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Phylogenetic study of some major Dendrobium species of Eastern Himalaya using internal transcribed spacer marker

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Supplementary Material

Supplementary Table 1: Patterns of nucleotide substitution, relative utility, and evolutionary history were calculated for both ITS regions using different algorithms of MEGA 11.		
Parameters	**Informative Readings**	**Data acquisition method/ model/ Algorithm**
DNA region	ITS-I-5.8S-ITS-II	Sequencing (Sanger method)
Range of bases in all samples	623- 644	Sequence statistics data
Average number of base	637.7	
Number of variable (Polymorphic) site	403	
Number of Invariable (Monomorphic/ Conserved) site	223	
Number of informative (Parsimony) sites	337	
Number of substitution	173	
Mean no of substitution /site	0.27	
Mean no of substitution /Informative site	0.51	
0-fold degenerate site	365	
Number of Single-ton sites	91	
Average GC% (ITS1 to ITS2)	52.82	Composition distance model
Average Transition (S) with SE in bracket	0.13 (0.01)	Distance measurement
Average Transversion (V) with SE in bracket	0.08 (0.01)	
S/V ratio	1.63	

Average Evolutionary Divergence (d) with SE in bracket	0.16 (0.02)	
Overall composition distance	0.32	
Percentage of A	23.7	Nucleotide substitution MCL model
Percentage of T	23.48	
Percentage of G	29.11	
Percentage of C	23.71	
Transition/ Transversion purine (K_1)	1.982	
Transition and Transversion pyrimidine (K_2)	4.008	
Transition and Transversion bias (R)	1.444	
Highest Log-likelihood (ML)	-8102.528	Maximum Likelihood Estimation method of Substitution
Range of Disparity Index (Mean)	0.00 to 1.89 (0.192)	Monte Carlo test for homogeneity
Tree length	1428	Maximum Parsimony analysis method
Mean Consistency index (parsimony-informative site)	0.5028 (0.4571)	
Mean Retention index (parsimony-informative site)	0.6545 (0.6545)	
Mean Composite index (parsimony-informative site)	0.3290 (0.2992)	
Synonymous (d_S) and nonsynonymous (d_N) d_N/d_S ratio (p-value)	-0.33 (0.74)	Z test for selection