



SHEDDING LIGHT ON THE HIDDEN LARVAE OF *BENTHESICYMUS LACINIATUS* RATHBUN, 1906 (DECAPODA, DENDROBRANCHIATA): AN INTEGRATIVE TAXONOMIC APPROACH

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INTRODUCTION

Benthescycymidae Wood-Mason in Wood-Mason & Alcock, 1891 comprises benthopelagic shrimps that inhabit deep-water habitats (500 - 2000 m depth). It is one of the least understood shrimp families given the rare occurrence and their difficult-to-access deep-sea habitats, and fragile body resulting in easily damaged specimens (Vereshchaka et al. 2021). The available knowledge for adults is limited and most larval stages are undescribed.

The systematics of the family changed throughout the years. Recently, Vereshchaka et al. (2020) presented the genus *Benthescycymus* as paraphyletic, and established four new genera. Two species were reported for the genus: *Benthescycymus crenatus* Spence Bate, 1881 and *Benthescycymus laciniatus* Rathbun, 1906. We report the description of larval stages of *B. laciniatus* detected in samples collected in the Madeira-Tore seamount complex, northeastern Atlantic.

METHODS

Neuston hauls were conducted after sunset with a Manta net (200 µm, 15 x 30 cm) in the Madeira-Tore area, northeastern Atlantic (Fig. 1), in September/October of 2022. The survey's main goal was to acquire oceanographic, biological and geological data to characterize the environmental baseline of the area. Samples were preserved in both ethanol and formaldehyde. After morphological analyses with a binocular stereomicroscope, the molecular analyses of the ethanol specimens involved the following steps:

01 Tissue sampling & DNA extraction;

02 Amplification of the COI-5P barcode region (primers pair Lobo F1-Lobo R1, In Lobo et al. 2013);

03 Purification of the PCR products & sequencing.

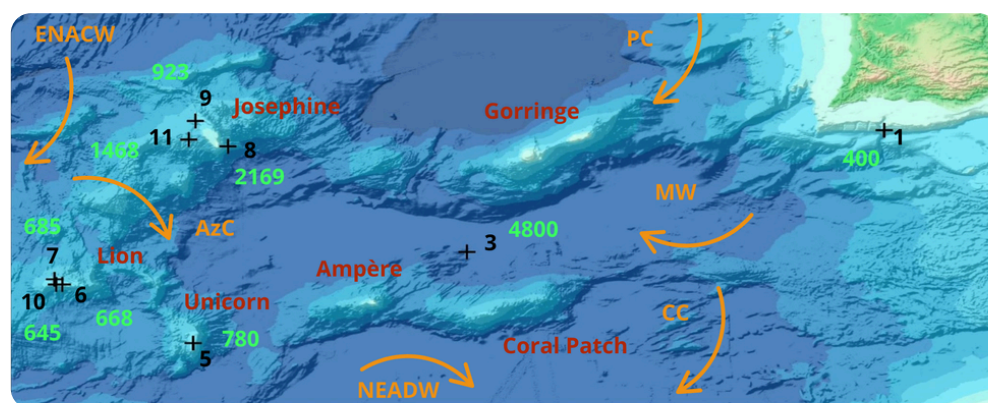


Fig. 1 - Madeira-Tore Rise. Sampling locations, main seamounts and station depth (green numbers).

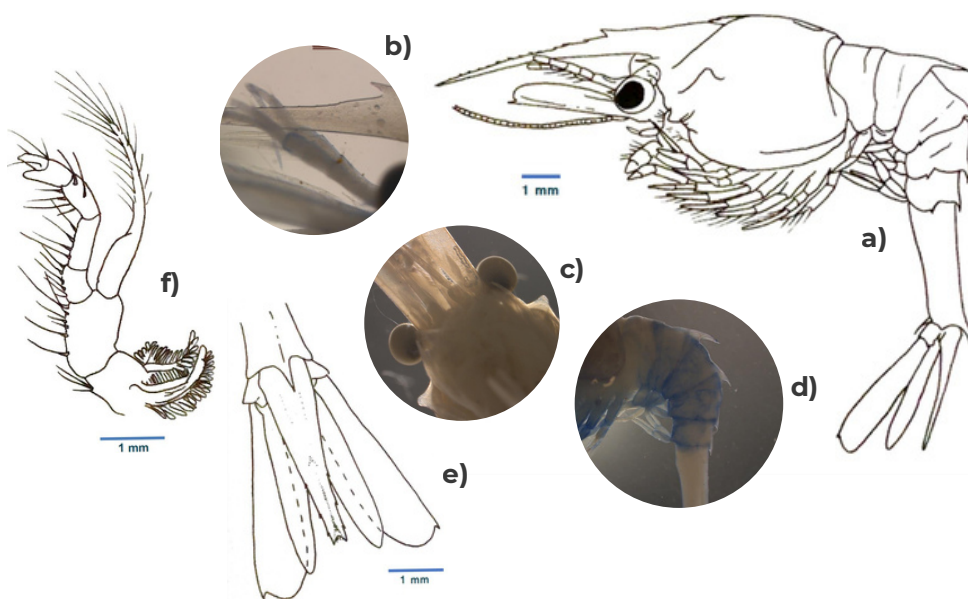


Fig. 2 - Advanced larval stage of *Benthescycymus laciniatus* Rathbun, 1906. a) General lateral view and details of b) rostrum, c) carapace, d) abdomen, e) telson and f) pereopod I.

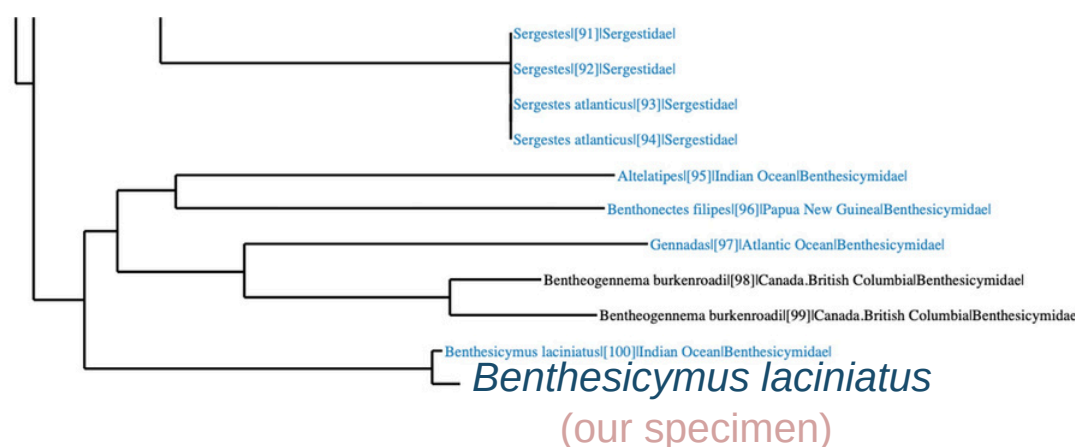


Fig. 3 - BOLD Taxon ID Tree: Neighbour-Joining tree based on K2P distances from COI sequences.

Fig. 4 - Early (upper image) & advanced larval stages of *Benthescycymus laciniatus* Rathbun, 1906.

RESULTS & DISCUSSION

Early and advanced larval stages of *B. laciniatus* were detected (Figs. 2 and 4) in samples of the Lion seamount (stations #7, #10). The taxon ID tree obtained in the molecular analyses, based on a complete sequence (658 bp) of the DNA barcode, is presented in Fig. 3. It indicated a 99.24% similarity to the GenBank sequence for the species (Indian Ocean).

The molecular data indicated low intraspecific divergence (< 1%), consistent with the species' broad geographic distribution and comparisons between distant regions (Indian vs. Atlantic oceans). The late *B. laciniatus* larvae showed blue chromatophores on the carapace, pereopods, somites, and telson tips, with the rest of the body nearly transparent. In the neuston, this pigmentation may reduce predation, offer protection from temperature and UV variability, and facilitate conspecific recognition.

The morphology of the larvae resembled existing descriptions of *Gennadas* (Heldt, 1938) and larvae previously attributed to *Benthescycymus* (Gurney, 1924), but with key differences: the armature of the abdominal somites and the morphology of the telson. The first abdominal somite lacked a dorsal spine, similarly to *Gennadas* and differing from the *Benthescycymus* descriptions. The second somite had a median dorsal spine, though shorter than in *Gennadas*. The median dorsal spine on somite 3 was longer and more robust than in both genera. These traits suggest that larvae previously assigned to *Benthescycymus* likely belong to another genus of family Benthescycymidae.

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