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**Circumscription of a monophyletic family for the tapaculos
(Aves: Rhinocryptidae): *Psiloramphus* in and *Melanopareia* out**

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ABSTRACT

31 The tapaculos (Rhinocryptidae) are tracheophone, suboscine birds restricted to South
32 and Central America. Most tapaculos share a number of internal and external
33 characteristics that have been used to define the family taxonomically. The genera
34 *Melanopareia* and *Psiloramphus* do not fully fit this pattern and have caused
35 considerable dispute among taxonomists since they were first described. In this paper
36 we delimit the systematic boundaries of the tapaculos and assess their generic
37 relationships by an analysis of molecular sequence data. The results show that while
38 *Psiloramphus* is nested well within the Rhinocryptidae, *Melanopareia* falls far outside
39 that clade. A new family is erected for *Melanopareia*.

41 INTRODUCTION

42 The impudently named tapaculos (Rhinocryptidae) are a small group of tracheophone,
43 suboscine passerines whose greatest generic diversity is in southern South America.
44 Most are large-footed, strong-legged ground birds reminiscent of some of the ground-
45 dwelling antthrushes (Formicariidae), with which they were often associated. The
46 family is generally well defined by the presence of operculate nostrils, a tracheophone
47 syrinx, a somewhat curved humerus and a four-notched sternum (Ames 1971,
48 Feduccia and Olson 1982, Maurício et al. 2008). Thus, Krabbe and Schulenberg
49 (2003: 748) considered that the "tapaculos constitute a well-knit group the members
50 of which are united by several derived characters. Only the genera *Melanopareia* and
51 *Psiloramphus* differ to such a degree that their systematic position as tapaculos could
52 be disputed." Furthermore, the phylogenetic relationships within the family
53 Rhinocryptidae are poorly known, particularly regarding the placement of *Liosceles*
54 and *Acropternis*, and the large austral species of *Pteroptochos* and *Scelorchilus*.

55 The early taxonomic history of the group was ably summarized by Sclater
56 (1874). d'Orbigny (1837) first erected a family "Rhinomyidaeae" (sic., p. 192) for
57 *Pteroptochos* and his *Rhinomya* (= *Rhinocrypta*) using the operculate nostril to
58 separate them from the Formicariidae. However, there was no coherent understanding
59 of the suboscine groups until their distinction from the oscines was established by the
60 pioneering work of Müller (1847) on the syrinx, Müller showed that *Scytalopus* was a
61 tracheophone suboscine and not a wren (Troglodytidae) and also that *Scytalopus* and
62 *Pteroptochus* differed from other known passerines in having a 4-notched sternum.

63 Sclater's (1874) "Pteroptochidae" comprised *Scytalopus* (including the type
64 species of what later became *Myornis* Chapman, 1915), *Merulaxis*, *Liosceles*,
65 *Pteroptochos* (including the type species of what later became *Teledromas* Wetmore
66 and Peters, 1922, and *Scelorchilus* Oberholser, 1923), *Rhinocrypta*, *Hylactes* (now
67 included in *Pteroptochos*), *Acropternis*, and *Triptorhinus* (= *Eugralla*). This
68 composition of the group was essentially maintained until Peters (1951), except for
69 the problem genera *Psiloramphus* and *Melanopareia*.

70 The three or four species of *Melanopareia* differ from other tapaculos by their
71 rather slender build and boldly and attractively patterned plumage, and by sharing a
72 semi-concealed white dorsal patch with various true antbirds (Thamnophilidae). They
73 were originally described in the genus *Synallaxis* (Furnariidae), in which Sclater
74 (1890) later submerged the genus. Salvin (1876) described a new species from
75 Ecuador as *Formicivora speciosa*, duly recognized in that combination by Sclater
76 (1890:251) and others until Hellmayr (1906:334) showed that this was a synonym of
77 *Synallaxis elegans* Lesson, in which genus Hellmayr continued to place it while
78 regarding Salvin's allocation of it to *Formicivora* with incredulity. Ridgway (1909)
79 appears to have overlooked this when he created a new genus *Rhoporchilis* for
80 *Formicivora speciosa*. It was Hellmayr (1921) who eventually established the modern
81 concept of the genus in showing that *Synallaxis elegans*, *S. torquata*, and *S.*
82 *maximiliani* were congeneric and would all fall under Reichenbach's earlier generic
83 name *Melanopareia* and "find their natural place in the Formicariidae", where they
84 stayed for only a few years (e.g. Cory and Hellmayr 1924). Next came the observation
85 of W.D.W. Miller that the sternum of *Melanopareia* was 4-notched – information that
86 was conveyed to and presented by Wetmore (1926: 292). On this basis, Peters (1951)
87 included *Melanopareia* in the Rhinocryptidae, where it has resided since.

88 The other problem species, the Bamboo-wren *Psilorhamphus guttatus*, is a
89 small bamboo specialist with a rather long, slender bill, a long tail and relatively weak
90 feet, so that it bears little resemblance to large-footed terrestrial tapaculos (Fig. 1).
91 From the beginning (Ménétriés 1835), it was placed with the antbirds in the
92 Myiotherinae (=Formicariidae). Sclater (1858:243) associated *Psilorhamphus* with
93 *Ramphocaenus* (which is now in the oscine family Polioptilidae) in the Formicariidae
94 with the comment that these genera "might perhaps be more naturally placed as a
95 distinct subfamily of Pteroptochidae [=Rhinocryptidae]" despite the fact that "there is
96 little external difference between the appearance of these birds and the true Wrens

97 [Troglodytidae]". We are not aware, however, of any instance in which
98 *Psilorhamphus* was placed in either the Troglodytidae or in a family with only
99 sylviid-like genera, as might be inferred from Krabbe and Schulenberg (2003).
100 *Psilorhamphus* continued to be associated with *Ramphocaenus* in the Formicariidae –
101 e.g. Sclater (1890) and Cory and Hellmayr (1924:205) – although in the latter
102 reference it was noted that W.D.W. Miller would show *Psilorhamphus* and
103 *Ramphocaenus* to "constitute a separate family" in "a paper shortly to be published."
104 Peters (1951: 213) later explained that Miller's death prevented publication of his
105 results but that Wetmore (1943:306) had shown *Ramphocaenus* to have an oscine
106 syrinx, and had told Peters that *Microbates* likewise was oscine and that he thought
107 based on external morphology that *Psilorhamphus* was also probably oscine.
108 Therefore, Peters postponed his treatment of those genera for a future volume treating
109 Sylviidae. Sick (1954) placed *Ramphocaenus* in the Sylviidae while provisionally
110 referring *Psilorhamphus* to the Formicariidae. Then, Plótnick (1958) revealed that
111 *Psilorhamphus* had a 4-notched sternum, a tracheophone syrinx, and had other
112 characters, including an operculate nostril, indicating that it should be placed in the
113 Rhinocryptidae. Thus, in Peters' Checklist *Psilorhamphus* appears as an addendum to
114 the Rhinocryptidae that appeared in the volume on Sylviidae (Paynter 1964).

115 Heimerdinger and Ames (1967) confirmed that the rhinocryptids they
116 examined all had a 4-notched sternum but also showed that this condition obtained in
117 at least two genera of grallarine Formicariidae, which was confirmed by Feduccia and
118 Olson (1982).

119 Ames (1971) made a thorough study of the anatomy of the syrinx in passerine
120 birds and examined *Melanopareia* first-hand but had to rely on the description of
121 Plótnick (1958) for *Psilorhamphus*. Although he noted that the cartilaginous elements
122 of *Melanopareia* differed from all other tapaculos examined, he found no grounds for
123 excluding either *Melanopareia* or *Psilorhamphus* from the Rhinocryptidae.

124 Feduccia and Olson (1982) made the much unexpected discovery that the
125 stapes in *Melanopareia* was of the primitive oscine type with a flattened footplate,
126 rather than having an expanded, bulbous, fenestrate footplate as in all other suboscine
127 birds. They went on to show other morphological similarities (which is all they ever
128 claimed they were) between some of the Rhinocryptidae and the oscine Menurae
129 (*Menura* and *Atrichornis*) of Australia. Although this observation was dismissed on
130 the grounds that the characters involved are either primitive or convergent (Krabbe

131 and Schulenberg 2003), the fact remains that the oscines and suboscines had to share a
132 common ancestor and that the ancestor very likely looked like *Atrichornis*,
133 *Melanopareia*, or one of the Rhinocryptidae such as *Scelorchilus*.

134 This paper aims to delimit the boundaries of the tapaculos and assess generic
135 relationships within the group, supplementing the very detailed ongoing studies of
136 relationships and speciation of small tapaculos (notably *Scytalopus*; Maurício et al.
137 2008, Cadena et al. unpublished) by providing a broader phylogenetic framework for
138 the family.

139

140 **MATERIALS AND METHODS**

141 *Taxon sampling, amplification and sequencing*

142 This study includes representatives of all genera traditionally recognized in
143 Rhinocryptidae (e.g. Ridgely and Tudor 1994, Krabbe and Schulenberg 2003),
144 including representatives of the large genus *Scytalopus*, including one representative
145 (*indigoticus*) of the “blue” species, which were recently placed in a separate genus
146 *Eleoscytalopus* (Maurício et al. 2008). Three of the authors have significant field
147 experience concerning the biology and vocalizations of tapaculos, and this was
148 supplemented with comments and analyses of sound archives by Niels Krabbe (pers.
149 comm.). Representatives of the main lineages within the tracheophone radiation serve
150 as outgroups (Ridgely and Tudor 1994, Irestedt et al. 2002, Krabbe and Schulenberg
151 2003, Chesser 2004).

152 Three nuclear gene regions, myoglobin intron 2, ornithine decarboxylase
153 (ODC) introns 6 to 7, and glyceraldehyde-3-phosphodehydrogenase (G3PDH) intron
154 11, were sequenced and used to estimate phylogenetic relationships. For each gene
155 and taxon, multiple sequence fragments were obtained by sequencing with different
156 primers. These sequences were assembled to complete sequences with SEQMAN II™
157 (DNASTAR Inc.). Positions where the nucleotide could not be determined with
158 certainty were coded with the appropriate IUPAC code. GenBank accession numbers
159 are given in Table 1. See Irestedt et al. (2002), Allen and Omland (2003), and Fjeldså
160 et al. (2003) for extractions, amplifications, and sequencing procedures for fresh
161 tissue/blood samples. Corresponding laboratory procedures for study skins are
162 detailed in Irestedt et al. (2006).

163

164 *Phylogenetic inference and model selection*

165 Due to the rather low number of insertions in the introns, the combined sequences
166 could easily be aligned by eye. All gaps have been treated as missing data in the
167 analyses. Bayesian inference (see, e.g., Holder and Lewis 2003; Huelsenbeck et al.
168 2001) was used to estimate the phylogenetic relationships. The models for nucleotide
169 substitutions used in the analyses were selected for each gene individually by
170 applying the Akaike Information Criterion (AIC, Akaike 1973) and the program
171 MrModeltest 2.2 (Nylander 2005) in conjunction with PAUP* (Swofford 1998).

172 Posterior probabilities of trees and parameters in the substitution models were
173 approximated with MCMC and Metropolis coupling using the program MrBayes
174 3.1.1 (Ronquist and Huelsenbeck 2003). Analyses were performed for both the
175 individual gene partitions and the combined data set. In the analysis of the combined
176 data set, the models selected for the individual gene partition were used. The chains
177 for the individual gene partitions were run for 5 million generations while the chains
178 for the combined data set were run for 10 million generations. Trees were sampled
179 every 100th generations, and the trees sampled during the burn-in phase (i.e., before
180 the chain had reached its apparent target distribution) were then discarded after
181 checking for convergence, final inference was made from the concatenated outputs.

182

183 *Sequence lengths and alignments*

184 We were able to sequence all three gene regions almost completely for all included
185 taxa (a few sequences miss some base pairs in the 3' or 5' ends in the myoglobin or the
186 ODC regions, and in the ODC region all sequences obtained from study skins lack a
187 short fragment of 22 bp in the exon 7). Taking into account the missing base pairs, the
188 sequences obtained varied in length between 667–701 bp for the myoglobin intron 2,
189 and between 313–363 bp for the G3PDH intron 11, except for the two antthrushes
190 *Chamaeza* and *Formicarius* which contains two large deletions in the G3PDH intron
191 11 which makes these sequences 251–252 bp long. In the ODC region all
192 Rhinocryptidae and Furnariidae taxa have a large deletion in intron 7 and the
193 sequences from these taxa range between 403 and 500 bp, while the sequences for all
194 other taxa range between 586 and 624 bp.

195 Most indels observed in the introns were autapomorphic and mainly found in
196 certain variable regions. Some indels vary in length between taxa, which makes it
197 difficult to know if these indels are homologous or represent independent evolutionary
198 events. Several apparently synapomorphic indels were also observed when mapping

199 the data onto the tree topology obtained from the Bayesian analyses of the combined
200 data set. A few indels were also found to be incongruent with the phylogenetic tree
201 obtained from the analysis of the combined data set. These were generally found in
202 the most variable regions and some of the single base pair insertions actually consist
203 of different bases. For more details of indel length and positions see the alignments of
204 the individual gene regions deposited at Genbank, accession numbers XX
205 (myoglobin), XX (G3PDH), and XX (ODC).

206

207 *Models for nucleotide substitutions*

208 The priori selection of nucleotide substitution models suggested that the GTR + Γ
209 model had the best fit for all three gene regions, but as the nucleotide state frequencies
210 and gamma distribution differed between the partitions we applied a partitioned
211 analysis of the combined data set. After discarding the burn-in phase the inference for
212 myoglobin and G3PDH were based on a total of 45,000 samples from the posterior,
213 the inference for ODC were based on a total of 40,000 samples, while the inference
214 for the combined data set were based on a total of 95,000 samples. The posterior
215 distribution of topologies is presented as a majority-rule consensus tree from the
216 combined analysis in Figure 2.

217

218 **RESULTS**

219 The trees obtained from the Bayesian analyses of the individual gene partitions (Fig.
220 3) are overall topologically congruent. *Melanopareia* clusters with Thamnophilidae
221 and Conopophagidae and we can therefore reject it as a member of the family
222 Rhinocryptidae with high confidence. Apart from this, all traditional tapaculo genera
223 form a monophyletic clade within a broader group which also contains Formicariidae
224 *sensu stricto* and Furnariidae, in agreement with previous molecular studies of
225 tracheophone suboscines (Irestedt et al. 2002, Chesser 2004).

226 Within the radiation of tapaculos there is also good support for two major
227 clades. Clade 1 includes *Teledromas*, *Acropternis*, *Rhinocrypta*, *Liosceles* and
228 *Psilorhamphus* and Clade 2 includes *Scytalopus*, *Eugralla*, *Myornis*, *Merulaxis* and
229 *Eleoscytalopus*. The only conflict within the rhinocryptid radiation supported by
230 posterior probabilities above 0.95 involves determining to which of the previous two
231 clades *Pteroptochos* and *Scelorchilus* belong. In the ODC tree they group with Clade
232 1 (0.97), whereas the myoglobin tree indicates that these two taxa are sister to the

233 Clade 2 (1.00). In the G3PDH tree this relationship is unresolved. Based on the
234 overall congruence of the individual gene trees we believe that the tree obtained from
235 the combined analysis (Fig. 2) represents the best estimate of the phylogenetic
236 relationship of the tapaculos and in this *Pteroptochos* and *Scelorchilus* fall out as
237 sister to Clade 2. This tree is fully congruent with the results of studies using other
238 genetic markers, but with focus on detailed relationships within Clade 2 (Maurício et
239 al. 2008 and Cadena et al., unpublished).

240

241 **DISCUSSION**

242 *Melanopareia* resembles members of the Rhinocryptidae in having the lacrimal bones
243 partly fused with the ectethmoid (but the lacrimals are lacking in Conopophagidae,
244 Thamnophilidae, Grallaridae and Formicariidae) and in having a 4-notched sternum.
245 The significance of these characters is uncertain because of the weak cranial
246 ossification in these groups and a considerable flexibility (including varying degrees
247 of developmental asymmetry) in the degree of ossification of the membranes serving
248 as attachment of pectoral muscles (Heimerdinger and Ames 1967). The molecular
249 data reject a close relationship of *Melanopareia* to the Rhinocryptidae. With four
250 closely related extant species, *Melanopareia* represents a long, unbroken phylogenetic
251 branch, and it may be difficult to tell with confidence whether this clade is nested
252 within the Conopophagidae-Thamnophilidae complex or represents a relictual, basal
253 tracheophone type of bird.

254 Irestedt et al. (2002) associated *Teledromas* with *Melanopareia* primarily
255 because their vocalizations are confusingly similar, and *Teledromas* was considered to
256 resemble a robust and pale version of *Melanopareia*. Both genera are reported to
257 share a peculiarity of the pterylography of the flank region, and details of the nasal
258 operculum and tarsal scutellation, and an X-ray photo suggested almost straight
259 humeri (approaching those of *Melanopareia*; Irestedt et al. 2002). However, our DNA
260 data and further examination of skeletal characters reject a closer relationship between
261 them and places *Teledromas* centrally in Clade 1 of the Rhinocryptidae.

262 *Psilorhamphus* was placed with Polioptiline oscines based on the acutiplantar
263 tarsus, but a similar tarsal scalation is also found in some antbirds, and osteology and
264 syringeal morphology suggested placement with Rhinocryptidae. We were able to
265 confirm from examination of skeletal specimens that *Psilorhamphus* – as well as

266 *Teledromas* – have the expanded footplate of the stapes typical of other suboscines
267 (except *Melanopareia*).

268 The distinctive appearance of *Psilorhamphus* may result from its divergent
269 habits (albeit shared with *Myornis*, N. Krabbe pers. comm.), as it generally feeds by
270 climbing in tangles of vine-like bamboo, occasionally up to 7 m, and it rarely feeds on
271 the ground. This species is also known for its unbelievably loud and low-pitched
272 vocalizations (for its small size, 13.5 cm): A fast series of hollow whistles at 0.9–1
273 kHz. Its sister taxon in Figure 2, *Liosceles*, also gives hollow whistles, but they are
274 higher pitched (1.3 kHz) and are given at a slower pace; the pace and quality of the
275 song notes of *Psilorhamphus* is most like the songs of larger species of *Pteroptochos*,
276 which are even lower pitched (0.5–0.6 kHz). Interestingly, *Psilorhamphus* shares with
277 *Liosceles* barred posterior underparts and distinctive whitish subterminal spots with a
278 black outline on the middle and greater wing-coverts. Apart from this, it is difficult to
279 see any external features supporting the suggested relationships within Clade 1.

280 The possible association of the large Chilean tapaculos (*Pteroptochos*,
281 *Scelorchilus*) with Clade 2 receives some morphological support, as *Pteroptochos* has
282 14 rectrices, something that is also found in some species or individuals of *Scytalopus*,
283 although other representatives of this genus have a reduced number of rectrices or
284 asymmetrical tails (Krabbe and Schulenberg 2003). Other suboscine birds typically
285 have 12 rectrices, although there are many cases of reduction. Molecular relationships
286 within *Pteroptochos* have been analyzed by Chesser (1999).

287 Within Clade 2, the *Myornis-Eugralla-Scytalopus* group is particularly well
288 defined morphologically by small size and sooty-grey to blackish plumage and
289 atrophied clavicles, which do not form a fused furcula (Maurício et al. 2008). This
290 may reflect reduced flying ability of these specialized birds, which tunnel through the
291 densest parts of the forest understorey. *Myornis* bears some resemblance to *Merulaxis*,
292 in shape and juvenile plumage (Krabbe and Schulenberg 2003), but our result does
293 not support such an association. On the other hand, *Myiornis* and *Eugralla* clearly fall
294 outside the group of species of *Scytalopus* that we studied (except with G3PDH) and
295 we therefore support keeping them in separate monotypic genera.

296 Under "Incertae sedis", Irestedt et al. (2002) introduced a family
297 "Melanopareiidae (new family, incl. *Melanopareia* and *Teledromas*)" and this family
298 name has been accepted by SACC (Proposal #239, 2006). These sources, however,
299 did not meet the requirements of the International Code of Zoological Nomenclature

300 (ICZN 1999) as it lacked any description purporting to differentiate the taxon from
301 other taxa, so the name was invalid at that point. The need still remains for separate
302 family status for the genus, which we re-propose here:

303

304 **Melanopareiidae, new family**

305 Type and only included genus: *Melanopareia* Reichenbach, 1853.

306 Diagnosis: Tracheophone suboscine passeriformes differing from other
307 Tracheophonae except Rhinocryptidae (and a few other taxa: *Myrmothera*, *Hylopezus*,
308 *Pittasoma*, *Conopophaga*) in having a 4-notched sternum and differing from the
309 Rhinocryptidae and all other suboscines in retaining the primitive morphology of the
310 stapes, with a flat, rather than inflated footplate.

311

312 **Zusammenfassung**

313

314 **Umschreibung einer monophyletischen Familie für die Bürzelstelzer (Aves:**

315 **Rhinocryptidae): *Psiloramphus* rein und *Melanopareia* raus**

316

317 Die Bürzelstelzer (Rhinocryptidae) sind tracheophone, suboscine Vögel, deren
318 Vorkommen auf Süd- und Mittelamerika beschränkt ist. Die meisten Bürzelstelzer
319 haben eine Reihe innerer und äußerer Merkmale gemeinsam, die benutzt worden sind,
320 um die Familie taxonomisch zu definieren. Die Gattungen *Melanopareia* and
321 *Psiloramphus* passen nicht vollständig in dieses Schema und haben zu beträchtlichen
322 Disputen unter Taxonomen geführt, seit sie erstmals beschrieben worden sind. In
323 diesem Artikel stecken wir die systematischen Grenzen der Bürzelstelzer ab und
324 bewerten ihre Gattungsbeziehungen mit Hilfe einer Analyse molekularer
325 Sequenzdaten. Die Ergebnisse zeigen, dass *Melanopareia* weit aus dieser Klade
326 herausfällt, während *Psiloramphus* gut in die Rhinocryptidae hineinpasst. Eine neue
327 Familie wird für *Melanopareia* eingerichtet.

328

329

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340

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455 **Figure 1.** The bamboo-wren *Psilorhamphus guttatus* bears little external resemblance
456 to typical members of the tapaculo family. With its grey iris, facial expression, bill
457 shape, and wing-coverts with white dots *Psilorhamphus* instead resembles some
458 antbirds (*Dysithamnus*, *Myrmotherula*) with which early ornithologists consequently
459 placed it. Unlike other tapaculos *Psilorhamphus* spends most of the time above the
460 ground. Photo: Edson Endrigo.

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463 **Figure 2.** Majority rule consensus tree obtained from the Bayesian analyses of the
464 combined data set (myoglobin intron 2, ODC introns 6 and 7, and G3PDH intron 11).
465 Posterior probability values are indicated at the node.

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468 **Figure 3.** The majority rule consensus trees obtained from the Bayesian analyses of
469 the individual genes. A) myoglobin intron 2; B) ornithine decarboxylase introns 6 to
470 7; and C) glyceraldehyde-3-phosphodehydrogenase intron 11. Posterior probability
471 values are indicated at the node.

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474 **Table 1:** Specimen data and GenBank accession numbers for samples used in the
475 study. Samples vouchered with a study skin are indicated by an asterisk. "TP"
476 indicates that the sample is obtained from toe-pads of an old study skin. Acronyms are
477 AMNH, American Museum of Natural History, FMNH, Field Museum of Natural
478 History, Chigaco, USA; NRM, Swedish Museum of Natural History; USNM,
479 University States National Museum, Washington, USA; ZMUC Zoological Museum
480 of Copenhagen. References: A, Irestedt et al. (2002); B: Ericson et al. (2002); C:
481 Irestedt et al. (2004); D: Ericson & Johansson (2003); E: Fjeldså et al. (2005); F:
482 Ericson et al. (2006); G: Fjeldså et al. (2003); H: Fjeldså et al. (2007).

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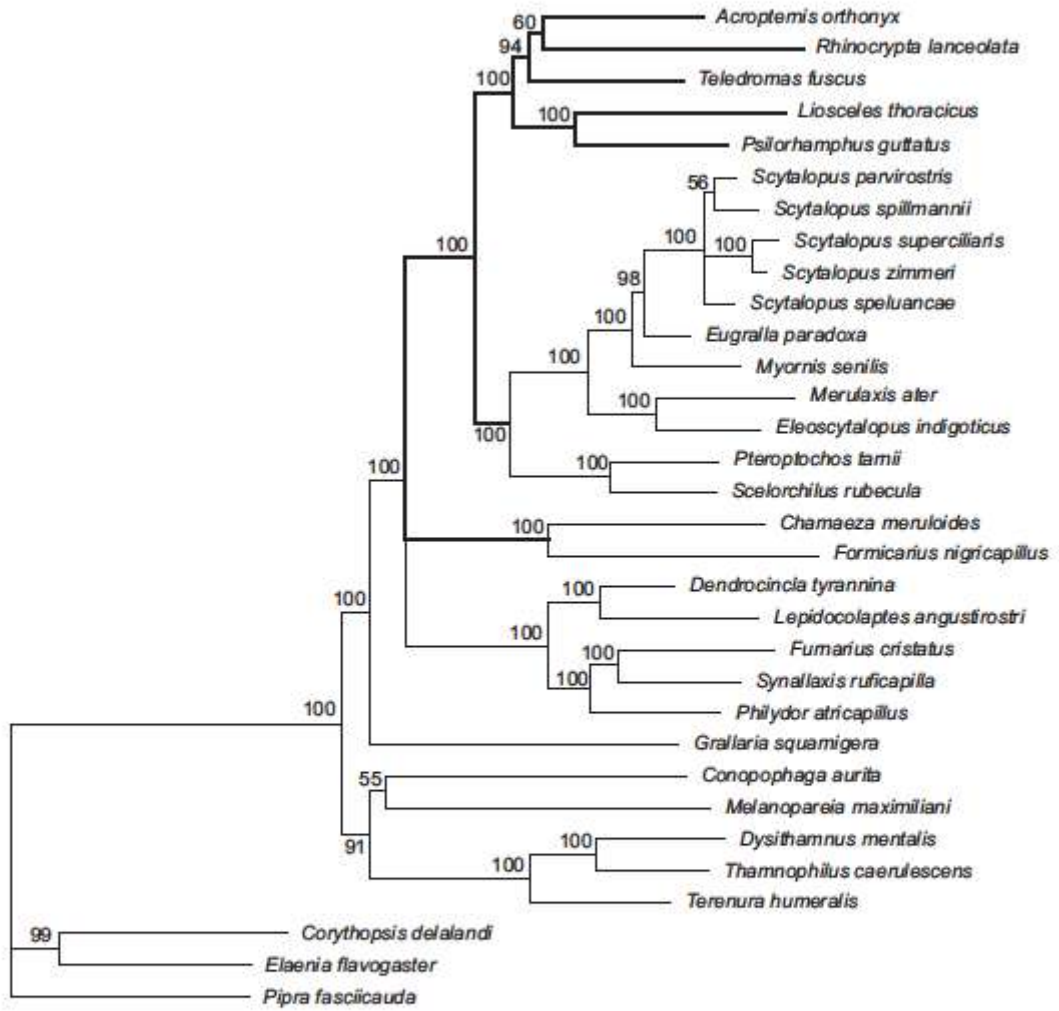
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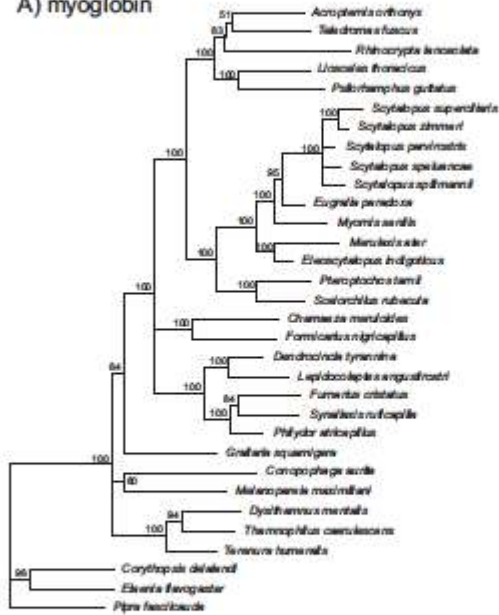


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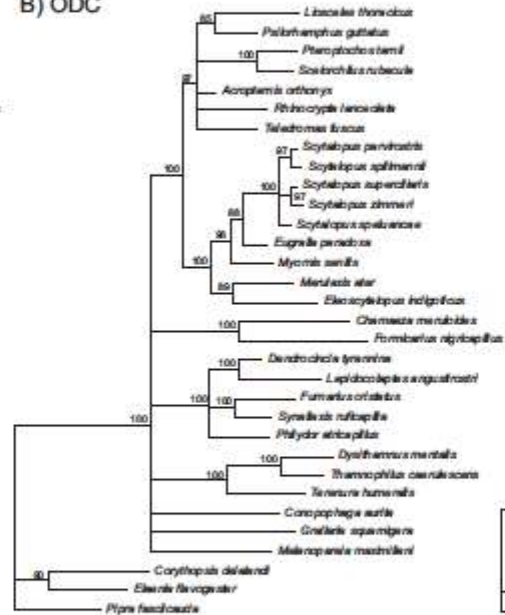


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A) myoglobin



B) ODC



C) G3PDH



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Table 1

Species	Family: Subfamily	Voucher / Sample No.	Myoglobin	G3PDH	ODC
<i>Acropternis orthonyx</i>	Rhinocryptidae	ZMUC 125695 *	new	new	new
<i>Merulaxis ater</i>	Rhinocryptidae	ZMUC 128820	new	new	new
<i>Pteroptochos tarnii</i>	Rhinocryptidae	AMNH RTC467 *	AY065774 ^{A)}	AY590096 ^{E)}	new
<i>Rhinocrypta lanceolata</i>	Rhinocryptidae	NRM 966793	AY065775 ^{A)}	DQ438953 ^{F)}	DQ435499 ^{F)}
<i>Teledromas fuscus</i>	Rhinocryptidae	USNM BKS3703 *	new	new	new
<i>Psilorhamphus guttatus</i>	Rhinocryptidae	ZMCU? Olson 2005	new	new	new
<i>Myornis senilis</i>	Rhinocryptidae	ZMUC 134967 *	new	new	new
<i>Scytalopus parvirostris</i>	Rhinocryptidae	ZMCU 128441	new	new	new
<i>Scytalopus speluancae</i>	Rhinocryptidae	ZMCU 128818	new	new	new
<i>Scytalopus spillmannii</i>	Rhinocryptidae	ZMUC 125091 *	AY065773 ^{A)}	AY590097 ^{E)}	new
<i>Scytalopus zimmeri</i>	Rhinocryptidae	ZMUC 126278 *	new	new	new
<i>Scytalopus superciliosus</i>	Rhinocryptidae	USNM BKS 3592 *	new	new	new
<i>Eugralla paradoxa</i>	Rhinocryptidae	NRM 570026 *, TP	new	new	new
<i>Scelorchilus rubecula</i>	Rhinocryptidae	NRM 570029 *, TP	new	new	new
<i>Liosceles thoracicus</i>	Rhinocryptidae	NRM 570027 *, TP	new	new	new
<i>Eleoscytalopus indigoticus</i>	Rhinocryptidae	NRM 570028 *, TP	new	new	new
<i>Melanopareia maximiliani</i>	Rhinocryptidae	ZMUC 125045 *	AY065785 ^{A)}	new	new
<i>Furnarius cristatus</i>	Furnariidae: Furnariinae	NRM 966772 *	AY064255 ^{B)}	AY590066 ^{E)}	DQ435482 ^{F)}
<i>Philydor atricapillus</i>	Furnariidae: Furnariinae	NRM 937334 *	AY065758 ^{A)}	AY590076 ^{E)}	EF212110 ^{H)}
<i>Synallaxis ruficapilla</i>	Furnariidae: Furnariinae	NRM 956643 *	AY065763 ^{A)}	AY590068 ^{E)}	EF212119 ^{H)}
<i>Lepidocolaptes angoustirostris</i>	Furnariidae: Dendrocolaptinae	NRM 937184 *	AY065767 ^{A)}	AY336576 ^{G)}	DQ435486 ^{F)}
<i>Dendrocincla tyrannina</i>	Furnariidae: Dendrocolaptinae	ZMUC 125661 *	AY442959 ^{C)}	AY590087 ^{E)}	EF212098 ^{H)}
<i>Chamaeza meruloides</i>	Formicariidae	ZMUC 126604 *	AY065776 ^{A)}	AY590095 ^{E)}	new
<i>Formicarius nigricapillus</i>	Formicariidae	ZMUC 125987 *	AY065777 ^{A)}	new	new
<i>Grallaria squamigera</i>	Grallariidae	ZMUC 124629 *	AY065778 ^{A)}	AY677078 ^{C)}	new
<i>Dysithamnus mentalis</i>	Thamnophilidae	NRM 956629 *	AY676995 ^{C)}	AY677042 ^{C)}	new
<i>Terenura humeralis</i>	Thamnophilidae	FMNH 389941	AY677004 ^{C)}	AY677051 ^{C)}	new
<i>Thamnophilus caerulescens</i>	Thamnophilidae	NRM 967007 *	AY065783 ^{A)}	AY336587 ^{G)}	DQ435504 ^{F)}
<i>Conopophaga aurita</i>	Conopophagidae	ZMUC 125796 *	AY065784 ^{A)}		DQ435478 ^{F)}
<i>Conopophaga lineata</i>	Conopophagidae	NRM 956653 *		AY336577 ^{G)}	
<i>Pipra fasciicauda</i>	Pipridae	NRM 947271 *	AY065787 ^{A)}	AY336583 ^{G)}	DQ435495 ^{F)}
<i>Corythopsis delalandi</i>	Tyrannidae	NRM 937282 *	AY065788 ^{A)}	DQ435463 ^{F)}	DQ435479 ^{F)}
<i>Elaenia flavogaster</i>	Tyrannidae	NRM 966970 *	AY228295 ^{D)}	new	new

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