

**Table S8:** Demographic parameters obtained by DIYABC analysis<sup>1</sup> of *Dipterocarpus turbinatus*. N1, N2, N3 and NA is effective population sizes of the corresponding populations CET, HIL, SOE and the ancestral population;  $\mu_{mic}$ , the mean mutation rate of SSR;  $p_{mic}$ , the mean distribution of the number of repeats of microsatellites;  $sn_{mic}$ , the mean rate of single nucleotide insertions/deletions; relative median absolute error values based on 500 psedo-observed datasets.

Parameter	Mean	Median	Mode	Quantile 2.5%	Quantile 5%	Quantile 25%	Quantile 75%	Quantile 95%	Quantile 97.5%	Relative median absolute errors
N1	1530	1080	686	174	232	639	1800	4560	6300	0.327
N2	4120	3580	1480	260	473	1830	6160	9150	9560	0.434
N3	1850	1360	728	258	349	814	2230	5380	6900	0.289
NA	5290	5360	9310	323	594	2960	7830	9550	9720	0.527
$t_1$	510	349	124	20.2	40.3	157	651	1490	2040	0.385
$t_2$	2630	2080	1190	400	519	1210	3480	6760	7820	0.253
$t_3$	6010	6440	9480	510	865	3840	8440	9700	9880	0.573
$\mu_{mic}$	1.59e-004	1.29e-004	1.00e-004	1.00e-004	1.00e-004	1.09e-004	1.76e-004	3.14e-004	4.01e-004	0.261
$p_{mic}$	0.258	0.268	0.3	0.151	0.177	0.238	0.29	0.3	0.3	0.223
$sn_{mic}$	6.18e-007	1.19e-007	1.00e-008	1.00e-008	1.06e-008	1.77e-008	5.67e-007	3.04e-006	4.76e-006	0.931

<sup>1</sup> Cornuet J.M., Pudlo P., Veyssier, J., Dehne-Garcia A., Gautier M., Leblois R., Marin J-M., Estoup A. (2014) DIYABC v.2.0: a software to make approximate Bayesian computation inferences about population history using single nucleotide polymorphism, DNA sequence and microsatellite data. *Bioinformatics* 30:1187-1189. doi: 10.1093/bioinformatics/btt763