

THE NON-NATIVE MONOGENEA *THAPAROCLEIDUS CAECUS* (MONOGENEA: DACTYLOGYRIDAE) IN INDIA ON ITS INTRODUCED HOST, *PANGASIANODON HYPOPHTHALMUS* (SAUVAGE, 1878): ABOUT TWO DECADES OF UNNOTICED PRESENCE

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Abstract

In the context of biological invasion, scientists increasingly aware the impact of invasive species on native communities. The introduced species can act as vector of non-native parasites with devastating effects. Exotic species tremendously cause economic loss, modify ecosystem functions and can threaten the native ones. During a survey of non-native monogenean parasites in Meerut region, India, the freshwater iridescent shark of family Pangasiidae, *Pangasianodon hypophthalmus* (Previously *Pangasius sutchi*) was found infected with monogenean parasites. *Pangasianodon hypophthalmus*, a freshwater fish popular for used as food in India which is also abundantly available in Vietnam, Bangladesh, Indonesia and Thailand. It is a native of Mekong River in Vietnam has been introduced in several ecosystems worldwide, reproduced at a high rate, resulting in dense population of small specimens. *P. hypophthalmus* has been proven adaptable for intensive production in many countries and culturing this fish to boost up aquaculture.

Parasitological examination of *P. sutchi* revealed the presence of a non-native monogenean parasite of genus *Thaparocleidus*. The large number of parasites (~200) on a single fish, suggests their successful reproduction in the non-native Indian geographical region. Morphology and morphometrics of the parasite showed similarity with *Thaparocleidus caecus* (Mizelle and Kritsky, 1969) Gussev, 1978 of Southeast Asia. After morphological analysis we have examined 28S rDNA sequences of the parasites to substantiate the findings. This represents the first record of *T. caecus* in India and provides a clear avenue for human-assisted introduction of *P. hypophthalmus*.

The 28S rDNA sequence of *T. caecus* (627 bps) did not show a close relationship with any other *Thaparocleidus* represented in GenBank, except *Thaparocleidus* sp. BDY (EF100555) (98%). The 28S tree showed a better resolution within the clade for *T. caecus* (high bootstrap values of 100%). This similarity might be revised in the future as no 28S sequence for *T. caecus* species is available now. *T. caecus* is differentiated among *Thaparocleidus* species by 2% generic difference in their nucleotide sequence calculated by NCBI BLAST and also through analysis of MEGA software. This is the first and only 28S sequence of *T. caecus* (KF361477) available on Genbank database. Thus, it seemed possible that this non-native monogenea has remained unnoticed over the past decades.

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