Table S3. Prior distributions of the parameters for simulated scenarios in DIYABC analysis[1] of *Dipterocarpus turbinatus.* A uniform distribution was applied for all parameters. N1, N2, N3 and *NA* is effective population sizes of the corresponding populations CET, HIL, SOE and the ancestral population

Parameter	Minimum	Maximum
Effective population size		
N1	10	10000
N2	10	10000
N3	10	10000
NA	10	10000
Time scale in generations		
$t1$	1	10000
$t2$	1	10000
$t3$	1	10000
db	1	10000
Admixture		
ra	0.001	0.999
Mutation model		
Mean mutation rate	1.00e-004	1.00e-003
Individual locus mutation rate	1.00e-005	1.00e-002
Mean coefficient P	1.00e-001	3.00e-001
Individual locus coefficient P	1.00e-002	9.00e001
Mean SNI rate	1.00e-008	1.00e-004
Individual locus SNI rate	1.00e-009	1.00e-003

[1] Cornuet JM, 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