



Correction to: Genetic structure and diversity in relation to the recently reduced population size of the rare conifer, *Pseudotsuga japonica*, endemic to Japan

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In the original publication, Table 3 was published with incorrect F_{IS} values for three populations Kawamata-kannonn, Ootousan and Senbonyama. The updated Table 3 with correct F_{IS} values are provided in this Correction.

The original article can be found online at <https://doi.org/10.1007/s10592-018-1092-5>.

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Table 3 Measurements of genetic diversity based on six SSR loci in seven populations of *Pseudotsuga japonica*

Region	Population	Code	N	A	A_p	RA^a	A_R	H_O	H_E	F_{IS}
Kii Peninsula	Sannokou	K-SAN	66	7.333	7	18	6.263	0.657	0.647	−0.011
	Oomata	K-OMA	90	5.333	2	12	4.669	0.547	0.538	−0.017
	Kawamatakannon	K-KAW	101	6.833	6	15	5.785	0.564	0.566	0.004
	Ootousan	K-OTO	55	6.667	4	14	5.939	0.647	0.655	0.012
Shikoku Island	Senbonnyama	S-SEN	30	5.167	3	10	5.167	0.467	0.472	0.011
	Yasudagawayama	S-YAS	59	5.333	3	10	4.791	0.558	0.548	−0.020
	Nishinokou	S-NIS	50	5.333	4	9	5.110	0.582	0.552	−0.054

N number of samples, A average number of alleles per locus, A_p number of private alleles, RA number of rare alleles, A_R allelic richness, H_O average observed heterozygosity, H_E average expected heterozygosity, F_{IS} fixation indices

^aRare alleles correspond to a frequency < 0.05