

Table 1. 134 individuals from 11 population used in this study

No.	Collection site	Species	Sample size	Population code	Longitude(E °)	Latitude(N °)
1	Changyi District, Jilin City, Jilin Prov.	<i>J. mandshurica</i>	11	JL	126.6193	43.8746
2	National walnut germplasm conservation center(Mt.Tai), Taian City, Shandong Prov.	<i>J. mandshurica</i>	42	TS	117.1509	36.2299
3	National walnut germplasm conservation center (Mt.Culai) , Taian City, Shandong Prov.	<i>J. mandshurica</i>	23	CL	117.2436	36.0467
4	Mt.Meng, Linyi City, Shandong Prov.	<i>J. mandshurica</i>	10	MS	117.9732	35.5642
5	Mt.Yangtian, Weifang City, Shandong Prov.	<i>J. mandshurica</i>	3	YT	118.2892	36.4583
6	Mt.Lu, Zibo City, Shandong Prov.	<i>J. mandshurica</i>	5		118.0550	36.3155
7	Mt.Daze Qingdao City, Shandong Prov.	<i>J. mandshurica</i>	2	LS	120.6256	36.1906
8	Mt.Lao,Qingdao City, Shandong Prov.	<i>J. mandshurica</i>	3		120.0221	37.0061
9	Mt.Kunyu,Yantai City, Shandong Prov.	<i>J. mandshurica</i>	11	KY	121.7426	37.2642
10	Mt.Que, Yantai City, Shandong Prov.	<i>J. mandshurica</i>	8	QS	121.2101	37.1427
11	Mt.Wulian, Rizhao City, Shandong Prov.	<i>J. mandshurica</i>	4	WL	119.4084	35.6921
12	National walnut germplasm conservation center,Taian City, Shandong Prov.	<i>J. regia</i>	3	HT	117.1194	36.2053
13	National walnut germplasm conservation center,Taian City, Shandong Prov.	<i>J. cathayensis</i> <i>var. formosana</i> (Hayata)	9	HDY	117.1192	36.2050

Table 2. Characterization of 9 microsatellite loci used in this study

Locus	Repeats	Primer sequence (5'—3')	Size range (bp)	T _m (°C)
JC5411	(GAT)7	F: AAGCTGTTTGTGCCAAAAGC R: TTCTAGCGAGAATTCCGGCC	300–315	55
JC1151	(AGT)7	F: AAGCTGTTTGTGCCAAAAGC R: TTCTAGCGAGAATTCCGGCC	213–249	53
JC4535	(ATA)7	F: CTTTGCTGGCCTTGTGGTC R: CATCACCCGAGTCCGTTTCA	174–186	53
JC7329	(TGA)8	F: TGCAGCGCATCAGTGAGTTA R: ACGCTCGAGTGATAGCAAG	330–363	55
JC8125	(TCT)7	F: AGCAACCAGAGCAGAGCATT R: AACCTCAACACCAACTATGCT	254–266	55
JC2995	(GA)10	F: AACTGTTGCCGGAGCTTTCT R: TGGGATAACACCACATGCAGT	248–268	55
JC3304	(CT)10	F: CGAAATGACCAAAGGCCAGC R: GCCATTGGTGATGCTGGAAG	270–284	53
JC4833	(GTC)7	F: GAGGAGTTGGTGAAGGAGGC R: CGCAAGGAAGCTAAAACCCA	214–226	53
JC3412	(AAAC)6	F: ACTAACGAACACGCCGGAAT R: CCCCAGAACTTTCCTCGGG	150–162	55

Table 3. Summary of genetic statistics and F-statistic for each locus

Locus	N _a	N _e	PIC	I	H _O	H _E	F _{IS}	F _{ST}	N _m
JC5411	8	2.3084	0.5194	1.1844	0.1045	0.5689	0.7109	0.4040	0.3689
JC1151	9	2.3087	0.5193	1.1742	0.0970	0.5690	0.6451	0.5190	0.2317
JC4535	4	1.3987	0.2621	0.5583	0.1642	0.2861	0.4484	0.3496	0.4651
JC7329	11	3.1893	0.6631	1.6008	0.5970	0.6890	0.1600	0.2543	0.7333
JC8125	9	4.0698	0.7163	1.5993	0.5896	0.7571	0.1849	0.1536	1.3773
JC2995	14	2.564	0.5916	1.5039	0.7313	0.6123	-0.3761	0.1480	1.4389
JC3304	11	2.0493	0.4491	0.9976	0.4776	0.5139	-0.0744	0.2038	0.9768
JC4833	6	2.1564	0.4616	0.9751	0.4701	0.5383	0.0490	0.3208	0.5294
JC3412	5	1.681	0.3806	0.8342	0.3433	0.4066	0.4180	0.2040	0.9755
Mean	8.5556	2.414	0.5070	1.1586	0.3972	0.5490	0.1758	0.2768	0.6532

N_a:number of observed alleles; N_e:effective number of alleles; PIC:polymorphism information content; I:Shannon's information index

H_O:observed heterozygosity; H_E:expected heterozygosity; F_{IS}:inbreeding coefficient;and N_m:gene flow.

Table4. Genetic diversity parameters among the 11 populations of *Juglans* L.

Population	Na	Ne	I	H _O	H _E	N _p	PPL
KY	3.3333	2.1325	0.8210	0.3333	0.4853	0.1111	88.89 %
QS	3.1111	2.1284	0.8472	0.4030	0.5100	0.3332	88.89 %
LS	3.0000	2.1556	0.7732	0.4028	0.5102	0.2222	88.89 %
YT	2.3333	1.7968	0.6129	0.3056	0.4065	0	88.89 %
MS	2.4444	1.6243	0.5266	0.2000	0.3010	0	77.78 %
WL	2.0000	1.7016	0.4873	0.2500	0.3413	0	55.56 %
CL	4.3333	2.1561	0.9018	0.5169	0.5241	0.8892	100%
TS	5.7778	2.2960	1.0207	0.4947	0.5232	0.6671	100%
Mean of Shandong	3.2917	1.9989	0.7488	0.3633	0.4502	0.2779	86.11%
JL	2.7778	1.9386	0.7051	0.3333	0.4367	0	77.78 %
HT	1.7778	1.6413	0.4723	0.1852	0.3852	0	66.67 %
HDY	2.3333	1.7437	0.5077	0.2593	0.3057	0.3333	55.56 %

Na: number of observed alleles; Ne: effective number of alleles; N_p: number of private alleles; H_O: observed heterozygosity; H_E: expected heterozygosity; I: Shannon's information index; PPL: percentage of polymorphic loci.

Table 5. Nei's genetic identity (above diagonal) and genetic distance (below diagonal) among the 11 populations of *Juglans* L. based on 9 EST-SSR loci

Population	HT	HDY	JL	CL	TS	YT	MS	LS	WL	QS	KY
HT	****	0.2606	0.3331	0.2862	0.2852	0.3428	0.3090	0.3562	0.3321	0.2839	0.3374
HDY	1.3449	****	0.6531	0.6177	0.6300	0.5914	0.7481	0.7066	0.6194	0.7132	0.6866
JL	1.0993	0.4260	****	0.8523	0.8582	0.8601	0.8724	0.8586	0.8406	0.8831	0.8798
CL	1.2509	0.4817	0.1598	****	0.9574	0.9061	0.7940	0.7878	0.8749	0.7551	0.8220
TS	1.2544	0.4621	0.1530	0.0435	****	0.9341	0.7905	0.7779	0.8988	0.7551	0.8570
YT	1.0706	0.5253	0.1507	0.0987	0.0682	****	0.7787	0.7857	0.9539	0.7165	0.8807
MS	1.1744	0.2902	0.1365	0.2306	0.2351	0.2501	****	0.9329	0.767	0.8888	0.9073
LS	1.0324	0.3473	0.1524	0.2385	0.2511	0.2411	0.0695	****	0.7753	0.8901	0.9077
WL	1.1024	0.4790	0.1672	0.1337	0.1067	0.0472	0.2652	0.2545	****	0.6931	0.8653
QS	1.2591	0.3381	0.1243	0.2809	0.2809	0.3334	0.1179	0.1164	0.3666	****	0.8745
KY	1.0864	0.3760	0.1281	0.1960	0.1543	0.1271	0.0973	0.0968	0.1446	0.1341	****

Table 6. Pairwise comparisons of N_m (above the diagonal) and F_{ST} (below the diagonal) for 11 populations of *Juglans* L.

Population	TS	CL	MS	YT	WL	LS	KY	QS
TS	****	12.463	1.604	5.395	2.858	1.950	3.254	2.017
CL	0.020	****	1.476	3.693	2.075	1.878	2.461	1.891
MS	0.135	0.145	****	1.265	1.069	4.229	3.094	2.654
YT	0.044	0.063	0.165	****	4.344	1.658	2.732	1.396
WL	0.080	0.108	0.190	0.054	****	1.246	1.870	1.032
LS	0.114	0.117	0.056	0.131	0.167	****	4.011	3.503
KY	0.071	0.092	0.075	0.084	0.118	0.059	****	3.912
QS	0.110	0.117	0.086	0.152	0.195	0.067	0.060	****

table 7. Analysis of molecular variance for 8 populations of *J. mandshurica* of Shandong Prov.

Source of variation	Degrees of freedom	Sum of squares	Variance component	Percentage of variation (%)
Among populations	7	63.006	0.263	11%
Within populations	214	465.724	2.187	89%
Total	221	528.730	2.450	100%