Herbarium-based phylogenomics reveals that the Andes are a biogeographic barrier for *Otoba* (Myristicaceae), an ecologically dominant Neotropical tree genus

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Abstract

• Premise of the study — Universal probesets for targeted sequence capture have facilitated phylogenomic research into diverse plant groups with limited genomic resources, including from low-quality DNA typical of herbarium specimens. Here, we leverage the Angiosperms353 loci to infer the first phylogeny of *Otoba* (Myristicaceae), a Neotropical tree genus that is ecologically dominant in low-to-mid elevation wet forests, exclusively from herbarium specimens.

• Methods— We use a combination of Angiosperms353 loci, obtained via targeted sequence capture, and plastid sequences to resolve the phylogeny of *Otoba* using concatenated and species tree methods. We subsequently use this phylogeny to infer biogeography and trait evolution using phylogenetic comparative methods.

• Key results— Recovery success of loci is correlated with age of herbarium specimens and average annual precipitation. Despite a large amount of missing data, we resolve the phylogeny of *Otoba* into three major subclades, each structured by geography. We show that *Otoba*'s crown radiation occurred on the western slopes of the Andes in the late Miocene, and from there, migrated into Central America at least twice; the genus was only able to cross to the eastern slopes of the Andes a single time. Trait evolution has been dynamic across vegetative and reproductive traits, with multiple origins of most discrete traits investigated, including ecologically important aril color.

• Conclusions — *Otoba* is recent, rapid radiation whose evolution is tied to landscape change, including Andean uplift, in the northern Neotropics. Its dynamic morphological evolution is consistent with sorting of ancestral traits during recent speciation events. In one of the first herbariomic studies exclusively using herbarium tissue from specimens collected in the wet tropics, this study demonstrates the promise of Angiosperms353 loci in resolving shallow species-level relationships, even from low-quality DNA.

Keywords

Amazonia; Chocó; herbariomics; Magnoliales; museum-based research; natural history collections; Neotropics; phylogeny; seed dispersal

The Northern Neotropics experience a dramatic recent geological history, punctuated by periods of rapid mountain uplift in the Andes (Hoorn et al., 2010) and Central America (De Boer et al., 1995) and a potentially gradual closing of the Isthmus of Panama (Bacon et al., 2015; O'Dea et al., 2016). Among the more notable geographic features of the Neotropics are the Andean mountains of western South America, the longest north-to-south oriented mountain chain in the world and the second tallest of any globally. These mountains began their rise in the Paleocene, but major bursts of mountain building occurred more recently, 4 to 12 My ago. This uplift not only changed local topography, but also impacted continental-scale climate and the entire landscape of the Neotropics (Hoorn et al., 2010). It is thus not surprising that the Andes are known to be important in structuring biogeography and species relationships in plants that occur in montane Andean habitats (Pennington et al., 2010; Särkinen, Pennington, et al., 2012; Lagomarsino et al., 2016; Hoorn et al., 2019), as well as in extra-Andean plants, including lowland tropical rainforest plants of the Amazon basin (Antonelli et al., 2009; Dick et al., 2012).

Both the Isthmus of Panama and the Andean mountains are important geological features of the northern Neotropics that promote speciation in allopatry following long distance dispersal (Gentry, 1982; Antonelli et al., 2009). Given their height and extreme habitat heterogeneity, the Andean mountains are a particularly important barrier to species movement, especially to tropical species that typically have relatively limited environmental preferences (Janzen, 1967). While there are widespread species that occur on either side of the Andes, including *Cordia alliodora* (Boraginaceae) (Rymer et al., 2013), *Symphonia globulifera* (Clusiaceae) (Dick and Heuertz, 2008), and *Schizolobium parahyba* (Fabaceae) (Turchetto-Zolet et al., 2012), it is more common that genera, not species, have trans-Andean distributions. Many of these groups are also found in Central America, which may have been facilitated by the closing of the Isthmus of Panama between 3 and 15 Mya (Coates and Stallard, 2013; Bacon et al., 2015). Myristicaceae, a pantropical family of mid-canopy and canopy trees with high species richness in the Neotropics (ter Steege et al., 2006), includes multiple genera with trans-Andean distributions.

Across their full diversity (comprising 21 genera and *ca.* 500 species), Myristicaceae are notable for their importance in ethnobotany, including as food plants (e.g., nutmeg and mace, *Myristica fragrans*), timber species (e.g., *Virola surinamensis*), and hallucinogenic drugs (e.g., epená, *Virola* sp. (Alrashedy and Molina, 2016)). Myristicaceae also have multidimensional ecological importance. For example, due to their large, arillate seeds, they are some of the most important food sources in the lowland tropics for large-bodied birds, such as toucans and mot-mots, primates, and bats, which, in turn, act as important seed dispersers (Forget et al., 2000;

Russo, 2003; Giraldo et al., 2007; Melo et al., 2009; Moreira et al., 2017). Though pollination is less well studied, the small, usually imperfect flowers, of which thousands can be in bloom at a single time on an individual plant (Kanstrup and Olesen, 2000), are known to be generalist pollinated by various small insects including beetles, flies, and thrips in *Myristica* (Armstrong and Irvine, 1989; Sharma and Armstrong, 2013), *Virola* (Jardim and Mota, 2007). A similar set of small, generalist pollinators is likely common throughout the distribution of the family. Myristicaceae are usually dioecious, with individual plants producing either carpellate or staminate flowers, which results in differential resource allocation, with pistillate plants (which give rise to the fruit) investing more in stem growth than staminate plants (Queenborough et al., 2007a). Further, the six Neotropical genera of Myristicaceae, *Bicuiba*, *Compsoneura*, *Iryanthera*, *Osteophloeum*, *Otoba*, and *Virola*, are important components of wet tropical forests at low to mid-elevations, and individual species can be among the most abundant in lowland tropical rainforests (ter Steege et al., 2006). Neotropical Myristicaceae are an important system for understanding the ecological processes that allow species co-existence in hyperdiverse communities in the western Amazon Basin (Queenborough et al., 2007b; c).

Despite its relatively low species richness, *Otoba* (Fig. 1) has among the broadest ecological tolerances of all Neotropical Myristicaceae. This genus of *ca.* 10 species are distributed from Nicaragua to Brazil, with the highest species richness in low Andean montane forests and lowland rainforests, especially of the Chocó region and western Amazon (Santamaría-Aguilar, Jiménez, et al., 2019). They are abundant in low Andean montane forest, and include the highest elevation occurrence of any member of Myristicaceae (Jaramillo-Vivanco and Balslev, 2020). However, species can also be found in lowland rainforests, and *Otoba* is one of the ten most abundant genera in western Amazonia (ter Steege et al., 2006; Guevara Andino et al., 2017). Individual species can be some of the most common in many forests, including *O. parvifolia* in Madre de Díos, Peru (Pitman et al., 2017; Swamy, 2017) and Madidí, Bolivia (Macía, 2008), *O. glycycarpa* in Yasuní, Ecuador (Guevara Andino et al., 2017), and high várzea forest of the Amazonian floodplain in Brazil and Bolivia (Wittmann et al., 2006). *Otoba parvifolia*, a wide-spread species of the Western Amazon, shows high intraspecific genetic differentiation (Honorio Coronado et al., 2019).

Otoba is distinct among Myristicaceae in many regards. Like other members of the nutmeg family, *Otoba* is characterized by a strong aromatic scent from essential oils, a pagoda-like growth form (i.e., “Myristicaceous growth”, or Massart’s model (Hallé et al., 1978)), dioeciousness with small, trimerous flowers (Armstrong and Tucker, 1986) (Fig. 1A-C), red, dilute latex (Fig. H), and a characteristic valvate capsule that opens to reveal a large, arillate

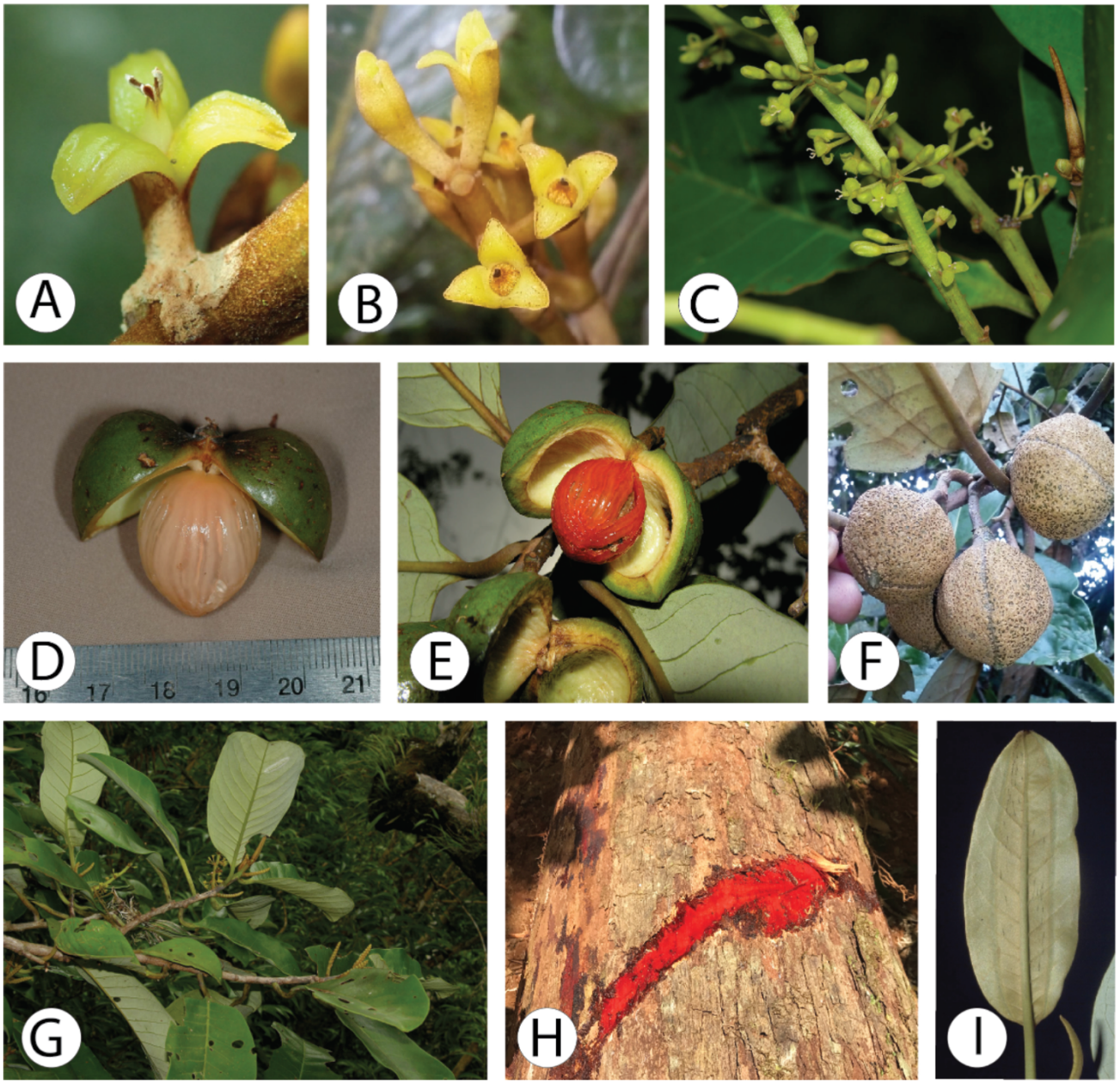

Figure 1. Morphological diversity of *Otoba*. A-C) Floral diversity. A) Staminate and B) pistillate flowers of O. gordoniifolia; C) Infloresence of Central American O. novogranatensis. D-F) Fruit diversity. D) Fruit from South American O. novogranatensis showing whitish aril and E) from Central American O. novogranatensis showing red aril. F) Unopened capsules of O. gordoniifolia. G-I) Vegetative diversity. G) Branch and H) stem cut of Central American O. novogranatensis, the latter showing characteristic red exudate. I) Leaf of O. parvifolia, showing vernation lines. (Photo credits: A, B, and F by Rudy Gelis, downloaded from iNaturalist with permission; C, E, G, and H by Reinaldo Aguilar; D by Timothy Paine; and I by John Janovec.)

seed (Fig. 1D-E). However, *Otoba* can be distinguished from these genera by a variety of traits. Within Neotropical Myristicaceae, *Otoba* is notable for its low-montane distribution (vs. the more common lowland rainforest) and seeds that most commonly have white arils (vs. typically brightly colored, as in mace). It has bifacial pollen with continuous tectum on the distal pole and reticulate tectum on the proximal pole (Sauquet and Le Thomas, 2003), a unique set of characters within Myristicaceae that is more similar to African members of the family than other Neotropical genera. It is also the only genus of Neotropical Myristicaceae with conduplicate vernation (Fig. 1).

These differences are perhaps not surprising given its relatively distant relationship to other Neotropical Myristicaceae. Myristicaceae is sister to the rest of Magnoliales (Qiu et al., 2006; Soltis et al., 2007; Massoni et al., 2014), a magnoliid clade that represents one of the oldest angiosperm orders (Magallón et al., 2015). Compared to other families within its order, Myristicaceae have low levels of genetic diversity. This may be a product of the relatively recent origin of extant Myristicaceae, compared to other Magnoliales, in the Miocene or late Oligocene (15–18 My: (Doyle et al., 2004; Massoni et al., 2015). This is corroborated by recent molecular dating analyses across angiosperms that suggest that the family originated at least 20 My after the crown-group of Magnoliales at 109 My (Magallón et al., 2015). Despite these young molecular age estimates, fossil evidence suggests that the family has existed since at least the early Eocene, though it is possible that *Myristicacarpum chandlerae* represents a stem lineage (Doyle et al., 2008). Within the family, Myristicaceae is split into three major clades: the Malouchoids, Pycnathoids, and Myristicoids (Doyle et al., 2004). While most Neotropical members of this family are included in the Myristicoids, *Otoba* is nested within the otherwise African Pycnathoids. This, with the relatively young crown age of Myristicaceae, suggests that it represents the product of long-distance dispersal to the Neotropics from Africa, followed by in-situ diversification (Sauquet et al., 2003; Doyle et al., 2004).

Despite their ecological importance and past work into the phylogeny of Magnoliales and Myristicaceae, there is no species-level phylogeny of *Otoba* to date. Further complicating this endeavor, species of *Otoba* are morphologically similar and, as is common for tropical trees, poorly represented in herbaria, making systematic treatment challenging (Gentry, 1979; Bebber et al., 2010).Like many other primarily tropical groups, Myristicaceae has few genomic resources, with only a single publicly available transcriptome (*Myristica fragrans*; (Carpenter et al., 2019). Luckily, the recent development of universal probe sets that target loci of phylogenetic utility across angiosperms, including Angiosperms353, has facilitated the phylogenomic analysis of such understudied lineages. Further, the molecular technique they

148 rely upon, targeted sequence capture, is robust to the low-quantity, low-quality DNA from
149 herbarium specimens. This is important, as inclusion of herbarium specimens is often necessary
150 to achieve robust taxon sampling for clades that grow in regions that are difficult to reach or to
151 collect in for a variety of reasons, including international collaborations, government permitting,
152 or regional unrest (Rabeler et al., 2019). While herbarium specimens serve as a valuable
153 resource to improve taxonomic sampling, DNA from herbarium specimens collected in the wet
154 tropics have been shown to perform relatively poorly due to preservation issues (Brewer et al.,
155 2019) posing a challenge to robust genetic sampling. We take advantage of the universal nature
156 of the Angiosperm353 probeset to infer the first phylogenetic hypotheses for *Otoba*. This is also
157 the first phylogenomic study that relies exclusive on DNA extracted from herbarium specimens
158 collected in the wet tropics. Using this phylogenetic framework, we discuss implications for
159 biogeography and trait evolution of *Otoba*.
160
161 MATERIALS AND METHODS
162 ***Taxon Sampling***
163 Twenty accessions of *Otoba* representing nine (*O. acuminata, O. cyclobasis, O. glycycarpa, O.*
164 *gordoniifolia, O. gracilipes, O. latialata, O. novogranatensis, O. parvifolia, and O. vespertilio*) of
165 the ten accepted species and two undescribed species (*Otoba* sp. nov.) were sampled. All
166 accessions came from herbarium specimens; voucher information may be found in Appendix S1
167 (see the Supplemental Data with this article). Herbarium acronyms follow Index Herbariorum
168 (Thiers, constantly updated: http://sweetgum.nybg.org/science/ih/). To serve as outgroups, data
169 from the following transcriptomes available on 1KP project (Carpenter et al., 2019; One
170 Thousand Plant Transcriptomes Initiative, 2019); <https://db.cngb.org/onekp/>) were gathered
171 for Myristicaceae (*Myristica fragrans*), the broader Magnoniales (*Magnolia maudiae*, *Annona*
172 *muricata*), and Laurales (*Cassytha filiformis*, *Sassafras albidum*, and *Persea borbonia*).
173
174 ***DNA extraction, library prep, target enrichment, and sequencing***
175 Dried leaf tissue was weighed to obtain 500 mg, and tissue was homogenized using an MP
176 Biomedicals FastPrep-24TM 5G Instrument. DNA extraction followed a modified sorbitol
177 extraction protocol (Štorchová et al., 2000). Double-stranded DNA concentration was quantified
178 using an Invitrogen Qubit 4 Fluorometer, and fragment size was assessed on a 1% agarose gel.
179 For samples with a high concentration of large fragments (>800 bp), the DNA was sheared
180 using a Bioruptor Pico (Diagenode Inc., Denville, New Jersey, United States) to obtain an
181 average fragment size of ~ 500 bp. Library preparation was carried out using KAPA Hyper Prep

182 and KAPA HiFi HS Library Amplification kits (F. Hoffmann-La Roche AG, Basel, Switzerland)
183 and with iTru i5 and i7 dual-indexing primers (BadDNA, University of Georgia, Athens, Georgia,
184 United States). Library preparation with KAPA Hyper Prep followed the manufacturer's protocol
185 (KR0961 – v8.20), except for the following modifications: reaction volumes were halved (25 µL
186 starting reaction, instead of 50 µL), and bead-based clean-ups were performed at 3X volume
187 rather than 1X volume to preserve more small fragments from degraded samples. Library
188 amplification reactions were performed at 50 µL. Target enrichment was carried out using the
189 MyBaits Angiosperms353 universal probe set (Däicel Arbor Biosciences, Ann Arbor, MI;
190 (Johnson et al., 2019)). Target enrichment followed the modifications to the manufacturer's
191 protocol outlined in (Hale et al., 2020); i.e., pool of 20-24 samples and RNA baits diluted to ¼
192 concentration). Unenriched DNA library was added to the cleaned, target enriched pool to
193 increase the amount of off-target, chloroplast fragments in the sequencing library. DNA libraries
194 were sent to Novogene Corportation Inc., (Sacramento, California, United States) for
195 sequencing on an Illumina Hiseq 3000 platform with 150 bp paired-end reads.
196
197 ***Sequence processing, assembly, and alignment***
198 Raw sequence reads were demultiplexed by Novogene Corportation Inc., (Sacramento,
199 California, United States). Adapter sequence removal and read trimming were performed using
200 illumiprocessor v2.0.9 (Faircloth et al., 2012; Faircloth, 2016), a wrapper for trimmomatic v0.39
201 (Bolger et al., 2014). The default settings were used and reads with a minimum length of 40 bp
202 kept.
203 HybPiper v. 1.3.1 (Johnson et al., 2016) was used to assemble and extract target
204 regions. Read mapping, contig assembly and coding sequence extraction were performed
205 running the reads_first.py script. The intronerate.py script was run to extract introns and
206 intergenic sequences flanking targeted exons. The retrieve_sequences.py script was run first
207 with the "dna" argument to extract coding regions and subsequently with the "supercontig"
208 argument to extract both coding and non-coding regions as a single concatenated sequence for
209 each target gene. Individual genes were aligned using MAFFT v. 7.310 (Katoh and Standley,
210 2013). Alignments were visually inspected in AliView v. 1.18.1 (Larsson, 2014) to identify
211 alignment errors, assembly errors, and areas that were difficult to align. Alignment errors were
212 manually corrected and assembly errors, as well as areas that were difficult to align, were
213 removed from individual alignments. Outgroup sequences were added to cleaned alignments
214 and aligned using MUSCLE v.3.8.31 (Edgar, 2004) as the default aligner program in AliView

215 (Larsson, 2014). Summary statistics on gene alignments were obtained using AMAS (Borowiec,
216 2016), including length, missing data, and number of parsimony informative sites.
217 Off-target chloroplast reads were extracted using FastPlast v1.2.6
218 (https://zenodo.org/record/973887). For all samples there was insufficient data to produce a
219 fully-assembled chloroplast genome. The SPAdes-assembler built into FastPlast iteratively used
220 k-mer lengths of 55, 87, and 121. Assembled contigs from the iteration using k-mer length 87
221 were mapped to a reference plastome obtained from GenBank (Clark et al., 2016): Horsfieldia
222 pandurifolia (GenBank accession number NC_042225.1). Once mapped, contigs were cleaned
223 by eye to remove assembly errors before generating a consensus sequence. Consensus
224 sequences for each sample were aligned visually against the *Horsfieldia* plastome, as alignment
225 algorithms performed poorly with the large amounts of missing data over long sequences.
226 Plastomes for *Annona muricata* (MT742546.1), *Cassytha filiformis* (MF592986.1), *Magnolia*
227 *maudiae* (MN990580.1), and an unverified plastome for *Myristica yunnanensis* (MK285565.1)
228 were added as additional outgroups.
229
230 ***Assessing the impact of specimen age and climate on capture success***
231 The collection year of each voucher specimen was recorded and the annual precipitation (mm)
232 at the collection locality extracted from the WorldClim 2.0 30s Bioclimatic variable layer (Fick
233 and Hijmans, 2017) using R package raster (Hijmans et al., 2015). Linear regressions were
234 performed for collection year and annual precipitation number versus number of target loci
235 recovered and average sequence length recovered for each sample to determine if the age of
236 specimen and/or the amount rainfall at the collection locality affected the success of target
237 sequence capture. The relationship between age, precipitation, and the number of ungapped
238 basepairs in cleaned chloroplast sequences was also examined to assess the effect of these
239 factors on off-target sequence capture.
240
241 ***Phylogenetic analyses***
242 *Gene tree reconstruction*- Maximum likelihood (ML) estimation of gene trees was performed for
243 each nuclear locus, a dataset with all nuclear loci combined, the chloroplast genome, and a
244 dataset with chloroplast and nuclear data combined. Alignments were processed with trimAl
245 (Capella-Gutiérrez and Silla-Martínez, 2009) assigning a gap threshold of 15% or 20% to each
246 column, depending on the number of taxa in the alignment. Thresholds were chosen to maintain
247 columns with data for four or more individuals. Alignments were analyzed using RAxML v8.2.12
248 (Stamatakis, 2014) under the GTR model with optimization of substitution rates and site-specific

evolutionary rates. For combined datasets and the chloroplast, analyses were first run with all individuals and the program RogueNaRok v.1.0 (Aberer et al., 2011) was used to identify individuals that negatively impacted phylogenetic inference. Individuals identified by RogueNaRok and or those with little data (total bp <1% of aligned length) were excluded from further analyses.

Multispecies Coalescent **-** Trees were generated under the multispecies coalescent model in ASTRAL-III (Zhang et al., 2018). Twenty random bootstrap trees were selected from each gene tree analysis of the Angiosperm353 loci, and used as the input for ASTRAL.

Divergence time estimation

Divergence times were estimated on the ML chloroplast-nuclear combined tree using penalized likelihood via the chronos() function in the R package ape (Paradis and Schliep, 2019). Crown ages from the literature (Magallón et al., 2015; Massoni et al., 2015) for Laurales + Magnoliales, Laurales, Magnoliales, and Myristicaceae were applied as secondary calibrations (Table 2). Because (Massoni et al., 2015) presented five different calibration schemes, and therefore five sets of dates for each node, we calculated the mean age for our calibrations as the average of their mean ages estimated by BEAST across the different schemes. The minimum and maximum for each node were selected as the youngest and oldest date, respectively, in the 95% confidence interval of any scheme across the different analyses. To estimate the error surrounding dates at uncalibrated nodes, like the crown age of *Otoba*, the median/mean, minimum and maximum value from each study was applied as an absolute age at the corresponding nodes.

Ancestral State Reconstruction

Ancestral character estimation was performed using the morphological characters scored in a recently published taxonomic revision *of Otoba* (Jaramillo-Vivanco and Balslev, 2020), including 10 discrete characters and 18 continuous characters. Character states were applied to the ML chloroplast and nuclear combined topology calibrated to maximum ages in (Magallón et al., 2015) and trimmed to include one representative of each species. *Otoba vespertilio* was not included in ancestral state reconstructions due to the uncertainty surrounding its phylogenetic placement.

Because *Otoba* is small genus, and our phylogeny included 8 species, the following discrete characters were simplified from (Jaramillo-Vivanco and Balslev, 2020) to reduce the

number of possible characters states: petiole wingedness; pubescence on the underside of leaves; anther shape and attachment; aril color. The degree to which the petiole is winged was simplified from four categories ("obscurely", "somewhat", "winged", and "not winged"; (Jaramillo-Vivanco and Balslev, 2020) to three (obscurely to somewhat winged, winged, and not winged). Pubescence on the underside of leaves was similarly simplified from "pubescent", "glabrescent", "somewhat pubescent", and "densely pubescent" (Jaramillo-Vivanco and Balslev, 2020) to just two character states: glabrescent to somewhat pubescent and pubescent to densely pubescent; *O. novogranatensis* ranges from glabrescent to densely pubescent and was thus coded as occupying both states. Anther shape and attachment did not vary (i.e, anthers were either globose and dorsally attached or reniform and basally attached, but never reniform and dorsally attached or globose and basally attached), so they were combined into a single character. Aril color was altered to have one state representing pale arils ("white", "white-yellow", and "yellow") and one representing darker arils ("orange-reddish" and "red"). Aril lacination was excluded from this study as information is only available for *O. acuminata*, *O. lehmannii*, and *O. vespertilio*. For continuous characters, the midpoint was taken for measurements given as a range in (Jaramillo-Vivanco and Balslev, 2020) and two-dimensional traits (e.g., ovary size [length x width (mm)] and seed size [length x width (mm)]) were separated into two traits (e.g., ovary length and ovary width).

Since *O. novogranatensis* was recovered as polyphyletic, the state for the broadly described *O. novograntensis* was applied to both *O. novogranatensis* populations in our tree, with the exception of aril color, which we know differs across inferred lineages (see (Santamaría-Aguilar, Jiménez, et al., 2019). Ancestral characters were estimated using the R package phytools (Revell, 2012); the ace() and the fastAnc() functions were used for discrete and continuous traits, respectively.

Biogeographic inference

We modeled biogeographic movements using BioGeoBEARS (Matzke, 2013, 2014; Massana et al., 2015) implemented in RASP v.4.0 (Yu et al., 2015). The same time-calibrated, trimmed topology used in ancestral state reconstructions was used for biogeographic reconstructions. To better understand how major geologic events, like the closure of the Isthmus of Panama and Andean orogeny, correlate with biogeographic events in the evolutionary history of Otoba, movement both between continents, as well as distribution on either side of the Andes were modeled. Each species was coded for occurrence in (A) Central America, (B) South America, or (AB) both. Species were also coded for their distribution on (A) the western side of

317 Andes, including the Darién gap and Central America or (B) the eastern side of the Andes and
318 western Amazonia. Six biogeographic models were tested with BioGeoBEARS (Matzke, 2013,
319 2014; Massana et al., 2015); the DIVA-like model was selected for reconstruction of continental
320 movements and the BAYArea-like model with jump dispersal was selected for reconstruction of
321 distribution around the Andes. A maximum of two ancestral areas was allowed for both
322 analyses.
323
324 RESULTS
325 ***Summary statistics of data assembly***— The number of Angiosperm353 loci captured,
326 average sequence length, number of ungapped basepairs of chloroplast DNA (cpDNA) for each
327 sample, collection year, and annual precipitation at the collection locality are listed in Table 1. A
328 heatmap of the percent of the reference protein length recovered for each sample at each locus
329 can be found in Appendix S2 and summary statistics for each locus in Appendix S3.
330
331 *Capture success from herbarium specimens*—We found variable success from hybrid enriched
332 target sequence capture across samples. Half of the 20 samples submitted for sequencing
333 recovered fewer than 10 Angiosperm353 loci; only 3 samples recovered more than 100 loci
334 (Table 1). Success in gathering off-target chloroplast data did not necessarily correspond to
335 success in capturing nuclear loci. For example, the sample with the most nuclear data– *O.*
336 *novogranatensis*_WS36336 with 217 of the 353 targeted loci– did not recover useful chloroplast
337 data. On the other hand, nearly half of the chloroplast genome was obtained for *O.*
338 *parvifolia*_MS1182, despite recovering only 6 nuclear loci.
339 Specimens used for DNA extraction were collected between 1983 and 2015, and annual
340 precipitation ranged from 1449 mm/year to 3870 mm/year (Table 1). There was a positive
341 correlation with collection year and both the number of loci recovered and the average
342 sequence length recovered--more recently collected specimens tended to recover longer
343 sequences for more loci--though only the correlation between age and average sequence length
344 was significant (Fig. 2). *Otoba novogranatensis*_LG20482 was an outlier; despite being the
345 oldest specimen, this sample performed well in both target sequence capture and off-target
346 capture of the chloroplast (Table 1; Figure 2). Annual precipitation was negatively, but not
347 significantly, correlated with the number of loci, average sequence length. Higher rainfall in the
348 collection locality reduced the performance of extracted DNA with target sequence capture.
349 There was very little correlation between age or rainfall and off-target capture success (Fig. 2);
350 the outlying sample *Otoba novogranatensis*_LG20482 did influence results. Without this
351

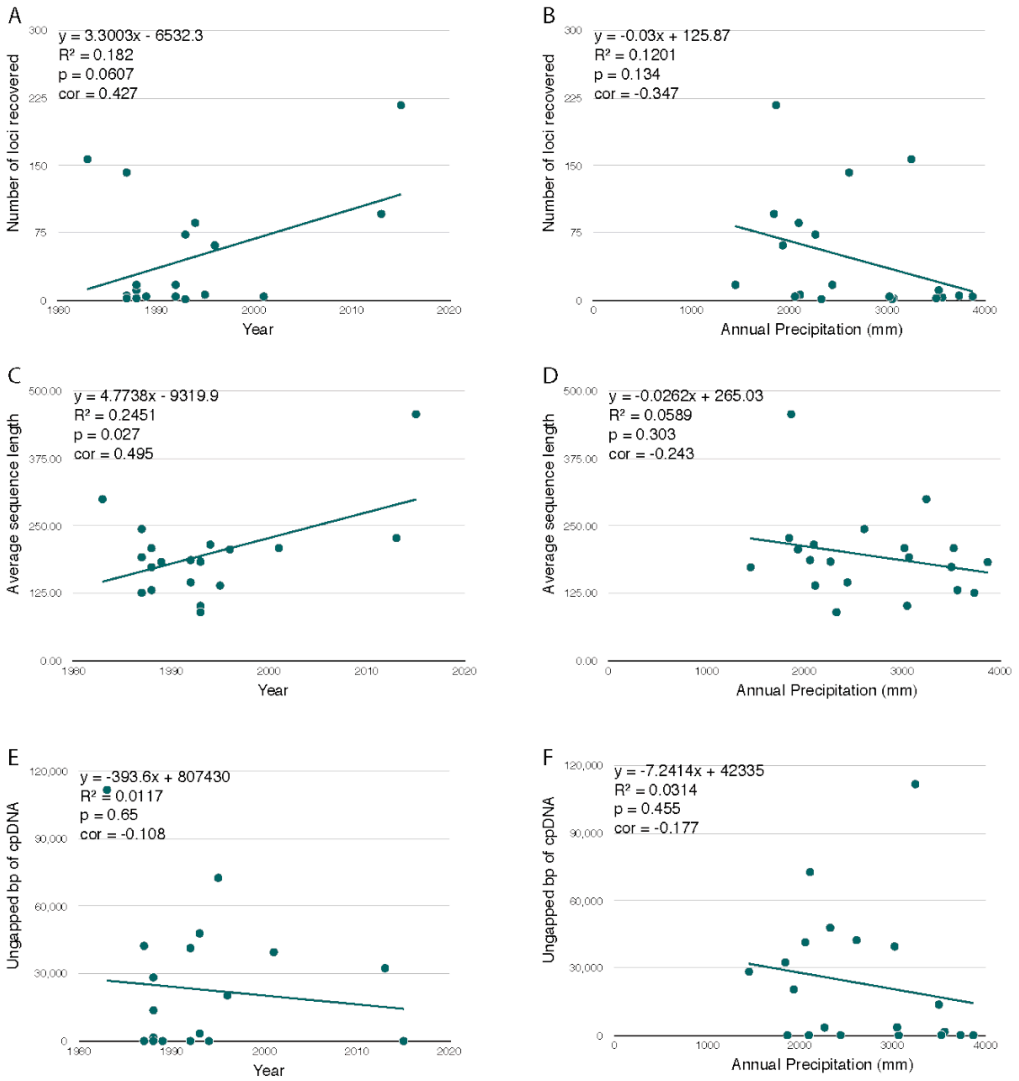

Figure 2. Linear regressions for (A) collection year and (B) annual precipitation versus number of loci recovered; (C) collection year and (D) annual precipitation versus average sequence length; (E) collection year and (F) annual precipitation versus number of ungapped basepairs (bp) of chloroplast DNA (cpDNA) recovered from the 20 samples of *Otoba*. The equation, R squared value, and p value (Pr(>|t|) for the linear regression as well as correlation of the two variables are shown in the top left corner of each graph.

sample, the weak negative correlation between collection year and off-target capture success became weakly positive and remained insignificant (cor=0.136, p-0.578). Meanwhile, the weak negative correlation between annual precipitation and off-target capture success became more negative, but remained insignificant (cor=-0.431, p=0.065).

Due to large amounts of missing data in both nuclear and chloroplast regions, the following samples were excluded from all analyses: *O. gracilipes*_DC884, *O. novogranatensis*_EB500, *O. parvifolia*_DN9151, *O. sp. nov.*_RC5752, *O. sp. nov.*_JP16902.

Otoba vespertilio, a recently described species from the Caribbean coast of Costa Rica and Panama (Santamaría-Aguilar, Jiménez, et al., 2019), was included in some analyses, despite large amounts of missing data, in an effort to place the species in the phylogeny (Figs. 3 and 4; Appenidces S4-S6). Maximum likelihood analyses were run with and without this species (Figs. 3 and 4; Appendices S4-S6). Overall, we were able to include 8 of the 10 described species of *Otoba* in phylogenetic analyses and 7 in comparative analyses.

Phylogenetic analyses

We found strong support for the monophyly of *Otoba* within Myristicaceae, albeit with limited outgroup sampling within the family (nuclear ML: 100, nuclear MSC: 1, chloroplast: 78, cp and nuclear combined ML: 100). Though the exact relationship between species varies across our individual analyses, we have strong support for three major clades of *Otoba* (Figs. 3 and 4). The first includes *O. acuminata*, *O. cylclobasis, O. gordoniifolia*, *O. latialata*, and *O. novogranatensis* specimens collected in Central America (nuclear ML: 94, nuclear MSC: 0.9, chloroplast: n/a, cp and nuclear combined ML: 100). The second includes *O*. *parvifolia* and *O*. *glycycarpa* (nuclear ML: n/a, nuclear MSC: 1, chloroplast: n/a, cp and nuclear combined ML: 75). The third includes individuals of *O. novogranatensis* collected in South America (nuclear ML: n/a, nuclear MSC: n/a, chloroplast: 63, cp and nuclear combined ML: 88).

Maximum likelihood analyses of concatenated nuclear loci recovered a poorly-supported grade of *O. glycycarpa* and *O. parvifolia* successively sister to a well-supported clade including *O*. *cyclobasis*, *O*. *latialata*, *O*. *gordoniifolia*, and *O*. *novogranatensis* (Fig. 3A). With *O. vespertilio* included, the widespread species *O. parvifolia* is paraphyletic with respect to *O. vespertilio*. Samples for another widespread species, *O. novogranatensis*, are monophyletic, but the nuclear dataset only included individuals from Central America. The ASTRAL-III tree also found a clade with *O*. *cyclobasis*, *O*. *latialata*,*O*. *gordoniifolia*, and *O*. *novogranatensis* with high support as well as a strongly-supported clade of *O. glycycarpa*, *O. parvifolia*, and *O. vespertilio* (Fig. 1B). *Otoba parvifolia* remains non-monophyletic in the ASTRAL-III results; however, relationships within the clade are poorly supported (Fig. 3B).

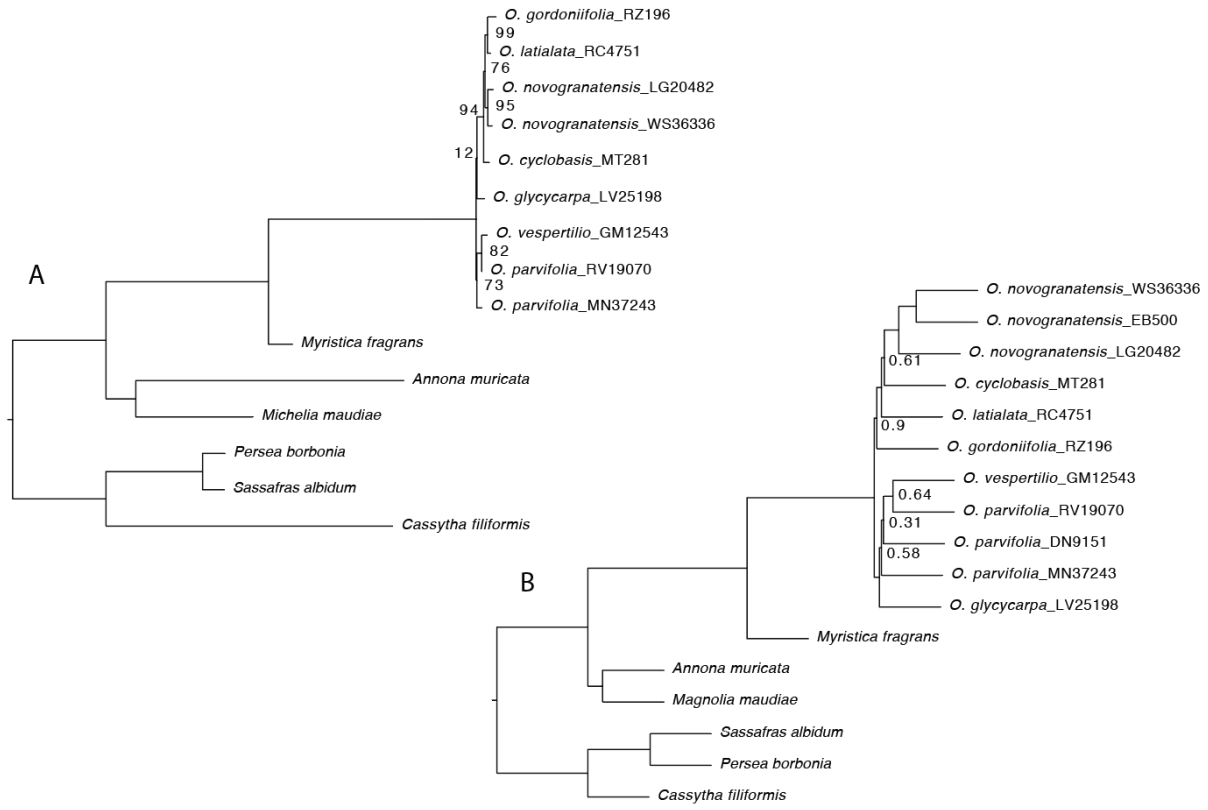

Figure 3. Results of phylogenetic analyses with nuclear data; (A) ML analysis of concatenated loci using RAxML and (B) multispecies coalescent analysis of 20 random bootstrap trees from each gene tree analysis using ASTRAL. Support values are listed at nodes for those with <100 bootstrap support and <1.0 local posterior probability for the RAxML and the ASTRAL tree, respectively.

The topology of the ML chloroplast tree did not agree with either of the nuclear topologies; however, relationships in the chloroplast tree are, overall, poorly supported (Appendix S5). The strongly-supported nodes in the ingroup included *Otoba* as a clade (bootstrap support=78) and the sister pair *O. acuminata* and *O. novogranatensis* (CA, sample LG20482; bootstrap support=85). Albeit with weak support along the backbone, the South American samples of *O. novogranatensis* are inferred to be sister to the rest of the genus. The clade of South American *O. novogranatensis* samples is resolved as sister to the rest of the genus in the combined chloroplast and nuclear analyses (bootstrap support=88; Fig. 4). The topology for the remainder of *Otoba* from the chloroplast and nuclear combined dataset is congruent with analyses of nuclear data (Figs. 3 and 4). The clade including *O. cyclobasis*, *O. latialata*, *O. gordoniifolia*, and the Central American *O. novogranatensis* is again found with high support; a well-supported clade including *O. glycycarpa*, *O. parvifolia* is also recovered (Fig. 4).

405 However, when *O. vespertilio* was included in the combined dataset, *O. vespertilio* nests within
406 the South American *O. novogranatensis* rather than *O. parvifolia* (Appendix S5).
407 *Otoba lehmannii* was not sampled in this study and we did not recover sufficient data to
408 include *O. gracilipes* in our phylogenetic analyses. Based on the geographical structure of
409 clades within *Otoba*, these species likely either belong to the larger western Andean/Central
410 American clade or in the South American *O. novogranatensis* clade.

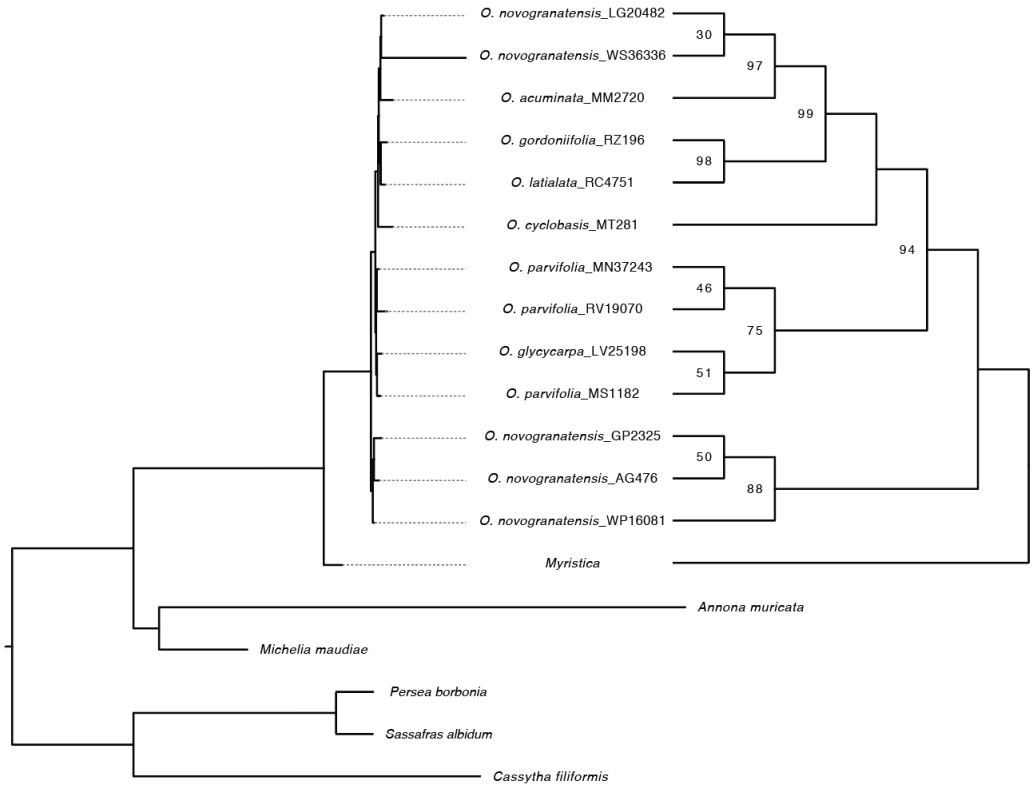

Figure 4. Results of ML analyses of concatenated chloroplast and nuclear data. The tree on the right shows branch lengths; the cladogram on the left shows the branching pattern for the ingroup + *Mryistica* and support values at nodes with <100 bootstrap support (all outgroup relationships were fully supported).

411
412
413 ***Divergence Time Estimation***
414 Divergence times estimated from different calibrations across studies (Magallón et al., 2015;
415 Massoni et al., 2015) were largely congruent (Table 2; Appendices S7-S12). The mean
416 estimated ages based on (Massoni et al., 2015) were older than those based on (Magallón et
417 al., 2015) and had a broader estimated minimum and maximum range. This is expected as
418 (Massoni et al., 2015) estimated ages under five different timelines for the crown radiation of

angiosperms: 130 Ma, 140 Ma, 150 Ma, 170 Ma, and 200 Ma. The estimated age of angiosperms from (Magallón et al., 2015) was 139.4 Ma. All estimates support the radiation of *Otoba* in the late Miocene (Fig. 6). The crown age for *Otoba* based on calibrations from Magallón et al. (2015) is estimated to be 7.28 Ma (7.04-7.51 Ma); whereas dates based on (Massoni et al., 2015) are 8.69 Ma (6.5 -11.36 Ma). The divergence between the western Andean/Central American clade and the eastern Andean/Amazonian clade is inferred to have occurred around 6.54 Ma (6.32-6.75 Ma) and 7.67 Ma (5.98-9.83 Ma) based on (Magallón et al., 2015) and (Massoni et al., 2015), respectively.

Ancestral State Reconstruction

Many of the discrete characters exhibited frequent transitions between states along the tree (Figure 5; Appendices S13-S22). These frequent shifts in character state among closely-related individuals, combined with short divergence times along the backbone of the tree, produced near-equivocal reconstructions of character states at ancestral nodes (Appendices S9-S18). Similarly, closely-related species exhibited marked differences in continuous traits (Figure 5; Appendices S23-S40). All estimations of continuous characters resulted in a value at the root close to the average of the observed states in the genus (Appendices S19 - S36).

Traits with a resolved evolutionary history include: the presence of secondary to tertiary intramarginal veins, the shape and fusion of filaments, the presence of extrastaminal discs, the presence of prickles at the apex of the seed, and aril color (Appendices S10, S11, S12, S17, and S18). Within the more-resolved character histories, multiple derivations of traits are inferred. The presence of secondary to tertiary intramarginal veins emerged at least three times; they are present in *O. gordoniifolia*, populations of *O. novogranatenis*, and *O. lehmannii* (not sampled). Fused, bottle-shaped filament columns are the most common state in *Otoba*. Filament shape transitioned from the tapered bottle shape to cylindrical in *O. cyclobasis*. Fusion of filaments was lost multiple times in populations of *O. novogranatensis*. Extrastaminal discs evolved twice: once in *O. acuminata* and once in *O. cyclobasis*. Prickles at the apex of the seed were partially lost in *O. cyclobasis* and *O. parvifolia* and lost completely in *O. glycycarpa*; *Otoba vespertilio* (not included in ancestral reconstructions) also displays a reduction in seed prickles. Finally, arils are ancestrally pale (white to yellow) in *Otoba*; red arils have evolved at least once in Central American *O. novogranatensis*. One additional species not included in ancestral reconstructions, *O. gracilipes*, also has red arils.

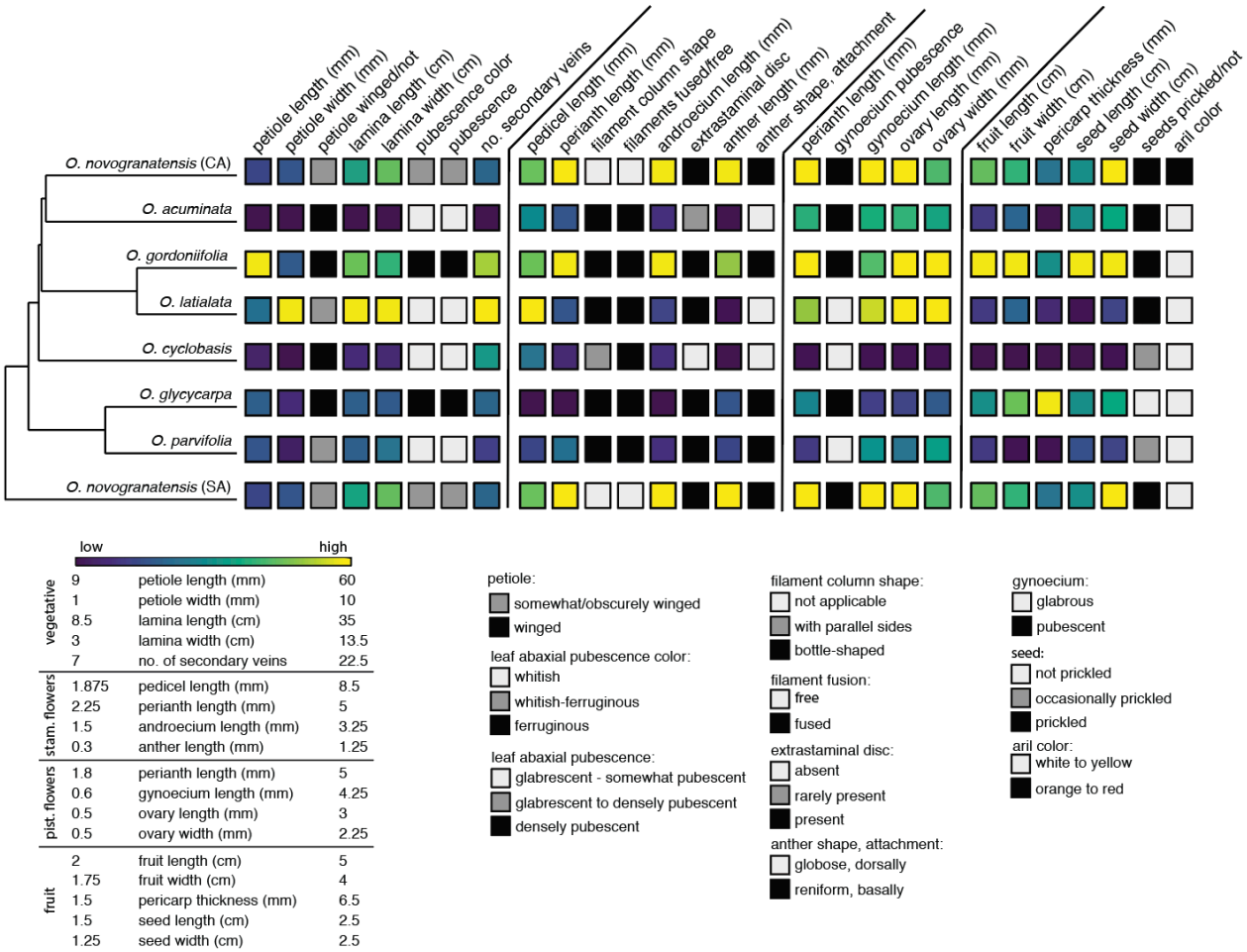

Figure 5. Summary of tip states from ancestral character reconstruction for species included in the phylogeny. Traits are sectioned into vegetative, staminate floral, pistillate floral, and fruit traits. Discrete traits are color-coded in grayscale with the scoring system for each trait described below. Continuous characters are coded along a colored gradient from low values (dark purple) to high values (yellow). The numerical range for each trait is listed below; color values for each tip were extracted from the output of ancestral character estimations in R (Appendices S9 – S37).

Biogeographic Reconstruction

South America and, more specifically, the western side of the Andes is inferred to be the ancestral area of *Otoba* (Fig. 6). Jump dispersal to the eastern side and the Amazonian basin best explains the divergence of the *O. glycycarpa*-*O. parvifolia clade* (Fig. 6B). In the western-Andean clade including *O. acuminata* and *O. cyclobasis*, a South American ancestor is inferred with expansion into Central America via widespread ancestors (Fig. 6A).

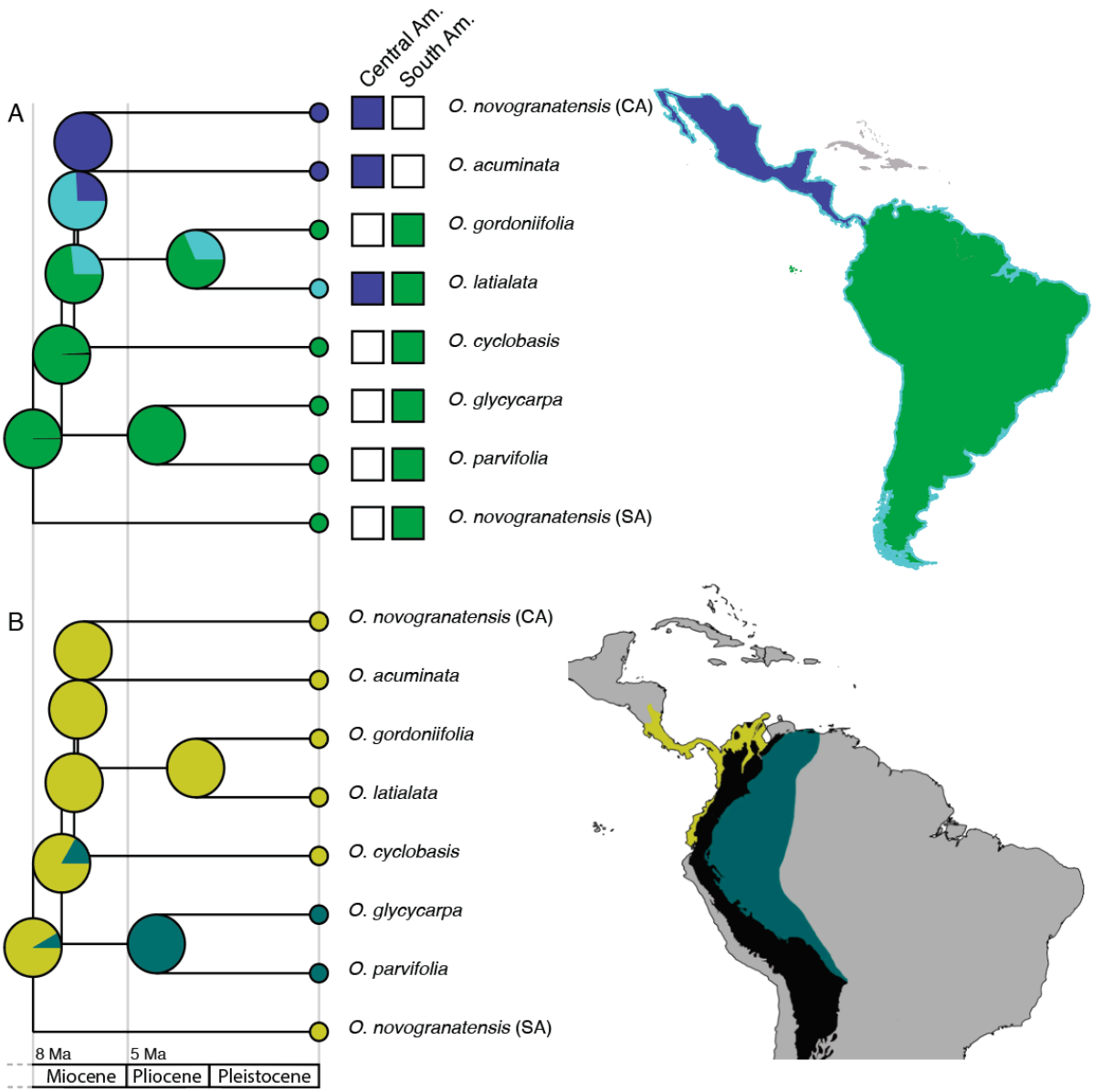

Figure 6. Ancestral area reconstructions for (A) Central America versus South America and (B) western Andes and Central America versus eastern Andes and the Amazon. Pie charts at nodes display the probability that the ancestor occupied a given range. Maps to the left of each tree are color coded to correspond with the geographic areas coded on the tree. In (A), green = South America, royal blue = Central America, and light blue = both Central and South America; the distribution of each species in Central and/or South America is additionally reflected in the color-coded boxes at the tips of the tree. In (B), chartreuse = western Andes and Central America, and teal = eastern Andes and the Amazon; the Andes are represented in black.

465

466 **DISCUSSION**

467 There were many challenges, both methodological and biological, inherent to our goal of
468 inferring the first phylogeny of the ecologically dominant Neotropical tree genus *Otoba*. Our use
469 of a universal probe set meant lower specificity in target capture, and that variation within loci
470 would potentially be low. Methodological challenges extended to our exclusive use of degraded,
471 low quantity DNA extracted from herbarium specimens— a challenge exacerbated by *Otoba*'s
472 distribution in low- to-mid-elevation moist tropical forests, where specimens are particularly
473 difficult to preserve and dry. Biologically, *Otoba*'s Andean-centered distribution suggests that it
474 is likely a young clade with a phylogeny characterized by short branch lengths and young
475 speciation events, a result borne out in our analyses. Despite these significant challenges, we
476 were able to produce a framework phylogeny for *Otoba*— the first phylogeny for any Neotropical
477 group of Myristicaceae. Our phylogenetic results consistently included two subclades: 1) an
478 eastern Andean/Amazonian clade comprising *O. parvifolia and O. glycycarpa* and 2) a northern
479 Andean/Central American clade comprising *O. acuminata*, *O. cyclobasis*, *O. gordoniifolia*, *O.*
480 *latialata*, and some individuals of *O. novogranatensis*. The 6-9 Ma divergence of the eastern
481 Andean/Amazionian clade from the western Andean/Central American clade suggests that long-
482 distance dispersal across the Andes, rather than vicariance via mountain uplift, produced the
483 present distribution.

484

485 ***Landscape evolution and dispersal limitation drive biogeography in* Otoba**

486 The Neotropics have a complex geological history (Hoorn et al., 2010), including the
487 rapid uplift of the Andes and the closure of the Isthmus of Panama. These events have had
488 dramatic impacts on the evolution of the taxa that inhabit this region (Hughes et al., 2006;
489 Antonelli et al., 2009; Bacon et al., 2015). We find compelling evidence that both have played
490 important roles in the shaping biogeographic history of *Otoba*.

491 *Otoba* is a product of long-distance dispersal from Africa to the Neotropics. It is likely
492 that the dispersal event that resulted in stem lineage *Otoba* was from western Africa, where the
493 closest relatives of *Otoba*, *Pycnanthus and Ceolocaryon*, occur today, to eastern South America
494 (Doyle et al., 2004) in the last 19-7.2MA (Table 1). During this time period, range expansion
495 across the northern Neotropics would have been facilitated by a more-or-less contiguous
496 swathe of lowland rainforest and a relatively low height of the Andes, including a low elevation
497 gap in the region that comprises the current border area between Ecuador and Peru (Hoorn et
498 al., 2010). By the time that crown *Otoba* originated *ca.* 7.2Ma, we infer that this lineage was

restricted to the western side of the Andes; the long, empty stem lineage of *Otoba* is consistent with high rates of past extinction explaining this pattern. Our ancestral state reconstructions and divergence time estimates point to a western Andean origin of *Otoba* (Fig. 6) in the late Miocene to early Pliocene. This is a region of origin shared with relatively few other Neotropical tree groups, including a clade of Annonaceae (Pirie et al., 2018); more tree clades that have been investigated have Amazonian origins, including the *Brownea* clade (Fabaceae; (Schley et al., 2018) and Neotropical Chrysobalanaceae (Chave et al., 2020). Following establishment, *Otoba* seem to be one of few lineages that experience *in situ* diversification within the Chocó biogeographic region (Pérez-Escobar et al., 2019).

The Andes structure the ranges of species and clades in crown *Otoba*. Species either occur on the eastern slopes of Andes, extending into the western Amazon basin, or on the western slopes of the Andes and/or in Central America. The same pattern is observed within subclades, with closest relatives sharing distribution on one side of the Andes. During the time that elapsed between the dispersal from Africa and the origin of crown *Otoba,* the northern Andes gained approximately half their elevation (Garzione et al. 2017) and analogs to modern montane cloud forests formed (Hughes, 2016; Martínez et al., 2020). Thus, even though they had not yet reached their full height (Hoorn et al., 2010), the Andes would have represented a significant barrier to dispersal for low- to-mid-elevation groups like *Otoba*. Consistent with this scenario, we infer only a single dispersal event from the western side of the Andes to the eastern side; this dispersal occurred in the late Miocene to early Pliocene, resulting in two widespread, lowland species, *O. glycycarpa* and *O. parvifolia* (Fig. 6). It is unlikely that Andean uplift served as a vicariant event that split widespread populations; instead, we posit that long-distance dispersal across the mountains, likely mediated by bird or mammal seed dispersers, facilitated this disjunct distribution.

Movement between Central and South America has occurred more frequently than movement across the Andes during the evolutionary history of *Otoba.* Range expansion and long-distance dispersal have both played a role in movement into Central America. A widespread distribution in South and Central America is inferred for the most recent common ancestor of *O. acuminata*, *O. novogranatensis* (CA), *O. gordoniifolia*, and *O. latialata* in the late Miocene (Fig. 6). The current, widespread distribution of *O. latialata* in the Chocó-Darién moist forest from Colombia to Panama suggests the common ancestor of the clade may have occupied a similar distribution. If this is the case, a pattern of subset sympatry—when one daughter lineage inherits the ancestral range and the other daughter(s) inherit a portion of the ancestral range (Ree et al., 2005)—is consistent with our inferred biogeographic history. An

additional long-distance dispersal event is assumed for *O. vespertilio*. While the phylogenetic position of *O. vespertilio* differs across our analyses (Fig. 3; Appendix S6), all possible placements are consistent with it representing a long distance dispersal event from South America to Central America. These events occurred within the last 10 million years, a time-frame that supports the role of the closure of the Isthmus of Panama in facilitating these movements (Montes et al., 2012; Bacon et al., 2013).

The observed biogeography patterns are likely explained by dispersal limitation. *Otoba*'s relatively large seeds are dispersed birds, primates, and bats (Giraldo et al., 2007; Nuñez-Iturri and Howe, 2007; Melo et al., 2009; Santamaría-Aguilar, Jiménez, et al., 2019), with a potential role of small mammals as secondary seed dispersers (Forget et al., 2002). These groups can often be dispersal limited, including across riverine barriers and fragmented habitats (Eberhard and Bermingham, 2005; Ripperger et al., 2013; Boubli et al., 2015) (though this is not always the case; see (Holbrook, 2011). The potential for dispersal limitation is observed within communities in which the relatively large seeds of *Otoba parvifolia* are dispersed at low frequency over typically short distances (Terborgh et al., 2011). On a continental scale and over evolutionary time, this has resulted in relatively few long distance biogeographic movements. *Otoba*'s two migrations into Central American were potentially facilitated by the continuous land bridge of more-or-less suitable habitat, while cold high-elevation habitats likely prevented more frequent traversing of the Andes. Further, the range of *Otoba* does not occupy all of the suitable habitat it presumably could based on distributions of extant species. Otoba does not occur in other low to mid-elevation moist forest habitats in the Neotropics, like the Atlantic coast forest in Brazil and the Caribbean islands, a pattern mirroring ecologically similar and closely related *Virola* (Santamaría-Aguilar, Aguilar, et al., 2019). Again, dispersal limitation may explain *Otoba*'s absence from these regions: the relatively large seeds of *Otoba* likely make dispersal events over water barriers or large stretches of unsuitable terrestrial habitat uncommon compared to groups that are dispersed by wind (Pérez-Escobar et al., 2017) or migratory passerine birds (Nathan et al., 2008). This is likely coupled to time limitation, given the young age of the genus and the stochastic nature of long-distance dispersal events (Nathan et al., 2008). However, high levels of seed-set, both in closed canopy forests and in treefall gaps, may make *Otoba* an effective colonizer of new habitats once they do arrive in a new region (Myster, 2020).

Dynamic evolution of morphological traits is common

We observe a dynamic pattern of character evolution across a broad suite of traits in *Otoba*. While frequent transitions between morphological characters often results in unresolved

567 ancestral state reconstructions, mapping tip states reveals that no two species share a set of
568 discrete traits (Fig. 5). Further, even though ancestral states were equivocal, the majority of the
569 discrete traits that we investigated underwent convergent evolution within the genus, including:
570 winged petioles, pubescence presence and color, filament fusion, anther shape and attachment,
571 and gynoecium pubescence (Fig. 4). Coupled with short divergence times between speciation
572 events after the crown age of *Otoba* (Fig. 6; Appendices S7 and S8), the observed variation
573 across all traits is consistent with rapid morphological evolution coinciding with rapid lineage
574 divergence upon establishment in South America. This pattern may also be explained by the
575 sorting of ancestral variation (Pease et al., 2016), and it is likely that hemiplasy or parallel
576 evolution underlie morphological evolution. Ecological opportunities on a new continent may
577 have served to differentially select standing ancestral variation, resulting in the repeated
578 evolution of many traits in *Otoba*.

579 An unconfirmed, but likely case of convergent evolution is aril color. Most species in
580 Myristicaceae produce red arils that cover seeds to varying degrees. These bright, red arils that
581 contrast with the green and brown of the capsule and seeds (Fig. 1E) serve as an attractant to
582 frugivores who consume the nutritious aril, either with or without consuming the seed (Howe and
583 Vande Kerckhove, 1981; Gautier-Hion et al., 1985). Most species of *Otoba*, however, produce
584 white to yellow arils (Fig 1F); these pale colors still contrast the seed and capsule and attract
585 frugivores (Gautier-Hion et al., 1985; Wheelwright and Janson, 1985). Two species have red
586 arils: *O. gracilipes* and the Central American members of *O. novagranatensis* (supported as a
587 distinct lineage in our analyses). Our field observations suggest that these differences in aril
588 color coincide with differences in texture: red arils are generally thick and waxy, while whitish
589 arils are thin and gelatinous. On a broad phylogenetic scale, this represents convergent
590 evolution of red arils within Myristicaceae and likely serves as a shared ecological signal with
591 other Neotropical members of the family, including the widespread *Virola*. Within the genus,
592 bright red arils have presumably evolved twice independently (Fig. 5), though the exact
593 phylogenetic placement of these independent origins remains unknown as *O. gracilipes* was not
594 included in our analyses. We also see convergence in seed size and shape (Fig. 5), additional
595 traits that are likely related to the mechanics of seed dispersal.

596 Convergence in fruit traits, including seed size and aril color and texture, may be linked
597 to a specialized dispersal syndromes in *Otoba*. Differences in overall seed morphology
598 throughout the genus, including size, aril color and texture, potentially represent specialization
599 with different classes of dispersers. For example, species with bright red arils, including *Virola*
600 *surinamensis*, are consumed by birds (Howe and Kerckhove, 1980; Howe and Vande

601 Kerckhove, 1981), while species with whitish arils are consumed by bats (Melo et al., 2009;
602 Santamaría-Aguilar, Jiménez, et al., 2019); while more comparative field studies are needed to
603 confirm the most effective dispersers across species, these observations are broadly consistent
604 with global patterns of mammal- and bird-dispersed fruits (Sinnott-Armstrong et al., 2018). While
605 seed dispersal is not directly tied to reproductive isolation, theoretical models support
606 mutualisms between animal dispersers and flowering plants coupled with repeated habitat
607 fragmentation as a mechanism that promotes speciation during range contractions, allowing for
608 coexistence of diverged populations upon habitat reunification (Kakishima et al., 2015). This is a
609 likely potential scenario in *Otoba*, given that major mountain-building events were occurring the
610 northern Andes and, along with them, reorganization of river systems, were occurring during the
611 late Miocene and early Pliocene, when many of the divergence times between species are
612 inferred (Hoorn et al., 1995, 2010; Struth et al., 2015). Fluctuating landscapes and fluvial
613 barriers at the time may have fragmented populations, promoting divergence between those
614 populations and securing species boundaries upon secondary contact. Supporting this, large
615 rivers are important barriers to dispersal and gene flow in tropical birds (Hayes and Sewlal,
616 2004; Burney and Brumfield, 2009; Fernandes et al., 2014; Oliveira et al., 2017; Sandoval-H et
617 al., 2017); by extension, they should also be significant barriers to the plants that they disperse
618 as well (Nazareno et al., 2017; Dambros et al., 2020).
619
620 ***The need for future phylogeography of widespread species***
621 *Otoba* includes a combination of narrowly endemic and widespread species. We find
622 strong evidence for polyphyly of one widespread taxon, *O. novogranatensis,* and for paraphyly
623 of another, *O. parvifolia*. This non-monophyly is likely both a product of biological processes
624 (e.g., very large population sizes maintained over very large distances in *O. novogranatensis*
625 (Pennington and Lavin, 2016) and an artifact of insufficient taxonomic study (Lagomarsino and
626 Frost, 2020).
627 The polyphyletic *Otoba novogranatensis* is one of the most collected species of its
628 genus. A preliminary revision of the resulting specimens shows variation across many traits. For
629 example, South American specimens differ from Central American specimens in their thicker
630 pericarp, pubescent ovaries, anthers that can be unfused to the base (de Candolle, 1856;
631 Jaramillo et al., 2004; Jaramillo-Vivanco and Balslev, 2020), and generally white arils. Thus, the
632 two distinct lineages of *O. novogranatensis* that we resolve (Fig. 4), corresponding to South
633 American and Central American accessions, are supported by morphology. There are additional
634 differences within Central American *O. novogranatensis* that are likely to be taxonomically

informative as well, including the size, shape, and pubescence of leaves, as well as the length of staminate inflorescences, perianth, and anthers varies across the Pacific (e.g., *R. Aguilar 638* [INB/CR]) and Caribbean slopes (e.g., *I. Chacón* 1360 [INB/CR]) of Costa Rica; montane populations within Costa Rica exhibit additional differentiation. Together, these observations suggest that phylogeographic analysis of *O. novogranatensis* is necessary to adequately determine the number of lineages that are currently described under this umbrella taxon. This would facilitate future taxonomic efforts to recircumscribe this species complex to reflect evolutionary relationships, which will likely entail the description of at least one new Central American species.

Similarly, the paraphyly of *O. parvifolia* is not surprising, but for different reasons. Our phylogenetic results suggest that *O. glycycarpa* has recently diverged from *O. parvifolia*, and has since become widespread as well. Our taxon sampling includes multiple accessions of *O. parvifolia* and a single accession of *O. glycycarpa*; these species determinations were based on differences in pericarp thickness, gynoecium pubescence, and color of foliar pubescence (Jaramillo et al., 2000). In all analyses, these accessions are each others' closest relatives, though *O. parvifolia* is almost always resolved as a grade (Fig. 3, 4; but see Appendix S4 where it is resolved as a clade). The geographic structure of these species are unresolved across our analyses; while Bolivian and Peruvian accessions of *O. parvifolia* are often resolved as sister lineages that are more distantly related from Ecuadoran and Brazilian accessions *O. parvifolia* and *O. glycycarpa*, there is variation across our analyses and support for these relationships is often low. A previous study based on limited genetic data has suggested that *O. parvifolia* and *O. glycycarpa* are genetically indistinguishable, with the implication that they represent a single species (Honorio Coronado et al., 2019). This low genetic variability between species, which is consistent with the short branch lengths in our analyses, may be the product of species misidentification, lack of informative variation in the loci used, introgression, or sorting of ancestral variation in the short time since speciation (*ca.* 3.7 Ma). The latter two mechanisms would not be surprising: our analyses suggest that these species are recently diverged, overlapping in both geographic occurrence, and have overall similar morphology. While our sampling did not allow us to test the monophyly of *O. glycycarpa*, morphological evidence supports the distinctness of these species (Jaramillo et al., 2000). Of particular note, *O. glycycarpa* has one of the thickest pericarps of all *Otoba*, which has implications for potential efficacy of seed dispersers. We consider *O. parvifolia* to be a distinct species form *O. glycycarpa*, and its paraphyly is indicative of its complex evolutionary history (Freudenstein et al., 2016). Future ecological and phylogeographic research could target what allows

669 morphologically similar closest-related species to co-occur throughout large swathes of western
670 Amazonia.
671
672 ***Targeted sequence capture promotes herbariomics— with caveats***
673 Hybrid-enriched target sequence capture with Angiosperms353 has proven useful for
674 generating phylogenetically informative data at multiple taxonomic scales and from different
675 sources of DNA (i.e., silica-dried tissue versus herbarium specimens; (Brewer et al., 2019; Shee
676 et al., 2020; Valderrama et al., 2020). To our knowledge, our study represents a new milestone
677 for Angiosperms353 phylogenomics: the first exclusively herbariomic dataset for a wet tropical
678 genus. DNA from herbarium specimens collected in the wet tropics performs poorly compared
679 extractions from other climates and silica-gel dried tissue (Brewer et al., 2019). This is because
680 high humidity in moist tropical forests and often remote localities extend drying times and/or
681 delay access to drying apparatuses. Resultantly, collections are often treated with ethanol to
682 prevent mold and decay until they can be dried. Both storage of tissues in humid conditions
683 after collection (Adams, 2011) and preservation in ethanol (Doyle and Dickson, 1987; Pyle and
684 Adams, 1989) degrades DNA, resulting in damaged and fragmented genetic material (Särkinen,
685 Staats, et al., 2012). Even though current short-read sequencing techniques perform well with
686 herbarium specimens as compared to conventional Sanger sequencing (Bakker et al., 2015),
687 the level of degradation common among wet tropical specimens led (Brewer et al., 2019) to
688 recommend the use of silica tissue for wet tropical groups. While we agree that this is a best-
689 practice, as in other herbarium-based studies (Brewer et al., 2019; Shee et al., 2020), we were
690 able to extract useful phylogenomic data from herbarium specimens using Angiosperms353.
691 Herbarium samples are an increasingly useful source of DNA for phylogenomic studies,
692 extending the utility of our historic natural history collections (Lendemer et al., 2020), but they
693 are not a panacea. Even high efficiency target capture will fail when DNA is low quality, as is
694 typical in herbarium specimens collected in the wet tropics (Brewer et al., 2019), especially
695 when they are collected in ethanol (Särkinen, Staats, et al., 2012)— a common scenario for
696 *Otoba*, and likely universal in the herbarium specimens that we sampled. The specimens we
697 included in our analyses span a breadth of age and environmental conditions at collecting
698 localities. The oldest specimen that we included was 37 years old, collected in 1983;
699 surprisingly, it resulted in the most genetic data (Fig. 2). However, not all of our samples
700 generated useful sequences; we had to remove some of our samples completely due to poor
701 quality reads and apparent contamination following visual inspection of alignments. In other

cases, we were able to extract a handful of useful loci, but at a much lower quality than the majority of our included species.

In agreement with past studies, we found that capture success, as measured by the total number of loci obtained as well as their average length, decreased with increasing age of the specimen; we further found a correlation between environmental conditions (i.e., annual precipitation) at the site of collection and the quality of phylogenomic data (Fig. 2). However, we were only able to capture more than 10 loci from half of our initial 20 samples, and only three *Otoba* samples were successful in recovering over 100 loci. This limited capture success is most likely a product of low input DNA quality and not due to sequence divergence from the probeset, especially considering that we had similarly variable success in capturing the high-copy, off-target chloroplast genome. Plastomes from wet tropical specimens have also been found to have higher fragmentation rates and lower sequencing success as compared to plastomes from specimens collected in other climates (Bakker et al., 2015; Brewer et al., 2019). This compounded with a lower depth of sequencing coverage in the off-target chloroplast regions and resulted in higher sequencing error, which led to conflicting phylogenetic signal and low support. The chloroplast data were able to complement our Angiosperms353 data and allowed the inclusion of additional samples in phylogenetic analyses, but stronger, more consistent signal was recovered in Angiosperm353 target loci.

To extend the potential utility of voucher specimens collected in the future for genomic research, efforts should be made to collect leaf tissue in silica gel or other preservation technique, following best practices, including unique IDs to connect the herbarium voucher to this secondary product (Funk et al., 2017). However, many studies of tropical groups rely on museum specimens, as it is not feasible to collect living material for the taxonomic and/or geographic breadth of many clades. As this is often the case, we urge botanical collectors to include information about how voucher specimens were treated (e.g., specifying that specimens were collected and dried in ethanol). We have demonstrated that even though it may not be ideal, it is still possible to generate phylogenomic datasets that can resolve rapid radiations of wet tropical plant clades using the Angiosperms353 probeset.

Utility of Angiosperms353 as universal loci for plant phylogenomics, even in rapid radiations

Despite the fact that the Angiosperms353 loci were designed to be phylogenetically useful across all angiosperms, we were able to resolve relationships within a clade estimated to be between 6.5–11.3 My old (Table 2). This adds to a growing number of rapid radiations whose

736 phylogenies have been resolved using these loci (Larridon et al., 2019). This performance goes
737 against a preconception that universal loci are not useful for species-level phylogenomic
738 analysis, probably borne of experience from the low-variation plastid loci that had universal
739 utility via PCR-based Sanger sequencing (Shaw et al., 2005), as well as related calls to move
740 away from the lofty goal of a universal set of loci for all flowering plants and instead develop
741 lineage-specific loci with more phylogenetic utility (Hughes et al., 2006). However, targeted
742 sequence capture allows the isolation of loci without finicky PCR probes at a percent-divergence
743 that allows for efficient capture over substantial evolutionary distances. Further, universal
744 probesets, including Angiosperms353, are designed such that multiple probe sequences for
745 each locus are included to account for sequencing variability across taxa. Instead of being
746 limiting, the universal nature of Angiosperms353 loci are proving to be informative for both very
747 deep (e.g, (Dodsworth et al., 2019) and very shallow (e.g., within populations of rice, (Van Andel
748 et al., 2019) phylogenetic splits. A further attractive aspect of Angiosperms353 data is that it is
749 cost-effective to generate, especially if pre-sequencing molecular labwork is completed by the
750 researcher and not outsourced (Hale et al., 2020).
751 While we were able to infer relationships in *Otoba* using Angiosperms353 loci, there was
752 very limited variation across our dataset (i.e., the proportion of variable sites in concatenated
753 target loci was 0.285). It has been shown in other taxa that custom bait kits are more informative
754 than Angiosperms353 loci for species-level phylogenetics (Jantzen et al., 2020), though this is
755 not always the case (Larridon et al., 2019). It is thus possible that a custom probe kit designed
756 for *Otoba* and close relatives would have outperformed the Angiosperms353 loci, either alone or
757 in combination. However, developing such custom loci is predicated on the existence of
758 genomic resources, either pre-existing or newly generated, which would have been difficult for
759 *Otoba*. While the number of angiosperms genomic resources is constantly growing (One
760 Thousand Plant Transcriptomes Initiative, 2019), there are still no transcriptomes or nuclear
761 genomes available for *Otoba* and data is limited for Myristicaceae overall: there is a single
762 transcriptome available in the 1KP database (nutmeg, *Myristica fragrans*) and no other genomic
763 resources. Further, we currently do not have access to fresh or silica-dried tissue from *Otoba*.
764 Because this scenario is common— especially in tropical plant groups, which tend to be
765 understudied (Goodwin et al., 2015), the universal utility and subsequent promise of assembling
766 a standardized set of loci across analyses is a very desirable property of the Angiosperms353
767 loci. To facilitate standardized loci that can be combined across studies, the plant systematics
768 community should strive for the development of searchable, long-term repositories for
769 Angiosperms353 datasets. Any such future repository would further benefit from being linked to

herbarium vouchers, which would help with reproducibility of research as well as continue to extend the use of herbarium specimens in science (Lendemer et al., 2020).

Conclusions

Otoba is a recent, rapid radiation with a trans-Andean distribution whose biogeographic history suggests that key aspects of the Neotropical landscape— namely the Andean mountains and the Isthmus of Panama— have been important barriers to dispersal. It is likely that traversing these barriers has happened only rarely in the history of the genus due to dispersal limitation, a product of its relatively large seeds that rely on large-bodied vertebrates for dispersal. Very short branch lengths separating species coincide with dynamic trait evolution— a pattern consistent with sorting of ancestral variation during rapid lineage diversification. Future research into *Otoba* would ideally tackle phylogeography of widespread species, including two species that we identify as non-monophyletic: *O. novogranatensis* and *O. parvifolia*, both of which can reach very high local abundance in the communities in which they occur. These insights were gained from a relatively small phylogenomic dataset obtained via targeted sequence capture of Angiosperms353 loci from DNA extracted from herbarium specimens. We observed an impact specimen age and the environmental conditions of their collection locality on data quality. While our study highlights the promise of Angiosperms353 in herbarium-based phylogenomics, it demonstrates the challenges inherent in studying rapid radiations broadly, and, more specifically, when using DNA extracted from herbarium specimens collected in the humid tropics.

Acknowledgements

This research was funded by a Louisiana Board of Regents Research Competitiveness Subprogram grant and by the LSU Department of Biological Sciences. We would like to thank the Missouri Botanical Garden (MO) for their access to their important collections, and Reinaldo Aguilar, Rudy Gelis, Timothy Paine, and John Janovec for permission to use their photographs. We thank Brant Faircloth, Matthew Johnson, Carl Oliveros, and Jessie Salter for their guidance in library preparation and Brant Faircloth for access to laboratory equipment. This manuscript benefited from feedback from Laymon Ball, Janet Mansaray, and Diego Paredes-Burneo.

Author Contributions

LAF, DASA, and LPL conceived of the research; LAF and DS collected data and performed analyses; LAF and LPL wrote the manuscript with significant feedback from DASA and DS.

Data Availability Statement

Illumina reads will be submitted to the NCBI Sequence Read Archive (SRA) and all other data formats (tree files, alignments, character matrices, etc.) will be uploaded on the Dryad Digital Repository and made available upon publication.

Additional Supporting Information may be found online in the supporting information.

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1182 **Table 1.** Summary of sequence data recovered for each sample for targeted and off-target
1183 (cpDNA) loci. Asterisks at sample names indicate samples that were not included in any
1184 phylogenetic analysis. Samples for which there was insufficient cpDNA data to include in
1185 phylogenetic analyses are marked with “n/a”.
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Sample	Avgerage sequence length	number of loci	ungapped bp cpDNA	Collection Year	Annual precipitation (mm)
***Otoba acuminata*_MM2720**	209.25	4	39,553	2001	3,021
***Otoba cyclobasis*_MT281**	183.9	73	3,399	1993	2,265
***Otoba glycycarpa*_LV25198**	227.88	96	32,401	2013	1,842
***Otoba gordoniifolia*_RZ196**	206.51	61	20,318	1996	1,933
Otoba_gracilipes_DC884*	192	2	n/a	1987	3,065
***Otoba latialata*_RC4751**	244.39	142	42,374	1987	2,610
***Otoba novogranatensis*_AG476**	102	1	3,533	1993	3,048
***Otoba novogranatensis*_CK681**	174	2	13,653	1988	3,499
Otoba novogranatensis*_EB500	208.91	11	n/a	1988	3,524
***Otoba novogranatensis*_GP2325**	186.75	4	41,378	1992	2,057
***Otoba novogranatensis*_LG20482**	299.92	157	111,863	1983	3,244
***Otoba novogranatensis*_WP16081**	90	1	47,902	1993	2,326
***Otoba novogranatensis*_WS36336**	457.56	217	n/a	2015	1,864
Otoba parvifolia*_DN9151	183	4	n/a	1989	3,870
***Otoba parvifolia*_MN37243**	173.47	17	28,315	1988	1,449
***Otoba parvifolia*_MS1182**	139.5	6	72,683	1995	2,109
***Otoba parvifolia*_RV19070**	215.62	86	n/a	1994	2,095

Otoba sp. nov.*_JP16902	145.41	17	n/a	1992	2,438
Otoba sp. nov*_RC5752	126	5	n/a	1987	3,732
***Otoba vespertilio*_GM12543**	131	3	1,532	1988	3,561

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Table 2. Divergence times (Ma) for major clades of Otoba estimated from penalized likelihood analyses based on different calibrations from Magallon et al. (2015) and Massoni et al. (2015).

	Magallon et al. (2015)						**Massoni et al. (2015)**					
	UCLN median		**UCLN min**		**UCLN max**		**UCLN mean**		**UCLN min**		**UCLN max**	
	calibration	**estimated age**	**calibration**	**estimated age**	**calibration**	**estimated age**	**calibration**	**estimated age**	**calibration**	**estimated age**	**calibration**	**estimated age**
Magnioliales + Laurales	127.70	—	121.80	—	131.77	—	134.15	—	121.34	—	161.65	—
Laurales	114.90	—	109.07	—	120.64	—	122.16	—	112.05	—	145.59	—
Magnoliales	109.59	—	108.14	—	112.32	—	123.86	—	114.75	—	145.66	—
Myristicaceae	—	19.09	—	18.55	—	19.66	29.07	—	14.70	—	51.51	—
Otoba	—	7.28	—	7.04	—	7.51	—	8.69	—	6.57	—	11.36
So. Am. *O. novogranatensis* clade	—	5.82	—	5.62	—	6.00	—	6.60	—	5.47	—	8.23
Eastern Andean/Amazonian + Western Andean/Cen. Am. clade	—	6.54	—	6.32	—	6.75	—	7.67	—	5.98	—	9.83
Eastern Andean/Amazion clade	—	4.13	—	3.99	—	4.27	—	4.57	—	4.01	—	5.61
Western Andean/Central American clade	—	6.21	—	6.00	—	6.41	—	7.25	—	5.71	—	9.26

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