Morphological and molecular characterization of *Henneguya* sp. infecting *Piaractus brachypomus* from the Amazon basin

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Mixosporids, belonging to the Cnidaria phylum, are obligate endoparasites, which mainly infect fish and which comprise more than 2,180 described species. They have a complex life cycle, involving an invertebrate and vertebrate host. Among the species of fish that harbor these parasites, the species *Piaractus brachypomus*, popularly known as pirapitinga, has great economic importance, especially in the region of the Amazon basin, where it is widely found. The objective of this study was to characterize, through morphological and molecular analyzes, the species of myxosporids found infecting *P. brachypomus*. In this study, 25 specimens of *P. brachypomus* were collected, of which 16 (64%) were infected in the gill filament with a *Henneguya* species no described. The morphological and morphometric analysis, performed by light microscopy, showed mature myxospores ellipsoid shaped, measuring 13.5 ± 0.4 μm length, 3.6 ± 0.2 μm width and 2.5 ± 0.4 μm thickness. Prolongation of the valves were lager than the length of the body, measuring 40.3 ± 2.7 μm, with a total spore length of 53.4 ± 2.8 μm. The polar capsules were elongated and occupied less than half of the body, measuring 5.0 ± 0.4 μm in length and 1.3 ± 0.2 μm in width. Among the species of myxosporids that infect fish of the Serrasalmidae family, the species *Henneguya piaractus* (Muller et al., 2013), observed in specimens of *Piaractus mesopotamicus* from fish farms in the state of São Paulo, presented the measures closest to *Henneguya* sp. 1 as: 14.2 ± 1.0 μm body length and 4.1 ± 0.3 μm body width. The capsules measured 6.8 ± 0.75 μm in length and 1.6 ± 0.2 in width. For the molecular analysis, parasite DNA was extracted using comercial kit. The 18S gene was amplified by Polymerase Chain Reaction (PCR), using specific primers, and sequenced, generated a partial sequence of 1946 bp, demonstrating a difference of 16.9% with the species *Henneguya piaractus*. Phylogenetic analysis was based in others South American myxosporids sequences deposited in the GenBank database, that revealed a cluster according to host order/family. *Henneguya* sp. 1 grouped as a sister species of *Henneguya leporinicola*, described infecting the gill filament of *Leporinus macrocephalus* (Characiformes: Anostomidae) from fish farms in the state of São Paulo, Brazil.

Keywords: myxosporids; *Henneguya*; Pirapitinga; 18S rDNA; Amazon river

* Scientific Initiation FAPESP (Proc. N ° 2016 / 19149-2 C. M. Meira)