

The tempo of trophic evolution in small-bodied primates

Running title: Trophic evolution in small-bodied primates

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Abstract

Objectives: As a primary trophic strategy, insectivory is uncommon and unevenly distributed across extant primates. This pattern is partly a function of the challenges that insectivory poses for large-bodied primates. In this study, I demonstrate that the uneven distribution is also a consequence of variation in the rate of trophic evolution among small-bodied lineages.

Methods: The sample consisted of 307 species classified by primary trophic strategy and body size, creating an ordered three-state character: small-insectivorous, small-herbivorous, and large-herbivorous. I tested for rate heterogeneity by partitioning major clades from the rest of the primate tree and estimating separate rates of transition between herbivory and insectivory for small-bodied lineages in each partition.

Results: Bayesian analysis of rate estimates indicates that a model with two rates of trophic evolution provides the best fit to the data. According to the model, lorisiforms have a trophic rate that is 4–6 times higher than the rate for other small-bodied lineages.

Conclusions: The rate heterogeneity detected here suggests that lorisiforms are characterized by traits that give them greater trophic flexibility than other primates. Previous discussions of trophic evolution in small-bodied primates focused on the low frequency of insectivory among anthropoids and the possibility that diurnality makes insectivory unlikely to evolve or persist. The present study challenges this idea by showing that a common transition rate can explain the distribution of insectivory in small-bodied anthropoids and nocturnal lemurs and tarsiers. The results of this study offer important clues for reconstructing trophic evolution in early primates.

Keywords body size, diet, insectivory, herbivory, heterotachy

44 **1 | INTRODUCTION**

45 Primates exhibit an impressive diversity of trophic strategies. Among extant members of the
46 order, frugivory is the most widespread primary strategy, but folivory is also common (Gómez &
47 Verdú, 2012; Kay & Covert, 1984). The clade also includes specialized lineages such as the
48 graminivorous gelada (*Theropithecus gelada*) of the Ethiopian Highlands, the tree-gouging,
49 exudativorous marmosets (genera *Callithrix*, *Mico*, *Callibella*, and *Cebuella*) of Amazonia and
50 the Atlantic Forest, and the exclusively faunivorous tarsiers (family Tarsiidae) of the Malay
51 Archipelago (Fleagle, 2013). Explaining how this diversity arose—and particularly how it has
52 been shaped by other aspects of primate biology—is a major goal of evolutionary primatology.

53 Body size has been recognized as an important influence on primate trophic evolution
54 since Kay (1975) noted that folivores are mostly large-bodied whereas insectivores are mostly
55 small. The correlation between body size and diet has been attributed to two other size-related
56 trends (Kay, 1975; Kay & Covert, 1984; Kay & Hylander, 1978; Kay & Simons, 1980). First,
57 because insects are small, dispersed, and often elusive, acquiring enough of them to meet
58 metabolic requirements becomes more challenging as body size increases and is probably
59 physiologically impossible above a certain threshold without specializing on social insects
60 (McNab, 1984). Second, as body size decreases, digestive retention time becomes shorter and
61 metabolic rate per unit mass increases, making it difficult for small-bodied primates to extract
62 sufficient nutrition from leaves, which are resistant to chemical digestion and must be slowly
63 fermented in the gut (Lambert, 1998). These arguments have also been invoked to explain why
64 large-bodied frugivorous primates rely on leaves as their main source of dietary protein whereas
65 small-bodied frugivores are dependent on insects (Kay & Simons, 1980; Kay & Covert, 1984).
66 Size differentiation between herbivores and faunivores is pervasive across mammals (Price &

67 Hopkins, 2015; Grossnickle, 2020), indicating that the pattern found in primates is a general
68 feature of mammalian biology.

69 The distribution of trophic strategies within small-bodied primates has generated
70 additional hypotheses of constraint on the evolution of insectivory. Although insects are an
71 important resource for many diurnal primates (e.g., Digby, Ferrari, & Saltzman, 2007; Kinzey,
72 1992; Souza-Alves, Fontes, Chagas, & Ferrari, 2011; Zimble-DeLorenzo & Stone, 2011),
73 insectivory as a primary trophic strategy (i.e., at least 50% a species' diet) is found mainly in
74 nocturnal lineages (Figure 1). The reason for the rarity of insectivory in small-bodied diurnal
75 lineages is unclear, but one hypothesis that has been proposed is that competition with diurnal
76 birds has limited the ability of primates to become established in the diurnal arboreal insectivore
77 niche (Cartmill, 1980; Charles-Dominique, 1975; Ross, 1996). This idea is difficult to test, but
78 direct interactions between the two clades certainly do occur (Heymann & Hsia, 2015), and there
79 is evidence that such interactions have had an influence on the distribution of species in each
80 clade (Beaudrot et al., 2013a, 2013b).

81 A long history of adaptation to herbivory has also been identified as a possible constraint.
82 In his discussion of primate origins, Rosenberger (2013) advocated for the idea that frugivory
83 was the formative trophic influence on early primate evolution, responsible for many of the
84 apomorphies that distinguish primates from other mammals (Sussman, 1991; Sussman,
85 Rasmussen, & Raven, 2013; Szalay, 1968). As a consequence, he argued, a primarily
86 insectivorous diet presents primates with “intense selective challenges” (Rosenberger, 2013, p.
87 886), making it difficult for them to switch from herbivory to insectivory. Studies of acidic
88 mammalian chitinase genes (*CHIAs*) provide support for the idea that some primate lineages
89 have experienced changes to their digestive biology that may decrease the likelihood of

90 insectivory evolving or persisting (Emerling, Delsuc, & Nachman, 2018; Janiak, Chaney, &
91 Tosi, 2018). However, in contrast to the global constraint proposed by Rosenberger, the
92 distribution of *CHIA* pseudogenes and deletions among extant species indicates that gene
93 functionality has been maintained by selection in some primate lineages and lost multiple times
94 in others (Emerling et al., 2018; Janiak et al., 2018). As noted by the authors of the *CHIA* studies,
95 this pattern of evolution is consistent with the hypothesis that insectivory was important for early
96 primates (Cartmill, 1974, 1992, 2012), with various clades becoming more specialized for
97 herbivory over time, perhaps resulting in variation across the primate tree in the ability to exploit
98 insects as a primary dietary resource.

99 If these constraints, or others, are operating in primates, then they should manifest at the
100 macroevolutionary level as heterogeneity among lineages in the rate of trophic evolution. For
101 example, the hypothesis that diurnality limits the evolution of insectivory predicts that small-
102 bodied anthropoids, which are mostly diurnal, will have a lower rate of transition between
103 trophic states than other small-bodied primate lineages, which are mostly nocturnal.
104 Evolutionary rates have been used to test hypotheses of constraint or to make a posteriori
105 inferences of constraint in a diverse set of organismal traits, including flower size in plants
106 (Barkman et al., 2008), forelimb morphology in marsupials (Cooper & Steppan, 2010), niche
107 evolution in damselfishes (Litsios et al., 2012), growth form in angiosperms (Beaulieu, O'Meara,
108 & Donoghue, 2013), and habitat shifts in diatoms (Nakov, Beaulieu, & Alverson, 2019). The
109 goal of the present study is to evaluate the idea that trophic evolution is constrained in some
110 small-bodied primate lineages by testing for variation in transition rates between insectivory and
111 herbivory against the null hypothesis that a single rate can explain the distribution of insectivory
112 and herbivory across the primate tree.

113

114 **2 | MATERIALS AND METHODS**

115 **2.1 | Tree and sample**

116 The analyses reported here were conducted using the phylogenetic topology estimated by
117 Springer et al. (2012) for 367 extant primate taxa. This tree was pruned so that only species-level
118 taxa recognized by Groves (2005) were included, resulting in a tree with 307 tips. Springer et al.
119 provided four sets of divergence dates for the tree based on different assumptions about variation
120 in rates of molecular evolution among lineages and the certainty of fossil calibrations. Two of the
121 timetrees were used for the present study: one that assumed autocorrelated rates of molecular
122 evolution with soft-bounded constraints on fossil calibrations, and one that assumed
123 autocorrelated rates but with hard-bounded constraints. These two trees were preferred over the
124 two that assumed independent rates of molecular evolution because autocorrelated rates provide
125 a much better fit to the primate molecular data and appear to be more biologically realistic (dos
126 Reis et al., 2018). The trees are available in the Supporting Information (Text S1 and Text S2).

127 Species were classified as insectivorous or herbivorous using primary field reports or
128 recent reviews that compiled information on dietary composition from such reports. A species
129 was considered insectivorous when insects and other small fauna constituted at least 50% of its
130 diet. For some species, dietary percentages were not available. In those cases, assignments were
131 made using qualitative descriptions from experts as long as the characterizations were
132 compatible with quantitative data for the species' closest living relatives. A total of 26 species
133 were identified as insectivorous (Table 1). The remaining taxa were categorized as herbivorous,
134 which subsumes frugivory, seed predation, folivory, exudativory, and graminivory (see Table S1
135 in the Supporting Information for the full list of taxa and character coding).

136 Species were further divided into small-bodied and large-bodied using literature
137 compilations of body mass (Smith and Jungers, 1997; Jones et al., 2009; Fleagle, 2013). Two
138 sets of analyses were performed using different size thresholds to evaluate whether the value
139 used to dichotomize body size affects interpretations: 800 g and 1 kg. All species were assigned
140 to a size category based on female body mass, given that females are considered more sensitive
141 to energetic constraints than males (e.g., Gordon, Johnson, & Louis, 2013). Taxa without data on
142 body mass were assigned to a size category when their position relative to the threshold could be
143 assumed with high confidence (e.g., all callitrichines are smaller than 800 g).

144 The size and diet classifications were combined to create a three-state character: small-
145 insectivorous, small-herbivorous, and large-herbivorous. This character was treated as ordered,
146 with direct transitions between small-insectivorous and large-herbivorous prohibited (i.e.,
147 SI↔SH↔LH). This coding scheme allowed transitions between trophic states within small-
148 bodied lineages to be isolated in the analysis without compromising phylogenetic sampling by
149 excluding large-bodied lineages.

150

151 **2.2 | Models of trait evolution**

152 Transition rates between character states were estimated using the multistate speciation and
153 extinction model (MuSSE) in the package diversitree (FitzJohn, 2012) for R (R Core Team,
154 2019). The hypothesis of variation in rates of trophic evolution was tested using diversitree's
155 make.musse.split function, which splits subclades (foreground clades) from the rest of the tree
156 (paraphyletic background) and allows each partition to have separate rate classes. The locations
157 of the splits are selected prior to analysis. Three foreground clades were used for this study:
158 Anthropoidea, Lemuriformes, and Lorisiformes. Initially, models with one split—one foreground

159 clade and the background—were examined. Depending on the results of those analyses, the
160 model set was expanded to include models with two foreground clades.

161 For each character state, MuSSE estimates up to three parameters: the transition rate out
162 of the state (q), the speciation rate for lineages in the state (λ), and the extinction rate for lineages
163 in the state (μ). Thus, a MuSSE model for an ordered three-state character and no splits will have
164 as many as $k = 10$ estimated parameters. Adding a single split will double that number to $k = 20$,
165 which is almost certainly too many for the size of the primate tree. To reduce the parameter set to
166 a more appropriate size, the following constraints were imposed. First, speciation and extinction
167 rates were not allowed to vary by character state or across partitions. Second, transition rates
168 between insectivory and herbivory in small-bodied lineages were set equal to each other within
169 partitions (i.e., $q_{IH} = q_{HI}$, where q_{IH} is the rate from insectivory to herbivory, and q_{HI} is the rate
170 from herbivory to insectivory). Previous analysis of this data set using an unpartitioned tree
171 found that the symmetric-rates model for transitions between trophic states provides a better fit
172 to the data than a model that allows rate asymmetry (i.e., $q_{IH} \neq q_{HI}$) (Scott, 2019). Preliminary
173 model comparisons using Akaike's information criterion indicated that the symmetric-rates
174 assumption is also justified within the partitions examined here. For transitions between size
175 classes among herbivores, there is strong support for rate asymmetry, with the rate into the large-
176 bodied state being several times higher than the rate into the small-bodied state across the
177 primate tree (Scott, 2019). Thus, size transition rates were allowed to vary within partitions.
178 These constraints resulted in two-partition models with $k = 8$ parameters: one trophic transition
179 rate for each partition, two size transition rates for each partition, and one speciation rate and one
180 extinction rate for the entire tree. A three-partition model (two foreground clades and the
181 paraphyletic background) has at least one more parameter ($k = 9$) for the second foreground

182 clade's trophic transition rate and, depending on the results, two additional parameters for that
183 clade's size transitions ($k = 11$).

184

185 **2.3 | Bayesian analysis of rate estimates**

186 Uncertainty in the maximum-likelihood estimate for each transition rate was examined
187 using a Bayesian approach to approximate each parameter's posterior distribution. This part of
188 the analysis was conducted with Markov chain Monte Carlo (MCMC) using diversitree's mcmc
189 function (FitzJohn, 2012). Markov chains were generated following the procedures outlined in
190 Johnson, FitzJohn, Smith, Rausher, & Otto (2011) and FitzJohn (2012), including their use of an
191 exponential prior distribution with a mean of twice the net diversification rate (i.e., speciation
192 rate minus extinction rate) for the entire tree. The chains were run for 120,000 generations, with
193 the first 20,000 being discarded as burn-in. The remaining generations were thinned by sampling
194 every tenth generation, resulting in a final sample of 10,000 generations for further analysis. The
195 R package coda (Plummer, Best, Cowles, & Vines, 2006) was used to examine MCMC
196 diagnostics on the thinned chains. Effective sample sizes for transition rates were high ($n > 8200$,
197 typically $n > 9000$), autocorrelation among generations for each parameter was low ($r < 0.07$,
198 typically $r < 0.03$), and trace plots indicated convergence.

199 The posterior distributions for the parameter estimates were used to compute posterior
200 probabilities for differences between transition rates. The posterior probability that q_i is greater
201 than q_j is simply the proportion of MCMC samples for which that statement is true (Goldberg et
202 al., 2010). Such comparisons were made across partitions (e.g., Anthropoidea versus the
203 background) and within partitions in the case of size transitions (e.g., the rate of transition into
204 the large-bodied state versus the rate into the small-bodied state in Anthropoidea). Because the

205 posterior distributions for Lorisiformes were strongly right-skewed, rates were log-transformed
206 (base e) for visual presentation, but all quantitative comparisons were made using the
207 untransformed rates.

208

209 **3 | RESULTS**

210 **3.1 | Two-partition models**

211 With Anthroidea split from the rest of the tree, there is moderate support for two rates of
212 transition between insectivory and herbivory in small-bodied lineages. Anthropoids have a lower
213 rate than other primates (Figure 2A): the maximum-likelihood estimate for the background rate
214 is approximately 5–7 times higher than the estimate for anthropoids (Table S2). The posterior
215 probabilities for rate heterogeneity in this partitioning scheme range from $PP = 0.906$ to 0.959 ,
216 depending on the tree and size threshold (Table 2). Support is highest when using a size
217 threshold of 1 kg and the tree with soft-bounded constraints on fossil calibrations.

218 There is strong support for asymmetry in size transition rates among anthropoids, where
219 transitions from small to large occur at a much higher rate than transitions in the reverse
220 direction ($PP > 0.99$; Figure 2B). In other primates, there is no evidence for such rate asymmetry
221 ($PP < 0.70$; Figure 2C). This difference in the pattern of size evolution is driven by the very low
222 transition rate out of the large-bodied state in anthropoids. This rate differs from the other size
223 transition rates with high posterior probability ($PP > 0.98$), whereas the other three rates cannot
224 be statistically distinguished from each other ($PP < 0.85$; compare Figure 2B and 2C).

225 Given the strong support for these contrasting patterns of size evolution, the remaining
226 two-partition models were modified to allow anthropoids to have their own set of size transition
227 rates while constraining the rest of the tree to have a second set of size transition rates, regardless

228 of how the tree was partitioned for the analysis of trophic transition rates. Thus, these models
229 have two partitions for trophic transition rates and two partitions for size transition rates. The
230 model that allowed Lorisiformes to have a distinct trophic rate produced the strongest support for
231 trophic rate heterogeneity among the two-partition models (Figure 3). In this case, lorisiforms
232 have a rate of trophic evolution that is approximately 4–6 times higher than the background rate
233 with high posterior probability ($PP > 0.98$; Table S3). The results from the model that allowed
234 Lemuriformes to have a distinct trophic rate indicate no support for trophic rate heterogeneity
235 ($PP < 0.70$; Figure 4; Table S4).

236

237 **3.2 | Three-partition model**

238 The two-partition analyses suggest three possibilities: (1) that anthropoids have a lower trophic
239 transition rate than other primates, (2) that lorisiforms have a higher rate than other primates, or
240 (3) that the two-partition models do not adequately describe the degree of rate heterogeneity in
241 primates. To distinguish among these alternatives, a three-partition model with anthropoids and
242 lorisiforms both foregrounded was constructed. This model allowed each partition to have its
243 own rate of trophic evolution, with size transition rates partitioned as above (i.e., anthropoids
244 versus all other primates, including lorisiforms; Table S5). Analysis of this model indicates that
245 the anthropoid trophic rate cannot be clearly distinguished from the background rate ($PP < 0.90$),
246 that there is moderate support for lorisiforms having a higher trophic rate than the background
247 ($0.90 < PP < 0.96$), and that anthropoids and lorisiforms are very unlikely to be characterized by
248 a common trophic rate ($PP > 0.98$) (Table 3; Figure 5). These results suggest that, of the models
249 considered here, the two-partition model with Lorisiformes as the foreground clade provides the
250 best description of primate trophic evolution.

251

252 **4 | DISCUSSION**

253 **4.1 | Activity pattern and trophic evolution**

254 The rate heterogeneity detected here supports the idea that trophic evolution has been more labile
255 in some small-bodied primate lineages than in others. The rarity of primarily insectivorous
256 anthropoids has focused attention on this clade and the possibility that some aspect of diurnal
257 ecology is a constraint on trophic evolution in primates (Cartmill, 1980; Charles-Dominique,
258 1975; Ross, 1996; Scott, 2019). The results of the present study challenge this idea by showing
259 that a single rate of transition between insectivory and herbivory can explain the distribution of
260 trophic strategies among small-bodied lineages of mostly diurnal anthropoids and nocturnal
261 lemurs and tarsiers. Insectivorous anthropoids and lemurs are nested deeply among herbivorous
262 lineages, indicating that insectivory is an evolutionarily recent phenomenon in these two clades
263 (Figure 1). Thus, despite differences in activity pattern, extant anthropoids and lemurs appear to
264 be characterized by similar trophic evolutionary histories where herbivory has predominated and
265 shifts to insectivory have been infrequent.

266 What distinguishes anthropoids in this analysis is their pattern of size evolution. In
267 contrast to other primates, which are characterized by symmetric rates of transition into and out
268 of the large-bodied state, anthropoids exhibit high rate asymmetry favoring shifts into the large-
269 bodied state. This result is not surprising in light of the well-known differences in the distribution
270 of body size among primate clades (e.g., Charles-Dominique, 1975; Fleagle, 1978, 2013;
271 Jungers, 1984). The prevalence of large body size (>1 kg) in anthropoids is thought to be one of
272 the solutions to the problem of trophic competition with diurnal birds, allowing anthropoids to
273 specialize on herbivorous resources that birds cannot typically access (e.g., leaves and

274 mechanically protected fruits; Charles-Dominique, 1975; Ross, 1996). The results of this study
275 are consistent with this idea, but they do not constitute additional evidence beyond the
276 observation that anthropoids tend to be larger than diurnal birds. Diurnality can be considered an
277 indirect influence on the distribution of insectivory across the primate tree to the extent that it
278 increases the likelihood that large body size will evolve and persist. This effect is magnified by
279 the tendency of diurnal lineages to diversify and accumulate at a higher rate than nocturnal
280 lineages (Magnuson-Ford & Otto, 2012; Santini, Rojas, & Donati, 2015; Scott, 2018, 2019).
281 However, the results of this study suggest that activity pattern does not have an effect on the rate
282 of transition between herbivory and insectivory among small-bodied primates.

283 Because the broad-scale phylogenetic approach adopted here does not address the
284 possibility that lineage-specific factors have produced similar patterns of trophic evolution in
285 diurnal anthropoids and nocturnal lemurs, these results should not be viewed as a decisive
286 rejection of the idea that diurnality is a constraint on primate trophic evolution. Studies
287 conducted at a much finer scale of resolution may reveal different processes operating in each
288 clade and establish equifinality. However, given the current state of knowledge, the low
289 frequency of insectivory among small-bodied diurnal anthropoids does not appear to be unusual
290 and therefore in need of explanation. Instead, it is the lorises and galagos that stand out relative
291 to other small-bodied primates in having a greater tendency to shift between trophic states.

292

293 **4.2 | Commitment to herbivory as a constraint on the evolution of insectivory**

294 The pattern of rate heterogeneity found in primates is consistent with the idea that
295 adaptive commitment to herbivory has reduced the likelihood that insectivory will evolve or
296 persist in some lineages. There are two ways to interpret the pattern of rate heterogeneity in this

297 context. The first posits that the low rate of transition between trophic states found in most of the
298 primate tree is plesiomorphic, meaning that trophic evolution has been conservative for much of
299 the clade's history. This inference, combined with the prevalence of herbivory among extant
300 lineages, aligns with the view that many of the apomorphies that unite primates originated as
301 adaptations for acquiring angiosperm products, and that this aspect of the clade's evolutionary
302 history has biased primates against adopting insectivory as a primary trophic strategy
303 (Rosenberger, 2013; Sussman et al., 2013). It follows that the higher rate of trophic evolution
304 found in loriforms represents a derived acceleration, suggesting that lineages in this group
305 evolved traits that allowed them to shift between trophic states more easily than other primates in
306 response to ecological conditions. The evolutionary importance of insects as a primary or
307 secondary dietary resource among loriforms was emphasized by Rasmussen & Nekaris (1998),
308 who argued that adaptive divergence between Lorisidae and Galagidae in aspects of locomotor
309 behavior, sensory systems, and life history was driven, in part, by specialization on insects with
310 different properties: cryptic or toxic prey in the case of lorids versus active and elusive prey in
311 the case of galagids. Notably, the ability to exploit insects has not necessarily channeled
312 loriform lineages toward obligate insectivory, as in tarsiers. The present-day expression of this
313 evolutionary history is the gradient of trophic strategies exhibited by galagids and the presence of
314 herbivorous and insectivorous lorid sister lineages found in both Africa and Asia (Nekaris and
315 Bearder, 2007).

316 The second scenario posits that the transition rate found in loriforms is plesiomorphic
317 and that other primate clades evolved slower rates in parallel as they became more committed to
318 a particular trophic strategy: herbivory in Anthropoidea and Lemuriformes, and insectivory in
319 tarsiers. This scenario is less parsimonious than the first, but there are two lines of evidence that

320 suggest convergent, herbivory-driven rate slowdowns in anthropoids and lemurs. First, as noted
321 above, studies of chitinase genes indicate pervasive homoplasy in loss of function in these genes
322 across primates (Emerling et al., 2018; Janiak et al., 2018). Emerling et al. (2018) inferred that
323 the plesiomorphic number of *CHIAs* for placental mammals is five functional genes, and that
324 tarsiers retain this condition, implying that the last common ancestors of Primates and Haplorhini
325 also had five. The anthropoids and lemurs that have been characterized so far, including small-
326 bodied species, have two or fewer functional *CHIAs*, and some large-bodied species in both
327 clades have lost function in all five genes, indicating separate histories of increasing commitment
328 to herbivory (Emerling et al., 2018; Janiak et al., 2018). This conclusion is further reinforced by
329 the observation that the lorisiform *Otolemur garnettii* has three functional *CHIAs* (Emerling et
330 al., 2018; Janiak et al., 2018).

331 The second line of evidence suggesting convergent rate slowdowns in Anthropeida and
332 Lemuriformes is the history of body-size evolution in each clade's smallest-bodied lineages. The
333 smallest anthropoids are the Callitrichinae, which have long been regarded as phyletic dwarfs
334 (e.g., Ford, 1980; Leutenegger, 1980; Rosenberger, 1992), descended from a common ancestor
335 shared with other platyrrhines that weighed approximately 1–2 kg (Ford & Davis, 1992;
336 Montgomery & Mundy, 2013; Silvestro et al., 2019). The closely related and slightly larger
337 squirrel monkeys (genus *Saimiri*) may also be dwarfed (Ford & Davis, 1992; Rosenberger, 1992;
338 Silvestro et al., 2019). Recent studies of size evolution in lemurs have concluded that the
339 smallest members of this clade—species of the family Cheirogaleidae—have experienced
340 episodes of size reduction similar to those reconstructed for callitrichines (Masters, Génin,
341 Silvestro, Lister, & DelPero, 2014; Montgomery & Mundy, 2013). If these inferences of phyletic
342 dwarfism are correct, then the evolutionary histories of small-bodied anthropoids and lemurs

343 may include long periods of relaxed selection on traits involved in extracting nutrition from
344 insects (e.g., chitinase genes) owing to the lesser importance of insects as a dietary resource at
345 large body size.

346 That most small-bodied anthropoids and lemurs have apparently entered their current size
347 range via phyletic dwarfism contrasts with the pattern evident in lorisiforms and tarsiers, where
348 small size appears to have prevailed throughout their histories (Beard, 1998; Beard, Qi, Dawson,
349 Wang, & Li, 1994; Jaeger et al., 2010; Rossie, Ni, & Beard, 2006; Steiper & Seiffert, 2012;
350 Seiffert, Simons, & Attia, 2003; Seiffert, Simons, Ryan, & Attia, 2005). The observation that
351 tarsiers and at least some lorisiforms retain more functional *CHIAs* than other primates also
352 suggests long histories of small body size with selection to maintain some of the primitive
353 digestive machinery assembled in early insectivorous mammals (Emerling et al., 2018; Janiak et
354 al., 2018). *Otolemur garnettii* is the only lorisiform in which *CHIAs* have been investigated so
355 far (Emerling et al., 2018; Janiak et al., 2018). It is unclear how typical this galagid is of other
356 lorisiforms, but the fact that the number of functional genes retained by *O. garnettii* (three) is
357 intermediate between tarsiers (five) and anthropoids and lemurs (two or fewer) is consistent with
358 the idea that lorisiforms have experienced episodes of adaptation to herbivory without becoming
359 too specialized, resulting in a clade that has been more flexible than crown anthropoids,
360 lemuriforms, and tarsiers with regard to shifting between trophic strategies.

361 Thus, whereas the first scenario outlined above views a slow rate of trophic evolution and
362 commitment to herbivory as evolutionarily ancient and tied to the origin of crown primates, the
363 second scenario raises the possibility that trophic evolution in early crown primates was more
364 labile—similar to lorisiforms—before herbivory came to predominate in the case of crown
365 anthropoids and lemurs, and insectivory in the case of tarsiers. Such trophic flexibility is

366 compatible with a last common ancestor of crown primates that was either primarily herbivorous
367 (Rosenberger, 2013; Sussman et al., 2013) or primarily insectivorous (Cartmill, 1974, 1992,
368 2012), and it implies that the ancestor's feeding adaptations did not necessarily constrain or bias
369 trophic evolution as the crown clade began to diversify in the late Paleocene and early Eocene.

370

371 **4.3 | Evidence for trophic lability in the primate fossil record**

372 The primate fossil record provides some evidence that early small-bodied primates had a
373 greater tendency to shift between trophic states than would be inferred from the distribution of
374 states among extant anthropoids, lemurs, and tarsiers of similar size. Most of the small-bodied
375 primates known from the early and middle Eocene are omomyiforms (e.g., Covert, 1986;
376 Fleagle, 1978, 2013; Gilbert, 2005; Gingerich, 1981). Studies that have examined functional
377 aspects of molar form in this group indicate that it was characterized by a level of trophic
378 diversity similar to that found in extant lorisiforms (Strait, 2001). The evolutionary history of this
379 diversity is difficult to reconstruct with confidence, given uncertainties in the relationships
380 among omomyiform lineages (e.g., Morse et al., 2019; Tornow, 2008; Williams, 1994). Mapping
381 inferred diets onto the phylogenetic tree generated by Seiffert et al. (2018) indicates a minimum
382 of 5–7 shifts between trophic states over the course of approximately 20 million years (Figure 6).
383 By comparison, the minimum number of shifts required to explain the distribution of states
384 among extant primates is 10 across 60 million years or more of evolution (Scott, 2019),
385 suggesting a relatively high rate of trophic evolution in omomyiforms. This conclusion is also
386 supported by evidence for trophic diversity within two of the earliest genera—*Teilhardina* and
387 *Steinicus* (Figure 6; Ni et al., 2004; Strait, 2001; Williams & Covert, 1994).

388 The broader significance of trophic evolution in omomyiforms is unclear owing to a lack
389 of consensus regarding their phylogenetic relationships to the crown clades. Omomyiforms have
390 been interpreted as stem tarsiers, stem haplorhines, or stem primates (see reviews in Fleagle,
391 2013; Martin, 1993; Miller, Gunnell, & Martin, 2005). Rosenberger (2013), adopting the first of
392 these alternatives as a working hypothesis, argued that trophic diversity within omomyiforms
393 reflects different stages in a shift from frugivory to the highly specialized form of insectivory
394 found in extant tarsiers. According to this view, the implications of omomyiform trophic
395 diversity are limited to the tarsier lineage, and the pattern of diversity mostly indicates a
396 directional macroevolutionary trend of increasing insectivory and its attendant morphological
397 adaptations. However, if omomyiforms are stem haplorhines (e.g., Kay, Ross, & Williams, 1997)
398 or representatives of an early radiation of primates not uniquely related to any of the crown
399 clades (e.g., Martin, 1993; Miller et al., 2005), then their pattern of trophic diversity can be
400 plausibly interpreted as consistent with the hypothesis that trophic evolution in early primates
401 was more labile in comparison to crown Anthroidea, Tarsiidae, and Lemuriformes.

402 Other groups of Eocene primates appear to have been less trophically diverse than
403 omomyiforms and more specialized for herbivory. Adapiformes—the other major radiation of
404 primates known from the early and middle Eocene—are mostly large-bodied and are thought to
405 have filled the ecological niches that are now dominated by extant large-bodied anthropoids and
406 lemurs (i.e., diurnal herbivores) (Covert, 1986; Fleagle, 1978, 2013; Gilbert, 2005).
407 Nevertheless, there is some evidence for trophic diversity among early small-bodied members of
408 this group (e.g., *Donrussellia*, *Asiadapis*, and *Marcgodinotius*; Bajpai et al., 2008; Gilbert,
409 2005). A similar pattern may hold in anthropoids, especially if Eosimiidae are stem anthropoids
410 (Beard, Qi, Dawson, Wang, & Li, 1994; Kay et al., 1997; Williams, Kay, & Kirk, 2010; but see

411 Miller et al., 2005). Small-bodied anthropoids from the late Eocene and early Oligocene have
412 been reconstructed as primarily frugivorous (Kirk & Simons, 2001). In contrast, the molars of
413 middle Eocene eosimiids exhibit morphologies suggesting that these species were more
414 insectivorous than later anthropoids (cf. Heesy & Ross, 2004; Kirk & Simons, 2001) and perhaps
415 comparable to *Saimiri*, the most insectivorous extant anthropoid (Zimble-DeLorenzo & Stone,
416 2011; Table 1). Thus, although adapiforms and early anthropoids appear to have been largely
417 herbivorous radiations, there are hints of greater trophic diversity in the earliest members of
418 these clades, suggesting that trophic evolution may have been more labile before herbivory
419 became the dominant trophic strategy.

420

421 5 | CONCLUSIONS

422 The results of this study indicate that the rate of trophic evolution in small-bodied
423 primates varies among clades. Contrary to expectations, small-bodied anthropoids do not have an
424 unusually low rate in comparison to other lineages. This finding challenges the hypothesis that
425 there is a direct connection between diurnality and the low frequency of insectivorous
426 anthropoids. The main contrast detected here involves lorisiforms, which have a much greater
427 tendency to shift between insectivory and herbivory than other primates. The implications of this
428 pattern of rate heterogeneity are unclear. The most parsimonious interpretation is that the
429 lorisiform rate is apomorphic, implying that primate trophic evolution has been conservative
430 throughout much of the clade's history. However, various lines of evidence suggest the
431 possibility of convergent rate slowdowns in anthropoids, lemuriforms, and tarsiers owing to
432 greater specialization for herbivory in the case of anthropoids and lemurs, and insectivory in the
433 case of tarsiers. These two scenarios can be tested as sampling of the earliest part of the primate

434 fossil record increases, and as our understanding of the Eocene primate phylogeny and trophic
435 adaptations improves.

436

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439 manuscript.

440

441 **DATA AVAILABILITY STATEMENT**

442 The data used for this study are available in Table S1 in the Supporting Information.

443

444

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- 682
- 683

684 **FIGURE CAPTIONS**

685 **FIGURE 1.** Primate phylogenetic tree from Springer et al. (2012) showing the distribution of
686 trophic states by activity pattern among small-bodied species (<1 kg) at the tips (Scott, 2019).
687 Cathemeral species are grouped with diurnal species. Large-bodied species, which are uniformly
688 herbivorous and mostly diurnal, are not labeled. The relative frequency of insectivorous species
689 is much greater among nocturnal lineages (41.5%) than among diurnal lineages (9.5%).

690

691 **FIGURE 2.** Posterior distributions of trophic transition rates (A) and size transition rates (B, C)
692 for the model with Anthroidea split from the rest of the tree and a size threshold of 800 g. The
693 results shown here were generated using the timetree that assumed autocorrelated rates and soft-
694 bounded constraints. Anth = Anthroidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor =
695 Lorisiformes, q = transition rate, SL = small to large, LS = large to small.

696

697 **FIGURE 3.** Posterior distributions of trophic transition rates for the model with Lorisiformes
698 split from the rest of the tree and a size threshold of 800 g. The results shown here were
699 generated using the timetree that assumed autocorrelated rates and soft-bounded constraints.

700 Anth = Anthroidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q =
701 transition rate.

702

703 **FIGURE 4.** Posterior distributions of trophic transition rates for the model with Lemuriformes
704 split from the rest of the tree and a size threshold of 800 g. The results shown here were
705 generated using the timetree that assumed autocorrelated rates and soft-bounded constraints.

706 Anth = Anthroidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q =
707 transition rate.

708

709 **FIGURE 5.** Posterior distributions of trophic transition rates for the model with Anthroidea
710 and Lorisiformes each split from the rest of the tree and a size threshold of 800 g. The results
711 shown here were generated using the timetree that assumed autocorrelated rates and soft-
712 bounded constraints. Anth = Anthroidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor =
713 Lorisiformes, q = transition rate.

714

715 **FIGURE 6.** Phylogenetic distribution of trophic strategies among early and middle Eocene
716 omomyiform genera. Dietary reconstructions for each genus are based mainly on the work of
717 Strait (2001), with additional information from Ni, Wang, Hu, & Li (2004) and Williams &
718 Covert (1994). Parsimony reconstructions of diet, obtained using Mesquite (v. 3.61; Maddison &
719 Maddison, 2019), indicate a minimum of 5–7 shifts between trophic states, depending on how
720 ambiguous taxa are coded. The reconstructions shown here are based on the data set where
721 *Bownomomys* and *Dyseolemur* were coded as ambiguous (see Strait, 2001). The tree was taken
722 from the Bayesian tip-dating phylogenetic analysis conducted by Seiffert et al. (2018; see their
723 figure 17). Branch lengths are proportional to time; the tree spans approximately 20 million years
724 from root to most recent tip (*Necrolemur*). *Teilhardina* includes *T. asiatica* and *T. belgica*;
725 *Steinius* includes *S. vespertinus* and *S. annectens*; the use of *Bownomomys* here follows Morse et
726 al. (2019) and is equivalent to *Teilhardina americana* in previous studies. See Strait (2001) and
727 Seiffert et al. (2018) for the complete lists of species-level taxa.

728

TABLE 1 Primates classified as insectivorous for this study

Species	% Faunivory	Source
<i>Galagoides thomasi</i>	70	Nekaris & Bearder, 2007
<i>Galagoides demidoff</i>	70	Nekaris & Bearder, 2007
<i>Galago matschiei</i>	qualitative [†]	Nash, Bearder, & Olson, 1989
<i>Galago moholi</i>	52	Nekaris & Bearder, 2007
<i>Galago gallarum</i>	qualitative [†]	Butynski & de Jong, 2004
<i>Galago senegalensis</i>	50	Burrows & Nash, 2010
<i>Paragalago orinus</i>	qualitative [†]	Rovero, Marshall, Jones, & Perkin, 2009
<i>Paragalago granti</i>	qualitative [†]	Génin et al., 2016
<i>Paragalago zanzibaricus</i>	70	Harcourt & Nash, 1986
<i>Otolemur garnettii</i>	50	Harcourt & Nash, 1986
<i>Loris lydekkerianus</i>	96	Nekaris & Bearder, 2007
<i>Loris tardigradus</i>	100	Nekaris & Bearder, 2007
<i>Arctocebus calabarensis</i>	85	Rothman et al., 2014
<i>Arctocebus aureus</i>	85	Rothman et al., 2014
<i>Allocebus trichotis</i>	70	Biebouw, 2013
<i>Mirza coquereli</i>	>50	Hladik, Charles-Dominique, & Petter, 1980
<i>Microcebus rufus</i>	54	Rothman et al., 2014
<i>Tarsius dentatus</i>	100	Niemitz, 1984
<i>Tarsius tarsier</i>	100	Niemitz, 1984
<i>Tarsius sangirensis</i>	100	Niemitz, 1984
<i>Cephalopachus bancanus</i>	100	Niemitz, 1984
<i>Carlito syrichta</i>	100	Niemitz, 1984
<i>Saimiri sciureus</i>	79–97	Zimble-DeLorenzo & Stone, 2011
<i>Saimiri oerstedii</i>	90	Zimble-DeLorenzo & Stone, 2011
<i>Saimiri boliviensis</i>	75	Zimble-DeLorenzo & Stone, 2011
<i>Saimiri ustus</i>	as for other <i>Saimiri</i>	Zimble-DeLorenzo & Stone, 2011

[†] For some species, dietary percentages were not available. In such cases, I used qualitative accounts from experts as long as the description was consistent with quantitative data for the species' closest living relatives. See Table S1 in the Supporting Information for the full sample.

TABLE 2 Support for trophic-rate differences in two-partition models

Model comparison	Posterior probability			
	AUTOsoft tree		AUTOhard tree	
	t.800	t.1000	t.800	t.1000
Anthropoidea < background	0.917	0.959	0.906	0.946
Lorisiformes > background	0.985	0.992	0.983	0.989
Lemuriformes > background	0.622	0.676	0.614	0.647

Notation: AUTOsoft = autocorrelated rates of molecular evolution and soft-bounded constraints; AUTOhard = autocorrelated rates of molecular evolution and hard-bounded constraints; t.800 = size threshold of 800 g; t.1000 = size threshold of 1 kg.

TABLE 3 Support for trophic-rate differences in the three-partition model

Model comparison	Posterior probability			
	AUTOsoft tree		AUTOhard tree	
	t.800	t.1000	t.800	t.1000
Anthropoidea < background	0.791	0.861	0.787	0.838
Lorisiformes > background	0.939	0.951	0.933	0.950
Lorisiformes > Anthropoidea	0.986	0.995	0.984	0.991

Notation: AUTOsoft = autocorrelated rates of molecular evolution and soft-bounded constraints; AUTOhard = autocorrelated rates of molecular evolution and hard-bounded constraints; t.800 = size threshold of 800 g; t.1000 = size threshold of 1 kg.

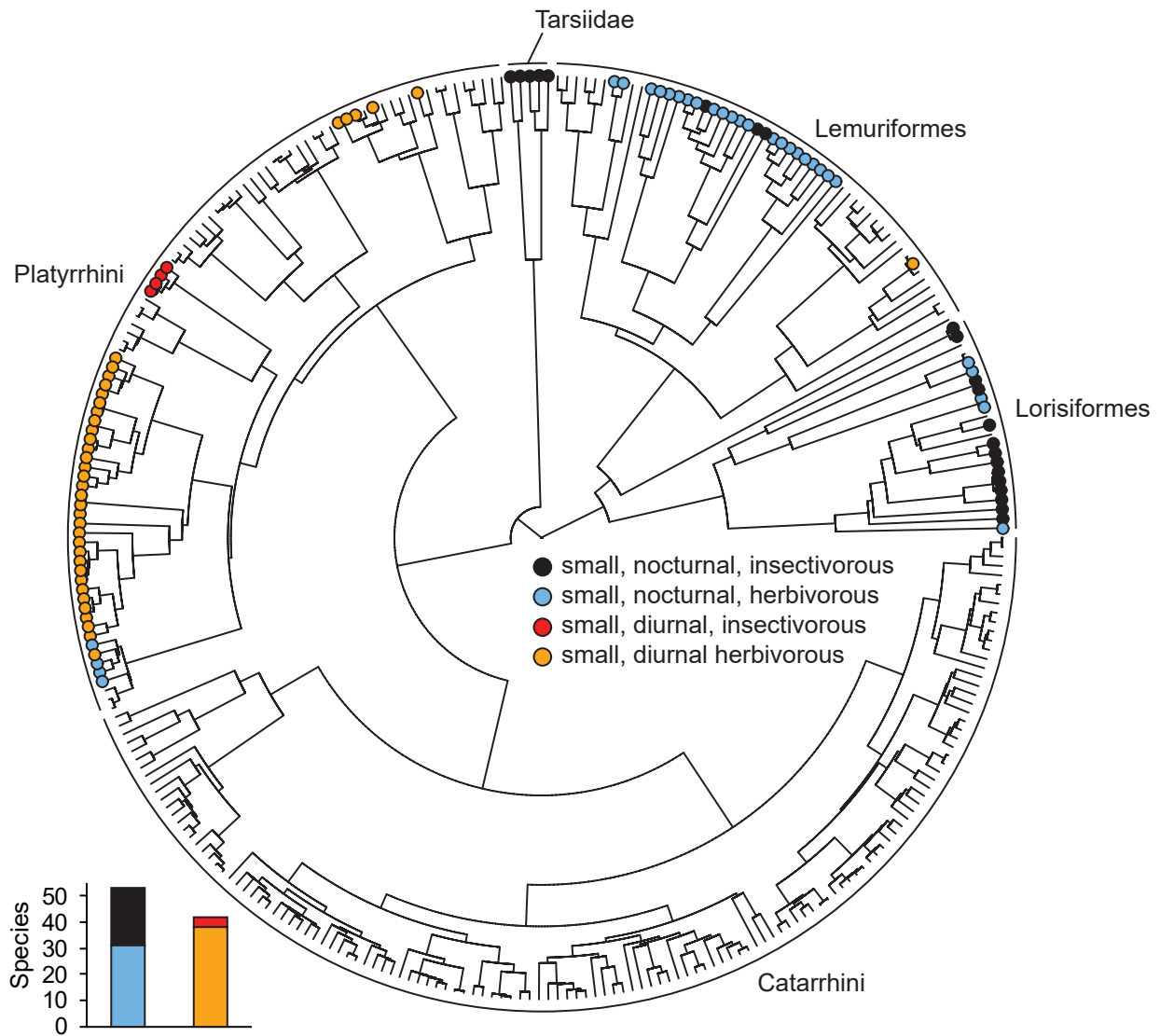


FIGURE 1. Primate phylogenetic tree from Springer et al. (2012) showing the distribution of trophic states by activity pattern among small-bodied species (<1 kg) at the tips (Scott, 2019). Cathemeral species are grouped with diurnal species. Large-bodied species, which are uniformly herbivorous and mostly diurnal, are not labeled. The relative frequency of insectivorous species is much greater among nocturnal lineages (41.5%) than among diurnal lineages (9.5%).

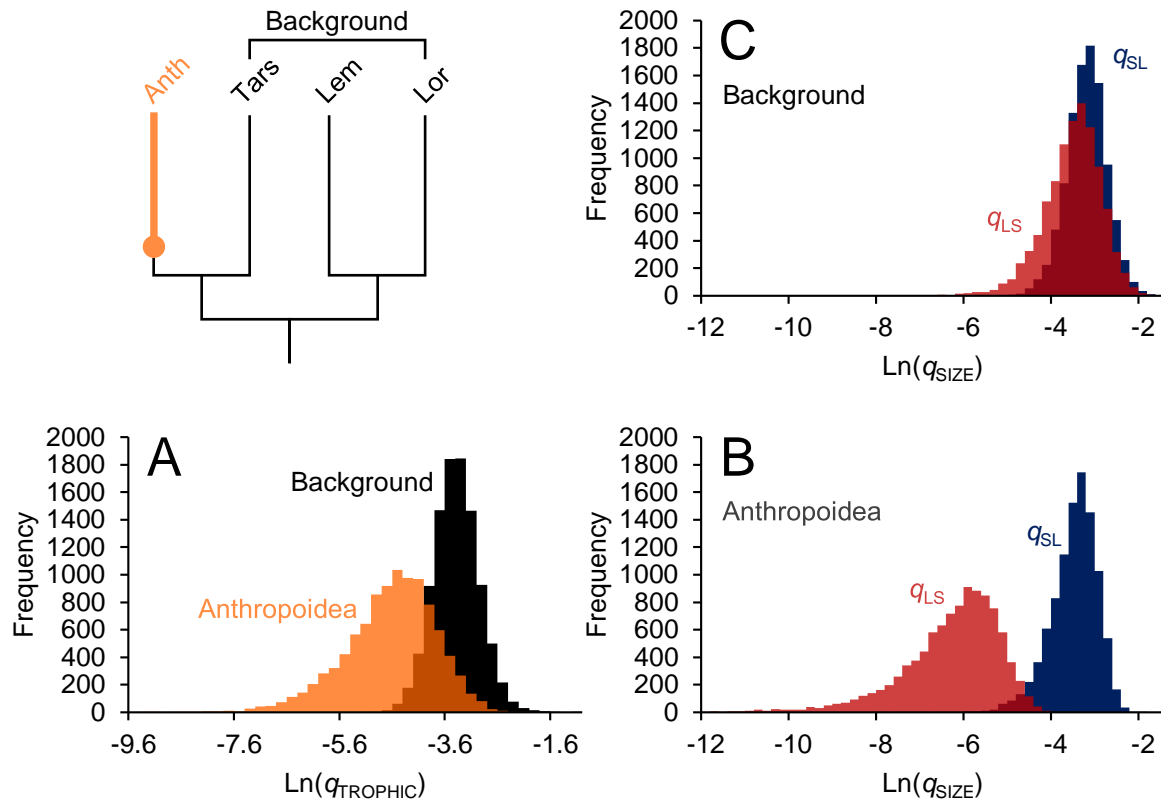


FIGURE 2. Posterior distributions of trophic transition rates (A) and size transition rates (B, C) for the model with Anthropoidea split from the rest of the tree and a size threshold of 800 g. The results shown here were generated using the timetree that assumed autocorrelated rates and soft-bounded constraints. Anth = Anthropoidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q = transition rate, SL = small to large, LS = large to small.

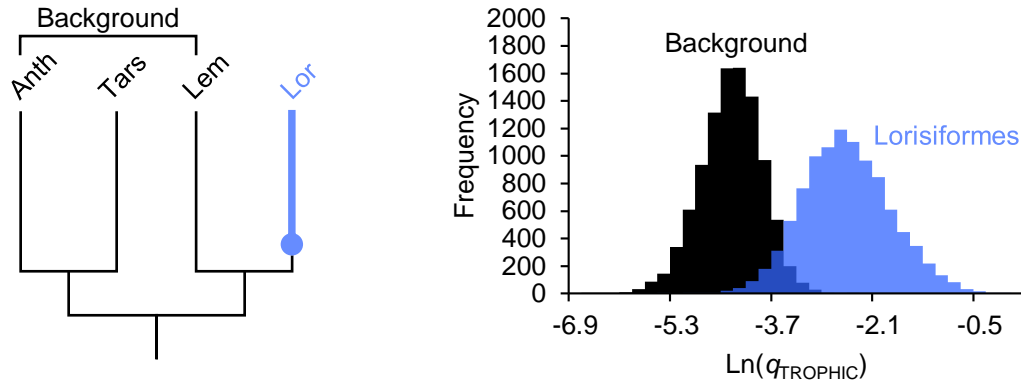


FIGURE 3. Posterior distributions of trophic transition rates for the model with Lorisiformes split from the rest of the tree and a size threshold of 800 g. The results shown here were generated using the timetree that assumed autocorrelated rates and soft-bounded constraints. Anth = Anthrozoidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q = transition rate.

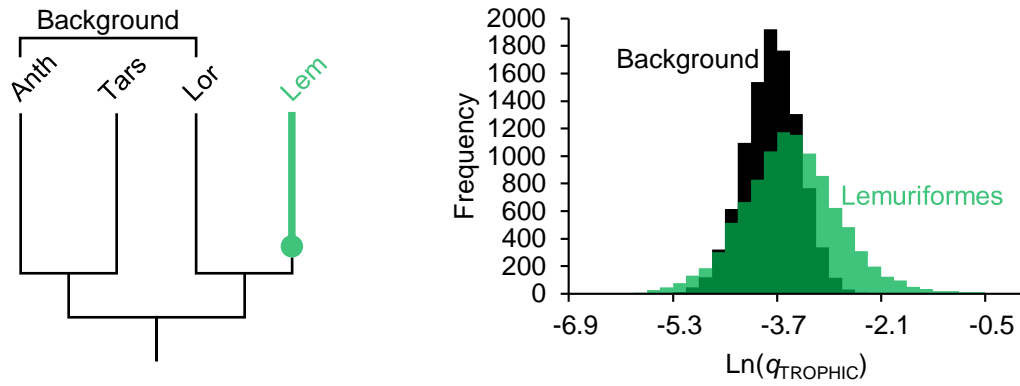


FIGURE 4. Posterior distributions of trophic transition rates for the model with Lemuriformes split from the rest of the tree and a size threshold of 800 g. The results shown here were generated using the timetree that assumed autocorrelated rates and soft-bounded constraints. Anth = Anthroidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q = transition rate.

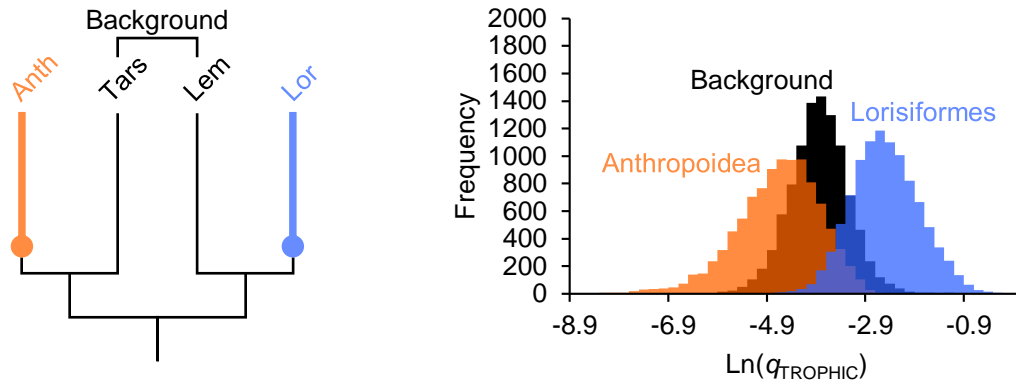


FIGURE 5. Posterior distributions of trophic transition rates for the model with Anthropoidea and Lorisiformes each split from the rest of the tree and a size threshold of 800 g. The results shown here were generated using the timetree that assumed autocorrelated rates and soft-bounded constraints. Anth = Anthropoidea, Tars = Tarsiiformes, Lem = Lemuriformes, Lor = Lorisiformes, q = transition rate.

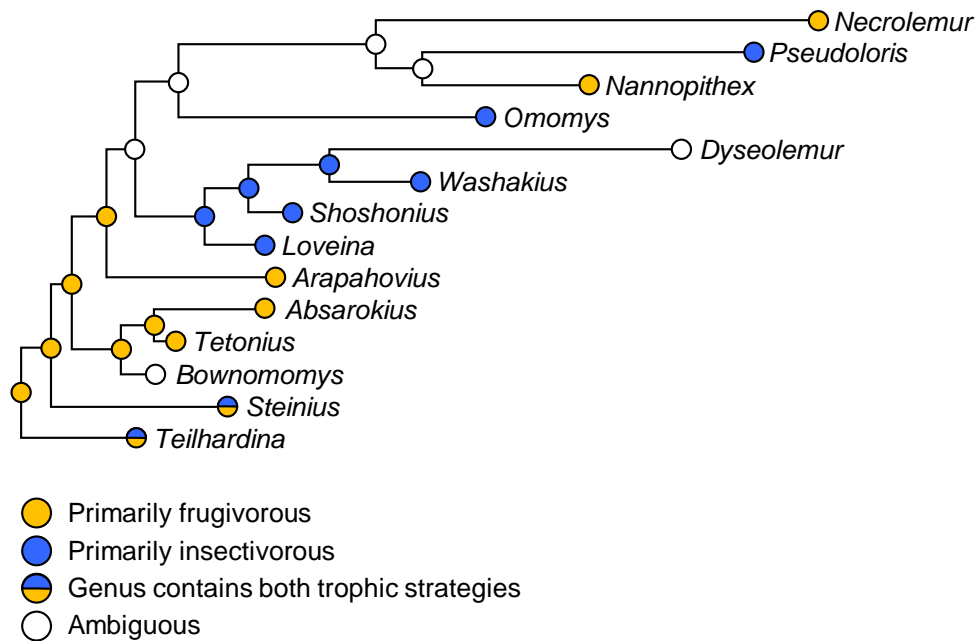


FIGURE 6. Phylogenetic distribution of trophic strategies among early and middle Eocene omomyiform genera. Dietary reconstructions for each genus are based mainly on the work of Strait (2001), with additional information from Ni, Wang, Hu, & Li (2004) and Williams & Covert (1994). Parsimony reconstructions of diet, obtained using Mesquite (v. 3.61; Maddison & Maddison, 2019), indicate a minimum of 5–7 shifts between trophic states, depending on how ambiguous taxa are coded. The reconstructions shown here are based on the data set where *Bownomomys* and *Dyseolemur* were coded as ambiguous (see Strait, 2001). The tree was taken from the Bayesian tip-dating phylogenetic analysis conducted by Seiffert et al. (2018; see their figure 17). Branch lengths are proportional to time; the tree spans approximately 20 million years from root to most recent tip (*Necrolemur*). *Teilhardina* includes *T. asiatica* and *T. belgica*; *Steinius* includes *S. vespertinus* and *S. annectens*; the use of *Bownomomys* here follows Morse et al. (2019) and is equivalent to *Teilhardina americana* in previous studies. See Strait (2001) and Seiffert et al. (2018) for the complete lists of species-level taxa.