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New species of *Ellipsomyxa* (Bivalvulida: Ceratomyxidae) parasitizing the gallbladder of *Ageneiosus ucayalensis* (Siluriformes: Auchenipteridae) in the Brazilian Amazon region

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ABSTRACT

The present study describes a new myxozoan species, *Ellipsomyxa matosi* n. sp. infecting the gallbladder of the catfish *Ageneiosus ucayalensis*, on Jutuba Island, municipality of Belém, state of Pará, Brazil. The new species was diagnosed based on morphological and molecular analyses. 33 specimens were examined between February and May 2023, and all (100 %) presented disporic plasmodia in the bile fluid, with ellipsoidal, slightly elongated mature myxospores, with a subtle valve projection in the apical region and a curved suture line, typical morphological characteristics of the genus *Ellipsomixa*. The polar capsules were pyriform and of equal size, with a subterminal opening and 6–7 polar tubule coils. No histopathological changes, lesions, or inflammatory responses were observed in the epithelial layer or any part of the tissue. PCA identified the proximity in spore length (SL) of the new species to *E. amazonensis* and *E. papantla*. The partial SSU rDNA sequence obtained was distinct from all other available sequences from species of this genus. The phylogenetic analysis obtained high nodal support, grouping the new species as an ancestor of the well-defined clade of *Ellipsomyxa* species described in the Amazon region.

1. Introduction

Myxozoans constitute a group of prominent parasites in fish, comprising a heterogeneous and widely distributed collection of endoparasites with pathogenic potential, with a considerable variety of forms, reported in different organs or tissues [1–4]. They belong to the Phylum Cnidaria, with more than 2600 species described worldwide in marine and freshwater environments, classified into 64 genera [1,5–7]

The myxosporean of the genus *Ellipsomyxa* Køie, 2003, a member of the family Ceratomyxidae Doflein, 1899, in the order Bivalvulida [8]. However, phylogenetic aspects show greater proximity to marine *Myxidium* than to *Ceratomyxa* species [2,8,9]. *Ellipsomyxa* species form plasmodia, monosporic or disporic, elongated myxospores, with polar capsules located at opposite ends, have a well-defined suture line in the transversal plane, which may be straight or sinuous, and show tropism for fish gallbladders [5,8–12]. At present, only seven species have been identified in the Amazon region based on morphological and phylogenetic traits, except *E. gobioides* [4,14–18].

In the Amazon region, the catfish *Ageneiosus ucayalensis* Castelnau, 1855, from the order Siluriformes, has a wide distribution in the river Brazilian amazon basin, with wide spatial distribution in the water column, carrying out annual reproductive migrations, being an

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important source of subsistence for riverside communities [19–21].

The present study describes a new species of myxozoan, *Ellipsomyxa matosi* n. sp., which was found in the gall bladder of specimens of catfish, *A. ucayalensis*, collected from Jutuba Island, in the municipality of Belém, in Pará state, Brazil, based on morphological and molecular analyses.

2. Materials and methods

2.1. Sample collection

A total of 33 *A. ucayalensis* specimens were collected from Jutuba Island (01°15′ S, 48°30′ W), in the northern Brazilian state of Pará, between February and May 2023. This island is located between Santo Antônio and Guajará bays, in the southeastern extreme of the estuary of the Amazon River.

The specimens were transported alive to the Carlos Azevedo Research Laboratory - LPCA, located on the Belém campus of the Federal Rural University of Amazonia- UFRA, in Pará state. In the laboratory, the fish were anaesthetized with 50 mg/L of tricaine (MS 222) and necropsied under a light stereomicroscope for the detection of myxozoans on the surface of the body and in the internal organs.

The analysis of the specimens presented here was authorized by the UFRA Ethics Committee for the Use of Animals in Research (CEUA 8323110522) and by a license from the Brazilian Institute for the Environment and Renewable Natural Resources, IBAMA (SISBIO/ICMBio license number 27119–1).

2.2. Morphological analysis

As myxospores were observed in the gall bladder, the organ was removed for histological analysis, for which it was fixed in Davidson solution (ethanol, formaldehyde, acetic acid, and distilled water) for 24 h. They were subsequently dehydrated in an increasing ethanol series, diaphanized in xylol, and included in paraffin. Then, 5 μm thick sections were obtained using a microtome and stained with special Ziehl-Neelsen technique [22].

The fresh myxospores and the stained slides were photographed under a Zeiss Primo Star Differential Interference Contrast (DIC) microscope attached to an AxiocamErc 5 camera equipped with AxioVision LE software. The fresh myxospores (n = 32) were measured (μm) following the protocol of [23], with the mean values being calculated for each parameter.

2.3. Phylogenetic analysis

For the molecular analysis, myxospores were fixed in 80 % ethanol for the extraction of the DNA using the PureLink Genomic kit (Invitrogen, USA), following the protocol provided by the manufacturer. The amplification of the Small Subunit of the ribosomal DNA (SSU rDNA) by Polymerase Chain Reaction (PCR) using the standard primers 18E and 18R in the first round of amplification [24,25]. The second amplification uses the primers MC5 and MC3 [25,26].

The reaction protocol for the 18E/18R primers consisted of an initial extension at 95 °C for 5 min, followed by 35 cycles of 94 °C for 50 s, 52 °C for 50 s, and 68 °C for 1 min and 30 s, with a final extension at 68 °C for 10 min. The protocol for the second sequencing reaction, with the MC3/MC5 primers, consisted of an initial extension at 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, 56 °C for 30 s, and 72 °C for 1 min, with a final extension at 72 °C for 10 min. Following these procedures, 5 μL of the amplicons was electrophoresed in 1 % agarose gel with Tris-borate-EDTA (TBE) and viewed under blue light. The PCR products were purified and sequenced using the Big Dye Terminator v3.1 sequence cycling kit (Applied Biosystems, USA), following the manufacturer's instructions.

The resulting sequences were aligned in BioEdit [27], with ambiguous bases being resolved using the respective chromatograms. The SSU rDNA sequences of the myxozoans that are most closely related to the new taxon were identified based on the highest similarity scores recovered using the Basic Local Alignment Search Tool (BLAST). These sequences were used for the subsequent phylogenetic analyses. The best nucleotide substitution model indicated for the data set, indicated in the jModelTest software, version 0.1.1, was GTR + G [28,29]. Phylogenetic analyzes by Bayesian inference analysis were performed in the multiplatform software BEAST v.1.8.4 [30], using a relaxed, uncorrelated lognormal model [31] based on the birth-death speciation process [32], with a principal tree being derived from the unweighted pair group method with arithmetic mean (UPGMA). The Markov Chain Monte Carlo (MCMC) was run for 10,000,000 generations and sampled every 10,000 steps [33]. The software Tracer [34], TreeAnnotator v1.8.4 [35], and FigTree v.1.4.3 [36] were used to verify the convergence of analysis results and generate the maximum redibility of the clade tree, with 10 % burn-in.

The reliability of the phylogeny was verified by a likelihood mapping analysis, which was run in Tree-Puzzle 5.2, following the approach of [37]. The genetic distances were calculated in PAUP*, 4.0b1 [38] using the standard p parameter for the SSU rDNA gene.

2.4. Data analysis

A principal component analysis (PCA) was carried out on the variable's length and width of the myxospores (SL and SW), as well as length and width of the polar capsules (PL and PW). Furthermore, the Pearson correlation approach was used to assess the relationship between the variables, both of which were performed using the Past Statistics software [39].

3. Results

3.1. Morphological description and taxonomic summary

The analysis of the 33 host specimens revealed the presence of several disporic plasmodia irregular morphology, observed free and attached to the gallbladder of all the individuals (Fig. 1A), that is, a prevalence of 100 %, varying only in the intensity of infection. Free mature myxospores, with extruded polar tubule that presented morphological characteristics typical of the genus *Ellipsomyxa* (Fig. 1B).

Mature myxospores that were slightly elongated and ellipsoid, measuring 13.1 ± 1.0 (11.9–14.4) μm in length and 8.0 ± 0.8 (7.2–9.4) μm in width, with a slight valvular projection in the apical region and curved suture line. Slightly pyriform polar capsules of equal size, 4.9 ± 0.3 (4.4–5.4) μm in length and 3.2 ± 0.6 (2.6–3.9) μm in width, with subterminal openings, in opposite extremities of the myxospores, space between polar capsules 3.4 ± 0.5 (31–3.7) μm in apical view, with 6–7 polar tubule coils was arranged perpendicularly to the longitudinal axis of each polar capsule (Fig. 1C and D) (Table 1).

The histological analysis with the ZN staining revealed myxospores with highlighted polar capsules floating freely in the bile or adhering to the epithelium of the organ (Fig. 1E and F). No histopathological alterations, lesions, or inflammatory responses, in the epithelial layer were observed or anywhere in the tissue.

Genus: *Ellipsomyxa* Køie, 2003.

Species: *Ellipsomyxa matosi* n. sp. (Fig. 2).

Host species: *A. ucayalensis* Castelnau, 1855.

Infection site: gallbladder.

Type locality: Brazil, state of Pará, municipality of Belém, Jutuba Island (01°15′0" S, 48°30′0" W).

Type specimens: A glass slide with a histological section, stained with ZN, containing a syntype of the new myxozoan species was deposited in the Museum of Zoology of the National Institute of Amazonian Research (INPA) in Manaus, Amazonas, Brazil – Number: 000106.

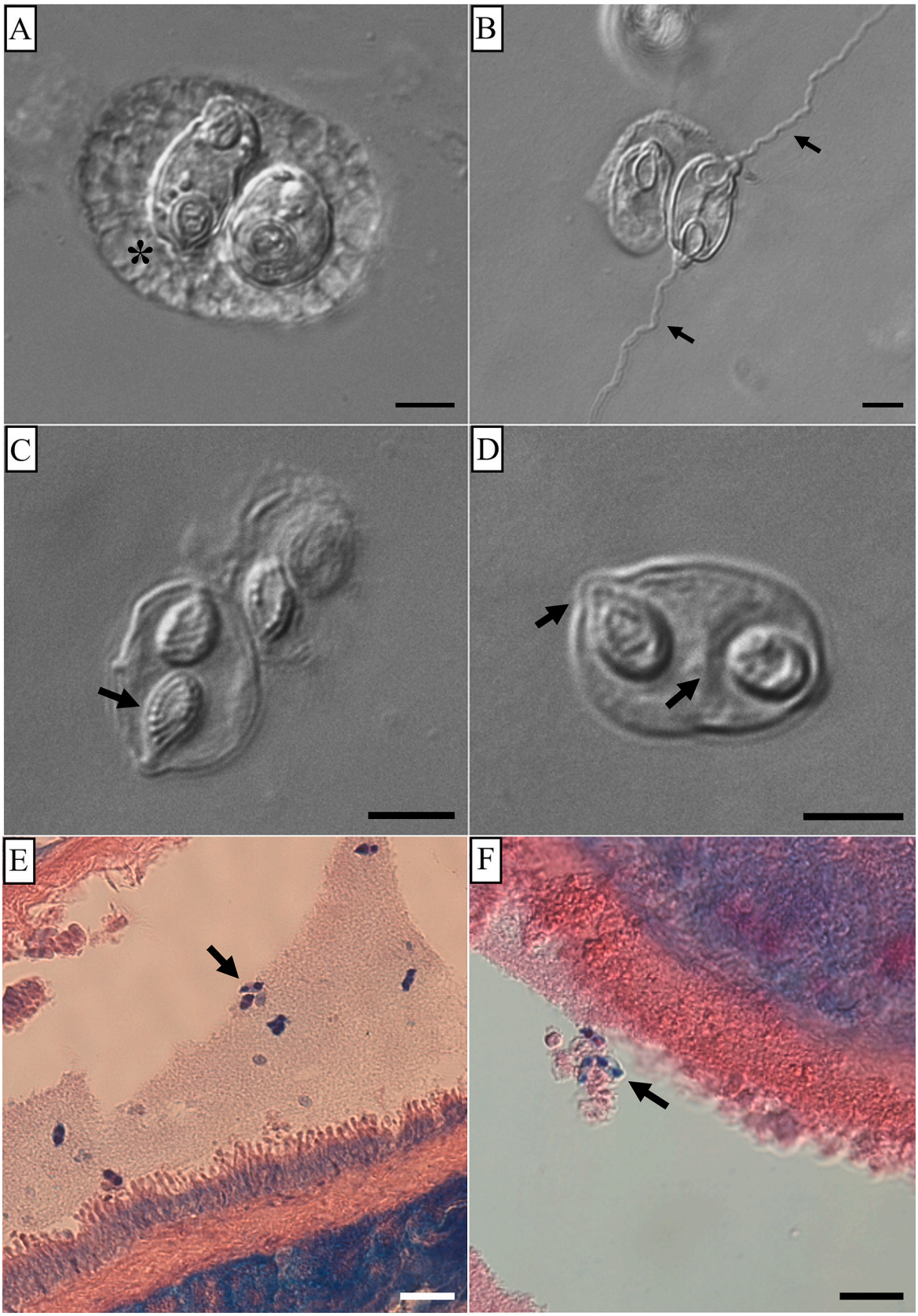

Fig. 1. Light photomicrographs (DIC) of *Ellipsomyxa matosi* n. sp. from the gall bladder of *A. ucayalensis*: (A) Plasmodium (*) containing two mature spores floating in the bile (Scale bar = 5 μm); (B) Spore undergoing the extrusion of the polar tubule (arrow) (Scale bar = 5 μm); (C) Spore showing the polar capsules in the opposite extremities, and the polar tubule, with 6–7 coils (arrow) (Scale bar = 5 μm); (D) Spore with valvular projection and curved suture line (arrow) (Scale bar = 5 μm). Histological section of the gall bladder of *A. ucayalensis*, prepared using the ZN staining technique (E) *Ellipsomyxa matosi* n. sp. spores floating in the bile (Scale bar = 20 μm); (F) Spores adhered to the wall of the gall bladder (Scale bar = 20 μm).

Table 1
Descriptive parameters of the spore and polar capsule (mean length and width, with standard deviation and amplitude) of *Ellipsomyxa matosi* n. sp. and comparisons with the same parameters recorded in other *Ellipsomyxa* species. N = number of coils of the polar tubule.

Species	Host	Spore shape	Spore (μm)		Spore (μm)		N	Country	References
			Long	Wide	Long	Wide			
Ellipsomyxa matosi n. sp.	*Ageneiosus ucayalensis*	ellipsoid	13.1 ± 1.0 (11.9–14.4)	8.0 ± 0.8 (7.2–9.4)	4.9 ± 0.3 (4.4–5.4)	3.2 ± 0.6 (26–3.9)	6–7	Brazil	Present study
Ellipsomyxa santarenensis	*Satanoperca jurupari*	ellipsoid	12.0 (10.7–13.7)	7.6 (5.6–8.2)	2.8 (2.0–3.6)	2.8 (2.1–3.7)	4–5	Brazil	[4]
Ellipsomyxa tucujuensis	*Satanoperca jurupari*	ellipsoid	10.11 ± 0.86	7.81 ± 1.14	3.1 ± 0.53	2.5 ± 0.32	5–6	Brazil	[17]
Ellipsomyxa paraensis	*Cichla monoculus*	ellipsoid	11.5 (10.5–12.4)	7.5 (6.6–8.6)	3.2 (2.1–3.9)	2.6 (2–3.3)	2–3	Brazil	[15]
Ellipsomyxa plagioscioni	*Plagioscion squamosissimus*	ovoid	11.1 (10.2–12.8)	6.6 (5.6–7.6)	3.8 (3.2–4.4)	2.8 (2.3–3.3)	5–6	Brazil	[15]
Ellipsomyxa arariensis	*Pigocentrus nattereri Pimelodus ornatus*	ellipsoid	12.6 (12.0–13.4)	7.3 (6.7–8.0)	3.5 (3.4–4.0)	2.6 (2.5–3.2)	5–6	Brazil	[18]
Ellipsomyxa amazonensis	*Brachyplatystoma rousseauxii*	ellipsoid	12.8 (12.3–13.6)	7.6 (6.7–8.7)	3.8 (3.8–4.0)	3.1 (2.5–3.4)	2–3	Brazil	[16]
Ellipsomyxa gobioides	*Gobioides broussonnetii*	ellipsoid	6.8 (6.5–7,0)	7.2 (6.9–7.5)	4.6 (4.3–4.8)	2.5 (2.1–2.7)	5–6	Brazil	[14]
Ellipsomyxa manilensis	*Arothron manilensis*	ovoid	11.8 ± 1.1 (10.2–13.3)	15.2 ± 1.1 (13.8–17.1)	5.6 ± 0.6 (4.6–6.6)	4.5 ± 0.3 (4.2–5.0)	3–4	Australia	[9]
Ellipsomyxa arothroni	*Arothron hispidus*	ovoid	11.7 ± 0.9 (9.9–13.6)	15.4 ± 1.3 (12.3–17.7)	6.6 ± 0.6 (5.4–7.9)	4.5 ± 0.4 (3.9–5.4)	4	Australia	[9]
Ellipsomyxa nigropunctatis	*Arothron nigropunctatus*	ovoid	9.9 ± 1.5 (8.0–12.9)	13.8 ± 1.1 (11.9–16.3)	4.7 ± 0.6 (3.5–5.7)	3.6 ± 0.5 (2.8–4.6)	5	Australia	[9]
Ellipsomyxa adlardi	*Gobiosoma bosc*	ellipsoid	12.4 (11.3–14.4)	7.7 (7.1–8.8)	4.3 (3.9–4.9)	3.6 (3.3–4.1)	5–6	USA	[10]
Ellipsomyxa syngnathi	*Syngnathus typhle*	ellipsoid	6.8 (6.3–7.2)	8.1 (7.2–8.6)	3.6 (3.2–4.1)	2.9 (2.7–3.2)	5–6	Denmark	[11]
Ellipsomyxa boleophthalmi	*Boleophthalmus dussumieri*	ellipsoid	9.8 ± 0.5 (9.0–10.7)	7.2 ± 0.6 (6.0–7.8)	2.8 ± 0.3 (2.6–2.8)	–	3–4	India	[12]
Ellipsomyxa gobii	*Pomatoschistus microps*	ellipsoid	7.0 (6.6–7.5)	8.7 (8.0–9.0)	3.1 (3.0–3.2)	–	6–7	Denmark	[8]
Ellipsomyxa mugili	*Liza saliens; Mugil cephalus; Liza ramada*	ovoid	11.5 (10–13.5)	6.8 (5.5–8.0)	2.9 (2.7–4.0)	–	5	Spain	[13]
Ellipsomyxa apogoni	*Apogon doederlein*	ellipsoid	10.2 (8.8–11.1)	6.9 (6.0–9.1)	3.7 (2.9–4.8)	2.7 (2.1–3.4)	2–3	Australia	[9]
Ellipsomyxa kalthoumi	*Liza saliens*	ellipsoid	17.2 (13–21)	13.2 (10–15)	5.5 (5.0–6.0)	–	9	Tunisia	[40]
Ellipsomyxa papantla	*Dormitator maculatus*	ovoid	12.9 ± 0.8 (11.6–15.0)	9.1 ± 0.5 (7.6–9.9)	3.8 ± 0.5 (2.6–4.6)	3.3 ± 0.5 (2.2–4.2)	3–4	México	[7]

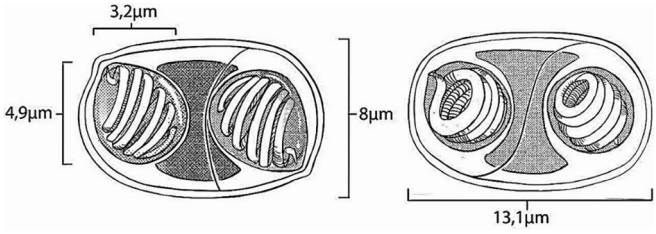

Fig. 2. Diagram of the spore of *Ellipsomyxa matosi* n. sp.

GenBank accession number: Partial sequence of 18S rDNA gene 1324 bp (PQ373927).

Etymology: The specific name is a homage to Dr. Edilson Matos, one of the pioneers in studying myxospores in the Brazilian Amazon Basin.

3.2. Morphometric analysis

In the PCA, component 1 accounted for 64.9 % of variance, whereas component 2 accounted for 34.4 %. *Ellipsomyxa matosi* n. sp. had a negative relationship with component 1 (Fig. 3), had been close to *E. amazonenis* and *E. papantia* due to its proximity to SL (Table 1). However, it can be shown that the main variable that influenced component 1 was SW, with the species *E. nigropuncatis*, *E. arothroni*, *E. manilensis*, and *E. kalthoumi* having the highest positive correlation, while PL and SL mainly influenced component 2, presenting respectively 32.2 % and 2.2 % of the variance. Overall, SW demonstrates a strong positive and significant relationship with both PW and PL, as has PL and PW (Fig. 4).

3.3. Phylogenetic analysis

The partial SSU rDNA sequence of *Ellipsomyxa matosi* n. sp. presented 1324 base pairs, differing from the available aligned sequences of other *Ellipsomyxa* species, available in GenBank. BLAST searches revealed that the greatest genetic identity with *E. paraensis* 92.12 % (MH364399), followed *by E. amazonensis* 92.04 % (MF193889).

Analysis of the genetic distances between *Ellipsomyxa* species, revealed smaller distance with *E.santarenensis* (OR142132) 5.82 %,and greater divergence with *E. tucujuensis* (MN999871) 13.48 %. (Table 2).

The phylogenetic analysis obtained high nodal support, grouping *E. matosi* n. sp. as an ancestor of the well-defined clade of *Ellipsomyxa* species described in the Amazon region, with hosts from freshwater. The molecular analysis presented here included 26 myxozoans and identified clades containing species of the genera Myxidum, *Tetracapsuloides, Buddenbrockia* and *Ellipsomyxa*. the outer group being formed by *Tetracapsuloides bryosalmonae* and *Buddenbrockia plumatellae* (Fig. 5).

4. Discussion

The general morphology of the myxospores of *Ellipsomyxa matosi* n. sp. is typical of that of the other species of the genus *Ellipsomyxa* described [8,9,10,11,12,13,36]. Mature Plasmodifusium disporic were also observed in *E. tucujuensis*, *E. arariensis*, *E. amazonensis*, *E. gobioides*, *E. kalthouni*, *E. gobii, E. syngnathi* [8,11,14,16,17,18,40]. All *Ellipsomyxa* species described from the Brazilian Amazon region have ellipsoid spores [4,14,15,16,17,18].

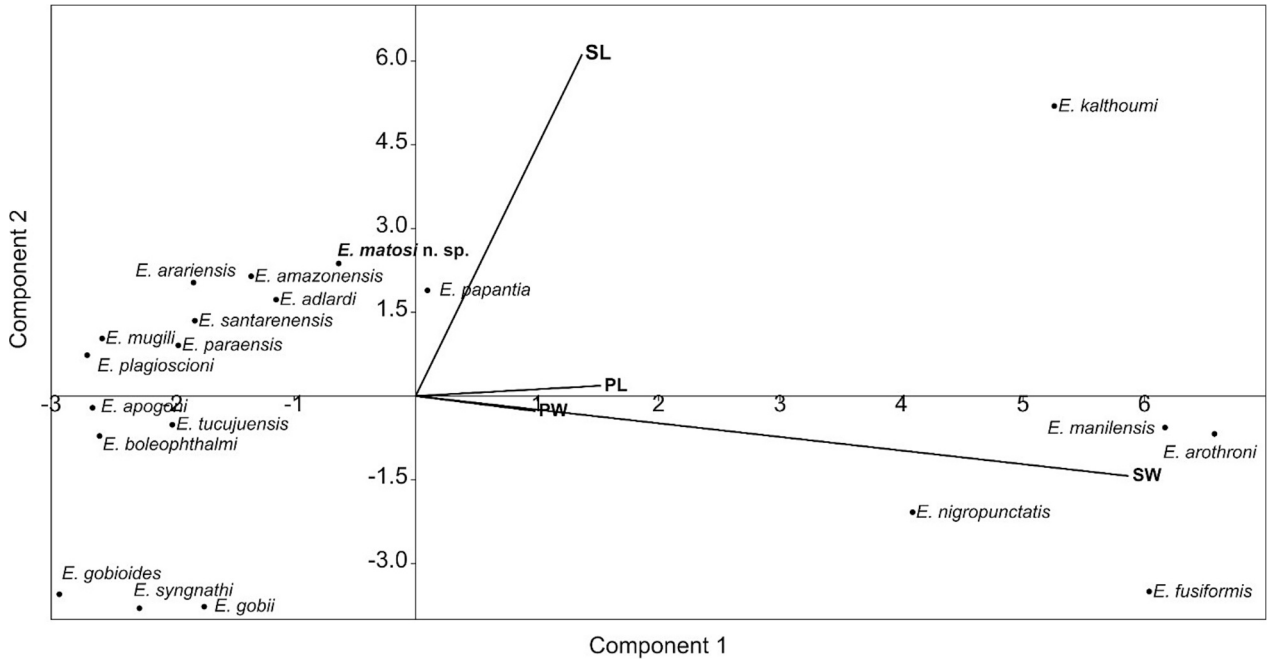

Fig. 3. PCA of *Ellipsomyxa* myxospores using the variables SL, SW, PL, and PW.

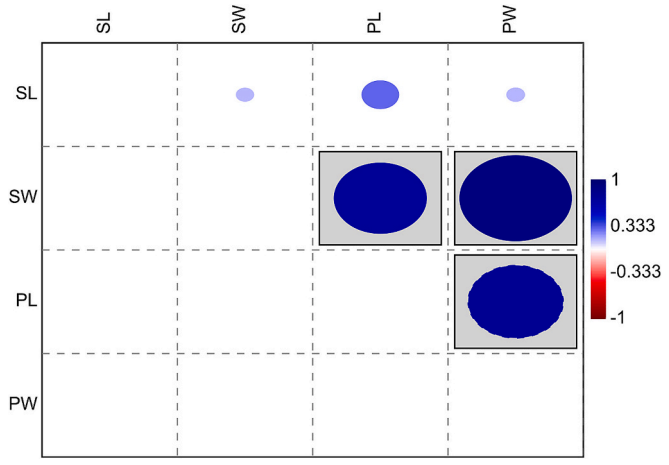

Fig. 4. Coefficient of relationship of the morphometric variables of myxospores, the boxes indicate positive correlations with significant value (p-value<0.05).

Table 2
Genetic distances (p distances) between pairs of *Ellipsomyxa* species from the Brazilian Amazon region.

Species	(1)	(2)	(3)	(4)	(5)	(6)	(7)
(1) *Ellipsomyxa matosi* n. sp.	–						
(2) *Ellipsomyxa santarenensis*	5.82 %	–					
(3) *Ellipsomyxa plagioscioni*	5.90 %	3.71 %	–				
(4) *Ellipsomyxa paraensis*	6.16 %	0.058 %	3.99 %	–			
(5) *Ellipsomyxa amazonensis*	6.16 %	0.070 %	3.87 %	0.11 %	–		
(6) *Ellipsomyxa arariensis*	6.84 %	2.11 %	5.37 %	2.01 %	2.13 %	–	
(7) *Ellipsomyxa tucujuensis*	13.48 %	8.50 %	11.27 %	7.90 %	8.02 %	10.17 %	–

The dimensions of the myxospores of *Ellipsomyxa matosi* n. sp. are similar to *E. amazonensis*, captured in the Tapajós rivers, municipality of Santarém, State of Pará, Brazil [16]. However, the polar capsule of the new species of this study is larger than that of the other *Ellipsomyxa* species described in the region, and its Polar tubule has a larger number of coils.

Most of the species described as *Ellipsomyxa* are parasites of marine fish, such as *E. gordey* (PP296411), *E. nigropunctatis* (KF179050) *E. arothroni* (KF179049) [9,41]. In the Amazon basin, only the species *E. paraensis* parasitizing *C. monoculus* [15], *E. tucujuensis* [17], and *E. santarinensis* [4] infecting the fish *S. jurupari* were considered species restricted to freshwater environments due to the distribution of their hosts. The new species was captured in a freshwater environment, but its host, *A. ucayalensis*, carries out migrations as observed in many other species of the Auchenipteridae family [20], therefore, we cannot state that *Ellipsomyxa matosi* n. sp. is an exclusive freshwater species.

Although the species *Ellipsomyxa matosi* n. sp. did not present pathological changes in its host, [42] observed changes in the epithelial layers of the gallbladder of the infected marine catfish, *Arius arius*, with swelling and vacuolization, in addition to changes in the color of the bile of infected individuals. Changes in bile color were also recorded in *E. gobioides* [14] and *E. kalthomi* [40], and were probably related to mucus reduction, due to the presence of parasites and necrotic cells. Modification of mucus production likely affects the activity of host digestive enzymes [42].

Ellipsomyxa species formed subclades, one composed species from freshwater hosts from the Amazon basin, only *E. plagioscioni* was not included in the clade of species from the Amazon, due to its host *P. squamosissimus*, grouping in a marine lineage [15], the present origin with migratory behavior, showing that freshwater species do not form a monophyletic group [4,10,12,15,17]. [43] demonstrated that the evolution of phylogenetic relationships between myxozoans identified in marine and freshwater environments is influenced by the characteristics of their definitive host, whether they are marine or freshwater species.

The morphological characteristics of the specimens and the molecular phylogeny confirmed the existence of a new species, *Ellipsomyxa matosi* n. sp. The discovery of this new species represents an important advance in the scientific understanding of the morphology, evolution, and distribution of microparasites in the Amazon region.

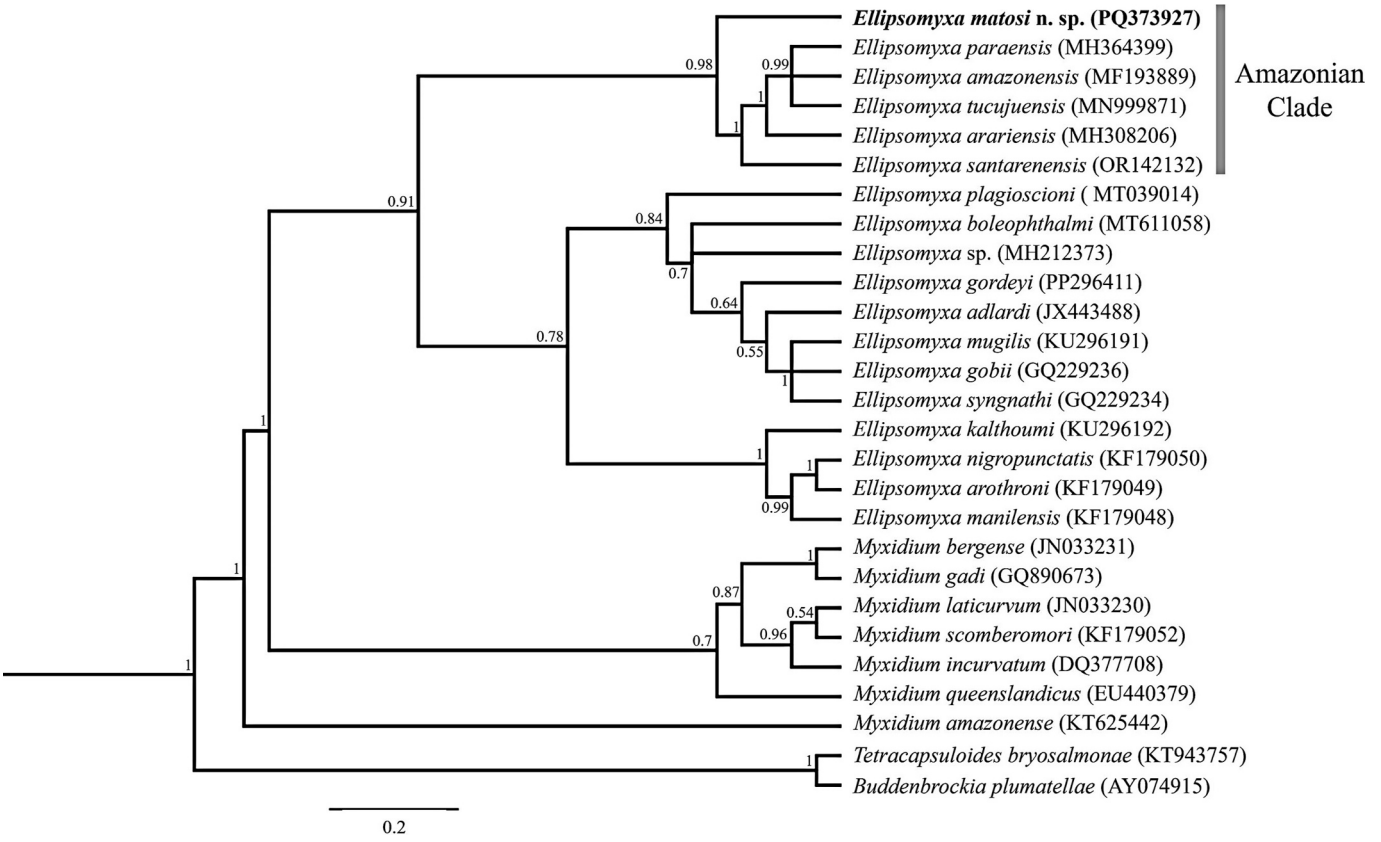

Fig. 5. Phylogenetic analysis of the partial sequence of *Ellipsomyxa matosi* n. sp. and other myxozoans. Numbers indicate Bayesian posterior probabilities. The new species is highlighted in bold and the clade of *Ellipsomyxa* species from the Brazilian Amazon region is highlighted.

CRediT authorship contribution statement

Camila Maria Barbosa Pereira: Writing – review & editing, Writing – original draft, Methodology, Investigation, Conceptualization. **Jhonata Eduard Farias de Oliveira:** Writing – review & editing, Methodology, Conceptualization. **Marcia de Nazaré Sacco dos Santos:** Methodology, Investigation. **Lana Priscila Barbosa Pereira:** Writing – review & editing, Investigation. **Igor Guerreiro Hamoy:** Methodology. **Marcelo Francisco da Silva:** Writing – review & editing, Writing – original draft, Methodology. **José Ledamir Sindeaux-Neto:** Writing – review & editing, Methodology, Conceptualization. **Michele Velasco Oliveira da Silva:** Writing – review & editing, Writing – original draft, Methodology, Investigation, Conceptualization.

Declaration of competing interest

The authors declare that there are no conflicts of interest.

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