Table S1 Frequency and diversities of cpSSR haplotypes within *Nothotsuga longibracteata* groups.

	Numbers of each haplotype														
Group	h1	h2	h3	h4	h5	h6	h7	h8	h9	h10	h11	h12	h13	N*	H_e
DY	6	0	13	2	0	0	0	0	1	0	33	9	0	7	0.271
NL	1	1	19	0	28	2	21	1	0	0	23	0	0	8	0.348
JXS	0	0	0	0	0	0	0	0	0	0	32	0	0	1	0.000
HNQ	0	0	0	0	0	0	0	0	0	0	32	0	0	1	0.000
HNH	0	0	0	0	0	0	0	0	0	0	26	0	0	1	0.000
GZF	0	1	0	0	1	0	0	0	1	1	26	2	0	6	0.157
GXM	0	0	0	0	2	0	0	0	0	0	23	3	4	4	0.174
Total	7	2	32	2	31	2	21	1	2	1	195	14	4		
Mean	1.0	0.3	4.6	0.3	4.4	0.3	3.0	0.1	0.3	0.1	27.9	2.0	0.6	4	0.136

N*, Number of different haplotypes; *H*e, haplotype diversity.

Table S2 Haplotypes and their distribution in populations of cpSSRs.

Haplotype	cpSSR locus			Groups
□	Pt15169	Pt63718	Pt71936	□
h1	139	99	153	DY, NL
h2	140	100	153	NL, GZF
h3	140	99	153	DY, NL
h4	140	99	154	DY
h5	141	100	153	NL, GZF, GXM
h6	141	100	154	NL
h7	141	101	153	NL
h8	141	102	153	NL
h9	141	98	153	DY, GZF
h10	141	98	154	GZF
h11	141	99	153	DY, NL, JXS, HNQ, HNH, GZF, GXM
h12	141	99	154	DY, GZF, GXM
h13	142	99	153	GXM

Geographical group NL (NanLing) consisted of populations HNZ, HNG and GDL; Group DY (Daiyun) consisted of populations FJM and FJT.

Table S3 Genetic differentiation (F_{ST}) between age classes of three populations estimated using the infinite alleles model.

		I	II	III	IV	V
FJM	II	0.032***				
	III	0.03***	0.001ns			
	IV	0.032***	0.007ns	0.006ns		
	V	0.016*	0.012ns	0.007ns	0.008ns	
	VI	0.018*	0.024**	0.005ns	0.036***	0.004ns
FJT	II	0.041*				
	III	0.037**	0.022***			
	IV	0.04*	0.026**	0.008ns		
	V	0.049*	0.009ns	0.009ns	0.016ns	
HNZ	II	0.008*				

One asterisk " *" indicates $P < 0.05$, two asterisks "**" indicate $P < 0.01$, three asterisks "***" indicate $P < 0.001$, and non-significant is indicated by "ns" .