

Baranow, P.; Rojek, J.; Dudek, M.; Szlachetko, D.; Bohdanowicz, J.; Kapusta, M.; Jedrzejczyk, I.; Rewers, M.; Moraes, A.P. Chromosome Number and Genome Size Evolution in *Brasolia* and *Sobralia* (Sobralieae, Orchidaceae). *Int. J. Mol. Sci.* **2022**, *23*, x. <https://doi.org/10.3390/xxxxx>

Supplementary Materials: The following supporting information can be downloaded at: www.mdpi.com/xxx/s1,

Figure S1: Maximum Likelihood (A) and Bayesian Inference (B) phylogenetic trees based on *matK*-*trnK* and ITS markers.

Figure S2. Chromosome complement of *Brasolia* and *Elleanthus* species. (a) *B. altissima* ($2n = 46$), (b) *B. cattleya* ($2n = 42$), (c) *B. dichotoma* ($2n = 46$), (d) *B. flava* ($2n = 46$), (e) *B. hirtzii* ($2n = 44$), (f) *B. portialle* ($2n = 48$), (g) *E. brasiliensis* ($2n = 50$), (h) *E. crinipes* ($2n = 50$). Each chromosome is indicated by a number. Bar in h correspond to 5 μ m.

Figure S3. Chromosome complement of *Sobralia* species. (a) *S. bimaculata* ($2n = 44$), (b) *S. decora* ($2n = 42$), (c) *S. decora* ($2n = 44$), (d) *S. fimbriata* ($2n = 46$), (e) *S. macrantha* ($2n = 48$), (f) *S. powelli* ($2n = 44$), (g) *S. vallecaucana* ($2n = 48$), (h) *S. wilsoniana* ($2n = 48$), (i) *S. yauaperyensis* ($2n = 46$), (j) *S. crocea* ($2n = 44$), (k) *S. fragans* ($2n = 42$), (l) *S. gloriosa* ($2n = 48$), (m) *S. luerorum* ($2n = 48$), (n) *S. rosea* ($2n = 48$). Each chromosome is indicated by a number. Bar in h correspond to 5 μ m.

Table S1. GenBank accession numbers of Internal Transcribed Sequences (ITS) and *matK* sequences used for the complete phylogenetic reconstruction. A total of 57 individuals from 53 species distributed in four genera were used: 11 *Brasolia*, four *Elleanthus*, 34 *Sobralia*, and four *Neottia* species, used as outgroup.

Table S2. Expectations probabilities considering the model Constant Rate without duplication for both phylogenetic analysis. The main mechanism of chromosome number rearrangement is indicated in bold (higher expectation on number of events).

Table S1. GenBank accession numbers of Internal Transcribed Sequences (ITS) and *matK* sequences used for the complete phylogenetic reconstruction. A total of 57 individuals from 53 species distributed in four genera were used: 11 *Brasolia*, four *Elleanthus*, 34 *Sobralia*, and four *Neottia* species, used as outgroup.

Taxa	ITS	<i>matK</i>
<i>Sobralia andreae</i>	KT923834.1	KT428828.1
<i>Sobralia atropubescens</i>	KT923842.1	KT428835.1
<i>Sobralia bimaculata</i>	KF612992.1	KF700346.1
<i>Sobralia callosa</i>	KT923833.1	KT428827.1
<i>Sobralia cobanensis</i>	KF612993.1	KF700347.1
<i>Sobralia crocea</i>	HM854644.1	HQ329050.1
<i>Sobralia decora</i>	KF612994.1	KF700348.1

<i>Sobralia fragrans</i>	KF612997.1	KF700351.1
<i>Sobralia fimbriata</i>	HM854631.1	HQ329037.1
<i>Sobralia gloriosa</i>	HM854629.1	HQ329035.1
<i>Sobralia klotzscheana</i>	HM854643.1	HQ329049.1
<i>Sobralia lancea</i>	KT923844.1	KT428837.1
<i>Sobralia lindleyana</i>	HM854624.1	HQ329030.1
<i>Sobralia luerorum</i>	MW628176.1	MZ170069.1
<i>Sobralia macrantha</i>	HM854651.1	HQ329058.1
<i>Sobralia macrophylla</i>	KT923840.1	KT428833.1
<i>Sobralia maduroi</i>	KT923828.1	KT428822.1
<i>Sobralia cf. madisonii</i>	HM854634.1	HQ329040.1
<i>Sobralia melantothrix</i>	KT923842.1	KT428835.1
<i>Sobralia mucronata</i>	KF612996.1	KF700350.1
<i>Sobralia powelli</i>	KF612986.1	KF700340.1
<i>Sobralia pulcherima</i>	KF612992.1	KF700346.1
<i>Sobralia rogersiana</i>	KT923830.1	KT428824.1
<i>Sobralia rosea</i>	KT923827.1	KT428821.1
<i>Sobralia sessilis</i>	MW628177.1	MZ170070.1
<i>Sobralia triandra</i>	KT923841.1	KT428834.1
<i>Sobralia tricolor</i>	KT923843.1	KT428836.1
<i>Sobralia undatocarinata</i>	KT923829.1	KT428823.1
<i>Sobralia vallecaucana</i>	KF613001.1	KF700355.1
<i>Sobralia virginalis</i>	KT923836.1	KT428829.1
<i>Sobralia warszewiczii</i>	KT923838.1	KT428831.1
<i>Sobralia wilsoniana</i>	KT923837.1	KT428830.1
<i>Sobralia withneri</i>	KT923839.1	KT428832.1
<i>Sobralia yauaperyensis</i>	HM854621.1	HQ329027.1
<i>Brasolia altissima</i>	HM854648.1	HQ329054.1
<i>Brasolia caloglossa</i>	KT923826.1	KT428820.1
<i>Brasolia cattleya</i>	KT923818.1	KT428817.1
<i>Brasolia dichotoma</i>	KT923814.1	KT428818.1

<i>Brasolia dichotoma</i>	HM854647.1	HQ329053.1
<i>Brasolia flava</i>	KT923817.1	KT428816.1
<i>Brasolia flava</i>	KT923816.1	KT428815.1
<i>Brasolia flava</i>	KT923815.1	KT428814.1
<i>Brasolia flava</i>	HM854637.1	HQ329043.1
<i>Brasolia hirtzii</i>	HM854641.1	HQ329047.1
<i>Brasolia hirtzii</i>	HM854640.1	HQ329046.1
<i>Brasolia portillae</i>	KT923813.1	KT428812.1
<i>Brasolia portillae</i>	KT923812.1	KT428811.1
<i>Brasolia roezlii</i>	KT923824.1	KT428819.1
<i>Elleanthus brasiliensis</i>	MZ153093.1	MZ170071.1
<i>Elleanthus crinipes</i>	MZ153094.1	-----
<i>Elleanthus oliganthus</i>	MH656420.1	MH733930.1
<i>Elleanthus purpureus</i>	HM854582.1	MH733936.1
<i>Neottia acuminata</i>	MH808060.1	KF695166.1
<i>Neottia cordata</i>	KX167869.1	KX677756.1
<i>Neottia nidusavis</i>	KX167909.1	AY368419.1
<i>Neottia pinetorum</i>	KT338759.1	KF262100.1

Table S2. Expectations probabilities considering the model Constant Rate without duplication for both phylogenetic analysis. The main mechanism of chromosome number rearrangment is indicated in bold (higher expectation on number of events).

Total number of:	Maximum Likelihood	Bayesian Inference
gain events (ascending dysploidy)	30.9113	15.2518
loss events (descending dysploidy)	49.1808	37.0653
duplication events	0	0
demi-duplications events	0	0