

1 **Exploring the possible role of hybridization in the evolution of photosynthetic pathways in**
2 ***Flaveria* (Asteraceae), the prime model of C₄ photosynthesis evolution**

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18 **Abstract**

19 *Flaveria* (Asteraceae) is the prime model for the study of C₄ photosynthesis evolution and seems
20 to support a stepwise acquisition of the pathway through C₃-C₄ intermediate phenotypes, still
21 existing in *Flaveria* today. Molecular phylogenies of *Flaveria* based on concatenated data
22 matrices are currently used to reconstruct the complex sequence of trait shifts during C₄
23 evolution. To assess the possible role of hybridization in C₄ evolution in *Flaveria*, we re-
24 analyzed transcriptome data of 17 *Flaveria* species to infer the extent of gene tree discordance
25 and possible reticulation events. We found massive gene tree discordance as well as reticulation
26 along the backbone and within clades containing C₃-C₄ intermediate and C₄-like species. An
27 early hybridization event between two C₃ species might have triggered C₄ evolution in the genus.
28 The clade containing all C₄ species plus the C₄-like species *F. vaginata* and *F. palmeri* is robust
29 but of hybrid origin involving *F. angustifolia* and *F. sonorensis* (both C₃-C₄ intermediate) as
30 parental lineages. Hybridization seems to be a driver of C₄ evolution in *Flaveria* and likely
31 promoted the fast acquisition of C₄ traits. This new insight can be used in further exploring C₄
32 evolution and can inform C₄ bioengineering efforts.

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34 **Keywords:** C₃-C₄ intermediates; C₄ photosynthesis evolution; Hybridization; HyDe analysis;
35 RNA-Seq; Reticulate evolution; Species network analysis.

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39 INTRODUCTION

40 The detection of gene tree discordance is common in the phylogenomic era. Discordance can be
41 the product of multiple processes and is commonly attributed to either incomplete lineage sorting
42 (ILS) and/or hybridization (Pamilo and Nei, 1988; Doyle, 1992; Galtier and Daubin, 2008).
43 Hybridization is a fundamental process in the evolution of animals, plants, and fungi (Giraud et
44 al., 2008; Schwenk et al., 2008; Soltis and Soltis, 2009; Payseur and Rieseberg, 2016), and
45 methods to investigate hybridization in a phylogenetic context recently have been developed
46 greatly. These include methods that estimate phylogenetic networks while accounting for ILS
47 and hybridization simultaneously (e.g., Solís-Lemus and Ané, 2016; Wen et al., 2018), and
48 methods that detect hybridization based on site patterns or phylogenetic invariants (e.g., (Green
49 et al., 2010; Durand et al., 2011; Kubatko and Chifman, 2019). The current ease to produce
50 phylogenomic data sets and the availability of new analytical methods facilitate the exploration
51 of reticulate evolution in any clade across the Tree of Life, including those that have particular
52 significance as model lineages, such as the flowering plant genus *Flaveria* (Asteraceae) for the
53 study of C₄ photosynthesis evolution.

54 *Flaveria* belongs to the sunflower tribe Heliantheae (Anderberg et al., 2007). According
55 to the most recent revision by Powell (1978), *Flaveria* includes 21 morphologically rather
56 similar species distributed mainly in southern USA and northern Mexico, with few species
57 occurring in the Caribbean and South America. The two weedy and self-compatible C₄ species,
58 *F. trinervia* and *F. bidentis*, have been introduced almost worldwide
59 (<https://powo.science.kew.org/>). Species of *Flaveria* usually show scattered occurrences in
60 unconnected, localized populations near rivers, creeks, irrigation canals, fields, roadsides, and
61 ponds, often on saline or gypseous soils (Powell, 1978). They are either robust shrubs or

62 herbaceous perennials, or annuals (mainly the C₄ species). The genus stands out in Asteraceae
63 for its reduced floral features and reduced and secondarily aggregated capitula (Anderberg et al.,
64 2007). Reduction is most evident in *F. trinervia* (C₄) and aggregation of capitula mimicking a
65 single capitulum in *F. anomala* (C₃-C₄). *Flaveria* is consistently diploid (see Powell, 1978 and
66 ref. therein; only exceptions are some tetraploid populations of *F. pringlei*) with a haploid
67 chromosome number of $n = 18$. Artificial hybridization among 16 species of *Flaveria* was
68 successful, and F1 hybrids could be obtained in most species' combinations (see Table 1 in
69 Powell, 1978). F2 and backcross crosses also resulted in offspring in a high number of
70 combinations, but only four of these were fertile. Powell (1978) excluded frequent natural
71 hybridization in *Flaveria* mainly because of geographical isolation.

72 C₄ photosynthesis in *Flaveria* was first recognized by Smith and Turner (1975), and the
73 presence of C₃-C₄ intermediate species was first noted by Brown (pers. comm. in Powell, 1978),
74 first verified by Apel and Maass (1981) and then studied in detail biochemically in four species
75 by Ku et al. (1983) and Nakamoto et al. (1983). Numerous publications characterizing the
76 physiology and biochemistry of C₃-C₄ intermediate species of *Flaveria* followed (Ku et al., 1991
77 and ref. therein). At the same time crossing experiments of C₃ and C₄ *Flaveria* species as well as
78 backcrosses or crosses between C₃-C₄ intermediate species revealed the transfer of C₄ properties
79 as well as the simultaneous functioning of C₃ and C₄ pathways in hybrids (see Apel et al., 1988
80 as an example and Kadereit et al., 2017 for review). Of all genera that contain C₃-C₄ intermediate
81 species, *Flaveria* has the highest diversity of C₃-C₄ phenotypes including C₂ photosynthesis
82 (Sage et al., 2012; briefly described in Table 1), and arguably is the only lineage that allows to
83 infer a detailed sequence of increasing C₄-ness (Sage et al., 2012). Against this background,
84 *Flaveria* qualified as the model group for the establishment (Monson and Moore, 1989) and

85 subsequent refinement of a model of stepwise acquisition of C₄ photosynthesis through
86 intermediate steps (Sage et al., 2014 and ref. therein).

87 One challenge of the *Flaveria* model is that C₃-C₄ intermediate phenotypes might also
88 have resulted from reticulation during the diversification of the genus, especially when
89 reproductive barriers are leaky among extant species as soon as they get into contact (Powell,
90 1978) and hybridization between C₃ and C₄ species is possible. Therefore, a phylogenetic study
91 exploring the occurrence and location of past reticulation events is needed. Comprehensive
92 molecular phylogenetic studies of *Flaveria* published so far were either based on few molecular
93 markers only (McKown et al., 2005), or on concatenated data matrices and inference methods
94 unable to reveal tree discordance, possible reticulation, or incomplete lineage sorting (Lyu et al.,
95 2015). Irrespective of this, numerous current studies of evolutionary change during the
96 establishment of the C₄ pathway rely on the *Flaveria* model (e.g., Lyu et al., 2021; Taniguchi et
97 al., 2021).

98 The aim of this study is to use available transcriptome data of 17 species of *Flaveria* to
99 assess the extent of reticulation during the diversification of the genus, and to evaluate these
100 findings with respect to the evolution of C₄ photosynthesis in the genus and its suitability as
101 general model of C₄ evolution.

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107 **Table 1.** Photosynthetic types in *Flaveria* according to Sage et al. (2014 and 2018 and ref.
 108 therein); species names marked * were not sampled in this study, mesophyll (M), bundle sheath
 109 (BS), glycine decarboxylase (GDC).

Photosynthetic type	Characteristics	<i>Flaveria</i> species representing this type ¹
C ₃	Photorespiratory cycle operates completely within single M cells, BS cells small ² with few organelles, veins widely spaced	<i>F. cronquistii</i> ² , <i>F. mcdougallii</i> *
C ₃ proto-kranz	Functionally C ₃ , activated BS cells, greater vein density, mitochondria localized at the inner BS wall adjacent to the vasculature	<i>F. pringlei</i> , <i>F. robusta</i>
C ₂ Type I	Low or no GDC expression in M cells, high number of centripetally located organelles in the BS cells, CO ₂ compensation point reduced in comparison to C ₃ , lack of any C ₄ cycle	<i>F. angustifolia</i> , <i>F. chlorifolia</i> , <i>F. sonorensis</i>
C ₂ Type II	In addition to type I, modest C ₄ cycle enhancement	<i>F. anomala</i> , <i>F. floridana</i> , <i>F. linearis</i> *, <i>F. pubescens</i> , <i>F. ramosissima</i>
C ₄ -like	Strong C ₄ metabolic cycle but also weak C ₃ cycle in the M cells	<i>F. brownii</i> , <i>F. palmeri</i> , <i>F. vaginata</i>
C ₄	No C ₃ cycle, CO ₂ -saturate photosynthesis below 500 ppm CO ₂	<i>F. bidentis</i> , <i>F. campestre</i> *, <i>F. kochiana</i> , <i>F. trinervia</i> , <i>F. australasica</i> ,

110 ¹ *Flaveria oppositifolia** so far only classified as C₂ without further specification.

111 ² *Flaveria cronquistii* qualifies as a C₃+ species (see Sage et al., 2018) because it has larger and
 112 photosynthetically more active BS cells (McKown and Dengler, 2007).

113

114 MATERIAL AND METHODS

115 Taxon sampling

116 We included publicly available transcriptomes from 17 species of *Flaveria* (Table S1). In
117 addition, we included outgroups from four genomes of Asteraceae (*Chrysanthemum*, *Helianthus*,
118 *Lactuca* and *Stevia*) following (Mandel et al., 2019; Table S1).

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120 Homology and orthology inference

121 Raw read processing, transcriptome assembly, low-quality and chimeric transcript
122 removal, transcript clustering into putative genes, translation, and final coding sequences (CDS)
123 redundancy assessment were carried out following Morales-Briones et al. (2021) with minor
124 modifications as follows. Sequencing errors in raw reads were corrected with Rcorrector (Song
125 and Florea, 2015) and reads flagged as uncorrectable were discarded. Sequencing adapters and
126 low-quality bases were removed with Trimmomatic v 0.39 (Bolger et al., 2014). Additionally,
127 chloroplast and mitochondrial reads were filtered out with Bowtie2 v 2.4.4 (Langmead and
128 Salzberg, 2012) using publicly available Asterales organelle genomes from the Organelle
129 Genome Resources database (RefSeq; [Pruitt et al., 2007]; last accessed on June 4, 2021) as
130 references. Read quality was assessed with FastQC v 0.11.9
131 (<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc>) and overrepresented sequences were
132 discarded. *De novo* assembly was carried out with Trinity v 2.13.2 (Grabherr et al., 2011) with
133 default settings, but without in silico normalization. Assembly quality was assessed with
134 Transrate v 1.0.3 (Smith-Unna et al., 2016). Low quality and poorly supported transcripts were
135 removed using individual cut-off values for three contig score components of Transrate: 1)
136 proportion of nucleotides in a contig that agrees in identity with the aligned read, $s(\text{Cnuc}) \leq 0.25$;

137 2) proportion of nucleotides in a contig that have one or more mapped reads, $s(\text{Ccov}) \leq 0.25$; and
138 3) proportion of reads that map to the contig in correct orientation, $s(\text{Cord}) \leq 0.5$. Furthermore,
139 chimeric transcripts (*trans*-self and *trans*-multi-gene) were removed following the approach
140 described in Yang and Smith (2013) using *Helianthus annuus* as the reference proteome, and a
141 percentage similarity and length cutoff of 30 and 100, respectively. To remove isoforms and
142 assembly artifacts, filtered reads were remapped to filtered transcripts with Salmon v 1.5.2 (Patro
143 et al., 2017) and putative genes were clustered with Corset v 1.09 (Davidson and Oshlack, 2014)
144 using default settings, except that we used a minimum of five reads as threshold to remove
145 transcripts with low coverage (-m 5). Only the longest transcript of each putative gene inferred
146 by Corset was retained as suggested in Chen et al. (2019). Filtered transcripts were translated
147 with TransDecoder v 5.3.0 (Haas et al., 2013) with default settings and the proteomes of
148 *Arabidopsis thaliana*, *Helianthus annuus*, and *Lactuca sativa* to identify open reading frames.
149 Finally, coding sequences (CDS) from translated amino acids were further reduced with CD-HIT
150 v 4.8.1 (-c 0.99; [Fu et al., 2012]) to remove near-identical sequences. Scripts used can be found
151 at https://bitbucket.org/yanglab/phylogenomic_dataset_construction/src/master/ (Morales-
152 Briones et al., 2021).

153 Homology inference was done with an all-by-all BLASTN search on CDS with an *E*
154 value cutoff of 10. BLAST hits were filtered with a minimal hit coverage of 40%. Homolog
155 groups were clustered with MCL v 14-137 (van Dongen, 2000) using a minimum minus log-
156 transformed *E* value cutoff of 5 and an inflation value of 1.4, and only clusters with at least 17
157 taxa were retained. Homolog cluster sequences were aligned using the OMM_MACSE v 11.05
158 pipeline (Scornavacca et al., 2019). Alignments were further trimmed to remove columns with
159 more than 90% missing data using Phyx (Brown et al., 2017). Homolog trees were inferred using

160 RAxML v 8.2.11 (Stamatakis, 2014) with the GTRCAT model and 200 rapid bootstrap (BS)
161 replicates. Monophyletic and paraphyletic tips of the same species were removed, keeping the tip
162 with the highest number of characters in the trimmed alignment following Yang and Smith
163 (2014). Spurious tips were detected and removed using TreeShrink v 1.3.9 (Mai and Mirarab,
164 2018) with the 'per-gene' mode, a false positive error rate threshold (α) of 0.05, and excluding the
165 outgroups. Trees were visually inspected, and deep paralogs producing internal branch lengths
166 longer than 0.20 were cut apart retaining subclades with at least 10 taxa to obtain final homolog
167 trees. Orthology inference was done using the 'monophyletic outgroup' (MO) approach from
168 Yang and Smith (2014). The MO approach filters for trees that have outgroup taxa being
169 monophyletic and single-copy, and therefore filters for single- and low-copy genes. This
170 approach roots the gene tree by the outgroups, traverses the rooted tree from root to tip, and
171 removes the side with less taxa when gene duplication is detected (Yang and Smith, 2014). If no
172 taxon duplication is detected in a homolog tree, the MO approach outputs a one-to-one ortholog.
173 We set all species of *Flaveria* as ingroups, and *Chrysanthemum*, *Helianthus*, *Lactuca*, and *Stevia*
174 as outgroups, keeping orthologs that included at least 10 taxa.

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176 **Tree inference and detection of gene tree conflict**

177 Sequences from individual orthologs were aligned using the OMM_MACSE pipeline.
178 Columns with more than 20% missing data were trimmed with Phyx, and only alignments with
179 at least 500 characters and all 21 taxa were retained and concatenated. We estimated a maximum
180 likelihood (ML) tree of the concatenated matrix with IQ-TREE v 2.1.3 (Minh et al., 2020)
181 searching for the best partition scheme (Lanfear et al., 2012) followed by ML gene tree inference
182 and 1000 ultrafast bootstrap replicates for clade support. To estimate a coalescent-based species

183 tree, first, we inferred individual gene trees with IQ-TREE using extended model selection
184 (Kalyaanamoorthy et al., 2017) and 200 non-parametric bootstrap replicates for clade support.
185 Gene trees were then used to infer a species tree with ASTRAL-III v 5.7.7 (Zhang et al., 2018)
186 using local posterior probabilities (LPP; Sayyari and Mirarab, 2016) to assess clade support.

187 We explored gene tree discordance by calculating the number of concordant and
188 discordant bipartitions on each node of the concatenated and ASTRAL trees using Phyparts
189 (Smith et al., 2015). We used individual gene trees with BS support of at least 50% for each
190 node. Additionally, to distinguish conflict from poorly supported branches, we carried out a
191 Quartet Sampling (QS; Pease et al., 2018) analysis using the concatenated matrix with a partition
192 by gene (--genetrees), the concatenated IQ-TREE and ASTRAL trees, and 1000 replicates. To
193 further visualize gene tree conflict, we built a cloudogram with the DensiTree function from
194 Phangorn v 2.7.1 (Schliep, 2011) in R (R Core Team 2021). We first time-calibrated individual
195 ortholog gene trees, for visualization purposes only, with TreePL v 1.0 (Smith and O'Meara,
196 2012). The most recent common ancestor (MRCA) of *Helianthus* and *Flaveria* was fixed to 21.5
197 MYA, and the MRCA of *Flaveria* was fixed to 4.3 MYA based on Mandel et al. (2019).

198

199 **Testing for potential reticulation**

200 First, to investigate if gene tree discordance can be explained by ILS alone, we performed
201 coalescent simulations like Cloutier et al. (2019). An ultrametric tree with branch lengths in
202 mutational units (μT) was inferred with PAUP v 4.0a (build 168; Swofford, 2002) by
203 constraining a ML tree search to the ASTRAL tree and using the concatenated alignment, a
204 GTRGAMMA model, and enforcing a strict molecular clock. The mutational branch lengths
205 from the constrained tree and branch lengths in coalescent units ($\tau = T/4N_e$) from the ASTRAL

206 tree were used to estimate the population size parameter theta ($\Theta = \mu T / \tau$; Degnan and Rosenberg,
207 2009) for internal branches. Terminal branches were set with $\Theta = 1$. We then used Phybase v 1.4
208 (Liu and Yu, 2010), that implements the formula from Rannala and Yang (2003), to simulate
209 10,000 gene trees using the constraint tree and the estimated theta values. Lastly, we calculated
210 the distribution of Robinson and Foulds (1981) tree-to-tree distances between the ASTRAL tree
211 and each original gene tree using Phangorn and compared this with the distribution of tree-to-tree
212 distances between the ASTRAL tree and the simulated gene trees.

213 To test for potential reticulation, we inferred species networks using maximum pseudo-
214 likelihood (Yu and Nakhleh, 2015) in PhyloNet v 3.8.2 (Than et al., 2008) with the command
215 "InferNetworks_MPL" and using individual ML gene trees as input. We included all 17 species
216 of *Flaveria* and *Helianthus* as an outgroup (18-taxon data set). Network searches were performed
217 allowing for up to ten reticulation events and using only nodes in the gene trees that have BS \geq
218 50%. To find the network with optimal number of reticulations, we plotted the number of
219 reticulations versus the pseudo-likelihood score to determine when the score stabilizes (Blair and
220 Ané, 2020). Given that the pseudo-likelihood scores did not stabilize after networks with ten
221 reticulation events (see results) and to reduce network complexity, we performed one additional
222 round of searches by removing taxa involved in reticulation from the previous search. We
223 removed *F. brownii* (C₄-like) and *F. pringlei* (C₃; 16-taxon data set). These two species were
224 inferred to be product of reticulation events in all ten original searches and were not involved in
225 additional reticulation events (i.e., they are not a parental lineage of other reticulation events; see
226 results). Network searches for the reduced data set were carried out similarly as with the original
227 data set.

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229 Additionally, we tested for hybridization with HyDe (Blischak et al., 2018), which uses
230 site pattern frequencies (Kubatko and Chifman, 2019) to quantify the hybridization parameter γ
231 between two parental lineages that form a hybrid lineage. We tested all triplet combinations
232 using the ‘run_hyde.py’ script, the concatenated alignment, and a mapping file to assign species.
233 Test significance was assessed with a Bonferroni correction ($\alpha= 0.05$) for the number of
234 hypothesis tests conducted with estimates of γ between 0 and 1 (Blischak et al., 2018). We
235 carried out HyDe hybridization test using all species and without *F. pringlei* (C₃), as it has been
236 identified as a potential artificial hybrid (Lyu et al., 2015).

237

238 **Assessment of whole genome duplication**

239 To investigate potential whole genome duplication, product of reticulation events in
240 *Flaveria* (see results), we mapped gene duplication events onto the inferred species tree
241 following (Yang et al., 2018). First, we extracted rooted ingroup clades (orthogroup) from the
242 final homolog trees by requiring at least 15 taxa and only orthogroups with an average BS ≥ 50
243 were used for mapping. Then gene duplication events were then mapped onto the MRCA on the
244 species tree when two or more taxa overlapped between the two daughter clades on the rooted
245 ingroup clade. Each node on a species tree can be counted only once from each gene tree to
246 avoid nested gene duplications inflating the number of recorded duplications (Yang et al., 2018).
247 Orthogroup extraction and mapping were carried out using the scripts “extract_clades.py” and
248 “map_dups_mrca.py” from <https://bitbucket.org/blackrim/clustering> (Yang et al., 2018).

249

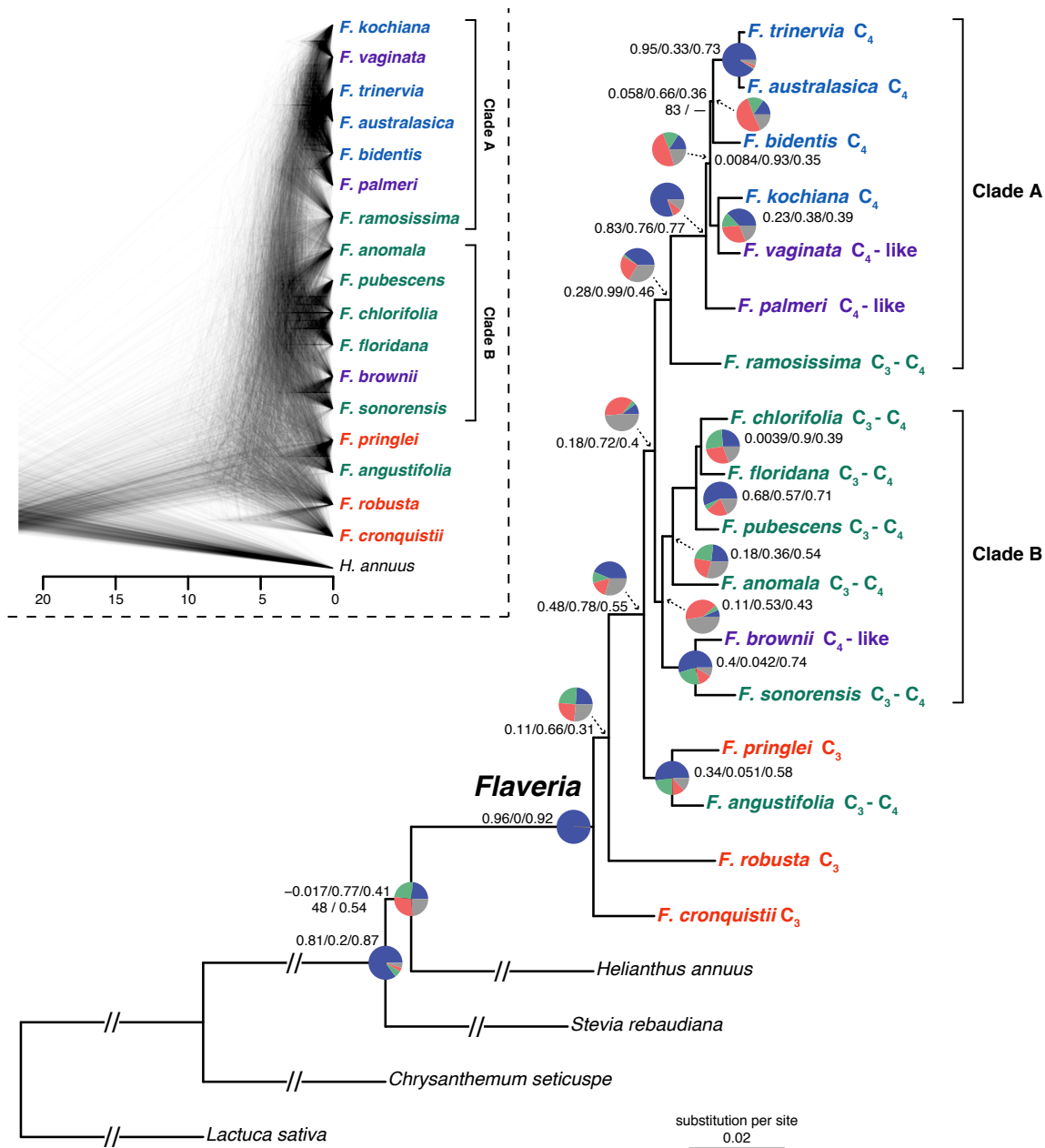
250 RESULTS

251 Orthology inference and phylogenetic analysis

252 The final number of orthologs with at least ten species was 5,374 with a mean of 4,809
253 orthologs per species (Table S1). The number of orthologs that included all 21 species was
254 1,295. The concatenated matrix (≥ 500 bp per ortholog) consisted of 1,582,170 aligned columns
255 with a character occupancy of 93% from 1,249 orthologs.

256 The topologies from the IQ-TREE and ASTRAL trees were similar and most nodes had
257 maximum support (BS = 100, LPP = 100; Fig. 1; Fig. S1). The two trees only differed in the
258 placement of *Flaveria bidentis* (C₄) which had lower support on both cases (Fig. 1; Fig. S1).
259 *Flaveria cronquistii* (C₃), *F. robusta* (C₃) and *F. pringlei* (C₃) + *F. angustifolia* (C₃-C₄) formed a
260 grade which is sister to Clade A + Clade B (clades names followed McKown et al., 2005). Clade
261 A from IQ-TREE comprised the same species and relationships as in Lyu et al. (2015). *Flaveria*
262 *ramosissima* (C₃-C₄) and *F. palmeri* (C₄-like) were successive sisters to *F. kochiana* (C₄) + *F.*
263 *vaginata* (C₄-like) and the C₄ clade [*F. bidentis*, *F. trinervia* + *F. australasica*]; BS = 83]. The
264 ASTRAL tree recovered *F. bidentis* (C₄) sister to *F. kochiana* (C₄) + *F. vaginata* (C₄-like; LLP =
265 0.96; Fig. S1). Clade B included the same species as in Lyu et al. (2015) but also included *F.*
266 *sonorensis* (C₃-C₄). Our analyses recovered *F. brownii* (C₄-like) + *F. sonorensis* (C₃-C₄) as sister
267 to the remaining species in Clade B. The remaining species, all C₃-C₄, had similar relationships
268 as in Lyu et al. (2015) with *F. anomala* as sister to the clade *F. pubescens*, *F. chlorifolia* + *F.*
269 *floridana*.

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271

272 **Fig. 1.** Maximum likelihood phylogeny of *Flaveria* inferred with IQ-TREE from the concatenated 1249-
 273 nuclear gene supermatrix. Species names are colored by photosynthetic type. Quartet Sampling (QS)
 274 scores are shown above branches. QS scores: Quartet concordance/Quartet differential/Quartet
 275 informativeness. All nodes have full bootstrap support (BS =100) and local posterior probability (LLP =1)
 276 unless noted next to branches. Em dashes (—) denotes an alternative topology compared to the ASTRAL
 277 tree (Fig. S1). Pie charts represent the proportion of ortholog trees that support a clade (blue), the main
 278 alternative bifurcation (green), the remaining alternatives (red), and bifurcations (conflict or support) with
 279 <50% bootstrap support (gray). Branch lengths as number of substitutions per site (scale bar).
 280 Exceptionally long branches were shortened with a broken segment (/) for illustration purposes (See Fig.
 281 S1 for original branch lengths). Inset: Cloudogram inferred from 1288 nuclear ortholog trees. Scale in
 282 millions of years ago (MA).

283 **Phylogenetic conflict**

284 Overall, conflict analyses and cloudogram visualization revealed rampant gene tree
285 discordance in *Flaveria* (Fig. 1; Fig S2). The cloudogram showed significant conflict along the
286 backbone of the phylogeny as well as within clades A and B (Fig. 1). The placement of *F.*
287 *robusta* (C₃) was supported only by 308 (of 947) informative gene trees and had low QS support
288 (0.11/0.66/0.3) with a clear signal of an alternative topology involving *F. cronquistii*. The sister
289 relationship of *F. pringlei* (C₃) and *F. angustifolia* (C₃-C₄) was supported by 677 (of 1,123) gene
290 trees and had moderate QS support (0.34/0.051/0.58) and a strong signal of an alternative
291 topology. The placement of *F. pringlei* (C₃) + *F. angustifolia* (C₃-C₄) as sister of Clade A +
292 Clade B was supported by 562 (of 909) gene trees and had strong QS support (0.48/0.78/0.55)
293 with moderate signal for an alternative topology. The clade composed of clades A and B was
294 supported only by 131 (of 661) gene trees and had low QS support (0.18/0.72/0.4) but had no
295 signals of an alternative topology. Clade A was supported by 505 (of 858) gene trees and had
296 moderate QS support (0.28/0.99/0.46) but showed no signals of alternative topologies. The
297 remaining species of Clade A [excluding *F. ramosissima* (C₃-C₄)] formed a clade supported by
298 most gene trees (1,037 of 1,151) and a strong QS score (0.83/0.76/0.77) with no signals of an
299 alternative topology. *Flaveria kochiana* (C₄) + *F. vaginata* (C₄-like) was supported by 479 (of
300 1,049) gene trees and had moderate QS support (0.23/0.38/0.39) with a clear signal of an
301 alternative topology. *Flaveria trinervia* (C₄) + *F. australasica* (C₄) was supported by most gene
302 trees (1,172 of 1,220) and had strong QS support with no signals of alternative topologies.
303 *Flaveria bidentis* (C₄) as sister to *F. trinervia* (C₄) + *F. australasica* (C₄; IQ-TREE) was
304 supported by 197 (of 1,054) and had very low QS support with a signal of an alternative
305 topology. When *F. bidentis* (C₄) was placed as sister to *F. kochiana* (C₄) + *F. vaginata* (C₄-like;

306 ASTRAL) the clade formed by these three species was supported by even fewer gene trees (170
307 of 1,037) and QS counter-support (-0.027/0.72/0.38; Fig. S3). The clade composed of *F.*
308 *kochiana* (C₄) + *F. vaginata* (C₄-like) and the C₄ clade *F. bidentis*, *F. trinervia* + *F. australasica*
309 was supported by 206 (of 1,028) gene trees and had very low QS support (0.0084/0.93/0.35) with
310 signals of alternative topologies. Clade B was supported by only 85 (of 679) gene trees and had
311 low QS support (0.11/0.53/0.43) with signals of an alternative topology. *Flaveria brownii* (C₄-
312 like) + *F. sonorensis* (C₃-C₄) was supported by 708 (of 1,180) gene trees and had moderate QS
313 support (0.4/0.042/0.74) with clear signals of an alternative topology. The four remaining species
314 of Clade B formed a clade supported by 299 (of 910) gene trees and had low QS support
315 (0.11/0.53/0.43) with signals of an alternative topology. *Flaveria chlorifolia* (C₃-C₄) + *F.*
316 *floridana* (C₃-C₄) was supported by 337 (of 1,042) gene trees and had very low QS support
317 (0.0039/0.9/0.39) with clear signals of an alternative topology. Lastly, the C₃-C₄ clade (*F.*
318 *pubescens*, *F. chlorifolia* + *F. floridana*) was supported by 727 (of 1,055) gene trees and had
319 strong QS support (0.68/0.57/0.71) with a slight signal of an alternative topology.

320

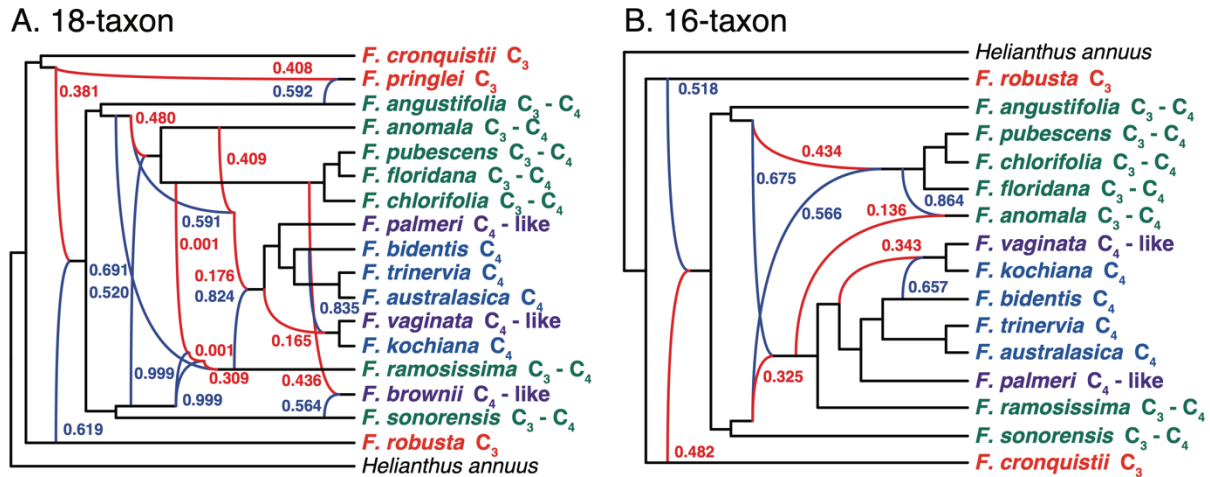
321 **Potential widespread reticulation**

322 The distribution of tree-to-tree distances of the empirical and simulated gene trees to the
323 ASTRAL tree showed some overlap (Fig. S4), but there was a skew towards larger distances in
324 the empirical trees (mean 16.61) compared to distances in the simulated trees (mean 11.80). This
325 suggested that ILS alone cannot explain most of the observed gene tree incongruence (Maureira-
326 Butler et al., 2008).

327

328 Species network analyses recovered topologies with up to ten reticulations events for the
329 18-taxon data set (Fig. S6). The pseudo-likelihood score (Fig. S5) continually improved with the
330 inclusion of additional reticulation events, and the network with ten reticulations (Fig. 2A) had
331 the best score. Although the best-scored network showed complicated and nested reticulation
332 patterns (Fig. 2A), there are several clear patterns among most networks (Fig. S6). *Flaveria*
333 *brownii* (C₄-like) and *F. pringlei* (C₃) were consistently recovered as hybrids in all ten networks
334 (Fig. S6). In both cases, parental lineages and inheritance probabilities were consistent across
335 networks. Other reticulation patterns recovered across networks were the hybrid origin of clades
336 A (mainly C₄ and C₄-like) and B (mainly C₃-C₄), which both had *F. sonorensis* (C₃-C₄; itself a
337 hybrid in some networks) and *F. angustifolia* (C₃-C₄; or closely related to lineage) as potential
338 parental lineages. The last reticulation event recovered in all networks involved the C₃ species *F.*
339 *cronquistii* and *F. robusta* which were potential parental lineages of all remaining *Flaveria*
340 species. The analyses of the 16-taxon data set (Fig. S6) resulted in a best-scoring network with
341 five reticulation events (Fig. 2B). This showed patterns like the 18-taxon dataset regarding the
342 hybrid origin of clades A and B, and the deep reticulation involving *F. cronquistii* (C₃) and *F.*
343 *robusta* (C₃). Also, it recovered a reticulation event (consistent with the 18-taxon dataset) where
344 *F. vaginata* (C₄-like) and *F. kochiana* (C₄) within Clade A had a hybrid origin.

345



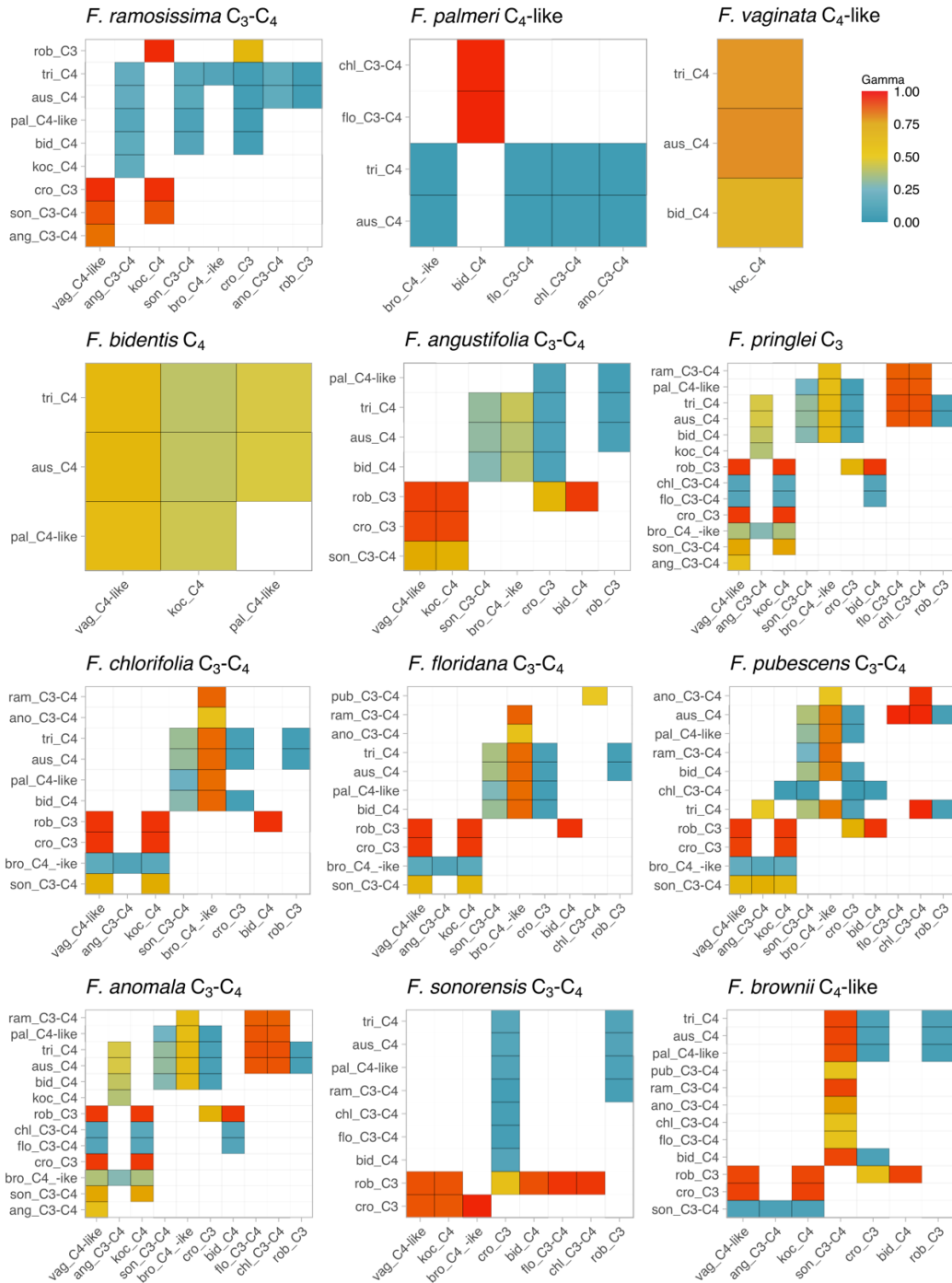
346

347 **Fig. 2.** *Flaveria* species networks with the best maximum pseudo-likelihood scores with PhyloNet for the
348 (A) 18-taxon and (B) 16-taxon data sets. Species names are colored by photosynthetic type. Red and blue
349 curved branches indicate the minor and major edges, respectively, of hybrid nodes. Numbers next to
350 curved branches indicate inheritance probabilities for each hybrid node.

351

352 The HyDe analysis of all possible triples using the 17 species of *Flaveria* resulted in
353 2,040 hybridization tests, of which 311 triples were significant (Table S2). The analyses without
354 *F. pringlei* (C_3) resulted in 247 significant hybridization tests of 1,680 overall tests (Table S3).
355 HyDe analyses detected 12 species as potential hybrids (Fig. 3). These species included all
356 members of Clade B which comprises five C_3 - C_4 and one C_4 -like species. Hybrids detected in
357 Clade B had several potential parental lineages from across *Flaveria* and admixture (γ) values
358 were either closer to zero or one (Fig. 3). *Flaveria chlorifolia*, *F. floridana*, *F. pubescens*, *F.*
359 *anomala* showed similar hybridization patterns consistent with a single ancient hybrid origin of
360 these species as shown in the PhyloNet analyses. On the other hand, *F. sonorensis* and *F.*
361 *brownii* showed hybridization patterns different from the rest of the species of the clade,
362 suggesting their independent hybrid origins as also seen in the PhyloNet analyses. In Clade A,
363 and unlike PhyloNet, HyDe detected only four instances of hybridization. These included the C_3 -
364 C_4 species *F. ramosissima* and the two C_4 -like species, *F. vaginata* and *F. palmeri*, of the clade.

365 In these three cases γ was consistent with ancient hybridization. *Flaveria vaginata* had notably
366 fewer potential parental lineages suggesting a more recent reticulation event. The fourth species,
367 *F. bidentis*, was the only C₄ member of the clade which was detected as a hybrid. In this case, all
368 potential parental lineages are members of Clade A, and γ values around 0.5 suggested a recent
369 reticulation event. Outside clades A and B, *F. angustifolia* (C₃-C₄) and *F. pringlei* (C₃) were
370 detected as hybrids. In both cases, the potential parental lineages come from across *Flaveria* with
371 γ values suggesting ancient reticulation. Overall, HyDe detected all C₃-C₄ and C₄-like species as
372 well as *F. bidentis* (C₄) and *F. pringlei* (C₃) as potential ancient hybrids.



373

374 **Fig. 3.** HyDe significant hybridization test for the 12 species of *Flaveria* identified as potential hybrids.
 375 Species on the x-axis are parental lineage 1 (P1) and species on the y-axis are parental lineage 2 (P2).
 376 Only colored boxes denote possible combinations of P1 and P2 as parents of hybrid species. The color
 377 scale represents the value of the hybridization parameter γ for each hybridization event. Recent 50:50
 378 hybrids would be represented by a $\gamma \sim 0.5$. Values of γ approaching 0 indicate a major hybrid contribution
 379 from P1, and values approaching 1 indicate a major hybrid contribution from P2, with both cases
 380 representing ancient hybridization.

381 **Lack of whole genome duplications**

382 The orthogroup mapping did not reveal any node in *Flaveria* with elevated levels of gene
383 duplication (Fig S7), showing the absence of whole genome duplication in the genus. In part this
384 is expected as *Flaveria* is consistently diploid (see Powell, 1978 and ref. therein) with a haploid
385 chromosome number of $n = 18$. Furthermore, the lack of whole genome duplication in *Flaveria*
386 suggests that reticulation events in this group are homoploid hybridizations.

387

388 **DISCUSSION**

389 In C_4 photosynthesis, high rates of net photosynthesis and a highly competitive water and
390 nitrogen use efficiency are achieved by spatially separated carbon fixation in the outer mesophyll
391 cells preceding the Calvin-Benson cycle, and by effectively fueling Rubisco with always high
392 CO_2 concentration in the controlled seclusion of the Kranz cells (Long, 1999). Resulting low
393 levels of photorespiration make C_4 plants competitive in various stressful environments where
394 carbon deficiency poses a problem to C_3 plants (Sage et al., 2012). C_4 evolved more than 60
395 times in angiosperms with hotspots of C_4 origins in Poaceae and Amaranthaceae (Sage et al.,
396 2018). Due to the anatomical and gene regulatory complexity of the C_4 pathway, it seems clear
397 that there must have been intermediate stable phenotypes during the evolution of C_4 from a C_3
398 ancestor (Monson and Moore, 1989). The established generalized model of C_4 evolution tries to
399 explain the sequence of intermediate adaptive events during the transition from the ancestral C_3
400 to C_4 using the naturally occurring C_3 - C_4 intermediate phenotypes of *Flaveria* (and other
401 lineages) as proxies of intermediate stages in C_4 evolution (Sage et al., 2014; Bräutigam and
402 Gowik, 2016). However, *Flaveria* is also known for rampant interfertility of its 21 (mostly
403 diploid) species (Long and Rhamstine, 1968; Powell, 1978), and for the transferability of

404 photosynthetic traits to hybrid offspring in hybridization experiments (Apel et al., 1988; Kadereit
405 et al., 2017 and ref. therein). Therefore, a clear understanding of the phylogenetic history of this
406 model lineage of C₄ evolution, including tests for possible reticulate evolution, is fundamental as
407 this might have strong implications for our understanding of the evolution of C₄ photosynthesis
408 in general.

409 Our analyses using transcriptome data of 17 *Flaveria* species revealed rampant gene tree
410 discordance along the backbone of the phylogeny as well as the clades containing most C₃-C₄
411 intermediate and C₄-like species (clades A and B; visualized in the cloudogram in Fig. 1).
412 Coalescence simulations showed that gene tree discordance in *Flaveria* cannot be attributed to
413 ILS alone. Our initial species network analyses including all 17 species sampled consistently
414 identified *Flaveria brownii* (C₄-like) and *F. pringlei* (C₃) as hybrids (Figs. 2 and 3). After
415 exclusion of these two most likely recent hybrids, deep reticulation events were recovered more
416 clearly. The network analyses of the remaining species suggested an early reticulation event
417 between two C₃ lineages (*F. robusta* and *F. cronquistii*) giving rise to the ancestor of the lineage
418 containing all C₃-C₄ intermediate species, C₄-like species and C₄ species. This result is supported
419 by the HyDe analysis which identified all C₃-C₄ and C₄-like species as potential ancient hybrids.
420 The ancestors of *F. robusta* and *F. cronquistii* seem to have contributed equally to the origin of
421 the hybrid lineage (Fig. 2). Within this lineage there exist two parental lineages, *F. angustifolia*
422 (C₃-C₄) and *F. sonorensis* (C₃-C₄), that seem to have contributed to a robust clade containing all
423 C₄ species plus *F. ramosissima* (C₃-C₄) and *F. vaginata* (C₄-like; clade A in Fig. 1), and also to
424 another robust clade of four C₃-C₄ intermediate species (*F. pubescens*, *F. chlorifolia*, *F.*
425 *floridana*, *F. anomala*; partial clade B in Fig. 1; supported also by the HyDe analysis). Of these
426 four species, *F. anomala* was introgressed by the ancestor of clade A (Fig. 2).

427 These results have several important implications that will be discussed in the following
428 three sections: 1) natural C₃-C₄ intermediates species in *Flaveria* do not seem to result from
429 hybridization between a C₃ and a C₄ lineage (as similar C₃-C₄ intermediate phenotypes resulting
430 from crossing experiments might suggest); 2) recurrent homoploid hybridization possibly played
431 a major role in the evolution of C₄ photosynthesis in *Flaveria* with an initial hybridization event
432 between two C₃ species (*F. robusta* and *F. cronquistii*) as a possible trigger, 3) only the ancestral
433 lineages of *F. angustifolia* and *F. sonorensis* (both C₃-C₄ intermediates) seem to be involved in
434 the formation of clades A and B, of which only clade A shows C₄ photosynthesis.

435 Hybridization is an important factor in plant evolution and speciation in general (Abbott
436 et al., 2013) and *Flaveria* is no exception to this but also shows hybridization in a more complex
437 way than we expected. From the phenotypic outcome of the numerous C₃ × C₄ hybridization
438 experiments in *Flaveria* it was conceivable that naturally occurring C₃-C₄ intermediate species
439 might be the result of crosses between parental lineages with different photosynthetic types
440 (Monson and Moore, 1989; Kadereit et al., 2017). However, our results indicate that origin of
441 C₃-C₄ intermediates might be more complex: in *Flaveria* there are several recent hybrids
442 expressing intermediate or deviating phenotypes compared to the parental lineages which perturb
443 phylogenetic reconstruction (in particular, *F. pringlei* and *F. brownii*). There also were ancient
444 hybridization events challenging the reconstruction of the backbone (Fig. 1; see below).
445 McKown et al. (2005) and Lyu et al., 2015 interpreted *F. brownii* as representing an independent
446 and recent origin of C₄-like photosynthesis from C₃-C₄ ancestors. According to our analyses, *F.*
447 *brownii* is a recent hybrid between *F. sonorensis* (C₃-C₄) and one of the other species in clade B
448 (all C₃-C₄; Fig. 1–3), probably *F. floridana* with which it forms fertile F1 and F2 hybrids
449 (Powell, 1978). This is an important finding for the interpretation of trait evolution in *Flaveria*.

450 The C₄-like photosynthesis in *F. brownii* seems to have resulted from a cross between a C₂ type I
451 (*F. sonorensis*) and C₂ type 2 species (possibly *F. floridana*; see Table 1) resulting in stronger
452 C₄-ness of *F. brownii*. Since *F. brownii* possesses C₃ isoforms of the key enzymes of the C₄
453 pathway (e.g., Kubien et al., 2008; Gowik and Westhoff, 2011; Ludwig, 2011), the C₄-like
454 metabolism in *F. brownii* seems to have resulted from a highly effective gene regulatory change
455 in comparison to its parental lineages rather than from the acquisition of C₄ isoforms. It clearly
456 outcompetes its parental lineages in terms of C₄ physiology. Taniguchi et al. (2021), studying
457 genome size evolution in *Flaveria*, showed dynamic alteration of genome size in the genus with
458 *F. brownii* having the largest genome size among the 11 species investigated. Rewiring the
459 parental genomes might have led to the C₄-like phenotype found in *F. brownii* and might have
460 facilitated adaptive divergence resulting in colonization of the coastal flats and islands of the
461 lower Texas Gulf Coast. Similarly, our analyses revealed *F. pringlei* (C₃ proto-kranz) as a recent
462 hybrid between *F. cronquistii* (C₃) and *F. angustifolia* (C₃-C₄; Fig. 1-3). Therefore, the proto-
463 kranz phenotype in this species might be of different origin than that of *F. robusta* (Table 1). In
464 fact, Lyu et al. (2015) showed the *F. pringlei* sample used in their study to be of artificial hybrid
465 origin (possibly resulting from unintended crosses in the greenhouse). Trait assessments in these
466 two species, e.g., of leaf anatomical and ultrastructural traits (McKown and Dengler, 2007; Sage
467 et al., 2013) might lead to re-evaluation of their assessment as evolutionary “basal” as they likely
468 acquired the proto-kranz phenotype differently. Also, the similarities between *F. cronquistii* and
469 *F. pringlei* found by McKown and Dengler (2007) and their differences to *F. robusta* can now be
470 explained. According to our analyses, *F. robusta* and *F. cronquistii* seem to be representatives of
471 ancient C₃ lineages in *Flaveria*, but not *F. pringlei*. The rare *Flaveria mcdougallii* (C₃, not
472 represented in this analysis), which is morphologically and geographically distinct and might be

473 sister to all other species of *Flaveria* (Powell, 1978; McKown et al., 2005), would be an
474 important species to add in further studies.

475 The most ancient hybridization event in *Flaveria* involved two C_3 lineages, *F. robusta*
476 and *F. cronquistii*. According to Powell (1978), *Flaveria cronquistii* most closely resembles *F.*
477 *robusta*. The two are geographically separated, and the former is distributed in the Tehuacán
478 Valley region and the latter in Colima and Michoacán (both Mexico). There are no reports of
479 artificial hybridization between these two species. The resulting ancient hybrid lineage seems to
480 include all C_3 - C_4 intermediate, C_4 -like and C_4 species (Fig. 2; Table 1). Concerning leaf
481 anatomy, *Flaveria robusta* differs from *F. cronquistii* by a higher vein density achieved through
482 higher vein branching, and by a higher number of organelles in the bundle sheath cells where the
483 organelles are located in a centripetal position along the cell wall connecting bundle sheath cells
484 and vascular tissue. Organelles are more evenly distributed in *F. cronquistii*, and its leaves are
485 more succulent and show larger bundle sheath cells (McKown and Dengler, 2007; Sage et al.,
486 2013). The combination of these traits in a hybrid lineage and subsequent segregation effectively
487 leading to a higher bundle sheath to mesophyll ratio and activated large bundle sheath cells may
488 have triggered the evolution of “pre kranz” cells in *Flaveria*. Possibly the strong leaf anatomical
489 differences between the two parental lineages promoted the origin of novel traits which then
490 allowed this lineage to occupy new niches eco-geographically separate from the parents. There
491 are multiple examples for plant lineages in which homoploid hybridization resulted in potentially
492 adaptive genotypes through transgressive segregation, eventually leading to speciation (Gross
493 and Rieseberg, 2005; Nieto Feliner et al., 2020). An increase of the bundle sheath to mesophyll
494 ratio has been suggested to play an initial role in the evolution of C_4 in several plant lineages

495 (Marshall et al., 2007; McKown and Dengler, 2007; Christin et al., 2013; Griffiths et al., 2013;
496 Lauterbach et al., 2019).

497 Two C₃-C₄ intermediate lineages, *F. angustifolia* and *F. sonorensis*, are involved in the
498 formation of clades A and B according to our results. It is remarkable that only these two and not
499 any other species (especially not the C₄-like species) contributed to the origin of these clades. In
500 their extant distribution the two species do not overlap. *Flaveria angustifolia* grows in
501 sclerophyllous scrub in Puebla and Oaxaca, while *F. sonorensis* is found only in the short-tree
502 forests of tropical Sonora (Powell, 1978). Looking more closely at these two descendants of the
503 lineages that seem to have hybridized in the past and possibly gave rise to C₄ photosynthesis
504 might give new insights into important preconditions for the evolution of C₄ in *Flaveria*. Both *F.*
505 *angustifolia* and *F. sonorensis* were categorized as C₂ Type I species (Table 1), but with weaker
506 C₂ photosynthesis (relatively high amounts of glycine decarboxylase in the mesophyll cells and
507 relatively high CO₂ compensation points) than other C₂ species of *Flaveria* (Sage et al., 2018).
508 This finding implies the evolution of a C₂ phenotype prior to C₄, supporting the ‘photorespiratory
509 bridge hypothesis’ (Sage et al., 2018) in case of *Flaveria*. However, it seems that C₄ evolution in
510 *Flaveria* was triggered by hybridization of C₂ lineages, a scenario never suggested before. For
511 *Flaveria* this somewhat shifts the focus to C₂ photosynthesis and under which selective
512 conditions this type of photosynthesis might have evolved. To gain further insights into the
513 evolution of C₂ photosynthesis, detailed studies of the origin, anatomy, and ecophysiology of *F.*
514 *angustifolia* and *F. sonorensis* might be rewarding. Organelle enrichment and their flux-
515 optimized positioning as well as glycine decarboxylase accumulation in the proto-kranz cells
516 (Khoshravesh et al., 2016) seem to be essential for C₂ photosynthesis (in eudicots and
517 monocots). These traits enable species to more efficiently re-cycle respired CO₂ and to longer

518 maintain a positive assimilation rate under carbon deficient conditions. Since the majority of C₄
519 lineages do not have any known C₂ relatives (see Sage et al., 2018 for an overview), and C₂
520 lineages without close C₄ relative are known as well (see Lundgren, 2020 for an overview), the
521 question remains whether there exist several evolutionary pathways to C₄ photosynthesis
522 (Edwards, 2019), and whether C₂ should be considered an independent carbon concentrating
523 mechanism not necessarily always intimately connected to C₄ photosynthesis (Lundgren, 2020
524 and ref. therein). Finally, a C₂ lineage might also be the result of ancient hybridization of a C₃
525 and a C₄ lineage, as has been suggested for *Salsola divaricata*, which then might have thrived
526 through the large plasticity of photosynthetic traits inherited from photosynthetically divergent
527 parental lineages (Tefarikis et al., 2021).

528

529 CONCLUSIONS

530 The young genus *Flaveria* which includes four C₃, four C₄, three C₄-like and c. ten C₃-C₄
531 intermediate species is remarkable for the high number of evolutionary reticulations creating an
532 enormous diversity of phenotypes with different photosynthetic traits. Due to this and its strictly
533 diploid chromosome number the genus is a highly interesting system to study the genetic basis of
534 the C₄ syndrome and the role of transgressive segregation in the origin of genotypes eventually
535 leading to the evolution of C₄ photosynthesis. We found evidence that homoploid hybridization
536 of C₃ lineages might have triggered the evolution of C₂ photosynthesis, and that homoploid
537 hybridization of C₂ lineages gave rise to C₄-like or C₄ photosynthesis. In both cases the hybrid
538 derivatives possibly surpassed the parental performance under conditions of high
539 photorespiration and had an adaptive advantage. However, since reticulation occurred in recent
540 as well as ancient lineages of the genus, the sequence of evolutionary events needs to be studied

541 in the light of a carefully reconstructed phylogenetic history of the genus. Comparison of the
542 entire genomes of parental and hybrid lineages should allow us to detect whether the origin of
543 new photosynthetic traits is indeed the result of transgressive segregation (de los Reyes, 2019),
544 as suggested here, or of stepwise mutational change of relevant genes.
545

546 **DATA AVAILABILITY STATEMENT**

547 Analysis and results files can be accessed at the Dryad repository XXXX

548

549 **CONFLICT OF INTEREST**

550 The authors declare no conflict of interest.

551

552 **AUTHOR CONTRIBUTIONS**

553 GK and DFM-B conceived the study. DFM-B performed all analyses. GK and DFM-B evaluated

554 the results and wrote the paper.

555

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568 **SUPPLEMENTARY MATERIAL**

569 **Table S1.** Taxon sampling and source of data

570

571 **Table S2.** HyDe significant hybridization tests for all species of *Flaveria*.

572

573 **Table S3.** HyDe significant hybridization tests for all species of *Flaveria* excluding *F. pringlei*

574 (C_3).

575

576 **Fig. S1.** A. Maximum likelihood phylogeny of *Flaveria* inferred with IQ-TREE from the
577 concatenated 1249-nuclear gene supermatrix. Numbers above branches represent bootstrap
578 support (BS). Branch lengths as substitutions per site (scale bar on the bottom). B. ASTRAL tree
579 of *Flaveria* inferred from the 1,295 nuclear gene trees. Local posterior probabilities (LLP) are
580 shown next to nodes. Internal branch lengths are in coalescent units (scale bar on the bottom).

581

582 **Fig. S2.** A. Maximum likelihood cladogram of *Flaveria* inferred with IQ-TREE from the
583 concatenated 1249-nuclear gene supermatrix. B. ASTRAL cladogram of *Flaveria* inferred from
584 the 1,295 nuclear gene trees. Pie charts represent the proportion of gene trees that support that
585 clade (blue), the main alternative bifurcation (green), the remaining alternatives (red), and
586 conflict or support that have <50% bootstrap support (gray). Number above and below branches
587 represent the number of concordant and discordant informative gene trees, respectively.

588

589 **Fig. S3.** A. Maximum likelihood cladogram of *Flaveria* inferred with IQ-TREE from the
590 concatenated 1249-nuclear gene supermatrix. B. ASTRAL cladogram of *Flaveria* inferred from

591 the 1,295 nuclear gene trees. Quartet Sampling (QS) scores are shown above branches. QS
592 scores: Quartet concordance/Quartet differential/Quartet informativeness. Circles at nodes are
593 colored by quartet concordance support.

594

595 **Fig. S4.** Distribution of tree-to-tree distances between empirical gene trees and the ASTRAL
596 tree, compared to the distribution of tree-to-tree distances between simulated trees and the
597 ASTRAL tree.

598

599 **Fig. S5.** Maximum pseudo-likelihood scores for species networks inferred with PhyloNet using
600 the (A) 18-taxon, (B) and 16-taxon data sets. The x-axis notes the maximum number of
601 reticulations for each of the network searches allowing up to ten reticulation events.

602

603 **Fig. S6.** Maximum pseudo-likelihood species networks inferred with PhyloNet using the (A) 18-
604 taxon, (B) and 16-taxon data sets and allowing up to ten reticulation events. Red and blue curved
605 branches indicate the minor and major edges, respectively of hybrid nodes. Numbers next to
606 curved branches indicate inheritance probabilities for each hybrid node.

607

608 **Fig. S7.** Maximum likelihood cladogram of *Flaveria* inferred with IQ-TREE from the
609 concatenated 1249-nuclear gene supermatrix. Numbers above branches are gene duplication
610 counts and numbers below branches are gene duplication percentages.

611

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