Henneguya sacacaensis n. sp. (Myxozoa: Myxosporea) parasitizing gills of the acará bicudo Satanoperca jurupari (Osteichthyes: Cichlidae) in eastern Amazon

Henneguya sacacaensis no. sp (Myxozoa: Myxosporea) parasitando brânquias do acará bicudo Satanoperca jurupari (Osteichthyes: Cichlidae) na Amazônia oriental

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Abstract

This study describes Henneguya sacacaensis n. sp. in specimens of the Osteichthyes Satanoperca jurupari (Heckel, 1840), collected in the Rio Curiaú Environmental Protection Area in the city of Macapá, state of Amapá Brazil. Using optical microscopy and molecular analysis, these cyst-shaped parasites were analyzed. The gills of 57.14% of the analyzed S. jurupari contained hundreds of spores. The cysts found on the gill lamellae were oval-shaped and whitish. The Henneguya spores had an average length of 46.5 (41.3-56.92) µm. The fusiform body of the Henneguya measured 16.5 (13.16-20.01) µm long and 5.1 (3.91-6.12) µm in width, the two polar capsules had a taper of 3.83 (3.4-4.32) µm and a width of 1.68 (1.4-1.99) µm, and the tail measured 30 (22.47-41.67) µm in length, containing a polar filament coiled seven to nine times. Morphological and phylogenetic analysis allowed the preposition of a new species, Henneguya sacacaensis n. sp, that belongs to the family Myxobolidae and the genus Henneguya.

Keywords: Freshwater, Myxobolidae, fish, parasite, Amazon, gill.

Resumo

Henneguya sacacaensis n. sp. é descrito em espécimes do Osteichthyes Satanoperca jurupari (Heckel, 1840), coletados na área de Proteção Ambiental do rio Curiaú na cidade de Macapá no estado do Amapá, Brasil. Com auxílio de microscopia óptica e análises moleculares, esses parasitos foram analisados e observados nas brânquias em forma de cistos, contendo centenas de esporos e apresentaram a prevalência de 57,14%. Os cistos encontrados nas lamelas branquiais tinham formatos ovais e esbranquiçados. Seus esporos apresentaram um comprimento médio de 46,5 (41.3-56,92) µm, corpo fusiforme medindo 16,5 (13.16-20,01) µm de comprimento e 5,1 (3.91-6,12) µm de largura, suas duas cápsulas polares apresentam uma conicidade de 3,83 (3,4-4,32) µm e sua largura 1,68 µm (1,4-1,99), a cauda 30 (22,47-41,67) µm de comprimento, contento um filamento polar de 7 a 9 voltas. Análises morfológicas e filogenéticas permitiram a preposição de uma nova espécie, Henneguya sacacaensis n. sp, que pertence à família Myxobolidae e ao gênero Henneguya.

Palavras-chave: Água doce, Myxobolidae, peixe, parasita, Amazônia, brânquia.
Introduction

Myxozoa are endoparasites that can infect various organs and present high specificity (László et al., 2002). The genus *Henneguya* Thélohan, 1892 (Cnidaria: Myxobolidae) is one of the most diverse for the described species (Lom & Dyková, 1992) within the Myxosporea class and is the second largest genus, with about 190 described species worldwide (Eiras & Adriano, 2012).

Knowledge of parasitic biodiversity in South America is limited, especially in the Amazon region, due to the high ichthyofauna diversity and remoteness (Reis et al., 2016; Zatti et al., 2018). Recently Zatti et al. (2018) claim that 55 species of *Henneguya* spp. infect fish in Brazil. Of these, about 20 were found infecting fish species in the Amazon region (Velasco et al., 2016; Naldoni et al., 2018; Abrunhosa et al., 2018; Zatti et al., 2018).

The species of the genus *Henneguya* are predominantly histozoic, can infect various organs, and can cause considerable pathological changes (Dyková & Lom, 1978; Molnár, 1998; Pote et al., 2000; Adriano et al., 2005; Naldoni et al., 2009; Barassa et al., 2012; Morsy et al., 2012; Mathews et al., 2016). When they infect the gills, they can cause filament destruction and respiratory failure (Lom & Dyková, 1992).

Matos et al. (2004) describe that these are parasites of very different morphology and structure, found mainly in fish. The parasites are characterized by a complex life cycle, alternating between hosts, fish and invertebrates (Holzer et al., 2018).

The morphology of this genus is characterized by the number and shape of the spore valves, the position, number, and shape of the polar capsules (round, piriform, or ellipsoid), the relative position of the suture line, the presence of grooves and superficial appendages, and the number of coiled polar filaments (Feist & Longshaw, 2006; Lom & Dyková, 2006; Kaur & Attri, 2015).

This study describes the morphological characteristics and molecular aspects of a new species of Myxozoa, *Henneguya sacacaensis* n. sp., found in the gills of *S. jurupari*. To date, no Myxobolidae has been recorded to infect this host.

Material and Methods

The 63 specimens used for this study were collected from the Curiaú River, Macapá, Amapá, Brazil (0°8’43.6”N, 51°2’30.3”W) (Figure 1). They were captured between September 2018 and September 2019 by the team at the Laboratory of Morphophysiology and Animal Health (LABMORSA) of the State University of Amapá (UEAP), with the help of local fishermen using a 30 mm cast net. The experiment was approved by the Animal Use Committee of the Brazilian Agricultural Research Company - Amapá (012-2018) and registered in the Biodiversity Authorization and Information System, IBAMA (SISBIO/ICMBIO License number 50376-1).

![Map of the collection site in Macapá, Amapá: Rio Curiaú Environmental Protection Area, Eastern Amazon region.](image-url)


The captured animals were conditioned and transported alive to LABMORSA/UEAP in refrigerated boxes with portable pumps. They were acclimatized and stored in glass aquariums with electric pumps for aeration. Subsequently, parasitological analyses were performed.

In the aquariums, the animals were anesthetized with tricaine methanesulfonate (MS222 SIGMA) at a concentration of 50 mg L\(^{-1}\). Their body surface was examined with binocular stereoscopic microscopy to detect lesions (cysts) or loss of coating (scales and epidermis). Infectious foci of parasites in their developing and spore phases were found in the gall bladder. Small fragments were removed and observed with light microscopy (LM) to confirm parasitosis. Gall bladder fragments were fixed in Davidson's solution (70% alcohol, formaldehyde, acetic acid, and distilled water) for 24 hours before paraffin embedding for histopathology. They were then stained with hematoxylin and eosin (H&E) and Ziehl-Neelsen (ZN) and photographed at Carlos Azevedo Research Laboratory at the Federal Rural University of the Amazon (LPCA/UFRA). The methodology proposed by Bush et al. (1997) was used to calculate prevalence.

Cysts of eukaryotic microparasites were collected and stored in 80% ethyl alcohol at 4 °C. The total DNA of each sample was extracted using the Wizard\textsuperscript{®} Genomic DNA. DNA samples were quantified by spectrophotometry (Biodrop DUO).

All molecular analyses were based on the 18S rDNA sequences, which were amplified using MC5/MC3 primers (Molnár, 2002). The final volume of the polymerase chain reaction (PCR) was of 25 μL using taq DNA polymerase Master Mix (PROMEGA, Madison, USA), with 0.5 μM of each primer and 2 μL of the DNA sample. With the initial amplification being initiated by denaturation of 10 s at 95 °C, followed by 40 cycles of denaturation at 95 °C for 1 min, hybridisation at 48 °C for 2 min, and polymerisation for 4 min 30 s at 72 °C, with final polymerisation of 10 min at 92 °C.

The amplicons were subjected to electrophoretic analyses through 1.5% agarose gel purified using GFX™ PCR DNA and Gel Band Purification Kit reagents were used to purify the material after PCR, as described by the manufacturer. These steps were performed at the Laboratory of Applied Genetics at the Federal Rural University of the Amazon (LGA/UFRA).

The amplification product was sequenced on an ABI 3730 automatic DNA analyzer using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). To confirm the observed mutations, the sample was sequenced with both forward and reverse primers. The nucleotide sequences obtained were edited and aligned using the BioEdit program (Hall, 1999). The phylogenetic relationship was obtained through maximum parsimony and Bayesian analyses, using the PAUP 4.0 b10 program (Swofford, 2003) for the former and the MrBayes 3.1.2 program (Ronquist & Huelsenbeck, 2003) for the latter. Maximum parsimony analysis was performed with a heuristic search algorithm, in which equal weight was given for transitions and transversions, while insertions and deletions (indels) were treated as lost data. The confidence level of the most parsimonious tree nodes was evaluated by 1,000 bootstrap replicates (Felsenstein, 2004).

In the Bayesian analysis (BI), two parallel runs of four simultaneous searches were performed using the Markov chain Monte Carlo method (MCMC) for 5,000,000 generations each, sampling one tree every 1,000 generations and discarding the results of the first 1,250 trees (25% of the sample). The remaining 3,750 trees were used to estimate the confidence level (subsequent probability) of each node in the phylogenetic reconstruction. In the cladogram analysis, the DNA sequences of the organisms used were obtained directly from GenBank.

As indicated by JMODELTEST 2.0.2 (Darriba et al., 2012), BI analysis assumed a GTR + G model of nucleotide substitution with estimated nucleotide frequencies (A = 0.2520, C = 0.1844, G = 0.2831, T = 0.2805), substitutions (A-C = 1.3916, A-G = 1.0936, A-T = 1.3916, C-G = 1, C-T = 4.3568, G-T = 1), and rates for variable sites following a gamma distribution (G = 0.4200) and p-inv 0.1990.

Results

Vegetative phase

*Henneguya* parasites can form cysts at various sites in the gill filaments, and infection can be characterized as lamellar (Molnár, 2002). Stereomicroscope analysis under incident light showed whitish cysts and ellipsoids in a thin layer of connective tissue (Figure 2A).
Henneguya sacacaensis n. sp. parasitizing Satanoperca jurupari in eastern Amazonia

Spores

Fresh spores were measured (n=31) (Figure 2B, C, D). Average total lengths were 46.5±5.47 µm; spores bodies averaged 16.5±2.64 µm in length and 5.1±0.94 µm in width. The two polar capsules have a taper 3.83±0.31 µm in length and 1.68±0.20 µm in width, with the tail measuring 30±6.87 µm long. Each capsule contained a polar filament coiled seven to nine times (Table 1).

Taxonomy

KINGDOM Metazoa Linnaeus, 1758
PHYLUM Cnidaria Hatscheck, 1888
SUBPHYLUM Myxozoa Grassé, 1970
CLASS Myxosporea Bütschli, 1881
ORDER Bivalvulida Shulman, 1959
FAMILY Myxobolidae Thélohan, 1892
GENUS Henneguya Thélohan, 1892
SPECIES Henneguya sacacaensis n. sp. (Figure 3)
HOST: Satanoperca jurupari Heckel, 1840
Site of infection: Henneguya cysts in the gill filaments.
Collection site: Rio Curiaú Environmental Protection Area, Macapá, Amapá (0°8’43.6” N, 51°2’30.3” W).
Prevalence: Forty-three of 63 specimens analyzed (68.25%)
Species deposit: Glass slide with H&E-stained spores was deposited in the collection of the Amazon Research Institute (INPA), Manaus, in the state of Amazonas, Brazil (accession number INPA 60).
Etymology: The epithet of this genus is in honor of Raimundo dos Santos Souza, popularly known as “Sacaca”, due to his contribution to Amapá popular culture.

The partial sequence of the SSU rDNA obtained from the species under study contains 1335 bp (GenBank accession number MT137652). For phylogenetic analysis, were used 38 South American sequences of Myxobolus spp. and Henneguya spp. available on Genbank. In the Bayesian inference analysis, Henneguya spp. formed a monophyletic group distributed in two clades, clade A, which includes Henneguya species that parasitize several fish species, mainly from the families Cichlidae and Pimelodidae, and clade B, which includes Myxobolus spp. parasites that infect organisms from the Amazon region (Figure 4). In comparisons between Henneguya spp. species that parasitize cichlids in the Amazon, there was a genetic p-distance ranging from 2.911 to 8.597% (Table 2).
Table 1. Comparative descriptive measures (means (μm) with ranges and standard deviation (SD) in parentheses) of *Henneguya sacacaensis* n. sp. and all *Henneguya* spp. registered in the Amazon region.

| Species              | Host                   | Locality | IS         | SPORE (μm) | POLAR CAPSULE (μm) | PF | References                  |
|----------------------|------------------------|----------|------------|------------|--------------------|----|-----------------------------|
| *H. sacacaensis* n. sp. | Satanoperca jurupari   | Amapá    | gills      | 46.5 (±5.47) | 30 (±6.87)          | 16.5 (±2.64) | 5.1 (±0.94) | 3.83 (±0.31) | 1.6 (±0.20) | 7-9 | Present study               |
| *H. santarenensis*    | Phractocephalus hemioliopterus | Pará     | gills      | 31.9 (±3)   | 21 (±3.1)          | 10.8 (±0.5) | 4.3 (±0.3) | 4.6 (±0.4) | 1.4 (±0.20) | 15 | Naldoni et al. (2018)       |
| *H. quelen*           | Rhamdia quelen         | Pará     | kidney     | 40.0 (±2.8) | 24.3 (±2.2)       | 15.5 (±0.8) | 4.1 (±0.3) | 5.5 (±0.5) | 1.68 (±0.20) | -  | Abrunhosa et al. (2018)     |
| *H. tucunarei*        | Cichla monoculus       | Pará     | gills      | 42.8 (±4.1) | 28.1 (±4.3)       | 14 (±0.8)    | 6.1 (±0.7) | 3.4 (±0.5) | 1.98 (±0.3) | 3-4 | Zatti et al. (2018)         |
| *H. tapajoensis*      | Cichla pinima          | Pará     | gills      | 54.6 (±3.9) | 39 (±3.9)         | 16.4 (±1.2) | 7 (±0.4)   | 4.2 (±0.5) | 2.1 (±0.4) | 4-5 | Zatti et al. (2018)         |
| *H. jariensis*        | Cichla monoculus       | Amapá    | gills      | 46.7 (±1.5) | 33.16 (±1.7)      | 13.4 (±0.7) | 6.5 (±0.5) | 4 (±0.5)   | 2 (±0.1)   | 4   | Zatti et al. (2018)         |
| *H. paraensis*        | Cichla temensis        | Pará     | gills      | 42.3 (±0.35) | 29.5 (±0.73)      | 12.8 (±0.42) | 8.6 (±0.32) | 7.4 (±0.16) | 2.6 (±0.08) | 5-7 | Velasco et al. (2016)       |
| *H. melini*           | Corydoras melini       | Pará     | gills      | 40.8 (±0.3) | 25.30 (±0.10)     | 15.5 (±0.2) | 4.7 (±0.1) | 4.8 (±0.5) | 1.7 (±0.3) | 5-6 | Mathews et al. (2016)       |
| *H. aequidens*        | Aequidens plagiozonatus | Pará     | gills      | 41 (±1.5)   | 27 (±0.6)        | 15 (±0.9)   | 6 (±0.8)   | 3 (±0.3)   | 3 (±0.3)   | 4-6 | Videira et al. (2015)       |
| *H. torpedo*          | Brachyhypomus pinnicauatus | Pará   | Brain and spinal cord | 48.62 (±0.51) | 19.64 (±0.44) | 28.53 (±0.36) | 7.25 (±0.31) | 6.41 (±0.26) | 1.84 (±0.19) | 5-6 | Azevedo et al. (2011)       |
| *H. rondoni*          | Gymnorhamphichthys rondoni | Pará   | Lateral nerve | 17.7 (16.9-18.1) | 10.7 (10.3-11) | 7 (6.8-7.3) | 3.6 (3.3-9) | 2.5 (2.2-2.8) | 0.85 (0.79-0.88) | 6-7 | Azevedo et al. (2008)       |
| *H. rhâdia*           | Rhamdia quelen         | Pará     | gills      | 50 (±1.81)  | 36.9 (±1.6)       | 13.1 (±1.1) | 5.2 (±0.5) | 4.7 (±0.4) | 1.1 (±0.2) | 10-11 | Matos et al. (2005)         |
| *H. schizodon*        | Schizodon fasciatum    | Amazonas | kidney     | 28.9 (27-30) | 16.3 (15-17)      | 13.1 (12-14) | 3.3 (3-4) | 5.4 (5-6) | 1.3 (1-1.5) | 8-10 | Eiras et al. (2004)         |
| *H. friderici*        | Leporinus friderici    | Pará     | gills, intestine and liver | 33.8 (28.7-39.3) | 23.3 (19.1-28.7) | 10.4 (9.6-11.8) | 5.7 (4.8-6.6) | 4.9 (4.25-5.9) | 2.1 (1.59-2.62) | 7-8 | Casal et al. (2003)         |

TL: total length; BL: body length; BW: body width; TA: tail length; PL: polar capsule length; PW: polar capsule width; PF: number of coils in the polar filament; IS: infection site.
Henneguya sacacaensis n. sp. parasitizing Satanoperca jurupari in eastern Amazonia

Table 1. Continued...

| Species          | Host                        | Locality | IS     | SPORE (μm) | POLAR CAPSULE (μm) | PF | References         |
|------------------|-----------------------------|----------|--------|------------|-------------------|----|-------------------|
|                  |                             |          |        | TL         | TA | BL | BW | PL | PW |                |
| H. astyanax      | Astyanax keith             | Pará     | gills  | 47.8 (±0.71) | 32.6 (±1.11) | 15.2 (±0.77) | 5.7 (±0.71) | 5 (±0.13) | 1.5 (±0.07) | 8-9 | Vita et al. (2003) |
| H. curimata      | Curimata inormata          | Pará     | Kidney | 35.4 (34.2-36.1) | 19.1 (18.3-19.9) | 16.6 (16-17.4) | 6.2 (5.8-6.6) | 3.33 (±0.02) | 1.5 (±0.04) | 10-11 | Azevedo & Matos (2002) |
| H. testicularis  | Moenkhausia oligolepis     | Pará     | testicules | 27.5 (27-28.5) | 13.5 (13-14.5) | 14 (14-14.5) | 6.5 (6-6.5) | 9 (8.5-9.5) | 2 (2-2.5) | 12-13 | Azevedo et al. (1997) |
| H. malabarica    | Hoplias malabaricus        | Pará     | gills  | 28.3 (26.6-29.8) | 17.1 (16.2-18.9) | 12.6 (11.8-13.1) | 4.8 x 3.6 | 3.7 (3-4.3) | 1.8 (1-1.6) | 6-7  | Azevedo & Matos (1996) |
| H. adherens      | Acestrorhynchus falcatus   | Amazonas | gills  | 32.3 (30.7-35.1) | 20.5 (18-21.7) | 12.4 (10.5-13.8) | 5.8 (5.1-6.5) | 3.1 (2.8-3.5) | 1.2 (1-1.6) | 3-4  | Azevedo & Matos (1995) |
| H. amazonica     | Crenicichla lepidota       | Amazonas | gills  | 59.3 (±0.56) | 45.4 (±0.01) | 13.9 (±0.16) | 5.7 (±0.06) | 3.3 (±0.02) | 1.5 (±0.04) | 6    | Rocha et al. (1992) |

TL: total length; BL: body length; BW: body width; TA: tail length; PL: polar capsule length; PW: polar capsule width; PF: number of coils in the polar filament; IS: infection site.
**Henneguya sacacaensis** n. sp. parasitizing *Satanoperca jurupari* in eastern Amazonia

**Discussion**

The characteristics of this myxosporian are typical of the myxospore morphology of histozoic infection and development of cysts in host gills described by Lom & Dyková (2006). The morphology of *Henneguya sacacaensis* n. sp. in this study was compared with other species of *Henneguya* described in the Amazon region.

In South America, about 100 species of the myxosporidian have been recorded in freshwater, being most of these species belonging to the Myxobolidae family, and the genera *Myxobolus* and *Henneguya* the most well-studied (Adriano & Oliveira, 2018; Naldoni et al., 2018). In the Amazon region, the most species for this genus have been recorded in the state of Pará with 75%, followed by Amazonas with 15%, and Amapá with 10%.

In the state of Amapá, only one species of myxosporidian has been described, *Henneguya jariensis* parasitizing the fin of *Cichla monoculus* (Agassiz, 1831) (Zatti et al., 2018). Therefore, *Henneguya sacacaensis* n. sp. is the second myxosporidian species described in Amapá.

**Figure 3.** Drawing of *Henneguya sacacaensis* n. sp. Apical view of spore and polar capsules. Scale bar, 10 µm.

**Figure 4.** Phylogenetic tree generated by Bayesian inference (IB) through partial alignment of *Henneguya sacacaensis* n. sp. with SSU rDNA gene sequences of selected *Henneguya* and *Myxobolus* species. GenBank accession numbers are shown next to species names. Node numbers are indicated for posterior probability values calculated by IB. The new species is highlighted in bold and within the clade of *Henneguya* spp. in Cichlidae.

**Table 2.** The uncorrected *p*-distances recorded between pairs of *Henneguya* spp. that comprise the clade of registered cichlids in the Amazon.

|   | 1   | 2   | 3   | 4   |
|---|-----|-----|-----|-----|
| (1) *Henneguya sacacaensis* n. sp. | 0.08597 |     |     |     |
| (2) *Henneguya jariensis*       | 0.08525 | 0.04455 |     |     |
| (3) *Henneguya tapajoensis*     | 0.06861 | 0.02911 | 0.03950 |     |
| (4) *Henneguya tucunarei*       | 0.08009 | 0.05006 | 0.07341 | 0.04783 |

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The *Henneguya* spp. have been described to infect various sites in Amazonian fish including gills, kidneys, gallbladder, medulla, testicles, and brain. Velasco et al. (2016) described that the genus *Henneguya* has a strong tendency to form clades, taking into consideration aspects such as environment, order, and family of host fish. Other researchers describe this trend in their studies as well (Fiala, 2006; Ferguson et al., 2008; Adriano et al., 2012; Carriero et al., 2013; Moreira et al., 2014; Abrunhosa et al., 2018). The *Henneguya sacacaensis* n. sp. behaves similarly and group together with others that parasitize the Cichlidae family.

Among the *Henneguya* spp. that infect fish from the Amazon, the *Henneguya amazonica* stands out (Rocha et al., 1992), with the longest total length (59.3 µm) and tail length (45.4 µm). Being that *Henneguya sacacaensis* n. sp. has a total length of 46.5 µm and tail length of 30 µm, only *Henneguya astyanax* (Vita et al., 2003) approaches it in relation to the total length (47.8 µm) and *Henneguya paraensis* (Velasco et al., 2016) is similar in tail length (29.5 µm).

Regarding spores, the total length of *Henneguya sacacaensis* n. sp. (16.5 µm) closely resembles *Henneguya curimata* (16.6 µm) (Azevedo & Matos, 2002), *Henneguya tapajoensis* (16.4 µm) (Zatti et al., 2018), *Henneguya quelen* (15.5 µm) (Abrunhosa et al., 2018), *Henneguya melini* (15.5 µm) (Mathews et al., 2016), and *Henneguya aequidens* (15.5 µm) (Videira et al., 2015). *Henneguya sacacaensis* n. sp. spore width (5.1 µm) was similar to *Henneguya rhamdia* (5.2 µm) (Matos et al., 2005).

Regarding polar capsule length, it is clear that *Henneguya malabarica* (Azevedo & Matos, 1996) is similar to *Henneguya sacacaensis* n. sp., with lengths of 3.7 µm and 3.8 µm, respectively, but the capsule width most closely resembled other species of the genus *Henneguya*. *Henneguya sacacaensis* n. sp. capsule width measure about 1.6 µm, which is more closely related to that of *H. melini* (1.70 µm) and *H. quelen* (1.68 µm).

Regarding the number of coils in the polar filament, *Henneguya sacacaensis* n. sp. has seven to nine coils. The number of coils in the polar filament varies from species to species: *H. paraensis* (5-7 coils), *H. rhamdia* (6-7 coils), *Henneguya schtzodon* (8-10 coils) (Eiras et al., 2004), *Henneguya friderici* (7-8 coils) (Casal et al., 2003), *H. astyanax* (8-9 coils), and *H. malabarica* (6-7 coils). *Henneguya santarenensis* (Naldoni et al., 2018) is recorded to have the highest known number of coils (15 coils).

Although the morphometric aspects are very similar to *H. astyanax*, the morphology of *Henneguya sacacaensis* n. sp. differs in the position of the binucleated cell. The binucleated cell of *H. astyanax* is just below the polar capsules, while in *Henneguya sacacaensis* n. sp., it is located at opposite ends in the sporoplasm. The sporoplasm also differs in its shape. Furthermore, the tail reinforces the difference in its arrangement, although there are no *H. astyanax* SSU rDNA data.

The gills of parasitized fish showed slight gill hyperplasia without lamellar fusion (Figure 2A and 5A); according to the classification by Molnár (2002), large cysts deform and press secondary lamellae laterally on both sides (Figure 5B).

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**Figure 5.** Gill tissue section of *Satanoperca jurupari* parasitized by *Henneguya sacacaensis* n. sp. (A) Cyst (*) between secondary lamellae with slight filamentous (intralamellar) hyperplasia. Insert: Cyst between secondary lamellae (arrows). Section stained with H&E. Scale bar, 10 µm; (B) Drawing of the *Henneguya* cyst (CY) between the secondary lamellae (arrows).
Henneguya sacacaensis n. sp. parasitizing Satanoperca jurupari in eastern Amazonia

Similar changes have been described previously in other Amazon hosts such as Astyanax keithi (Vita et al., 2003), Cichla temensis (Velasco et al., 2016), Phractocephalus hemioliopterus (Naldoni et al., 2018), and Metynnis hypsauchen (Figueredo et al., 2020).

Conclusion

Thorough analysis of the morphological, morphometric, and molecular aspects allow us to describe a new species, Henneguya sacacaensis n. sp., with characteristics that differ from all other species previously described.

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