Table 1S. Nucleotide sequences of the SSR primers, allele size range for two ginseng species *Panax vietnamensis* and *P. stipuleanatus.* F - forward primer; R - reverse primer; T_m - annealing temperature.

Locus	Nucleotide sequences (5'-3')	Repeat motif	T_m [°C]	PCR product length [bp]
PG281	F: AAACTCTCTTCTAGTCTTCTTGCC R: GTAGGTATACATACATGTACGGAA	$(CTAT)_{12}$	57	201
PG167	F: CTGAGAGTAGAGGCGAGGCTG R: TCATTTCTCAGCCACCTGGCGT	$(TGG)_5$	52	166
PG424	F: GTACGGAAGGATGGAAGAGGAG R: CCCTCCTCTGTCAATAAGTTAAA	$(TC)_{16}$	55	241
PG186	F: ATGCTCGGACTCAGTCCAATCA R: TACCACTATTCTCCATCTCTCAC	$(GGA)_7$	52	294
PG352	F: GTCGTTAATCGCTAGGTAGGCT R: TTGTCTCCTCTTGTTTAGCGCAC	$(TA)_7(TG)_8$	56	113
HPG132	F: CACTCAGCTTTTCCTTCTCAAGG R: ACTGAAAGTTAATAGAAATGCTTC	(TTG)7	56	231
PG450	F: GATCTTCTGGATGATTTCGACAT R: TTGCCCACCCCTTTCTCCACC	$(GA)_{13}$	52	172
HPG126	F: TGGAACCATCTGGGAAGAGGAA R: GTGGATAGATGCCTCGCCAGG	$(CA)_{10}$	55	159

Table 2S. Genetic parameters of the eight SSR loci for two gingseng species. N_A - number of alleles; N_R - allelic richness; N_E - effective alleles; N_P - private alleles; H_O and H_E - observed and expected heterozygosity; H_T - total expected heterozygosity; F_{IS} - fixation index; Null allele the average null allele frequency, F_{IT} - coefficient of total inbreeding; F_{ST} - genetic differentiation index of Weir and Cockerham (1984); P_{HWE} - *P* value test for Hardy-Weinberg equilibrium; ns - no significant; nd - not determined; * - $P<0.05$, ** - $P<0.01$.

Loci	N_A	N_R	N_E	*Null allele*	N_P	H_O	H_E	H_T	F_{IS}	F_{IT}	F_{ST}	P_{HWE}
P. vietnamensis												
PG281	4	3	1.9	0.157	2	0.346	0.466	0.526	0.257	0.342	0.114	**
PG167	5	4.1	1.7	0.104	2	0.323	0.403	0.421	0.198	0.233	0.043	ns
PG424	4	2.5	1.6	no	2	0.314	0.351	0.362	0.105	0.135	0.033	ns
PG186	3	2.9	1.4	no	-	0.301	0.249	0.267	-0.208	-0.127	0.067	nd
PG352	5	3.5	1.8	0.134	2	0.320	0.413	0.446	0.226	0.284	0.075	*
HPG132	3	3.0	1.8	no	-	0.436	0.419	0.459	-0.043	0.048	0.087	ns
PG450	3	3.0	2.1	no	-	0.533	0.51	0.544	-0.044	0.021	0.063	ns
HPG126	4	2.5	1.4	0.129	2	0.188	0.276	0.279	0.317	0.325	0.011	nd
Mean		3.1	1.7			0.345	0.386	0.413	0.101	0.158	0.062	
P. stipuleanatus												
PG281	3	2.7	1.4	no	1	0.237	0.250	0.266	0.054	0.111	0.061	nd
PG167	4	3.8	2.2	0.137	-	0.454	0.518	0.622	0.124	0.269	0.166	**
PG424	3	2.9	1.9	0.133	-	0.367	0.431	0.515	0.149	0.287	0.162	*
PG186	4	2.5	1.2	no	1	0.141	0.140	0.145	-0.003	0.030	0.032	nd
HPG126	3	2.6	1.4	no	-	0.283	0.278	0.299	-0.017	0.054	0.070	nd
PG352	5	3.9	1.7	no	1	0.414	0.377	0.413	-0.098	-0.002	0.087	ns
HPG132	3	3.0	1.4	0.107	-	0.224	0.248	0.285	0.097	0.215	0.131	nd
PG450	3	3.0	2.1	0.111	-	0.390	0.492	0.525	0.208	0.259	0.064	ns
Mean			1.7			0.316	0.346	0384.	0.064	0.153	0.097	

Table 3S. Pairwise genetic differentiation (F_{ST}) between populations for two gingseng species. * - *P<0.05,* ** - *P<0.01,* *** - *P<0.001.*

P. vietnamensis

Populations	Nam Tra My	Tu Mo Rong	Dak Glei
Tu Mo Rong	0.023*		
Dak Glei	0.022*	0.007	
Phuoc Loc	0.082***	0.075***	0.077***

P. stipuleanatus

Populations	Lao Chai	Ban Giang	Muong Nhe	Muong Hum
Ban Giang	0.124***			
Muong Nhe	0.147***	0.041**		
Muong Hum	0.09***	0.064***	0.062***	
Nam Dom	0.046***	0.028*	0.058***	0.06***

Table 4S. Number of individuals for each population assigned to a cluster.

Populations	Cluster 1	Cluster 2	Cluster 3
P. vietnamensis			
Nam Tra My	3	9	16
Tu Mo Rong	4	12	11
Dak Glei	3	14	13
Phuoc Loc	21	2	4
P. stipuleanatus			
Lao Chai	3	0	23
Ban Giang	2	13	11
Muong Nhe	10	13	2
Muong Hum	14	10	4
Nam Dom	3	7	19

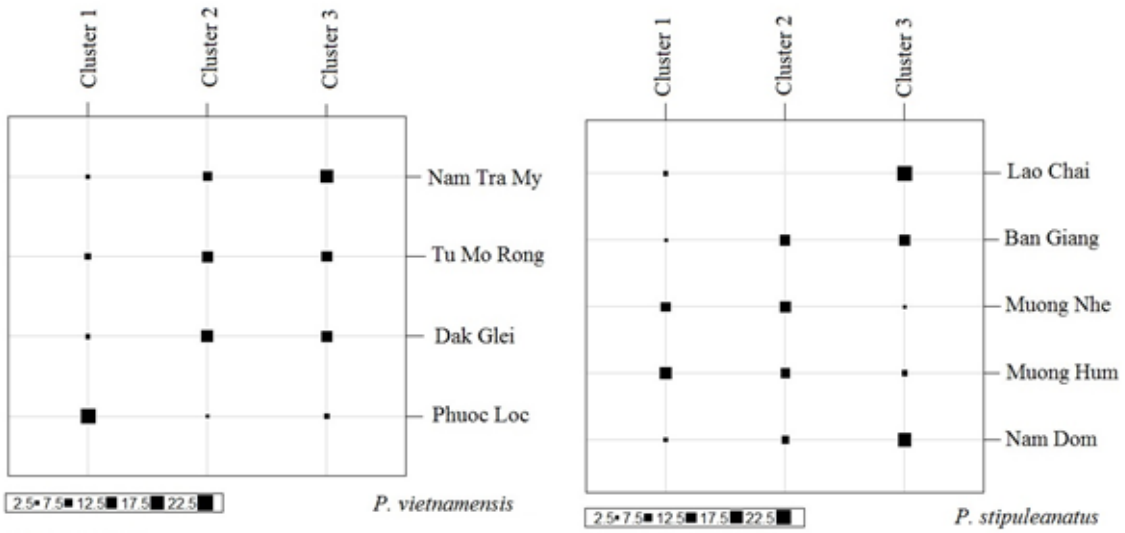

Fig. 1S. Number of individuals for each population (*rows*) assigned to each of the three inferred genetic clusters (*columns*) using *DAPC* without prior information.