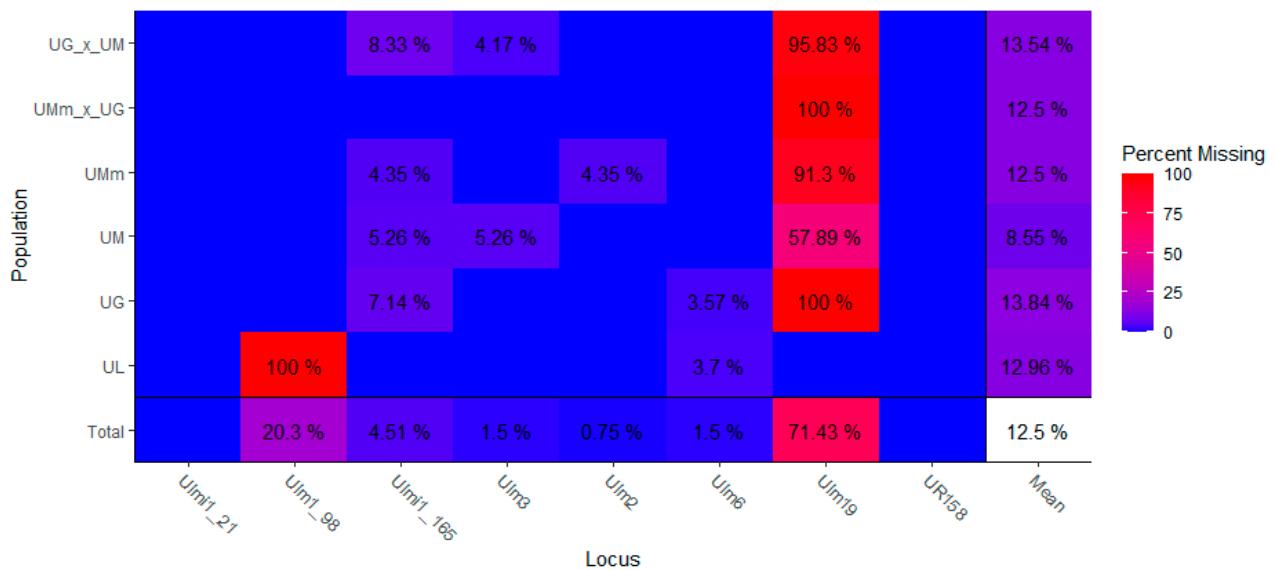


Figure S4. Missing data among six target *Ulmus* spp. groups and among eight nSSR loci (R package *poppr* [62]).

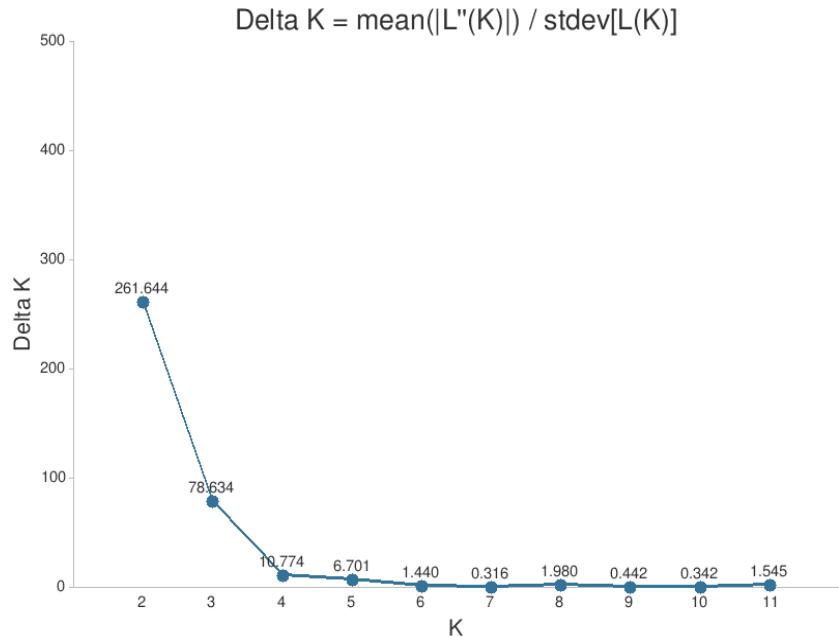


Figure S5. The results of Bayesian clustering (soft. STRUCTURE2.3.4 [67]) on the most likely number of genetic clusters within the studied six *Ulmus* spp. groups, indicated by the highest deltaK value at K = 2 (STRUCTURE HARVESTER soft. [69]).

Table S2. The Evanno table output results of Bayesian clustering (soft. STRUCTURE2.3.4 [67]) on the most likely number of genetic clusters within the studied populations, indicated by the highest deltaK value (STRUCTURE HARVESTER soft. [69]).

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	20	-3098.160	0.5365	-	-	-
2	20	-2747.370	0.7378	350.7900	193.0350	261.64388
3	20	-2589.615	0.7995	157.7550	62.8700	78.634397
4	20	-2494.730	3.2680	94.8850	35.2100	10.774032
5	20	-2435.055	4.5476	59.6750	30.4750	6.701364
6	20	-2405.855	6.9327	29.2000	9.9800	1.439550
7	20	-2386.635	11.0506	19.2200	3.4950	0.316272
8	20	-2363.920	25.0046	22.7150	49.5000	1.979634
9	20	-2390.705	39.7894	-26.7850	17.6050	0.442454
10	20	-2435.095	70.9670	-44.3900	24.2800	0.342131
11	20	-2455.205	41.4600	-20.1100	64.0400	1.544620
12	20	-2539.355	80.3063	-84.1500	-	-

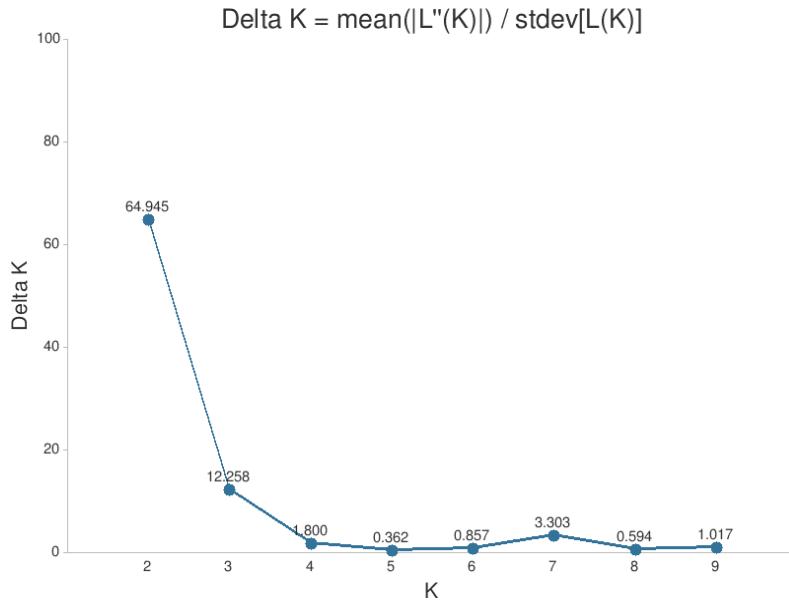


Figure S6. The results of Bayesian clustering (soft. STRUCTURE2.3.4 [67]) on the most likely number of genetic clusters within the studied five *Ulmus* spp. groups (106 individuals), indicated by the highest deltaK value at K = 2 (STRUCTURE HARVESTER soft. [69]).

Table S3. The Evanno table output results of Bayesian clustering (soft. STRUCTURE2.3.4 [67]) on the most likely number of genetic clusters within the studied populations, indicated by the highest deltaK value (STRUCTURE HARVESTER soft. [69]).

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	20	-2341.375	0.4278	-	-	-
2	20	-2193.755	0.8793	147.6200	57.1050	64.945255
3	20	-2103.240	3.6773	90.5150	45.0750	12.257639
4	20	-2057.800	16.3817	45.4400	29.4850	1.799878
5	20	-2041.845	32.1926	15.9550	11.6450	0.361729
6	20	-2014.245	22.2165	27.6000	19.0500	0.857472
7	20	-1967.595	38.7299	46.6500	127.9100	3.302616
8	20	-2048.855	54.3145	-81.2600	32.2500	0.593764
9	20	-2097.865	46.0609	-49.0100	46.8650	1.017458
10	20	-2100.010	53.4699	-2.1450	-	-