

Supplementary Data

Table S1: The Statistics of the partitions from the data that was used for the tree.

	<i>rbcLa</i>	<i>matK</i>	26s	Combined
Sequence coverage	76	57	33	76
Number of characters	545	659	882	2086
Number of unique characters	93	231	116	440
Number of informative characters	56 (10%)	140 (21%)	72 (8%)	266 (13%)
Number of constant characters	466	418	766	1643
Consistency index (CI)	0,607	0,789	0,576	0,668
Retention index (RI)	0,865	0,894	0,654	0,823
Number of trees	79	2346	324	503
Tree length	163	383	273	837

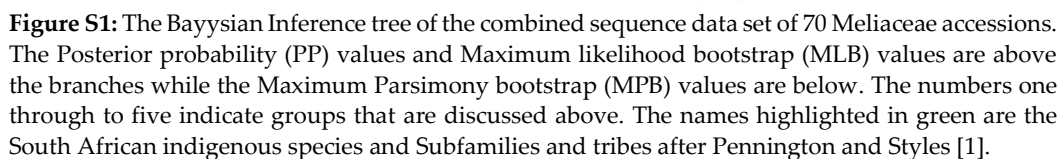


Figure S1: The Bayesian Inference tree of the combined sequence data set of 70 Meliaceae accessions. The Posterior probability (PP) values and Maximum likelihood bootstrap (MLB) values are above the branches while the Maximum Parsimony bootstrap (MPB) values are below. The numbers one through to five indicate groups that are discussed above. The names highlighted in green are the South African indigenous species and Subfamilies and tribes after Pennington and Styles [1].