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Commentary: Comparative omics analysis of a new deep-sea barnacle species (Cirripedia, Scalpellomorpha) and shallow-water barnacle species provides insights into deep-sea adaptation

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A Commentary on:

[Comparative omics analysis of a new deep-sea barnacle species \(Cirripedia, Scalpellomorpha\) and shallow-water barnacle species provides insights into deep-sea adaptation](#)

by Mao N, Shao W, Cai Y, Kong X, Ji N and Shen X (2024). *Front. Mar. Sci.* 10:1269411. doi: 10.3389/fmars.2023.1269411

Mao et al. (2024) recently published an article comparing the mitochondrial genome and transcriptome of the deep-sea hydrothermal vent barnacle *Vulcanolepas fijiensis* and the relatively shallower barnacle *Scalpellum stearnsi* (contradictory to the title, no new species was described). This paper concluded that the mitogenomes and key genes found in the transcriptomic analysis were subjected to positive selection related to high-temperature and high-pressure conditions, allowing *V. fijiensis* to adapt to the deep-sea environment. However, the neolepadid hydrothermal vent barnacle used in their study was misidentified and actually represents a different species, *Neolepas marisindica*. We present our evidence and reasoning for this below. Although the main conclusions presented by Mao et al. (2024) still stand because *N. marisindica* is also a deep-sea vent species, their misidentification has connotations on the context, interpretation, and of course future use of their data.

The deep-sea hydrothermal vent barnacle specimen referred to as *V. fijiensis* in Mao et al. (2024) was collected at Longqi hydrothermal vent field on the Southwest Indian Ridge at a depth of 2759 m in the Indian Ocean. *Vulcanolepas fijiensis* was originally described from the North Fiji Basin in the Southwest Pacific (Chan et al., 2019) and had never been reported in the Indian Ocean. Watanabe et al. (2018) were the first to explore the diversity of neolepadid hydrothermal vent barnacles in the Indian Ocean and found only one species, *Neolepas marisindica*, from

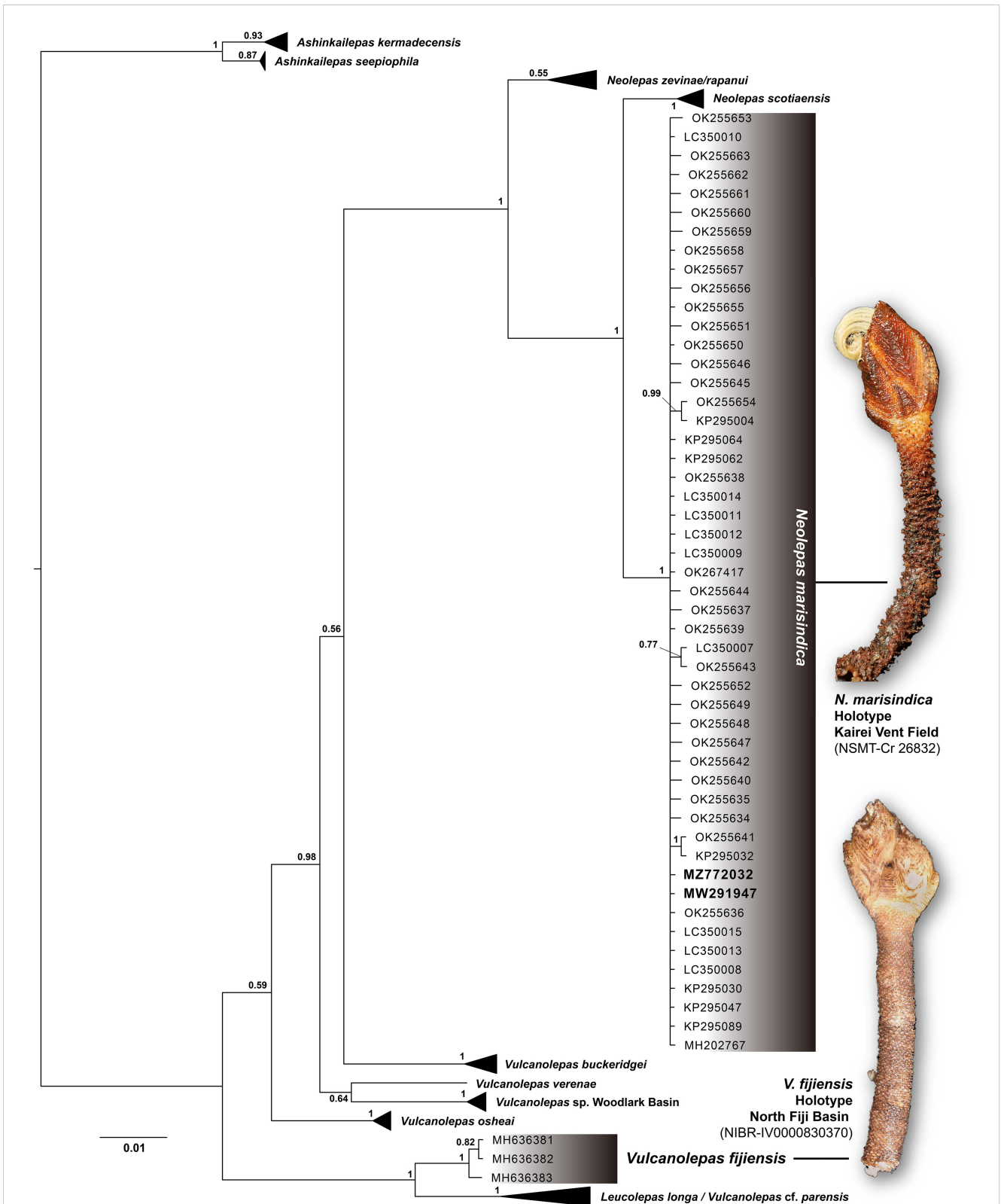


FIGURE 1
 Phylogenetic tree of neolepadid stalked barnacles reconstructed by Bayesian inference with the GTR+I+G model, following published methods in Watanabe et al. (2023). For simplicity, taxa other than *Vulcanolepas fijiensis* and *Neolepas marisindica* have been collapsed. Accession numbers in bold refer to sequences referred to as *V. fijiensis* in Mao et al. (2024). Node values indicate Bayesian posterior probability. The 528 bp alignment used contained all 202 COI barcoding sequences openly available on GenBank, accession numbers as follows: JX036420–JX036464, KF739820–KF739838, KP295001, KP295004–KP295005, KP295007–KP295009, KP295013–KP295014, KP295018–KP295019, KP295022, KP295026–KP295028, KP295030–KP295037, KP295039–KP295042, KP295045–KP295053, KP295055–KP295058, KP295060–KP295064, KP295067–KP295069, KP295073, KP295076, KP295078, KP295080, KP295082–KP295085, KP295089–KP295091, KP295094, KP295097–KP295098, KY502196–KY502197, LC350007–LC350015, MH202767, MH636381–MH636383, MN722546–MN722548, MN722550–MN722551, MT662001, MW291947, MW602536–MW602540, MW602548–MW602549, MW602552–MW602566, MZ772032, OK255634–OK255663, OK267417. Holotype of *V. fijiensis* (NIBR-IV0000830370; Korea National Institute for Biological Resources, Incheon, Korea) as well as *N. marisindica* (NSMT-Cr 26832; National Museum of Nature and Science, Tsukuba, Japan) shown in inset, photographs were taken by Benny K. K. Chan.

several vent fields including the Longqi vent field. Though *N. marisindica* exhibits two morphotypes, these have been shown to be the same species using molecular data (Watanabe et al., 2018).

Using the mitochondrial genome of *V. fijiensis* supplied by Mao et al. (2024) in GenBank (MZ772032), we show in a phylogenetic tree that the mitochondrial COI (cytochrome *c* oxidase subunit I) barcode sequence of *V. fijiensis* in Mao et al. (2023) is nested into a well-supported clade with other available sequences of *N. marisindica* and not with *V. fijiensis* sequences from the original description by Chan et al. (2019) that includes barcodes of the holotype (Figure 1). This sequence from Mao et al. (2024) was identical to published sequences of *N. marisindica* from both Kairei (type locality; LC350008, LC350015) and Solitaire (LC350013) vent fields on the Central Indian Ridge (CIR). Searching on GenBank revealed another mitogenome listed as *V. fijiensis* (MW291947) linked to the Mao et al. (2024) paper, but this too was nested within *N. marisindica* (Figure 1). Furthermore, a mitogenome of the real *V. fijiensis* from the North Fiji Basin had already been published (Lee et al., 2019; MN061491) using one of the original specimens sequenced in the description paper, and a BLAST comparison with the mitogenome (MZ772032) presented by Mao et al. (2024) revealed a percentage identity of only 88.84% between these two mitogenomes. Altogether, these evidences show that the species identification in Mao et al. (2024) was incorrect, and their hydrothermal vent barnacle was actually *N. marisindica*.

We also note that another layer of confusion came from an inset specimen photo used in Figure 1A of Mao et al. (2024), which shows a photo of the real *V. fijiensis* directly taken from figure 3F of Chan et al. (2019) (original authors were not consulted about this use prior to publication). This photograph is of the holotype of *V. fijiensis* housed in the collection of the Korea National Institute for Biological Resources (Incheon, Korea; NIBR-IV0000830370) where it still resides. As such, the photo of *V. fijiensis* presented in Mao et al. (2024) is misleadingly not linked to the actual specimen used in their study.

Hydrothermal vent field stalked barnacles in the family Neolepadidae often exhibit morphological variations in the capitular shells and peduncular scales (Watanabe et al., 2021), which may have contributed to the misidentification in Mao et al. (2024). A more reliable identification for deep-sea hydrothermal vent barnacles should be based on an integrative approach, a combination of morphological and barcoding sequence matching with reference sequences available in GenBank. With the misidentification in Mao et al. (2024) corrected, *Neolepas marisindica* remains the only neolepadid species known from the Indian Ocean so far (Watanabe et al., 2018; Kim et al., 2020; 2021; Zhou et al., 2018; 2022), known from nine vent fields across four ridges (SWIR, CIR, Southeast Indian Ridge, and Carlsberg Ridge). At present, the hydrothermal vent stalked barnacle species identified in the Pacific include *V. fijiensis*, *V. osheai*, *V. buckeridgei*, *V. veranae*, *Leucolepas longa*, *Neolepas rapanuii*, and *N. zeviniae* (see Watanabe et al., 2021); an undescribed species is also known from Woodlark Basin (Boulart et al., 2022). Such a contrasting diversity pattern between the Pacific and Indian Ocean vent fields supports the Dispersal Corridor Hypothesis, where the ancestors of the Indian Ocean neolepadid barnacles

originated from the Pacific Ocean and entered the Indian Ocean via the Southern Ocean (see Watanabe et al., 2018).

Correct species identification is of utmost importance to ensure the correct interpretation and usage of molecular and distribution data. The data in Mao et al. (2024) presents the first assembled and published mitogenome sequence for *N. marisindica*, a valuable piece of new data that will be useful in the future for understanding the evolutionary history of this species and vent barnacles as a whole. Although previously another transcriptome for this species was published using specimens from Onnuri vent field on the CIR (Ryu et al., 2019), this means the Longqi transcriptome data from Mao et al. (2024) provides an opportunity to make an interesting comparison with Onnuri to reveal potential differences between conspecific barnacles in two different vents across two ridge systems. We hope this case serves as an example for biologists working on difficult-to-identify deep-sea species to embrace integrative taxonomy and to ensure the species identification and taxonomy is correct prior to publication.

Author contributions

BC: Funding acquisition, Writing – original draft, Validation, Investigation, Conceptualization. HW: Writing – original draft, Visualization, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. CC: Writing – original draft, Visualization, Validation, Methodology, Investigation, Data curation, Conceptualization.

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Conflict of interest

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