



An Integrative Analysis to Resolve Taxonomic Deadlocks in Ergasilid Copepods in the Planet

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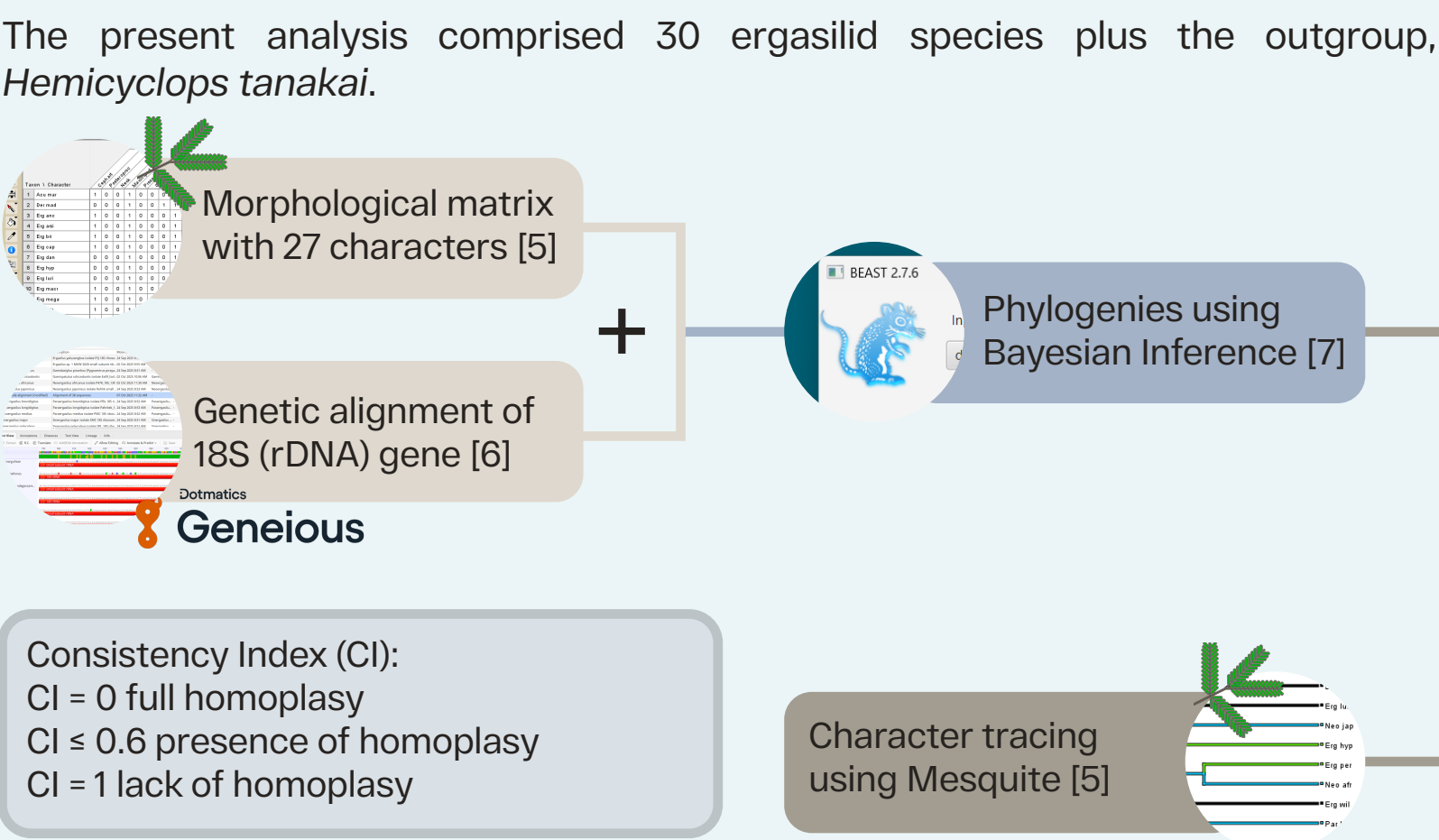
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1 Introduction

Ergasilidae is among the most commonly recorded families of parasitic copepods on fish worldwide [1]. Besides its impressive diversity of 281 species, morphological and molecular phylogenies have demonstrated the lack of monophyly in several genera, as well as other taxonomic deadlocks [1–4]. This highlights the need to conduct new analysis to better understand the evolutionary history of the family and to improve its systematics.

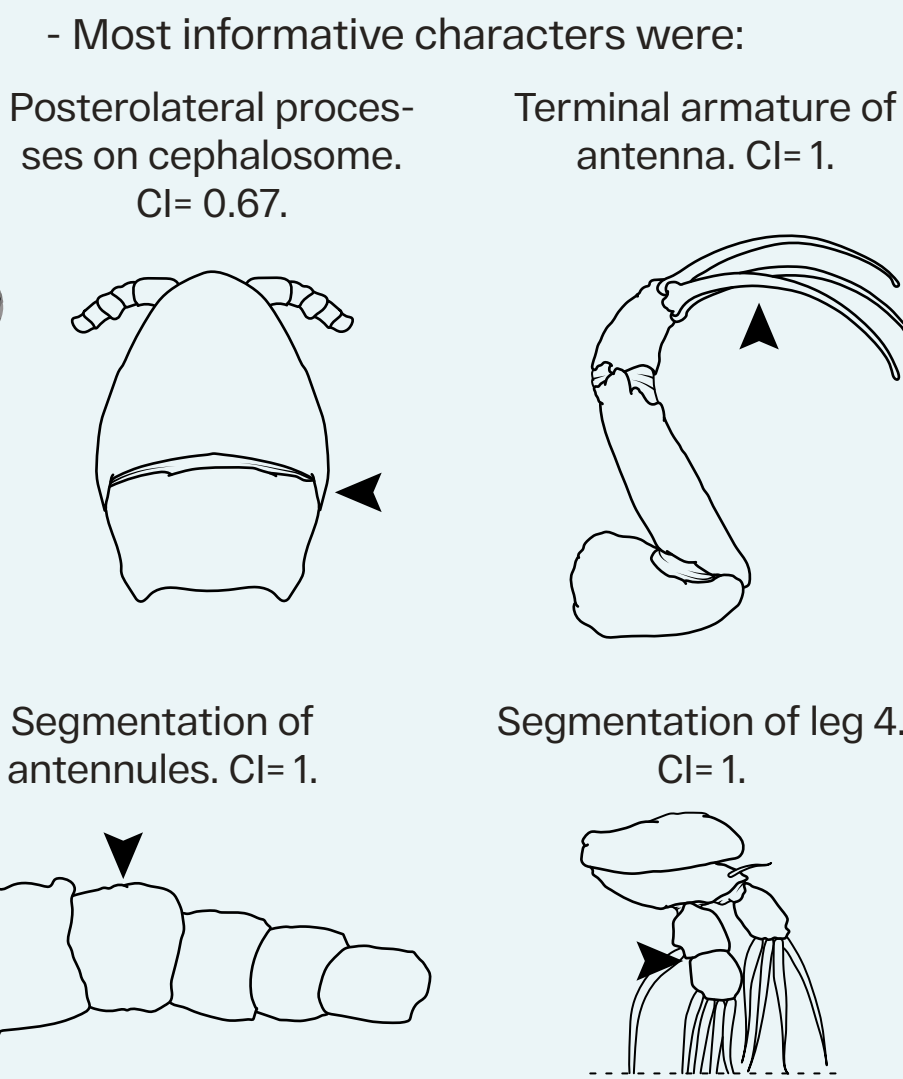
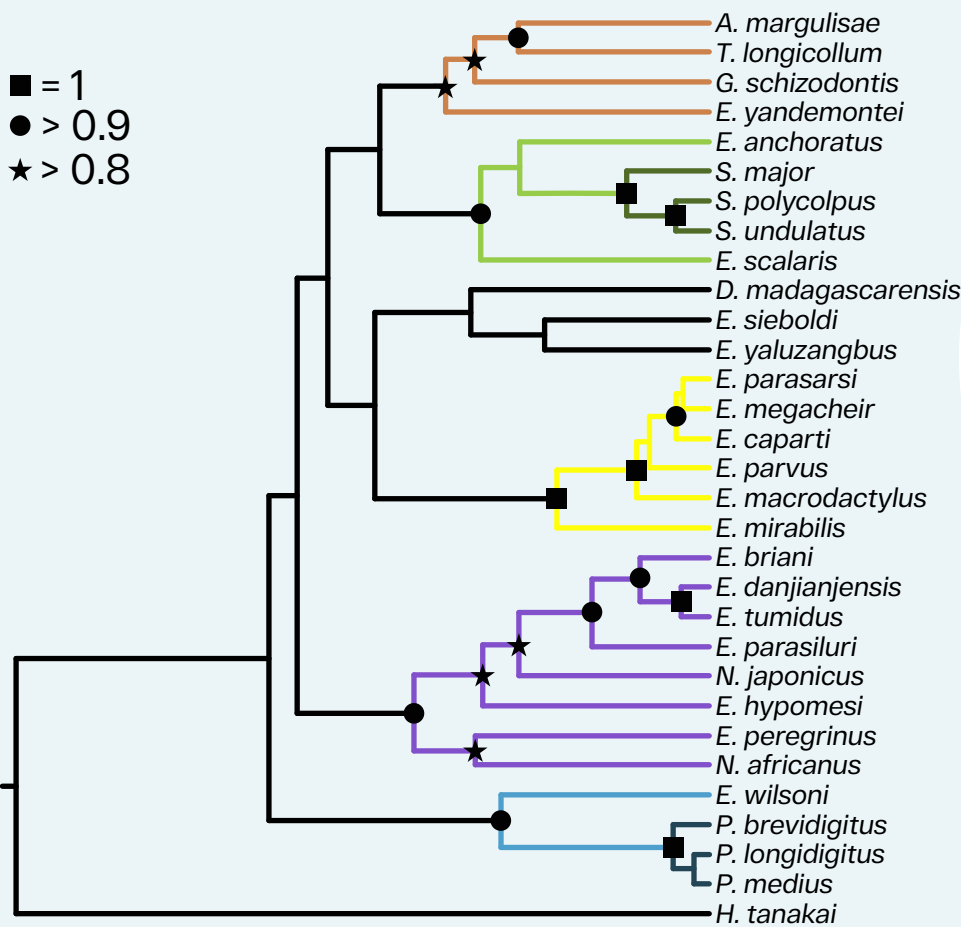
The aim of this study was to assess the evolutionary relationships within Ergasilidae using morphological and molecular data combined, to clarify their systematic and shed light on which criteria must be followed to enhance the taxonomic definitions in the family.

2 Methods



3 Results

- CI of integrated tree (below)= 0.55, being moderately infomative.

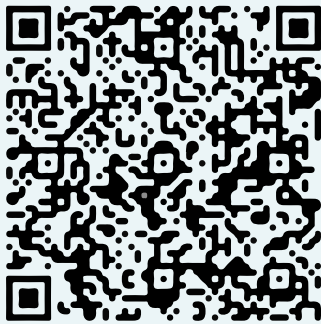


4 Discussion

Our integrated morphological and molecular analysis recovered a non-monophyletic *Ergasilus*, indicating that the current morphological diagnosis does not reflect its evolutionary history [1]. The same is true for *Neoergasilus*. Given the present results, at least 5 new genera would need to be erected to allocate *Ergasilus* spp. to monophyletic groups, but clear morphological characters supporting these subgroups have yet to be found. *Paraergasilus* and *Sinergasilus*, however, were monophyletic, supported mainly by morphological traits currently used in their diagnosis [8]. The present results reinforced some characters previously used to distinguish genera within the Ergasilidae, while revealing others, such as segmentation of rami on leg 4, which also have taxonomic value. Limited molecular data for ergasilid species have impeded taxonomic revision of the family, highlighting the need for increased taxon sampling in molecular analyses to produce a more comprehensive and stable revision of the family.

References

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