Genetic evaluation of the breeding population of a valuable reforestation conifer *Platycladus orientalis* (Cupressaceae)

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Supplementary Table S1. Characteristics of 87 polymorphic and monomorphic EST-SSR loci developed for *P. orientalis.*

Locus	Primer sequence (5'-3')	Repeat motif	Allele size (bp)	Functional annotation	Tm (°C)	HW
Po53	F: GTCGGGAGTTCTTGAACGAG	$(AG)_8$	186	no hit	54	ns
	R: AAACTCTCATCCCTTCTTGGG					
Po57	F: ATGGCTTTATTGCATCCGTC	$(AC)_7$	213	no hit	54	ns
	R: ACAGAACATAGCATTAAACACCCA					
Po73	F: TTGTGTCCCAGTTCAGTGGA	$(AT)_8$	284	no hit	54	ns
	R: ATAACTGGCCATCCAGCATC					
Po75	F: TGAAGCTTTCTTGAGGTAAGGG	$(AC)_8$	142	no hit	54	*
	R: TGAAGAGGCATAATACCGGG					
jc52	F: TCAATTGTCATGGGTCTAGGAA	$(AG)_6$	213	no hit	54	*
	R: GGTATCAAAGAACTTGGTGCTTG					
jc38	F: CGATGGCATCTTTGACCAAT	$(AAAG)_5$	289	no hit	54	**
	R: TTTCTTTGAAGTGTGATCGGG					
Po45	F: GCCTAACCGGAGGTATAGTTTG	$(AG)_9$	103	no hit	54	ns
	R: CACTGCGTGGAAAGACTTCA					
jc89	F: ATCCGGCCAAATAACACAAC	$(AC)_5$	230	no hit	54	ns
	R: TGAGCCTCCTTCTTTCTTGC					
jc90	F: GCTCGGCTTCTGAAGGACT	$(AAG)_5$	332	no hit	54	ns
	R: CACCTTCTGCCATCCCTTTA					
jc10	F: TTCTGTGTCACCTCTGTGGC	$(AG)_5$	146	PMT	54	ns
	R: GACGACAAGGAGTGGTGGTT					
jc20	F: GCATTCATGGACACATACAAGC	$(AC)_5$	236	no hit	54	ns
	R: TGAACAAATGAAGGCATGGA					
jc69	F: AGGACATTGAGAAGGCAACC	$(AG)_5$	297	no hit	54	*
	R: TATGCCCAAGGTAAAGGAGC					
Po165	F: CCGACACAAACTGTGTGCTT	$(AG)_5$	170	Gp37_Gp68	54	ns
	R: AATGGCAGAATGACAATCCC					
Po156	F: CCCAGAACCTCAAACCTTCC	$(AG)_5$	187	no hit	54	**
	R: TTCCGCTATACAACAATACGACA					

Po103	F: TGGCATAACCTACTTGCATCC R: CTGTAAATGATAAATTAGGAAAGCTG	$(AT)_8$	275	no hit	54	*
Po182	F: TCTTGCTCTCAAACCATCCC R: CCCATCATTCCCAATACCAA	$(AAG)_5$	191	DEC-1_N	54	ns
Po161	F: AATTTGTGCGCTTGAGCTTT R: TGTGGCTTTAATCTGAGCTTG	$(AG)_5$	118	p450	54	ns
Po171	F: CTCACTTCCTGCCATAAGCC R: CAAGTTGAACAGCCTCAGCA	$(AAAC)_5$	184	Mmp37	54	ns
Po159	F: TCCCGATAGTAAAGGAGCCC R: TGTTTAGCGTCAGAAGAAGCAA	$(AT)_6$	200	no hit	54	ns
Po107	F: TGAGAGTAACAGCAGCAGGG R: TAGGCCATTGTTTGAGATGG	$(AC)_5$	160	no hit	54	*
Po108	F: ATCATTCTCACTTGTGTCCAGC R: GGGAAGAGGCTAACTTCGCA	$(AG)_5$	244	no hit	54	ns
Po145	F: AAAGCAAGCATGAGAACCAA R: TCTCCCTCACTCCATCTTCC	$(AG)_5$	182	no hit	54	**
Po114	F: CTCCTGGATATTTATGCAATCG R: TATTGCCTTGTGGTGAGTCG	$(AT)_5$	153	no hit	54	ns
Po152	F: AGATGGAAAGGATATTCCCAGA R: ACATCTTCTCCCGACTTCCA	$(AAG)_5$	139	no hit	54	ns
Po135	F: GCTTCGAATTTGCTAGCCC R: GCTCAAATCAGTTATCCTTGCAG	$(AT)_5$	190	no hit	54	ns
Po173	F: TTGAAGGAATGATCAAGGCTG R: CAGACAAAGAACCACCACCA	$(AAC)_5$	161	no hit	54	ns
Po180	F: CCCTTTCTCTGAGCAAACCA R: GGACTGGAGCTATTTGCCTG	$(AGC)_6$	126	no hit	54	ns
jc1	F: AAAGTTCCATATCTGGCGGA R: TGGTATTCTTGGTATTCTTCTTCG	AAG	281	—	59	Monomorphic
jc14	F: TGAGTAGATGAGTGCGGGTG R: GGTTCTCACCATCTTCGAGC	AG	292	—	59	Monomorphic
jc15	F: AGCAGACATCGATGAAGGTTT	AC	284	—	59	Monomorphic

	R: GCCAATAAATTGCATCTCCC					
jc25	F: GTGCATGACCTCATTGATCG	AC	161	—	59	Monomorphic
	R: ACTCATTGTTTGGGCTTTGG					
jc26	F: CTCCACCGATCAGATCAAGC	CG	244	—	59	Monomorphic
	R: GGGAGAACCCTAAGGCCC					
jc27	F: GTCCATTGAGTGTTGAACCAAG	AT	255	—	59	Monomorphic
	R: GGTAGCTATGCCTCCAACCA					
jc30	F: TGCAAACAATTTGGTAACGG	AG	246	—	59	Monomorphic
	R: TGATACTTGGGAGAACTTGGG					
jc37	F: CGAGGATATTGCAGACGGAT	AG	299	—	59	Monomorphic
	R: TTCCACCAGGAGTAGCCTTC					
jc40	F: CACAATGATCTCCTTTCATTTCC	AT	170	—	59	Monomorphic
	R: AGGTAACTACAAGATCGCGAGG					
jc44	F: TGGTTTCCCTTGAGTGCTTT	AG	294	—	59	Monomorphic
	R: CCATTGTTGAAGATTTAATTGGTG					
jc46	F: ATCCAAATGCGTTGTTCCAT	AC	274	—	60	Monomorphic
	R: CCAGAGCAGCTGTAGGCAAT					
jc49	F: GATGATTGATTACCCAAAGCAA	AAG	242	—	59	Monomorphic
	R: TTGGAGGATATGTGGAGGAAA					
jc53	F: GCTGATTGGATCTCAAGCCT	AG	185	—	59	Monomorphic
	R: GGGTATTGAGTGCATGGAGG					
jc64	F: AATTGGGAAAGCCTCAAAGC	AC	171	—	59	Monomorphic
	R: TTGCATCCAAATAATCCCTTG					
jc65	F: TGAAACTTTCTTGAGACCTCCC	AG	250	—	59	Monomorphic
	R: GTTGTTACTGCCTCTTGCCC					
jc76	F: GCACTTGAATTGAAGCCACA	AAG	282	—	59	Monomorphic
	R: CAACACCCTCAACACCACC					
jc80	F: CCAGAAACTCCTTCAGTACCTCA	AT	299	—	59	Monomorphic
	R: ATGGAGAATGGAGGATGTGC					
jc82	F: TTGTCATGGAGAACTTGGGAG	AT	292	—	60	Monomorphic
	R: TCCAACCCATCAGACTATCCA					

jc84	F: ATTTCACTGCTCTGTGGAGGA R: AATAAGGCCAATGCTGATTCAT	AAT	341	—	59	Monomorphic
jc91	F: CTCATTCCAAGGCTCCAGAA R: GCTCAGAAACCTCTCACCCA	AG	327	—	60	Monomorphic
Po6	F: TTCCAGTAATGATCCGTGGAG R: CGTGGCAATACAAGACACAAA	AC	170	—	59	Monomorphic
Po17	F: GCGTTTGGATGTAAACTTGGA R: AGAACCTGAGTTCGTGTGGG	AG	113	—	59	Monomorphic
Po52	F: GTGAATCTTGCATCAGCAGC R: TTCACATGAAAGAGGCATGG	AT	229	—	59	Monomorphic
Po62	F: TGCCTTATGGTAAAGAACCCA R: TGTTGACATCTCAGGCTCAAA	AT	212	—	59	Monomorphic
Po80	F: GCTGTGTTTCGCTTTACCGT R: ACAGGAGTCAAGATCAGTGAAGG	AT	269	—	59	Monomorphic
Po87	F: GAGCAGTGGTACTGATTCCTTT R: GTAAACCCGTTCATGTGCCT	AT	249	—	58	Monomorphic
Po30	F: GAGTTTATTGCCTCCCACAAA R: ATTACGCATGCCCACAATTT	AG	126	—	59	Monomorphic
Po38	F: ATCTCACCCGATCAAAGCTC R: ATTGTGTAGCGTTACCAAGGG	AT	194	—	59	Monomorphic
Po78	F: CTTATGCTTTACCTAACCATGCG R: CAATCCTTTACTTGTAAGCGGC	AT	240	—	60	Monomorphic
Po68	F: AAATGCATTCAAACCAAGCC R: AAGACGAAGACTCTGGTGCAG	AT	216	—	59	Monomorphic
Po101	F: CCCTCCCTCCTCATATAATCTC R: AGGTAGACATAGAGAATGAATTCAAGA	AG	336	—	58	Monomorphic
Po104	F: AATAGGTTGGTGGTTGGTCG R: GGCATAGCACCTCTAGCCC	AT	139	—	59	Monomorphic
Po109	F: GGTCTACTGCTATCCTTCACCC R: ACAATGAGAAAGGTCCGCAT	AG	217	—	59	Monomorphic
Po113	F: GTTGATTTGCGGCTCAGG	AAC	118	—	60	Monomorphic

	R: CTCATCAAGTCCTCCCTCCA					
Po117	F: GTAGCAGGTAGCGCGGGT	ACT	191	—	59	Monomorphic
	R: CCTCGACTCTCGTCTTCGAC					
Po162	F: GCCCTTTAAACCCAATGCTT	CCG	133	—	60	Monomorphic
	R: CGGCGGAGTAAAGTGGTG					
Po166	F: GAGCAATCCACACCACCTTC	AAC	167	—	59	Monomorphic
	R: TGGATCATTGGTCTTCCCTT					
Po168	F: GGATCATGGGAGAATCGAGA	AC	125	—	59	Monomorphic
	R: TGCACTACTCCTTCGGTGG					
Po177	F: GTTGGCTGTATTGGGTTTGG	AGG	225	—	59	Monomorphic
	R: CAGCACTCAACTGATCGGAA					
Po178	F: AAGAAATGCCCTCTCAACGA	ATC	204	—	59	Monomorphic
	R: GGTTTGAAGTGTATGGCGGA					
Po184	F: TTCTCTCCCTCCACAACCAA	AG	140	—	59	Monomorphic
	R: CTCACATGCTGCTGTGGTTT					
Po185	F: CTTTCAGTCGCTCCTGCTTC	AT	139	—	60	Monomorphic
	R: CGGTTCCGTTTCATTAGCAT					
Po186	F: TTTGGAGAGTTTCTGGGCTG	AC	192	—	60	Monomorphic
	R: CTTCCCTACACTGCACCTGG					
Po189	F: TGTTTCCATCCTACCCTTGC	AG	126	—	60	Monomorphic
	R: CATTGGCTTTCCTACCTGGA					
Po138	F: GATTCTATGACGACAGCGGC	AG	115	—	60	Monomorphic
	R: TGATGGGTGGTATGATTCTCG					
Po140	F: CTTCTTGGTGATGTCAGAGGG	AAG	185	—	59	Monomorphic
	R: GAAGGAAGAGGAAGCCAAGG					
Po141	F: GAATTCAAGGAACCATGGGA	AG	181	—	59	Monomorphic
	R: TCCAATGTTGACCAAAGAAGG					
Po142	F: CCCAACTATCTCCAGCTTCG	AT	224	—	59	Monomorphic
	R: ATTAGTTGTGGTGGCAGGCT					
Po143	F: TAGCCTTTGGGCTTATCTGC	AG	239	—	59	Monomorphic
	R: AAAGCATCTTCCCTGTGAGC					

Po146	F: CTCCGTATACAAGTGGCGGT R: TTGCATCCGTTAGTATTCCAAA	AG	127	—	59	Monomorphic
Po147	F: ATGGCATCCTCCTCTTTCCT R: GAAAGGCCACAAAGAAACCA	AG	239	—	60	Monomorphic
Po148	F: GTTCTTTCCTACCAGCGCC R: CAGACCCAGAAATTGTTTCCA	AT	187	—	59	Monomorphic
Po150	F: AGTTCAGATTTGTCCAACACGA R: CGCAATTGTAAGGGTTCCAG	AC	153	—	59	Monomorphic
Po151	F: TTCCCAATCCGTAATACCCA R: AATGCAACCAGGAAGTAGGG	AG	177	—	59	Monomorphic
Po153	F: ATCCGACGACCTTCTGAGC R: AACACGCTTGACTTCCCTTG	AGG	178	—	60	Monomorphic
Po154	F: ATTGCTTCCGTACAAGGCAC R: TGAGAGGCTCACAAGTTACCG	AT	164	—	60	Monomorphic
Po155	F: GGATTGTTTGGTTTCATTTGC R: ACCAAGTTGCTAGAGACGCC	AG	170	—	59	Monomorphic
Po157	F: TATCCCGGAGAACAAATTGC R: CAAGTGACCATGAGTGGAGC	AG	176	—	59	Monomorphic
Po158	F: AAAGAAAGCGAAGAGAGGGC R: CAGTGTGCTTCTTCTGCCTG	AG	173	—	59	Monomorphic
Po102	F: TCTCATAAAGGTACAATGCATACACA R: TACAGCAGCGTAGTCCCATC	AT	350	—	59	Monomorphic

The locus names with "Po" indicate the locus developed from the transcriptome assembly of *P. orientalis*; the locus names with "jc" indicate the locus developed from the draft genome assembly of *Juniperus communis*. Protein family annotation are prepared by querying the protein family database, Pfam[1]; HW: ns = not significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

1 RD, F. *et al.* The Pfam protein families database. *Nucleic Acids Research* 28, 263-266(264) (2000).

Supplementary Table S2. Results of bottleneck test in the 3 populations under IAM and SMM models.

Population	IAM	SMM
North	0.784	0.997
Southwest	0.278	0.839
East	**0.014**	0.326

IAM: infinite allele model; SMM: stepwise mutation model. The significant value was indicated in bold type.

Supplementary Table S3. Origins of the *P. orientalis* samples.

Population	Forest stands	Sample Size	Longitude (E)	Latitude (N)	Accessions
North	Linxian, Huixian, Weihui, Huojia, Boai, Jiyuan	136	113.51º	35.42º	54-69, 71-73, 76-86, 89-95, 97-124, 126, 131, 133-151, 153-161, 163-165, 189, 190, 193, 196, 198-200, 215, 232, 43, 245, 246, 248, 250-253, 274, 275
East	Jiaxian, Xiangxian, Wugang, Leshanlinchang, Biyang	21	113.43º	33.33º	1, 3-11, 18, 20-25, 174, 177, 206, 209
Southwest	Yiyang, Luoning, Luanchuan, Luoyang, Longmen, Linru	35	112.17º	34.36º	13-17, 26, 27, 29, 30, 32-36, 39-45, 47-53, 178, 180, 181, 188, 192, 202, 212

Supplementary Data S1

>Po53

AGGGTGTATTTGTTACAGTTCAATAATTTGCCATAGAGAAGAACCAATTCGTTTGAGGATAGAGTGTGCTCCCTATATTCATCTATAGGAGGATG
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>Po57

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>Po73

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>Po75

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>Jc52

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>Po103
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>Po182
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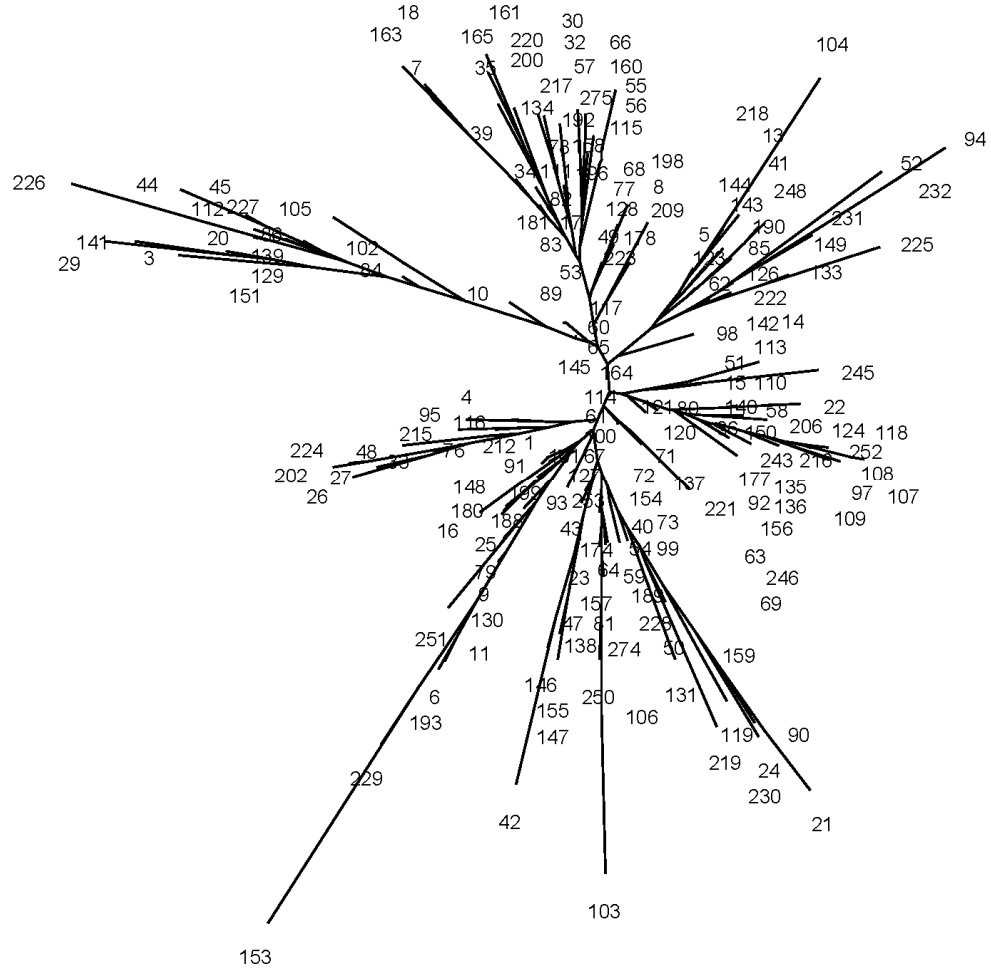
Supplementary Figure S1. Neighbour joining tree.



Phlylogenetic relationship of *P. orientalis* individuals.