Table S2: List of phylogenetic analyses performed on the alignments, with the partitioning method chosen, the number and identity of the resulting subsets and the substitution model applied (*: when applicable).

Alignment	Analysis	Partitioning method	No. subsets	Subsets	Model*
Section, concatenated	RAxML, Mr Bayes, BEAST	PartitionFinder, BIC	5	ITS 1 + ITS 2, ß-tubulin non-coding, IGS1	TrN + G
				5.8S, ß-tubulin 1st codon + 2nd codon, RPB1 2nd codon	JC + I
				EFT2.1 3rd codon + non-coding, RPB1 3rd codon, ß-tubulin 3rd codon, IGS3	HKY + G
				EFT2.1 1st codon + 2nd codon, RPB1 1st codon + non-coding, LSU	TrN + I + G
				IGS16	K80+G
	*BEAST	locus by locus	8	ITS	GTR+G
				LSU	GTR+I+G
				ß-tubulin	HKY+G
				EFT2.1	K80+G
				RPB1	SYM+G
				IGS1	HKY+G
				IGS3	HKY+G
				IGS16	K80+G
Section, ITS	RAxML,	ITS 1 + 2 vs 5.8S	2	ITS1+ITS2	
				5.8S	
Section, ß-tubulin	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Section, EFT2.1	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Section, RPB1	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Section, LSU	RAxML	all in one	1		/
Section, IGS1	RAxML	all in one	1		/
Section, IGS3	RAxML	all in one	1		/
Section, IGS16	RAxML	all in one	1		/

Alignment	Analysis	Partitioning method	No. subsets	Subsets	Model*
Dolichorhizoid, concatenated	RAxML, Mr Bayes, BEAST		4	IGS1, IGS16, IGS3, ITS1 + ITS 2, ß-tubulin 3rd codon	HKY + G
				LSU, ß-tubulin 1st codon + 2nd codon, EFT2.1 1st codon, RPB1 1st codon	HKY + I
				5.8S, EFT2.1 2nd codon, RPB1 2nd codon + non-codong	F81
				EFT2.1 3rd codon + non-codiong, RPB1 3rd codon	K80
	*BEAST	locus by locus	8	ITS	HKY+G
				LSU	GTR+G
				ß-tubulin	K80+G
				EFT2.1	K80
				RPB1	GTR
				IGS1	HKY+G
				IGS3	HKY
				IGS16	K80+G
Dolichorhizoid, ITS	RAxML, BEAST	ITS 1 + 2 vs 5.8S	2	5.8S	JC
				ITS1+ITS2	HKY+G
Dolichorhizoid, ß-tubulin	RAxML, BEAST	by codons/non-coding	4	1st codon	F81
				2nd codon	JC
				3rd codon	F81
				non-coding	K80
Dolichorhizoid, EFT2.1	RAxML, BEAST	by codons/non-coding	4	1st codon	F81
				2nd codon	F81
				3rd codon	HKY
				non-coding	JC
Dolichorhizoid, RPB1	RAxML, BEAST	by codons/non-coding	4	1st codon	F81
				2nd codon	F81
				3rd codon	HKY
				non-coding	JC
Dolichorhizoid, LSU	RAxML, BEAST	all in one	1	LSU	GTR+G
Dolichorhizoid, IGS1	RAxML, BEAST	all in one	1	IGS1	HKY+G
Dolichorhizoid, IGS3	RAxML, BEAST	all in one	1	IGS3	HKY
Dolichorhizoid, IGS16	RAxML, BEAST	all in one	1	IGS16	K80+G

Alignment	Analysis	Partitioning method	No. subsets	Subsets	Model*
Scabrosoid, concatenated	RAxML, Mr Bayes, BEAST	PartitionFinder, BIC	6	IGS3, ITS1 + ITS2, ß-tubulin non-coding, EFT2.1 non-coding	HKY+G
				ß-tubulin 1st codon, RPB1 1st codon, EFT2.1 1st codon	F81
				5.8S, ß-tubulin 2nd codon	JC
				IGS16, ß-tubulin 3rd codon, EFT2.1 3rd codon, RPB1 3rd codon	K80+G
				EFT2.1 2nd codon, RPB1 2nd codon	F81
				LSU, RPB1 non-coding	K80+I
	*BEAST	locus by locus	7	ITS	HKY+G
				LSU	HKY+I+G
				ß-tubulin	K80+G
				EFT2.1	K80
				RPB1	HKY
				IGS3	HKY
				IGS16	K80
Scabrosoid, ITS	BEAST	all in one	1	ITS	HKY+G
	RAxML	ITS1+ITS2 vs 5.8S	2		/
Scabrosoid, ß-tubulin	RAxML	by codons/non-coding	4		/
	BEAST	all in one	1	ß-tubulin	K80+G
Scabrosoid, EFT2.1	RAxML	by codons/non-coding	4		
	BEAST	all in one	1	EFT2.1	K80
Scabrosoid, RPB1	RAxML	by codons/non-coding	4		
	BEAST	all in one	1	RPB1	HKY
Scabrosoid, LSU	RAxML, BEAST	all in one	1	LSU	HKY+I+G
/					
Scabrosoid, IGS3	RAxML, BEAST	all in one	1	IGS3	HKY
Scabrosoid, IGS16	RAxML, BEAST	all in one	1	IGS16	K80

Alignment	Analysis	Partitioning method	No. subsets	Subsets	Model*
Concatenated, Polydactyloid	RAxML, MrBayes, BEAST	PartitionFinder, BIC	4	IGS1, IGS3, ß-tubulin non-coding ITS1 + ITS2, RPB1 3rd codon	HKY+I
				5.8S, EFT2.1 1st codon, LSU, ß-tubulin 1st codon, RPB1 1st codon + non-coding	HKY+I
				EFT2.1 2nd codon, RPB1 2nd codon, ß-tubulin 2nd codon	F81
				EFT2.1 3rd codon + non-coding, IGS16, ß-tubulin 3rd codon	K80
Polydactyloid, ITS	RAxML, BEAST	ITS1+ITS2vs5.8S	2	5.8S	JC
				ITS1+ITS2	HKY+G
Polydactyloid, ß-tubulin	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Polydactyloid, EFT2.1	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Polydactyloid, RPB1	RAxML	by codons/non-coding	4	1st codon	/
				2nd codon	/
				3rd codon	/
				non-coding	/
Polydactyloid, LSU	RAxML	all in one	1	LSU	/
Polydactyloid, IGS1	RAxML	all in one	1	IGS1	/
Polydactyloid, IGS3	RAxML	all in one	1	IGS3	/
Polydactyloid, IGS16	RAxML	all in one	1	IGS16	/