



# Toward resolving cryptic diversity in opisthorchiid flukes: Molecular clarification of an *Opisthorchis viverrini*-like parasite in Myanmar is urgently needed



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We read with deep interest the recent article by Sohn et al. [1], who reported the discovery of an *Opisthorchis viverrini*-like liver fluke in snakehead fish (*Channa lucius* and *Channa striata*) from the Yangon Region, Myanmar. Based on a detailed morphological examination of both metacercariae and experimentally recovered adult worms, the authors proposed that the parasite may represent a distinct taxon, provisionally referred to as an “*O. viverrini*-like” species. This important contribution sheds light on the largely underexplored opisthorchiid fauna of Myanmar and raises key questions regarding species boundaries and host specificity in the Greater Mekong Subregion.

The observed morphological differences—including the highly spiraled seminal vesicle, a uterus occupying more than 50% of the body length, ungrouped vitellaria, and smaller metacercariae—support the authors’ view that the parasite diverges from both *O. viverrini* sensu stricto and *Opisthorchis lobatus* [1]. However, certain features are shared with these species, particularly *O. lobatus*, which was originally described in birds and later recovered from experimentally infected hamsters in Laos [2], and with the cat-specific lineage of *O. viverrini* reported in Thailand [3]. In the absence of molecular data, it remains unclear whether these traits represent a novel species, cryptic diversity within *O. viverrini*, or phenotypic plasticity influenced by host or environmental conditions.

Molecular evidence is essential to resolve this ambiguity. Recent studies using mitochondrial (cox1 and nad1) and nuclear (ITS2 and 28S) markers have clarified population-level divergence within *O. viverrini*, revealing distinct human- and cat-specific lineages with different transmission dynamics and zoonotic potential [3,4]. Agustina et al. [3] showed that *O. viverrini*-like metacercariae in snakehead fish could belong to either lineage, whereas Sota et al. [4] demonstrated cross-transmission between cats and humans. Given the overlapping fish hosts, the Myanmar fluke may be a member of this complex.

We therefore encourage the authors and the broader research community to prioritize the molecular sequencing of adult flukes from future experimental infections. Such data, integrated with host-range and ecological studies, could establish whether this fluke naturally infects mammals, birds, or both. Emerging tools, including environmental DNA screening and metagenomic analysis, could complement classical parasitology and expedite definitive host identification.

Determining the natural definitive host is not a minor taxonomic detail—it is critical for disease control. If the fluke parasitizes birds, interventions will differ markedly from those

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targeting zoonotic transmission via domestic cats or humans. Clarifying its phylogenetic position would inform the development of diagnostics and surveillance strategies that rely on species-specific molecular targets.

Although Myanmar has previously been considered an area of low-grade *O. viverrini* endemicity in humans [5–7], this newly described form may account for undiagnosed or misidentified infections and could represent an overlooked public health risk, particularly if zoonotic. Conversely, if it is non-zoonotic or restricted to avian hosts, it would still contribute significantly to our understanding of opisthorchiid diversity in the region.

In conclusion, we commend the authors for their rigorous morphological investigation and valuable contribution to regional parasitology. Completing the molecular characterization of this fluke—ideally through an integrative One Health lens—will clarify its taxonomic identity and health significance. We hope that this correspondence catalyzes collaborative efforts to resolve opisthorchiid taxonomy and transmission in Myanmar and the Greater Mekong Subregion.

**Reply from Dr. Jong-Yil Chai (corresponding author: [cjy@snu.ac.kr](mailto:cjy@snu.ac.kr))**

We sincerely appreciate the valuable comments and suggestions provided by Rattanapitoon et al. (see above) on our recent publication [1]. They acknowledged the status of our '*Opisthorchis viverrini*-like liver fluke in Myanmar' as a distinct taxon, based on morphological features of the metacercariae and adults. However, they also stated that, without molecular data, it remains unclear whether these traits indicate a new species, cryptic diversity within *O. viverrini*, or phenotypic plasticity influenced by host or environmental conditions. We completely agree with them and are currently conducting some molecular studies.

Considering the morphology of the adult flukes and the fish host species (snakehead fish), our specimens appear to be a divergent form of both *O. viverrini* sensu stricto and *Opisthorchis lobatus* [2]. Conversely, Rattanapitoon et al. suggested that our specimens might belong to the *O. viverrini* complex, including human-specific and cat-specific *O. viverrini*-like populations reported in Thailand and Laos [3,4]. However, cross-transmission between human- and cat-specific *O. viverrini* populations could occur, as observed in an endemic area in Thailand [4]. Therefore, there is likely high genetic diversity among *O. viverrini*-like liver flukes in the Greater Mekong Subregion, and the taxonomic status of *O. lobatus* in Laos, as well as the human-specific and cat-specific populations of *O. viverrini* in Thailand and Laos, and the *O. viverrini*-like liver fluke in Myanmar, needs to be clarified soon.

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