

1 **A Hotspot Atop: Rivers of the Guyana Highlands Hold High Diversity of Endemic Pencil**
2 **Catfish**

3
4 Running Title: *Trichomycterus* of the Guyana highlands

5
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23
24 **ABSTRACT**

25 **Aim**

26 The Pakaraima Mountains are an ancient mountain range along the borders of Guyana, Brazil,
27 and Venezuela. The high plateau is drained by multiple river systems in all directions. Although
28 hypotheses have been presented for the biogeographic relationships of lowland rivers, the
29 interconnectivity of rivers on the top of the plateau is unknown. With multiple complex rivers in
30 a small, upland area we predicted a high level of endemism for stream fishes and complex
31 biogeographic relationships. We explore this with the incredibly diverse pencil catfish genus

32 *Trichomycterus*. Only two species are known from the region. In this study, we 1) confirm the
33 discovery of multiple endemic *Trichomycterus* species in the region, 2) determine the
34 phylogenetic placement of our samples to posit biogeographical scenarios, and 3) provide
35 clarification for the identification of *T. guianensis* based on morphology.

36 **Location**

37 Pakaraima Mountains, a part of the Guiana Shield in Guyana, South America

38 **Taxon**

39 Pencil catfish genus *Trichomycterus*

40 **Methods**

41 Using collections from recent expeditions to the Pakaraima Mountains of Guyana, we amplified
42 three mitochondrial (16S, COI, and cytb) and two nuclear markers (myh6 and RAG2). We
43 constructed individual gene trees as well as a concatenated tree to determine the placement of
44 these taxa within the *Trichomycterus* of the Trans-andean/Amazonian clade.

45 **Results**

46 Our results identify six unique lineages in the highlands of Guyana. Only two species,
47 *Trichomycterus guianensis* and *T. conradi*, were previously known to science.

48 **Main Conclusions**

49 The Pakaraima Mountains of South America are a region of high endemism, as demonstrated
50 here in *Trichomycterus* catfishes. We find two species occupying multiple basins, suggesting that
51 Pakaraima streams either maintain or had some degree of recent connectivity. We identify six
52 endemic lineages of *Trichomycterus* from the highlands of the Pakaraima Mountains. The upper
53 portions of the study rivers have been connected either through surface flow or by stream
54 capture. Both processes have occurred on multiple time scales and are independent of the
55 patterns seen in the lowlands.

56 **Keywords:** catfish, fishes, freshwater, Guiana shield, neotropics, systematics, *Trichomycterus*,

57

58 **INTRODUCTION**

59 The Pakaraima Mountains run along the borders of Guyana, Brazil, and
60 Venezuela. These ancient mountains have been the subject of diverse lore of the
61 indigenous inhabitants of the region as well as the western world. Sir Arthur Conan
62 Doyle (1912), in *The Lost World*, imagined dinosaurs and other ancient organisms on the

63 high plateau and Pixar Animation Studios, in the movie *Up* (Docter & Peterson, 2009), imagined
64 a house perched on top of “Paradise Falls” and an undescribed, endemic species of flightless
65 bird. The artists that designed Paradise Falls recognized that many of the rivers of the region fall
66 off of the escarpment in dramatic waterfalls such as Kaieteur, Amaila, and Orinduik Falls.

67 Although dinosaurs and large, flightless birds do not appear to be denizens of the
68 Pakaraimas, the streams there hold a high degree of endemism (Alofs, Liverpool, Taphorn, &
69 Bernard, 2014; Armbruster & Taphorn, 2011; Hardman, Page, Sabaj, Armbruster, & Knouft,
70 2002). The Pakaraimas (Figure 1) are drained to the north by the Mazaruni and Cuyuni rivers, to
71 the east by the Potaro River (Essequibo River drainage), to the southwest by the Ireng and
72 Uraricoera rivers (Amazon River drainage), and to the west and northwest by the Caroni River
73 (Orinoco River drainage). The mountains are the remains of Archaean and Proterozoic rocks
74 whose lighter sediments have eroded to fill formerly lacustrine basins such as the Venezuelan
75 Llanos and the Rupununi Savanna of Guyana (see Lujan & Armbruster, 2011, for review). This
76 erosion has left behind a durable core that often has steep faces that the rivers run off of in
77 spectacular waterfalls. Below the falls, the rivers often have some rapids complexes, but quickly
78 reach lowland conditions (Lujan & Armbruster, 2011).



79
80 **Figure 1.** A topographical map of the Pakaraima highlands depicting the physiography of rivers.
81 Major rivers are labelled along their flow. Country names are listed horizontally in all capital
82 letters
83

84 Current evidence for the relationships of the rivers draining the Pakaraima Mountains
85 involves, in part, the development and subsequent fragmentation of a paleo-river drainage called
86 the proto-Berbice (Lujan & Armbruster, 2011; Schaefer & do Vale, 1997; Sinha, 1968). The
87 proto-Berbice contained what are now tributaries of the upper rio Branco (Amazon drainage,
88 including the Ireng), the upper Essequibo, the Berbice, and parts of the Courantyne and Orinoco.
89 Meanwhile, the middle and lower Essequibo (including the Potaro/Kuribrong) likely joined the
90 Mazaruni and Cuyuni near where the current mouths are. Slowly, the Amazon River has been
91 capturing streams from the proto-Berbice in an east-west manner. This pattern would suggest a
92 similarity between the faunas of the Potaro/Kuribrong and the upper Mazaruni with the Ireng
93 being more distantly related as it appears to have never been connected into the middle and lower
94 Essequibo + Mazaruni.

95 However, the upper courses of the rivers have not been explored
96 biogeographically. The likely complex relationships of the upper courses of the rivers
97 were suggested by the description of the crenuchid *Apareiodon agmatos*, and the
98 loricariid taxa *Paulasquama callis*, *Neblinichthys brevibraccium*, and *N. echinasus* in the
99 upper Mazaruni (Armbruster & Taphorn, 2011; Taphorn, Armbruster, López-Fernández,
100 & Bernard, 2010; Taphorn, López-Fernández, & Bernard, 2008), all of which share
101 affinities with the Orinoco River basin. Given the absence of these taxa in lowland
102 streams, it is likely that these highland taxa were moving via stream capture or other
103 events that connected these highland tributaries. Thus far, the relationships of the
104 highland regions have been scarcely explored systematically. Lujan et al. (2018) found
105 that *Paralithoxus bovallii* (Loricariidae) from the Ireng was more closely related to an
106 undescribed species in the Courantyne than one from the lower Potaro in support of the
107 proto-Berbice hypothesis; however, *Paralithoxus* is not found elsewhere in the Pakaraima
108 highlands. Lujan et al. (in press) found that *Corymbophanes* (Loricariidae), an upper
109 Potaro/Kuribrong endemic, was sister to an undescribed genus from the upper Ireng with
110 the two clades separated by long branch lengths suggesting an ancient relationship.

111 Coupled with the lack of basic information on the fauna of the region, the area is
112 also under extreme threat by gold and diamond mining with a strong potential of mining
113 eliminating species before they are even discovered (Alofs et al., 2014). In this study, we
114 explore the potential interconnectedness of the high Pakaraima streams by examining the

115 relationships of the pencil catfishes of the genus *Trichomycterus* in order to identify pertinent
116 diversity and to uncover biogeographic patterns that could be duplicated in other Pakaraima
117 organisms.

118 Trichomycteridae represents a diverse family of freshwater catfishes distributed across
119 the Neotropics. Of the more than 300 recognized species (Fricke, Eschmeyer, & van der Laan,
120 2018), the majority of species (219) are found in the Trichomycterinae, which contains the
121 genera *Bullockia*, *Cambeva*, *Eremophilus*, *Hatcheria*, *Ituglanis*, *Rhizosomichthys*, *Scleronema*,
122 *Silvinichthys*, and *Trichomycterus*. Most of the diversity within Trichomycterinae can be
123 attributed to *Trichomycterus*, with all other genera except *Ituglanis* (28 species), *Cambeva* (25
124 species), *Silvinichthys* (seven species), and *Scleronema* (three species) being monotypic (Fricke
125 et al., 2018). While other genera exhibit apomorphic specializations, the lack of specializations
126 unique to *Trichomycterus* has long made researchers suspect, and later confirm with molecular
127 studies, the non-monophyly of the genus (Baskin, 2016; de Pinna, 2016; Henschel, Mattos, Katz,
128 & Costa, 2018; Katz et al., 2018; Ochoa et al., 2017).

129 The emerging phylogenetic pattern matches those of other similarly distributed fishes,
130 such as doradid catfishes, characins, and armored catfishes, where distinct clades are
131 geographically linked to a Trans-andean/Amazonian distribution or to south Atlantic coastal
132 drainages (Katz et al., 2018; Ochoa et al., 2017; Ribeiro, 2006). Katz et al. (2018) attempted to
133 solve some of the taxonomic problems of the Trichomycterinae by restricting *Trichomycterus* to
134 a clade that contained the type species (south Atlantic coastal drainages), describing *Cambeva*
135 for a clade sister to *Scleronema*, a clade that is sister to *Trichomycterus sensu stricto*, and
136 referring the Andean, Pagaonian, Amazonian, and Guiana Shield species to “*Trichomycterus*” in
137 quotation marks. “*Trichomycterus*” is paraphyletic and part of a clade that includes *Bullockia*,
138 *Eremophilus sensu stricto*, and *Ituglanis*. Results were similar to those in Ochoa et al. (2017).
139 These patterns are not surprising, given the tectonic and geologic history of the continent that
140 highlights the importance of the Guiana and Brazilian Shields as original uplands of South
141 America, formation of the Andes, and uplift of the Eastern Cordillera (to name a few) with
142 shaping the biogeography of neotropical fishes (Lujan & Armbruster, 2011; Lundberg et al.,
143 1998; Ribeiro, 2006). For ease, we will not be referring to *Trichomycterus* in quotation marks.

144 *Trichomycterus* are long, slender catfishes generally found only in swift waters. Such
145 habitat, even in the mountains, is patchy, and we suspect that the fishes would be more likely to

146 be isolated to drainages. Recent collections from this region have identified all specimens
147 as *T. guianensis* (Eigenmann, 1912), but we noted significant differences in color and
148 morphology in samples that we have made. Preliminary external visual examinations
149 indicate the possibility for unrecognized diversity and perhaps misidentification of *T.*
150 *guianensis* in the rivers of this region. The only other species recognized in the region is
151 *T. conradi* (Eigenmann, 1912), and we have found some specimens from the Ireng and
152 Kuribrong rivers that correspond to this species.

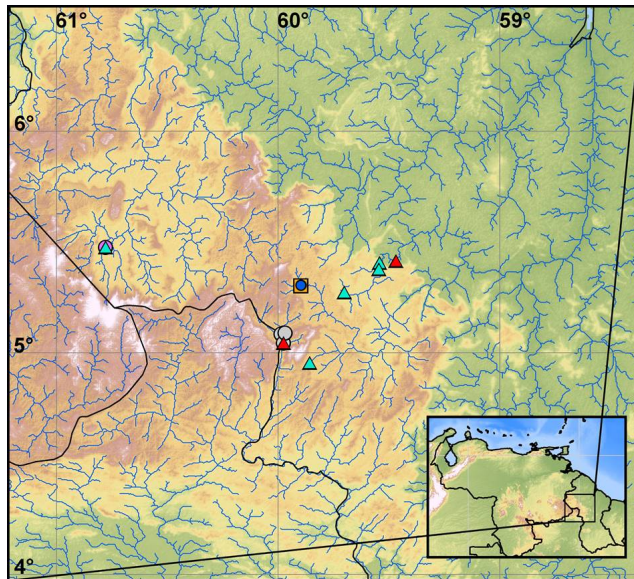
153 Recent studies have illuminated the need to identify unrecognized diversity
154 within *Trichomycterus* and have highlighted the important role that geology and
155 topography play in contributing to that diversity (Katz et al., 2018; Ochoa et al., 2017;
156 Unmack, Bennin, Habit, Victoriano, & Johnson, 2009). In this study, we 1) confirm the
157 discovery of multiple endemic *Trichomycterus* species in the region, 2) examine the
158 diversity and endemism of *Trichomycterus* in the Pakaraima Mountain region with
159 respect to the unique geologic features that have likely influenced their genetic structure,
160 and 3) provide clarification for the identification of *T. guianensis* and *T. conradi* based on
161 morphology.

162 **METHODS**

163 **Taxon Sampling, DNA Extraction and Sequencing**

164 Collections ranged across multiple years with research permits from Environmental
165 Protection Agency of Guyana as follows, listed as year, reference number: 2011, 030510 BR
166 130; 2008, 300408 SP: 004; 2014, 040414 SP: 003; 2015, 123115 BR031; 2016, 012016 SP:
167 003. Fish were either collected with six-foot by ten-foot nylon coated seines with 1/8" mesh, or
168 we joined fishing expeditions of the Patamona who used hiari, a root native to the area around
169 the collection site and a natural source of rotenone (Figure 2). After capture, fish were
170 euthanized in a solution of tricaine methanesulfonate (MS-222) until no sign of respiration was
171 observed for five minutes. Tissue samples were taken from the right pectoral fin or right axial
172 musculature and placed into 1.5 mL vials containing RNALater or ethanol for preservation. Once
173 tissue samples were taken, voucher specimens were fixed in a 3.7% formaldehyde solution for
174 seven days, then rinsed in water for three days, and finally stored in 70% ethanol. Vouchers and

175 tissue samples were deposited in the AUM Fish Collection. Additional materials not collected by
176 the authors were requested from the Royal Ontario Museum (ROM, Table 1).



177
178 **Figure 2.** Collection localities for species of *Trichomycterus* found in this study. Color codes
179 correspond to images in Figure 7 and are as follows: red triangles, *T. conradi*; blue circle, *T.*
180 *guianensis*; teal triangles, *T. cf. guianensis*; purple circle, Mazaruni, plain form; orange square,
181 Potaro elongate; gray circle, Ireng, spotted form.

182
183 Whole genomic DNA was extracted from tissues using either Chelex or an E.Z.N.A
184 Tissue DNA Kit (Omega BioTek, Norcross, GA). The four genes 16S, COI, cytb, and RAG2
185 were amplified through 25 μ L polymerase chain reactions using primers described in Ochoa et al.
186 (2017). The 16S gene was amplified using the following protocol: initial denaturation step of 180
187 s at 94°C then 30 cycles of denaturation (45 s at 95°C), annealing (30 s at 54°C), and extension
188 (60 s at 68°C) followed by a final extension of 600 s at 68°C. The COI gene was amplified using
189 the following protocol: initial denaturation step of 180 s at 94°C then 30 cycles of denaturation
190 (45 s at 94°C), annealing (30 s at 54°C), and extension (60 s at 68°C) followed by a final
191 extension of 60 s at 68°C. The cytb gene was amplified using the following protocol: initial
192 denaturation step of 180 s at 94°C then 30 cycles of denaturation (45 s at 95°C), annealing (30 s
193 at 54°C), and extension (60 s at 68°C) followed by a final extension of 60 s at 68°C. The RAG2
194 gene was amplified using a two-step protocol. The first reaction was performed using the
195 touchdown protocol described in Lovejoy & Collette (2001) with RAG164F and RAG2R6
196 primers. The second PCR used 1.5 μ L of template from the first run and primers 176R and
197 RAG2Ri under the following conditions: initial denaturation step of 30 s at 95°C then 35 cycles

198 of denaturation (30 s at 95°C), annealing (45 s at 56°C), and extension (90 s at 72°C).
199 Primers used for PCR amplification were also used for DNA sequencing for all genes,
200 with 176R and RAG2Ri used for sequencing RAG2.

201 The products were visualized and size-verified on a 0.8% agarose gel. PCR
202 purification, sample preparation, and Sanger sequencing were performed at GeneWiz
203 (South Plainfield, NJ). Chromatographs from forward and reverse reads were imported
204 into Geneious v. 10.2.3 (Kearse et al., 2012) for assembly. Assembled contiguous
205 sequences were aligned using the MUSCLE algorithm (Edgar, 2004), and results were
206 checked by eye. Due to length variation among sequences generated in this study and
207 those of Ochoa et al (2017), alignments were trimmed to the following lengths: 16S: 466;
208 COI 522; cyt b: 858; myh6: 543; and RAG2: 885. Each individual gene tree was analyzed
209 with *Scleronema minutum* as an outgroup, while the concatenated dataset (3579bp)
210 included members from Ochoa et al's (2017) clades D1, D2, D3, and E with *S. minutum*
211 as an outgroup. Data were exported both as individual alignments and as a concatenated
212 dataset for phylogenetic analysis.

213

214 **Phylogenetic Analysis**

215 Best-fit models of evolution were tested using PARTITIONFINDER2 (Lanfear, Frandsen,
216 Wright, Senfeld, & Calcott, 2017). Models were tested on individual gene trees, and then on the
217 concatenated dataset. The resulting data blocks were then used in Bayesian Inference analysis.
218 Bayesian Inference was performed using MrBayes v. 3.2.6 on XSEDE via CIPRES Science
219 Gateway (Miller, Pfeiffer, & Schwartz, 2010). Each dataset had 2 runs with 4 chains run for 15
220 million generations, sampling once every 1,000 generations. The parameters and trees were
221 summed in MrBayes v. 3.2.6 using the default 25% burn-in. The resulting 50% majority
222 consensus rule phylogeny is reported.

223

224 **Maps**

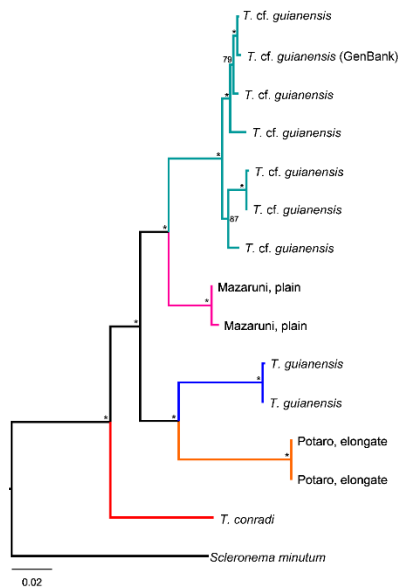
225 The maps produced for this paper were created in ARCGIS, ARCMAP V. 10.3.1; ESRI, 2011).
226 Digital elevation models and rivers are from HydroSHEDS by the United States Geological
227 Service and World Wildlife Federation (<https://www.worldwildlife.org/pages/hydrosheds>;
228 <https://hydrosheds.cr.usgs.gov/>). Width of rivers is by Strahler number (stream order).

229 Bathymetry is ETOPO1 from the National Geophysical Data Center
230 (<https://www.ngdc.noaa.gov/mgg/global/>). Color ramps for elevation and bathymetry are from
231 Environmental Systems Research Institute's Color Ramps v. 3.0 ([https://www.esri.com/arcgis-
232 blog/products/product/imagery/esri-color-ramps-version-3-0/](https://www.esri.com/arcgis-blog/products/product/imagery/esri-color-ramps-version-3-0/)). Country borders and graticules
233 are from Natural Earth (<https://www.naturalearthdata.com/>).

234

235 RESULTS

236 Four genes trees were analyzed separately, then combined into a concatenated analysis.
237 The first individual gene tree is cytochrome b (cytb, Figure 3), which results in a well-supported
238 clade of Pakaraima *Trichomycterus*. Members of true *Trichomycterus guianensis* are found sister
239 to the Potaro, elongate form. This clade is sister to another well-supported clade of *T. cf.*
240 *guianensis* + Mazaruni, plain form. These are all sister to a single representative of the *T.*
241 *conradi*. This analysis did not include the Ireng, spotted form that is present in other analyses.



242

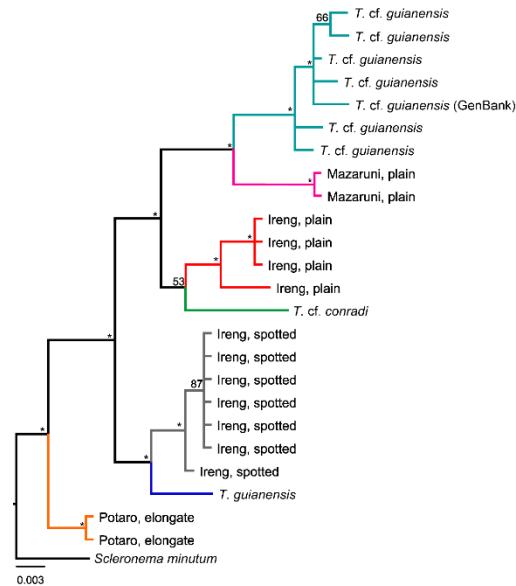
243

244 **Figure 3.** Fifty per cent majority rule consensus tree from Bayesian inference of cytochrome b
245 sequences. Nodes labelled with an asterisk (*) indicate posterior probabilities >90%. Values less
246 than 90% are written on the trees. Branches are colored to match localities as seen in Figure 1.
247 Tip labels correspond to individuals as denoted in Table 1.

248

249

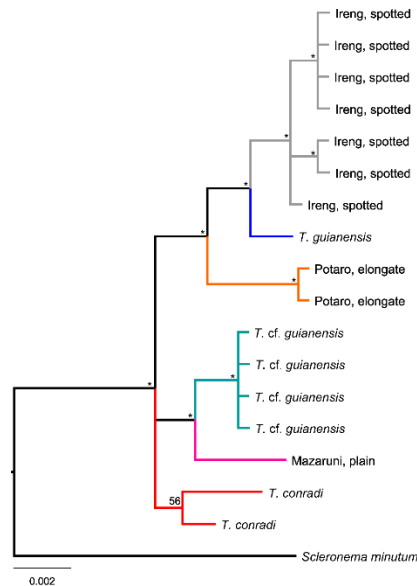
250 The second gene tree generated from our data is based on COI (Figure 4). This analysis
251 again places *T. cf. guianensis* sister to the Mazaruni, plain form. In contrast to the cytb
phylogeny, this clade is sister to the *T. conradi*; however, this relationship is weakly supported.



274

275 **Figure 5.** Fifty per cent majority rule consensus tree from Bayesian inference of 16S sequences.
276 Nodes labelled with an asterisk (*) indicate posterior probabilities >90%. Values less than 90%
277 are written on the trees. Branches are colored to match localities as seen in Figure 1. Tip labels
278 correspond to individuals as denoted in Table 1.

279



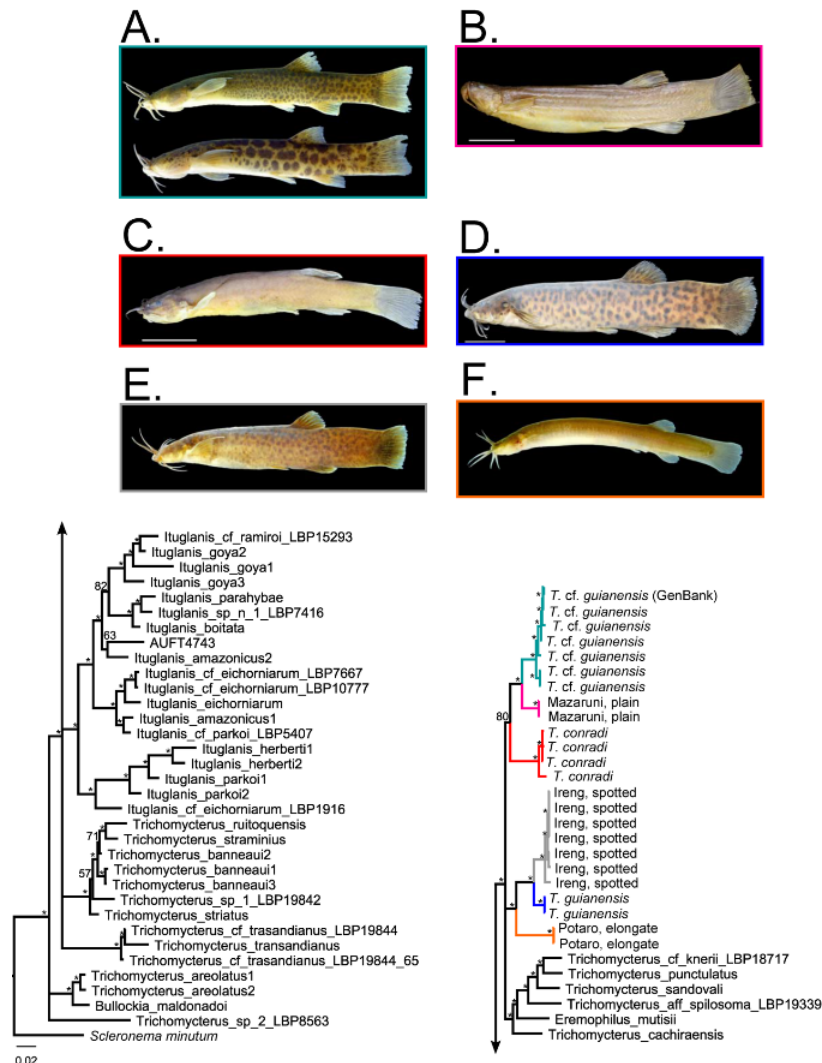
280

281 **Figure 6.** Fifty per cent majority rule consensus tree from Bayesian inference of RAG2
282 sequences. Nodes labelled with an asterisk (*) indicate posterior probabilities >90%. Values less
283 than 90% are written on the trees. Branches are colored to match localities as seen in Figure 1.
284 Tip labels correspond to individuals as denoted in Table 1.

285

286 With gene tree heterogeneity rampant in this analysis, the four genes were concatenated
287 and analyzed with the D1, D2, D3, and E clades from Ochoa et al (2017, Figure 7). This tree,

288 with 24 individuals from our analysis, shows that all morphotypes we identified *a priori*
 289 are monophyletic. Two distinct clades compose Pakaraima *Trichomycterus*:
 290 *Trichomycterus cf. guianensis* + Mazaruni, plain form are sister to the *T. conradi*. This
 291 clade is sister to another clade consisting of *Trichomycterus guianensis* + Ireng, spotted
 292 which are sister to the Potaro, elongate form. Each of these relationships are supported
 293 with >90% posterior probability, while deeper relationships remain unresolved.



294

295 **Figure 7.** Fifty per cent majority rule consensus tree from Bayesian inference of concatenated
 296 sequences. Nodes labelled with an asterisk (*) indicate posterior probabilities >90%. Values less
 297 than 90% are written on the trees. Branches are colored to match localities as seen in Figure 1.
 298 Tip labels correspond to individuals as denoted in Table 1. These sequences are combined with
 299 the D1, D2, D3, and E clades from Ochoa et al (2017). Arrows connect disconnected branches in
 300 the phylogeny. Outlines of the photographs of specimens correspond to clade color and symbol
 301 color in Figure 1. A. *T. cf. guianensis*. B. Mazaruni, plain form. C. *T. conradi*. D. true *T.*
 302 *guianensis*. E. Ireng, spotted form. F. Potaro, elongate form.

303 DISCUSSION

304 Our results demonstrate the presence of multiple species of *Trichomycterus* in the
305 Pakaraima Mountains of Guyana. There were two major clades, one consisting of *T. guianensis*
306 and two undescribed species, and the other of *T. conradi* and two undescribed species. Both *T.*
307 *guianensis* and *T. conradi* appear to be the rarer species in the region (based on collections), and
308 *T. guianensis* is not as widespread as previously believed. Based on examination of the types and
309 comparison with specimens we have collected, *Trichomycterus guianensis* is a deep bodied
310 species with irregular blotches (Figure 7D). *Trichomycterus* sp. Ireng Spotted (Figure 7E) is the
311 dominant species in the Ireng, and it is similar in morphology to *T. guianensis* and was recovered
312 as sister to it. In morphology, the Ireng Spotted species is even shorter and deeper-bodied than *T.*
313 *guianensis*. Sister to the clade of *T. guianensis* and the Ireng Spotted species is a very elongate,
314 almost entirely brown species from near Ayangana in the far upper Potaro with miniscule pelvic
315 fins (*Trichomycterus* sp. Potaro Elongate, Figure 7F). It was found in sluggish, swampy areas,
316 which is habitat more indicative of *Ituglanis*, but the species lacks the diagnostic characters of
317 *Ituglanis* (JWA pers. obs.), and we found it to be a member of *Trichomycterus* in the molecular
318 analysis. *Trichomycterus* sp. Potaro Elongate and *Trichomycterus* sp. Ireng Spotted are at the
319 opposite extreme of *Trichomycterus* morphology, suggesting a strong capacity for body
320 rearrangement in the genus.

321 The other major clade contains a wide-spread, elongate species with dark, small or large,
322 regular spots (*Trichomycterus* cf. *guianensis*, Figure 7A). This species is found in the upper
323 Potaro, Kuribrong, and Mazaruni rivers. Little geographic structure was present in the specimens
324 examined, suggesting fairly recent movement between the basins. Sister to this species is a
325 similar but unspotted species from the Mazaruni River (*Trichomycterus* sp. Mazaruni Plain,
326 Figure 7B). Finally, sister to the other two species is a clade that consists of a few individuals
327 from the Ireng as well as a specimen from the lower Kuribrong of a plain-colored species that
328 appears to be *T. conradi* (Figure 7C).

329 Two species of *Trichomycterus* have been described from the upper Caroni, Orinoco
330 River drainage section of the Pakaraima Mountains: *T. celsae* Lasso and Provenzano 2002 and *T.*
331 *lewi* Lasso and Provenzano 2002. The Orinoco species do appear to be different from the species
332 analyzed here, and it appears that there are additional undescribed species from that region.
333 Unfortunately, we do not have tissue samples from these species.

334

335 **Biogeography of the Pakaraima Mountains**

336 The biogeographic story that the species of *Trichomycterus* of the Pakaraimas tell is a
337 complex one. *Trichomycterus* cf. *guianensis* appears to have moved between river systems
338 relatively easily. Mazaruni samples are sister to those in the Kuribrong and Potaro rivers, but the
339 Mazaruni samples are paraphyletic. Tributaries of the Mazaruni interdigitate with the Kuribrong
340 and Potaro rivers, and species living as high in their drainages as *Trichomycterus* would be more
341 likely to be able to move via river capture events where tributaries erode their divides and switch
342 from one system to the next. Anecdotal reports suggest that the upper courses of at least the
343 Potaro and Kuribrong connect during particularly rainy times; flying over the area reveals
344 numerous fissures that seem to run between the two rivers (JWA pers. obs.). These drainages
345 also interdigitate with Caroni and Ireng tributaries. Some of the specimens from the Caroni do
346 appear similar to the elongate, spotted species of Guyana, but we did not find anything similar in
347 the Ireng despite extensive searching.

348 The upper Caroni and the Ireng were once part of the proto-Berbice paleodrainage basin
349 along with the upper Branco, upper Essequibo, Berbice, and Courantyne rivers while the
350 Mazaruni was likely independent (Lujan and Armbruster, 2011). The Essequibo makes a
351 westward bend near Massara and away from a nearby Berbice tributary (Gibbs & Barron, 1993),
352 suggesting a likely point of demarcation between the upper Essequibo as part of the proto-
353 Berbice and the lower Essequibo, which probably joined with the Mazaruni at the present mouth
354 of the Essequibo. This would mean that the Potaro and Mazaruni were part of the same system
355 and not part of the proto-Berbice. However, the mixing of Ireng, Potaro, and Mazaruni
356 *Trichomycterus* in the phylogeny suggests that there likely existed faunal exchange between the
357 proto-Berbice, Potaro, and Mazaruni rivers at least in the highlands prior to the breakup of the
358 proto-Berbice during the Pliocene and Pleistocene potentially leading to complex
359 interrelationships between these basins. A similar finding was made in Lujan et al. (in press) who
360 found that *Corymbophanes* was sister to a new genus from the Ireng; however, the branch
361 lengths were much longer than what was observed here. Further exploration into the
362 relationships of *Trichomycterus* along with a molecular clock will likely lead to fascinating
363 insights into the biogeography of the Pakaraima Mountains, but this further insight will require

364 extensive collecting in the difficult to explore Brazilian tributaries of the Pakaraima Mountains
365 and further collecting in Venezuela, that is difficult now because of civil strife.

366 *Trichomycterus conradi* appears to be a more lowland form found in the rapids below
367 Kaieteur and Amaila Falls on the Potaro and Kuribrong, respectively, as well as in the Ireng. The
368 shallow nodes between the Kuribrong and Ireng samples sequenced suggest that movement has
369 been relatively recent. We were only able to obtain 16S sequences for a specimen of *T. cf.*
370 *conradi* from the Maroni River of eastern Suriname, and it was sister to *T. conradi*. A similar
371 distribution across the northern Guiana Shield was found for *Paralithoxus bovallii* from the Ireng
372 River and hypothesized new species related to it in the Potaro, Courantyne, and Coppename
373 rivers (Lujan et al. 2018). The distributions of *T. conradi* and *P. bovallii sensu lato* suggest
374 interconnectivity across the Guiana Shield even for small fishes restricted to fast-flowing
375 streams. Clearly, we are just beginning to understand the complexities of the biogeography of the
376 western Guiana Shield and the interconnectedness of it with the eastern portion of the shield.

377

378 **Threats to Biodiversity in the Guyana Highlands**

379 The Pakaraimas represent the cores of ancient mountains, which are among the main
380 sources of gold and diamonds. Alofs et al. (2014) review some of the issues with gold mining in
381 the upper Mazaruni River, and we have observed similar issues in the Kuribrong and Potaro
382 Rivers as well. Large swaths of forest have been removed from around the rivers with the
383 sediment pumped through sieves to extract gold and diamonds. Gold is removed with mercury
384 amalgamation leading to high mercury levels in the water, fishes, and humans (Miller et al.
385 2003) and large swaths of forest replaced by denuded landscapes and toxic spoil ponds. On
386 larger rivers like the lower Potaro, large dredging machines suck up sediment and process it
387 directly in the river leaving behind piles of gravel in the river that alter the natural hydrology.
388 Although Hardman et al. (2002) did not find significant differences between their study of the
389 fishes of the Potaro River and Eigenmann (1912), certain species that had been present and
390 common in Eigenmann's survey were absent 90 years later. Mol & Ouboter (2004) and Brosse,
391 Grenouillet, Gevrey, Khazraie, & Tudesque (2011) found that the erosion related to gold mining
392 has reduced fish diversity. As of our 2014 trip to the upper Kuribrong and 2016 trip to the Ireng,
393 there was little impact to the rivers from mining; however, a recently completed road now
394 provides easier access to the upper Kuribrong, and one small mine was observed. The lower

395 Kuribrong has been heavily impacted, and after flying over the Potaro River in 2014, JWA can
396 state that the Potaro looks less clear than it had during the 1998 expedition reported in Hardman
397 et al. (2002).

398 As expressed by Alofs et al. (2014) for the upper Mazaruni, the whole high plateau of the
399 Pakaraimas supports an endemic fauna as is evidenced here. Although there is some
400 interconnectivity of the river systems, narrow endemic *Trichomycterus* are found in each of the
401 rivers in this study. Conservation of this unique landscape that has become part of our shared
402 cultural heritage is important, and further studies on the unique fauna of the region are needed.

403

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491

492

493 **DATA ACCESSIBILITY STATEMENT**

494 Sequence data are available on GenBank. Accession numbers for each specimen and gene are
495 listed in Table 1.

496 *Note: Accession numbers will be included upon acceptance of the paper.*

497

498 **TABLES** (each table complete with title and footnotes)

499 **Table 1.** Collection information for *Trichomycterus* species used in this study. GenBank

500 Accession numbers are provided for each gene and individual.

Tissue Catalog	Species ID	Voucher Number	Latitude	Longitude	16S	COI	Cytb	RAG2
AUFT10166	Ireng, spotted	67129	5.08955	-59.97514	Y	Y	Y	Y
AUFT10168	Ireng, spotted	67129	5.08955	-59.97514	Y	Y	-	Y
AUFT10169	Ireng, spotted	67129	5.08955	-59.97514	Y	Y	Y	Y
AUFT10170	Ireng, spotted	67129	5.08955	-59.97514	Y	Y	Y	Y
AUFT10212	T. conradi	67138	5.04398	-59.97717	Y	Y	Y	Y
AUFT10213	T. conradi	67138	5.04398	-59.97717	Y	Y	Y	-
AUFT10234	Ireng, spotted	67154	5.08388	-59.98762	Y	Y	Y	Y
AUFT10276	Ireng, spotted	67179	5.04398	-59.97717	Y	Y	-	Y
AUFT10294	T. conradi	67194	5.08867	-59.96952	Y	Y	Y	-
AUFT10310	Ireng, spotted	67172	5.08955	-59.97514	Y	Y	Y	Y
AUFT2110	T. guianensis	63677	5.30181	-59.89838	Y	Y	-	-
AUFT2186	T. cf. guianensis	62902	5.40532	-59.5439	Y	Y	-	Y
AUFT4743	T. cf. conradi	51758	4.767118	-54.56462	Y	Y	Y	-
AUFT6563	T. guianensis	62932	5.30181	-59.89838	-	Y	-	Y
AUFT6596	Potaro, elongate	62949	5.304	-59.89819	Y	-	-	Y
AUFT6597	Potaro, elongate	62949	5.304	-59.89819	Y	-	-	Y
ROMT06183	Mazaruni, plain	83791	5.4755	-60.77967	Y	Y	Y	Y
ROMT06184	Mazaruni, plain	83791	5.4755	-60.77967	Y	Y	Y	-
ROMT06185	T. cf. guianensis	83790	5.4755	-60.77967	Y	Y	Y	-
ROMT06186	T. cf. guianensis	83790	5.4755	-60.77967	Y	Y	Y	-
ROMT12696	T. cf. guianensis	89932	4.95407	-59.85882	Y	Y	Y	Y
ROMT15527	T. cf. guianensis	91392	5.272085861	-59.7026908	Y	Y	Y	Y
ROMT15575	T. cf. guianensis	91500	5.3759978	-59.5472803	Y	Y	Y	Y
ROMT15595	T. conradi	91436	5.413958782	-59.470252	Y	Y	Y	Y