

**Molecular characterization of *Platynosomum illiciens* (= *P. fastosum*) (Trematoda: Dicrocoeliidae) confirms the host non-specificity and wide distribution of the species**

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Although studies on a feline platynosomosis have become more common in recent years, the taxonomy and epidemiology of the fluke involved in this biliary disease in cats remains controversial. In this sense, the use of molecular tools is an approach that may be useful to accomplish this task. In this study, *Platynosomum illiciens* (adult and metacercariae) obtained from naturally infected marmosets (*Callithrix penicilata*), cats (*Felis catus*), and lizard (*Hemidactylus mabouia*) from Brazil were used for molecular analyses by PCR and sequencing of partial region of the nuclear gene 28S ( $\approx$  1200bp) and complete region of the gene ITS rDNA ( $\approx$  1000bp). The data obtained reveals no molecular differences between these different developmental stages or specimens from different vertebrate hosts found in Brazil. Moreover, ITS sequences obtained from Brazilian hosts were compared with ITS-1-5.8S sequences (990bp) from adult parasites recovered from cats from Vietnam recently available in GenBank, revealing that these isolates are also conspecifics despite great geographic distance (molecular divergence of 0.0-0.3%). The molecular data obtained, besides supporting the previous morphology-based synonymies between *P. illiciens* and *P. fastosum*, confirm the wide distribution and host non-specificity of this biliary trematode to its definitive hosts.

Key-words: *Platynosomum*, sequences, distribution, trematodes, cats.