

## Unraveling the molecular mechanisms of diversification: Comparative genomics of the monogeneans infecting the gills of the marine barramundi, at both micro and macro evolutionary levels

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Biological diversity varies significantly across the tree of life: some clades are highly species-rich, and others remarkably species-poor<sup>1</sup>. Despite our growing understanding of the conditions and processes that lead to the formation of new species, we still struggle to identify what hinders diversification<sup>2</sup>. Lates perches (Latidae) are fishes with a unique dichotomous distribution pattern. The euryhaline species of lates perches can be found in the Indo-Pacific region, with barramundi (*Lates calcarifer*) being the most widespread representative with significant relevance to the aquaculture and fisheries sector. On the other hand, freshwater representatives are found solely in African river basins and lakes. Interestingly, while marine barramundi hosts a variety of monogenean gill parasites, the monogenean fauna of African lates perches is species poor with a single species being reported, *Dolicirroplectanum lacustre*<sup>3, 4</sup>. This contrast in parasite species richness is counterintuitive, because typically parasites diverge faster than their hosts because of their shorter generation time and faster mutation rate<sup>5</sup>.

In this study, we want to understand the constraints on species diversification by delving into the genomic diversity of the monogenean parasites infecting lates perches. We integrate a comparative genomic study encompassing both micro-evolutionary (intraspecific) and macro-evolutionary (interspecific) levels (between Indo-Pacific monogeneans and *D. lacustre*). This approach aims to identify genomic signatures associated with diversification at both evolutionary levels, shedding light on the intricate interplay of host-parasite-environment interactions in shaping evolutionary outcomes.

Specimens of barramundi were obtained from the coast of China (n=22) and Sri Lanka (n=16). Their gills were collected and preserved in absolute ethanol. Gills were screened for monogenean gill parasites under a dissecting microscope using entomological needles. A total number of 125 parasites were retrieved from 11 screened hosts. The average infection intensity was 10.9 parasite individuals per infected host with the overall prevalence of 81.8%. The DNA of the parasites was extracted using an in-house protocol for low-input samples<sup>6</sup>. Species composition of monogenean communities was determined via barcoding approach using the part of 28S rDNA fragment. Genomic libraries were sequenced on the Illumina NovaSeq platform at 50x sequencing depth.

The resulting genomic data were adapter-trimmed and quality-filtered, and will consecutively be analyzed to identify outlier loci, evaluate genetic diversity indices, and estimate fixation indices ( $F_{ST}$ ) for intra- and interspecific comparisons. This study aims to contribute novel insights into the mechanisms driving diversification in soft-bodied organisms, addressing a critical gap in our understanding of micro- and macro-evolutionary processes.

### References

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### Keywords

Comparative genomics; Monogenea; Diversification; Speciation; Biodiversity