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1 **Molecular Phylogeny and taxonomy of a new *Myxobolus* species from the**
2 **endangered ornamental fish, *Otocinclus cocama* endemic to Peru: A host-parasite**
3 **coextinction approach**

4 Patrick D. Mathews^{a,b*}, Omar Mertins^c, Tiago Milanin^d, Luis L. Espinoza^e, Anai P.
5 Gonzales-Flores^f, Fabienne Audebert^b, André C. Morandini^a

6 ^a Department of Zoology, Institute of Biosciences, University of São Paulo, 05508-090,
7 São Paulo, Brazil

8 ^b Unité Biologie des Organismes et Écosystèmes Aquatiques, Sorbonne Université,
9 MNHN, CNRS, IRD, UCA, CP 26, 75231 Paris, France

10 ^c Department of Biophysics, Paulista Medical Scholl, Federal University of São Paulo,
11 04023-062 São Paulo, Brazil

12 ^d Department of Basic Sciences, Faculty of Animal Science and Food Technology,
13 University of São Paulo, 13635-900, Brazil

14 ^e Laboratory of Biology and Molecular Genetics, Faculty of Veterinary Medicine,
15 National University of San Marcos, 2800 San Borja, Lima, Peru

16 ^f Post-Graduate Program in Tropical Biodiversity, Federal University of Amapá, 68903-
17 419 Macapá, Brazil

18 *Corresponding author at: Department of Zoology, Institute of Biosciences, University
19 of São Paulo, 05508-090 São Paulo, Brazil. E-mail address:
20 patrickmathews83@gmail.com (P.D. Mathews).

21 **ABSTRACT**

22 A new *Myxobolus* species is described infecting gill filaments of the endangered
23 ornamental fish *Otocinclus cocama* from Peruvian Amazon. In a total of 35 fish

24 examined, five (14.3%) had myxozoan plasmodia. Taxonomic analysis was performed
25 integrating multiple characters, including morphometrical, biological traits, ssrDNA
26 sequence data and host ecological characters. Myxospores of *M. iquitoensis* n. sp. were
27 ovoid in shape from the frontal view and measured $17.6\pm 1.2\ \mu\text{m}$ (16.2–19.8 μm) in
28 length and $10.5\pm 0.7\ \mu\text{m}$ (9.8–12 μm) in width. The two polar capsules were elongate in
29 shape, equal in size and occupying almost half of the myxospore body. They measured
30 $8.7\pm 0.4\ \mu\text{m}$ (6.9–9.3 μm) in length and $3.3\pm 0.2\ \mu\text{m}$ (3–3.6 μm) in width. The **polar**
31 **tubules** presented six to seven turns. Molecular phylogenetic analysis revealed that the
32 obtained ssrDNA sequence did not match any existing sequences in GenBank but
33 showed *M. iquitoensis* n. sp. to be a close species of *M. figueirae*. Nonetheless, the
34 ssrDNA sequences of those species show large genetic divergence. This is the first
35 description and phylogenetic study of a myxozoan parasitizing fish of the genus
36 *Otocinclus* from South America, as well the first report of these parasites infecting a
37 fish belonging to the Loricariidae family from Amazon basin. Considering the
38 endangered status of the host, the high degree of host-specificity of freshwater histozoic
39 myxobolids, the low occurrence shown by the new myxozoan, and the fact that this is
40 the only host known for this myxozoan, the conservation status of the new species of
41 myxozoan is likely to be connected to the future survival of its host.

42 **Keywords:** Cnidaria; Myxosporea; *Myxobolus iquitoensis* n. sp.; Peruvian Amazon

43 **1. Introduction**

44 The worldwide aquarium industry moves millions of fishes each year around the world
45 and is an important source of income in many local markets (Prang, 2007). Nonetheless,
46 as a function of growing global demand of the pet trade, exports of species that are
47 biologically unsuited to heavy exploitation has increased. This has resulted in dramatic

48 reductions of natural populations, and contributed to local extinctions (Ng and Tan,
49 1997; Moreau and Coomes, 2006; Mohanty and Measey, 2019). In this context, over-
50 exploitation of wild ornamental fish for the aquarium trade has become an important
51 conservation menace (Moreau and Coomes, 2007).

52 The Amazon basin is the most important source of ornamental freshwater fishes for the
53 international aquarium industry (Prang, 2007; Moreau and Coomes, 2007). Among
54 countries of the Amazon region, Peru is the second largest exporter of ornamental fish,
55 with about 14,000 people depending directly on the aquarium trade (Moreau and
56 Coomes, 2007). This activity is centralized in the city of Iquitos in the Department of
57 Loreto, Peru with approximately 28 established aquarium fish exporter firms, exporting
58 ornamental fish to 24 countries (Moreau and Coomes, 2007). Virtually all fishes in the
59 trade are taken from a variety of wild aquatic habitats such as main river channels, small
60 tributaries, floodplain oxbow lakes, swamps, flooded moriche palm forest, and remote
61 upland streams (Moreau and Coomes, 2007).

62 The plecocs are members of the family Loricariidae. With more than 830 valid species,
63 they are the most species-rich family within the Order Siluriformes. These neotropical
64 freshwater catfishes are distributed throughout South America (Ribeiro et al., 2012).
65 Within Loricariidae, species belonging to the genus *Otocinclus* Cope, 1871 are small
66 loricariids not exceeding 5 cm in length and represent one of the most important
67 aquarium fish exported from Peruvian Amazon, comprising over 29% of the total
68 volume of the international export (Moreau and Coomes, 2007). Species of *Otocinclus*
69 are widely distributed in South America, specifically east of the Andes, and often
70 inhabit small lowland tributaries of the main rivers associated with marginal vegetation
71 (Schaefer, 1997). Among these, *Otocinclus cocama* Reis, 2004 known as “zebra
72 otocinclus” is very popular in the aquarium trade and it is one the most important

73 aquarium fish exports from Iquitos based on international sales (Moreau and Coomes,
74 2007). *O. cocama* is endemic to Peruvian Amazon, specifically from the Yanayacu
75 small stream, near district Jenaro Herrera, Department of Loreto (Reis, 2004). As a
76 direct consequence of the increasing exploitation by the ornamental trade, with
77 continuing decline of mature individuals, *O. cocama* is currently considered an
78 endangered species in Peru and it is included on the Red List of Threatened Species-
79 IUCN (Hidalgo and Chocano, 2016).

80 Models of coextinction have suggested parasites to be one the most menaced ecological
81 groups (Strona et al., 2013). According to Dallas and Cornelius (2015) extinction and
82 declining of wild hosts could result in secondary extinctions of their parasites,
83 especially parasites endemic to a small subset of host species. Following the fine scale
84 of host-parasite coextinction, parasites of *O. cocama* are likely to be similarly
85 vulnerable. However, little is known about parasites that infect this Amazonian
86 ornamental fish, especially the myxozoan parasites. Thus, it is important to clarify the
87 parasite fauna of *O. cocama*.

88 Myxozoans are microscopic parasitic cnidarians of worldwide distribution and they
89 represent about 20% of the cnidarian biodiversity known to date (Atkinson et al., 2018).
90 Although predominantly known to infect wild and cultured fishes, myxozoans can
91 infect virtually all vertebrate groups, including amphibians, reptiles, birds, and
92 terrestrial mammals (Okamura et al., 2015; Lisnerová et al., 2019). Among the
93 myxozoans, the genus *Myxobolus* Bütschli, 1882 is the most abundant, accounting for
94 around 905 species described within a wide geographical range (Eiras et al., 2014).
95 Freshwater histozoic *Myxobolus* species are widely recognized for their strict or high
96 host-specificity (Molnár and Eszterbauer, 2015).

97 In this study, we described a new host-specific freshwater histozoic myxozoan,
98 *Myxobolus iquitoensis* n. sp. infecting the gill filaments of the endangered fish *O.*
99 *cocama* from the Peruvian Amazon. Morphological and molecular features of the
100 parasite are provided herein.

101 **2. Materials and methods**

102 A total of 35 specimens of *Otocinclus cocama* were acquired from local fisherfolk of
103 aquarium ornamental fishes in September 2019, for parasitological survey. According to
104 the fisherfolk, the fishes were caught in the marginal vegetation in the small stream
105 Yanayacu, near Jenaro Herrera district, Loreto, Peru (4°58'58"S, 74°19'38"W). The fish
106 were transported live to the field laboratory at the Research Institute of the Peruvian
107 Amazon, where they were euthanized by pit transaction and examined using a light
108 microscope to verify the presence of lesions and parasites. The euthanasia method was
109 approved by Federal University of São Paulo—UNIFESP Ethics Committee (CEUA
110 No. 9209080214; Federal Law No. 11794, dated 8 October 2008), in accordance to
111 international procedures.

112 For morphological and morphometric characterization, the mature myxospores were
113 fixed in 10% formalin and transported to Department of Zoology, University of São
114 Paulo, Brazil. The analyses were performed based on the criteria outlined by Lom and
115 Arthur (1989). Measurements and photographs were taken from 30 myxospores using a
116 compound microscope Leica DM1000 LED equipped with Leica Application Suite
117 version 1.6.0 image capture software. Smears containing free myxospores were air
118 dried, fixed with methanol and stained with Giemsa solution to mount on permanent
119 slides that were deposited in the collections of the Museum of Zoology of the
120 University of São Paulo - USP, São Paulo, Brazil.

121 For molecular characterization, plasmodia were removed from the infected tissue and
122 preserved in absolute ethanol. Extraction of genomic DNA (gDNA) was carried out
123 from a single plasmodium and was performed using a DNeasy® Blood & Tissue Kit
124 (animal tissue protocol) (Qiagen Inc., California, USA), in accordance with the
125 manufacturer's instructions. gDNA concentration was quantified in a NanoDrop 2000
126 spectrophotometer (Thermo Scientific, Wilmington, USA) at 260 nm. Small-subunit
127 ribosomal DNA (**SSU rDNA**) was amplified using a two-round polymerase chain
128 reaction (PCR) according to Naldoni et al. (2019). The initial PCR was performed using
129 universal eukaryotic primers ERIB1, ACCTGGTTGATCCTGCCAG and ERIB10,
130 CTTCCGCAGGTTACCTACGG (Barta et al., 1997), followed by a second round
131 with primer pairs ERIB1 with ACT1r, AATTTACCTCTCGCTGCCA (Hallet and
132 Diamant, 2001) and BOBF, TGTTACAGCATGGAACGAAC (Capodifoglio et al.,
133 2019) with ERIB10. PCR was carried out in a total volume of 25 µl consisting of 1 µl of
134 DNA (10 to 50 ng), 0.5 µl of each specific primer (0.2 µM), 12.5 µl DreamTaq 2x PCR
135 Master Mix (Thermo Scientific, Massachusetts, USA) and 10.5 µl of ultrapure water.
136 The amplification of the partial **SSU rDNA** was performed in the Mastercycler® nexus
137 (Eppendorf, Hamburg, Germany) and the PCR cycle consisted of an initial denaturation
138 step at 95 °C for 5 min, followed by 35 denaturation cycles at 95 °C for 60 s, annealing
139 at 60 °C for 60 s, and extension at 72 °C for 120 s, following by a terminal extension at
140 72 °C for 5 min. A control reaction was processed in order to check for possible
141 contamination. The amplified products were subjected to electrophoresis in 1.0%
142 agarose gel (BioAmerica, California, USA) in a TAE buffer (Tris–Acetate EDTA: Tris
143 40 mM, acetic acid 20 mM, EDTA 1 mM), stained with Sybr Safe DNA gel stain
144 (Invitrogen by Life Technologies, California, USA), and then analyzed with a
145 Stratagene 2020E trans illuminator. For sizing and approximate quantification of

146 fragments, 1 Kb Plus DNA Ladder (Invitrogen by Life Technologies, USA) was used.
147 PCR products were purified using USB® ExoSap-IT® (Thermo Fisher Scientific,
148 Massachusetts, USA) in accordance with the manufacturer's instructions. PCR products
149 were sequenced using the same PCR primers. Additional primers MC5,
150 CCTGAGAAACGGCTACCACATCCA and MC3, GATTAGCCTGACAGATC
151 ACTCCACGA (Molnár et al., 2002) were used to connect overlapping fragments.
152 Sequencing was performed with a BigDye® Terminator v3.1 cycle sequencing kit
153 (Applied Biosystems Inc., California, USA) in an ABI 3730 DNA sequencing analyzer.
154 The obtained sequences were visualized, assembled and edited using BioEdit 7.1.3.0
155 software (Hall, 1999). A basic local alignment search was conducted (BLASTn) to
156 verify the similarity of our sequence with other sequences of myxozoans available in the
157 National Center for Biotechnology non-redundant nucleotide database (Altschul et al.,
158 1997). Phylogenetic analysis was conducted using the 53 most closely related
159 myxobolid myxosporeans sequences with BLAST similarity > 80%, included 29
160 sequences of *Myxobolus* species, 23 sequences of *Henneguya* species and 1 of
161 *Thelohanellus* species. *Parvicapsula bicornis* (EF429097) sequence was used as
162 outgroup. The sequences were edited and aligned with ClustalW within BioEdit version
163 7.1.3.0 (Hall, 1999) and phylogenetic relationships were performed using maximum
164 likelihood (ML) methods with a Kimura 2-parameter (K2P) evolution sequence model
165 in the MEGA 6.0 program (Tamura et al., 2013). Bootstrap analysis (1000 replicates)
166 was employed to assess the relative robustness of the tree branches. Other alignments,
167 including species that clustered together with the *O. cocama* isolate in the phylogenetic
168 tree, were used to produce a pairwise similarity using MEGA 6.0.

169 **3. Results**

170 Among the 35 specimens of *O. cocama* examined in the present study, the gill filaments
171 of five (14.3%) harbored plasmodia of an unknown parasite belonging to the genus
172 *Myxobolus*. Plasmodia were not found in any other organ and no clinical signs were
173 observed in the parasitized organ. The description of the novel species is provided
174 below.

175 Taxonomic summary

176 Phylum: Cnidaria Verrill, 1865

177 Class: Myxosporea Bütschli, 1881

178 Order: Bivalvulida Shulman, 1959

179 Family: Myxobolidae Thélohan, 1892

180 Genus: *Myxobolus* Bütschli, 1882

181 Species: *Myxobolus iquitoensis* n. sp.

182 Type host: *Otocinclus cocama* (Siluriformes: Loriicaridae)

183 Site of infection: Gill filaments

184 Type locality: Yanayacu brook, Municipality of Jenaro Herrera (4°58'58"S,
185 74°19'38"W), Department of Loreto, Peru.

186 Prevalence: From 35 examined fish, five were infected (14.3%).

187 Type of material: Syntypes-Air-dried slide stained with Giemsa (MZUSP 8507)
188 deposited in the collection of Museum of Zoology of the University of São Paulo - USP,
189 São Paulo, Brazil. The **SSU rDNA** sequence was deposited in GenBank under accession
190 number MN995338.

191 Etymology: The specific name (*M. iquitoensis*) is based on the geographic area (Iquitos
192 city), which is the center of aquarium fish trade of the Peruvian Amazon.

193 **Morphological description**

194 Plasmodia of rounded shape and measuring up to 45 μm in diameter were found in the
195 distal region of the gill filaments. Mature myxospores featured an ovoid shape from the
196 frontal view and measured 17.6 ± 1.2 μm (16.2–19.8 μm) in length and 10.5 ± 0.7 μm
197 (9.8–12 μm) in width (Fig. 1A-C). The two polar capsules were elongated in shape,
198 equal in size, occupying almost half of the myxospore body (Fig. 1A-B). They
199 measured 8.7 ± 0.4 μm (6.9–9.3 μm) in length and 3.3 ± 0.2 μm (3–3.6 μm) in width. The
200 **polar tubules** presented six to seven turns (Fig. 1B and 2).

201 **Molecular characterization and phylogenetic analysis**

202 The sequencing of the **SSU rDNA** from the myxospores of *M. iquitoensis* n. sp.,
203 resulted in sequence of 1926 bp with a GC content of 48.3%. BLASTn search revealed
204 that the sequence obtained did not match any known myxozoan species sequences
205 available in the GenBank database. The highest percentage of identity belonged to
206 *Myxobolus figueirae* Naldoni, Maia, Correa, Da Silva and Adriano, 2018 (query
207 coverage 93%, maximum identities 88%), a parasite of the Amazon pimelodid fish
208 *Phractocephalus hemiliopterus*. Phylogenetic analysis based on the most closely
209 related myxozoan sequences placed the sequence within a subclade containing
210 myxobolid parasite species of native South American fishes. In this same subclade, *M.*
211 *iquitoensis* n. sp. appears as a close species of *M. figueirae* (GenBank accession
212 MG181226). Genetic distance analysis considering only of **SSU rDNA** sequences of the
213 myxobolids that cluster together in the same clade (Fig. 3) with the new parasite herein
214 described showed the largest genetic divergence among these species, with a difference

215 of 11% to *M. figueirae*, 14.9% to *Myxobolus porofilus* Adriano, Arana, Ceccarelli and
216 Cordeiro, 2002, 15.7% to *Myxobolus curimatae* Zatti, Naldoni, Silva, Adriano, 2015
217 and 17.1% to *Myxobolus prochilodus* Zatti, Arana, Maia and Adriano, 2016.

218 **4. Discussion**

219 Although, several myxosporean species have been described in South American fishes
220 (Mathews et al., 2016; Velasco et al., 2019; Naldoni et al., 2020), there are few studies
221 about the occurrence of this enigmatic group of parasites infecting ornamental fishes,
222 particularly on native and endemic species from Amazon basin (Mathews et al., 2020).
223 Indeed, from the Peruvian Amazon, a key source of wild freshwater fishes to the global
224 aquarium market, only two myxozoan species have been described (Mathews et al.,
225 2017; Mathews et al., 2018). In the present study, based on integrating morphological,
226 ecological (host endemism and geography locality), biological traits (host/organ-tissue
227 specificity), and molecular phylogenetic analysis, we describe a new species of
228 freshwater histozoic myxobolid, *Myxobolus iquitoensis* n. sp. infecting gill filaments of
229 the endangered fish *O. cocama*.

230 To our knowledge, this study reports for the first time a myxosporean infecting a fish of
231 the genus *Otocinclus* from South America, being notably as well the first report of these
232 parasites infecting a fish belonging to the Loricariidae family from Amazon basin.
233 Thus, our results contribute to freshwater platysporines taxonomy and extend the
234 knowledge about myxosporean parasites of ornamental fish from the Amazon basin.
235 The morphological and morphometric comparison of mature myxospores of *M.*
236 *iquitoensis* n. sp. with those from the other *Myxobolus* species described that infect
237 siluriform fish from the Amazon basin, showed remarkable differences as reported in
238 Table 1. Differences could also be observed in the genus/family of the parasitized host.

239 Indeed, it has been reported that the host fish represents an important taxonomic clue
240 and that *Myxobolus* species display a strong tendency to cluster, based on host
241 phylogenies (Fiala, 2006; Carriero et al., 2013). Thus, a single species is typically
242 limited to closely related hosts within Genus/Family/Order, which is another important
243 feature of *M. iquitoensis* n. sp as a new species, since *O. cocama* represents its unique
244 host.

245 Compared with other known *Myxobolus* species previously described from South
246 American freshwater fishes, the new species resembles *Myxobolus aureus* Carriero,
247 Adriano, Silva, Cecarelli and Maia, 2013, a parasite of *Salminus brasiliensis*. However,
248 the comparison showed that myxospores are slightly larger in length and width, being
249 $17.6\pm 1.2 \times 10.5\pm 0.7 \mu\text{m}$ for the new species, while $12.6\pm 0.5 \times 8.3\pm 0.3 \mu\text{m}$ for *M. aureus*.
250 The two polar capsules of *M. iquitoensis* n. sp. are substantially larger at $8.7\pm 0.4 \mu\text{m} \times$
251 $3.3\pm 0.2 \mu\text{m}$ compared to those of *M. aureus* $5.7\pm 0.3 \mu\text{m} \times 2.9\pm 0.2 \mu\text{m}$ and number of
252 coils in polar tubule are 6-7 turns to 7-8 for *M. aureus*. Furthermore, these species
253 demonstrated a large genetic divergence of 12.2% in their SSU rDNA. In addition, the
254 hosts of these two species are different, with *M. iquitoensis* n. sp. parasitizing a
255 siluriform fish belonging to the Loricariidae family, while *M. aureus* infects a
256 characiform fish from the Bryconidae family. Finally, the species infect different
257 organs, with *M. iquitoensis* n. sp. parasitizing gill filaments and *M. aureus* parasitizing
258 the liver.

259 The phylogenetic analysis performed in our study showed SSU rDNA sequences of
260 *Heneguya* and *Myxobolus* species grouped together (Fig. 3). The absence of
261 phylogenetic separation between these two genera agrees with several other studies
262 conducted in many regions of the world (Kent et al., 2001; Carriero et al., 2013; Milanin

263 et al., 2018). This trend is noticeably observed in clade B, where *Henneguya*
264 *basifilamentalis* Molnar, Szekely, Mohamed and Shaharom-Harrison, 2006 and
265 *Henneguya mystusia* Sarkar, 1985 parasites of Siluriform bagrid catfishes, are
266 positioned in a clade composed mostly of species belonging to the genus *Myxobolus*.
267 Our phylogeny also evidenced a strong affinity of *Myxobolus* and *Henneguya* species to
268 cluster, based on the order and/or family of the host, as previously pointed out by other
269 authors (Fiala, 2006; Naldoni et al., 2011; Carriero et al., 2013). In the phylogenetic
270 tree, *M. iquitoensis* n. sp. appears weakly supported in a subclade as a close species of
271 *M. figueirae*, a parasite of the Amazonian catfish from the Pimelodidae family (Naldoni
272 et al., 2018). Although this data reveals geographic affinity, these two species showed a
273 large genetic divergence of 11% as revealed by the pairwise analysis. Furthermore, the
274 two species show noticeable differences in morphology, genus/family and the host
275 organ they infect, as reported in Table 1. It is important to highlight that this is the first
276 phylogenetic study of a myxobolid parasite of *Otocinclus* genera and Loricariidae
277 family from Amazon basin and, as a matter of fact, there are few **SSU rDNA** data
278 available from myxosporeans infecting Amazonian siluriform hosts. Thus, future
279 molecular data and phylogenetic studies of the many yet-to-be-discovered *Myxobolus*
280 species from these underrepresented hosts and other groups of native and endemic
281 Amazonian fishes should help resolve the evolutionary context of *M. iquitoensis* n. sp.

282 Moreover, it is now recognized that parasitic fauna can decline with biodiversity losses
283 (Koh et al., 2004; Dobson et al., 2008; Lafferty et al., 2012). Indeed, models of
284 coextinction have identified parasites as one of the most menaced ecological groups,
285 representing an unseen majority of species extinctions (Dobson et al., 2008; Strona et
286 al., 2013). Although, *O. cocama* is currently considered an endangered species in the
287 IUCN, little or nothing is known about its parasitic fauna, and the *Myxobolus* species

288 described herein represents the only platysporine **myxozoan reported to parasite** this
289 ornamental fish. According to previous studies, the relationship between parasite
290 specialization and host vulnerability are important factors that predict the risk of a
291 parasite species becoming extinct together with its host (McKinney, 1999; Dobson et
292 al., 2008; Strona et al., 2013). Considering the endangered status of the host fish and
293 that the same is the only known habitat for *M. iquitoensis* n. sp., together with the low
294 occurrence shown by this new myxozoan and the high degree of host-specificity of
295 freshwater histozoic myxobolids, *M. iquitoensis* n. sp. may face the danger of
296 coextinction with its host. In this context, the establishment and implementation of a
297 conservation programme in order to minimize impacts on wild populations of *O.*
298 *cocama* would also benefit the survival of their endemic myxozoan.

299 **Conflicts of interest**

300 The authors declare that they have no conflict of interest.

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465 **Legends**

466 Fig.1. Light photomicrograph of mature myxospores of *Myxobolus iquitoensis* n. sp.,
467 parasite of gill filaments of *Otocinclus cocama*. A, Fresh mature myxospore. Scale bar:
468 50 μm . B, Formalin-fixed mature myxospore showing two equal elongated polar
469 capsules. Scale bar: 15 μm . C, Mature myxospores in frontal view stained in May-
470 Grünwald-Giemsa. Scale bar: 30 μm .

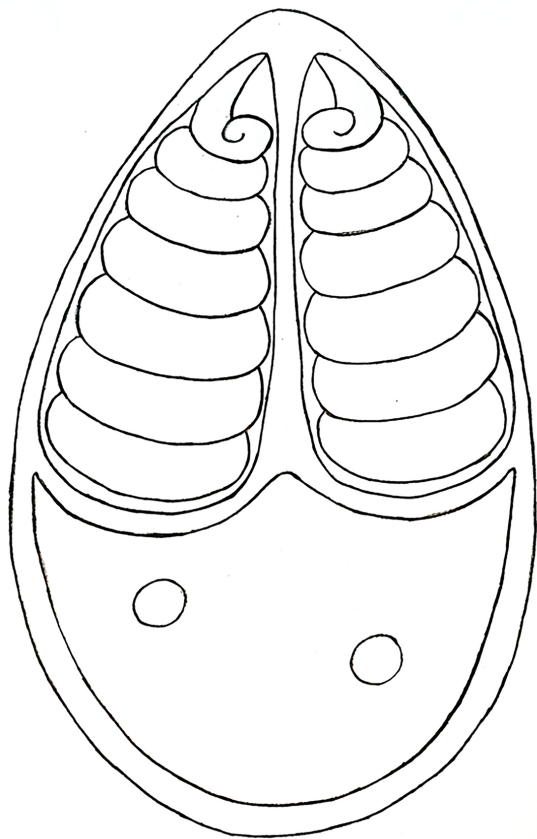
471 Fig. 2. Schematic representation of mature myxospore of *Myxobolus iquitoensis* n. sp.
472 parasite of gill filaments of *Otocinclus cocama*. Scale bar: 5 μm .

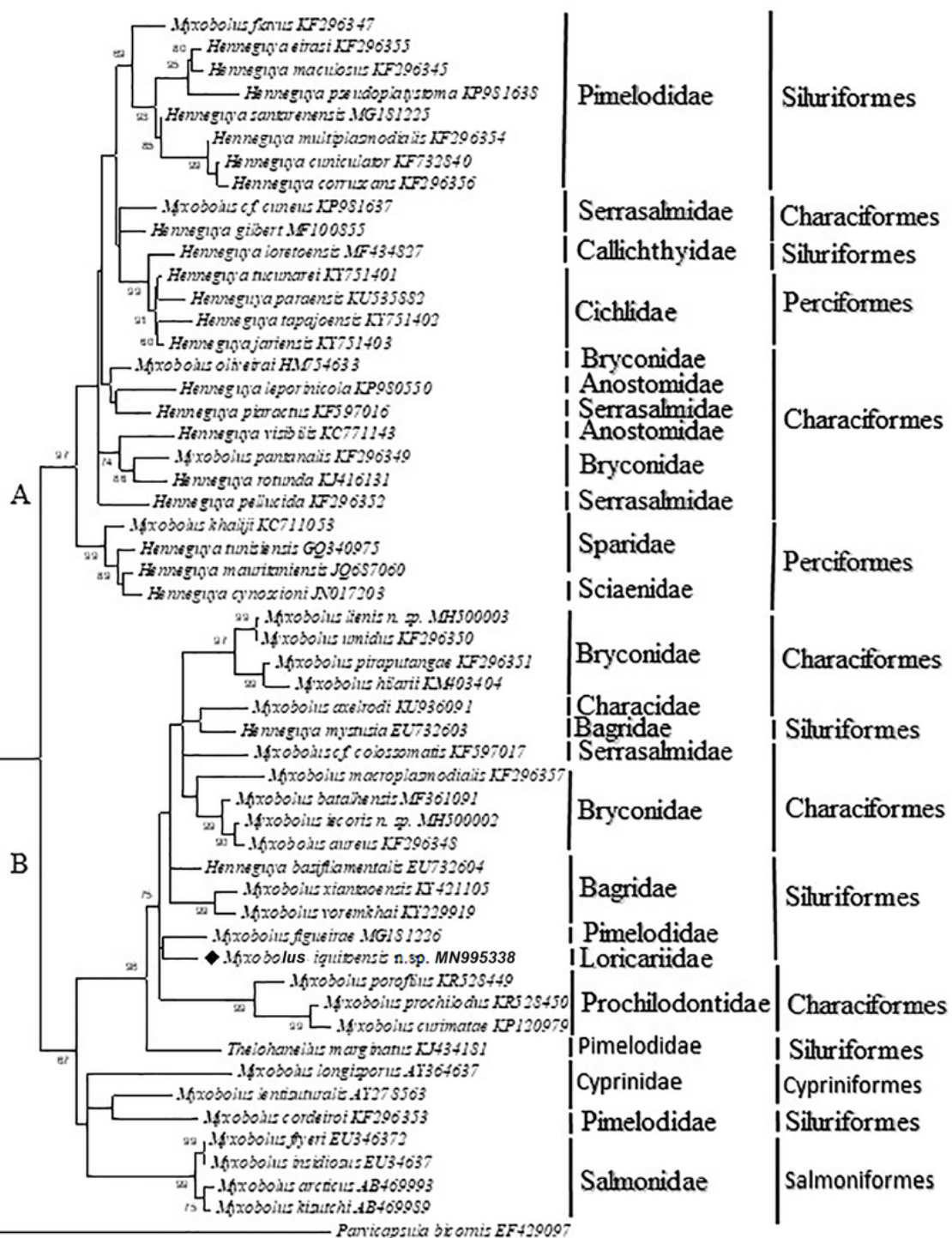
473 Fig. 3. Maximum Likelihood (ML) tree containing *Myxobolus iquitoensis* n. sp. and
474 closely related myxosporeans sequences deposited in GenBank based on partial small
475 subunit ribosomal DNA. The numbers above the nodes indicate bootstrap confidence
476 levels.

477 Table 1. Comparison of *Myxobolus iquitoensis* n. sp. with other *Myxobolus* species
478 described parasitizing siluriform fishes from Amazon basin. Spore dimensions, hosts,
479 infection sites, and collection sites are given. SL: spore length, SW: spore width, ST:
480 spore thickness, PCL: polar capsules length, PCW: polar capsules width, NCT: number
481 of coils in polar tubule, dashes: no data. All measurements are in μm .

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A50 μm **B****C**





Species	SL	SW	ST	PCL	PCW	NCT	Host	Family	Site of infection	Locality	References
<i>Myxobolus iquitoensis</i> n. sp.	17.6±1.2 (16.2-19.8)	10.5±0.7 (9.8-12)	-	8.7±0.43 (6.9-9.3)	3±0.2 (3-3.6)	6-7	<i>Otocinclus cocama</i>	Loricariidae	Gill filaments	Yanayacu brook, Peru	This study
<i>Myxobolus adrianoi</i>	22.4±0.3	16.3 ± 0.1	-	14.3 ±0.2	6.5 ± 0.1	5	<i>Corydoras schwartzi</i>	Callichthyidae	Intestine	Purus River, Brazil	Mathews et al. 2020
<i>Myxobolus figueirae</i>	9.5 (9.1-10)	6.4 (5.8-6.9)	4.5 (4.4-4.5)	4.1 (3.5-4.6)	2.1 (1.7-2.6)	7-8	<i>Phractocephalus hemioliopterus</i>	Pimelodidae	Skin	Tapajós River, Brazil	Naldoni et al. 2018
<i>Myxobolus tapajosi</i>	15 (13.5-17)	10.7 (9.6-11.4)	-	5.8 (4.6-7.1)	3 (2.3-3.8)	6-7	<i>Brachyplatystoma rousseauxii</i>	Pimelodidae	Gill filaments	Tapajos River, Brazil	Zatti et al. 2018
<i>Myxobolus marajoensis</i>	10.9 (10.0- 11.6)	5.1 (4.2-5.4)	-	5.3 ± 0.6	1.6 ± 0.36	-	<i>Rhamdia quelen</i>	Heptapteridae	Intestine	Marajó Island, Brazil	Abrunhosa et al. 2017
<i>Myxobolus niger</i>	11.3±0.4	6.8 ±0.2	4.1 ± 0.2	5.0 ± 0.3	2.0 ± 0.1	6-7	<i>Corydoras melini</i>	Callichthyidae	Gill arch	Negro River, Brazil	Mathews et al. 2016
<i>Myxobolus</i> sp.	8 ± 0.2	5.8 ± 0.4	3.4 ±0.2	3.6 ± 0.3	1.2 ± 0.2	-	<i>Pimelodus ornatus</i>	Pimelodidae	Heart	Arari River, Brazil	Matos et al. 2014

