

Supplementary Material to “Cytological and genome size data analyzed in a phylogenetic frame: evolutionary implications concerning *Sisyrinchium* taxa (Iridaceae: Iridoideae)”

Table S2: Dataset partitions for Maximum Likelihood (ML) and Bayesian Inference (BI) analyses and evolutionary models used in BI

Data partition	No. of positions (without primers)	Partition by codon position	Model
<u>cpDNA partition</u>			
<i>rpoC1</i> (partial sequence)	508	X	HKY
<i>rpoB</i> (partial sequence)	472	X	HKY+I
<i>matK</i> (partial sequence)	1572	X	GTR+I
<i>matK</i> -5' <i>trnK</i> intron (complete sequence)	242		F81
<i>psbA</i> (partial sequence)	53	X	K80
<i>psbA-rps19</i> spacer (complete sequence)	124		HKY
<i>rps19</i> (complete sequence - negative strand)	279	X	HKY
<i>rps19-trnH</i> spacer (complete sequence)	137		F81
<i>trnQ</i> (partial sequence)	49		K80
<i>trnQ-rps16</i> spacer (partial sequence)	1185		GTR
<u>mtDNA partition</u>			
5'- <i>nad1</i> exon 2 (partial sequence)	57		HKY
<i>nad1</i> exon 2 (complete sequence)	82	X	HKY
<i>nad1</i> intron 2 (complete sequence)	1458		HKY
<i>nad4</i> intron 1 (complete sequence)	1386		GTR+I
<i>nad4</i> exon 2 (partial sequence)	271	X	HKY
<u>nuDNA partition</u>			
Internal Transcribed Spacer 1 (complete sequence)	232		GTR+ Γ
5.8S ribosomal RNA (complete sequence)	164		K80
Internal Transcribed Spacer 2 (complete sequence)	246		HKY+I
28S ribosomal RNA (partial sequence)	42		JC

Notes: partition by codon position = partition coding for protein.