Table S2: Phylogenetic analyses realized on the matrices, with the partitioning method chosen, the number and list of selected subsets, and the models applied to them.

Analysis: RaxML Matrix 1	List of subsets	Model
Partitioning method:	• 3rd codons ; EFT2.1, ß-tubulin introns	GTR+G
PartitionFinder (BIC, All)	• 1st codons ; LSU	GTR+G
No. subsets: 4	• 2nd codons	GTR+G
	• RPB1 intron	GTR+G
Analysis: MrBayes Matrix 1	List of subsets	Model
Partitioning method:	• 3rd codons, EFT2.1, ß-tubulin introns	HKY+I+G
PartitionFinder (BIC, All)	• 1st codons, LSU	GTR+I+G
No. subsets: 4	• 2nd codons	HKY+I+G
	• RPB1 intron	K80
Analysis : RaxML Matrix 2	List of subsets	Model
Partitioning method:	• ITS1, ITS2, ß-tubulin and EFT2.1 introns	GTR+G
PartitionFinder (AICc, ALL)	• ß-tubulin 1st codon	GTR+G
No. subsets: 11	• ß-tubulin and RPB1 2nd codons	GTR+G
	• ß-tubulin and EFT2.1 3rd codons	GTR+G
	• EFT2.1 1st codon	GTR+G
	• EFT2.1 2nd codon	GTR+G
	• RPB1 1st codon	GTR+G
	• RPB1 3rd codon	GTR+G
	• RPB1 intron	GTR+G
	• 5.8S	GTR+G
	• LSU	GTR+G
Analysis: MrBayes Matrix 2	List of subsets	Model
Partitioning method:	• 1st codons	HKY+I
Arbitrary	• 2nd codons	HKY+I+G
No. subsets : 7	• 3rd codons	HKY+I
	• introns	HKY+G
	• LSU	GTR+I+G
	• ITS1, ITS2	K80+G
	• 5.8S	constant, excluded
Analysis: BEAST Matrix 2	List of subsets	Model
Partitioning method:	• ß-tubulin coding	HKY+I+G
Arbitrary	• EFT2.1 coding	HKY+G
No. subsets: 6	• RPB1 coding	GTR+G
	• introns	HKY+G
	• LSU	GTR+I+G
	• ITS	HKY+G
Analysis: RaxML : Mr Bayes, Matrix 3	List of subsets	Model
Partitioning method:	• 1st codon	GTR+G
Arbitrary	• 2nd codon	GTR+G
No. subsets: 3	• 3rd codon	GTR+G