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Supplementary Data

Table S1: Sequence characteristics from multiple sequence alignment of *ITS* and *matK*

Characteristics	<i>ITS</i>	<i>matK</i>
Number of samples	24	24
PCR success (%)	100	100
Sequencing success (%)	100	100
Aligned sequence length (bp)	711	846
Mean Interspecific K2P distances	0.024 ± 0.006	0.005 ± 0.002
Mean Intraspecific K2P distances	0.007 ± 0.002	0.002 ± 0.001

Table S2: Wilcoxon two-sample test for interspecific and intraspecific divergences of *ITS* and *matK*

Parameter	<i>ITS</i>	<i>matK</i>
Number of interspecific	360	362
Number of intraspecific	168	166
Wilcoxon W	23 250.00	23 550.000
p value	0	0