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

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KEYWORDS

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A Corrigendum on

Comparative omics analysis of a 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

Error in the Article Title

In the published article, there was an error in the article title. Instead of “*Comparative omics analysis of a new deep-sea barnacle species (Cirripedia, Scalpellomorpha) and shallow-water barnacle species provides insights into deep-sea adaptation*”, it should be “*Comparative omics analysis of a deep-sea barnacle species (Cirripedia, Scalpellomorpha) and shallow-water barnacle species provides insights into deep-sea adaptation*”.

Text Correction

In the published article, there was an error. We provisionally identified the deep-water species *Vulcanolepas fijiensis*. As a result of the Chan et al. Commentary Paper (2024), we became aware that our initial identification of *Vulcanolepas fijiensis* was incorrect. We have confirmed that the barnacle is actually *Neolepas marisindica* and have revised this paper to include the correct species indentation.

The change to “*Neolepas marisindica*” or “*N. marisindica*” applies to all instances of the words “*Vulcanolepas fijiensis*” and “*V. fijiensis*” respectively, which appear in the

Keywords, Abstract, Introduction, Materials and methods, Results, Discussion, and Conclusions.

A correction has been made to **Introduction**. This sentence previously stated:

“While studies on other organisms inhabiting extreme deep-sea environments have identified several potential mechanisms, the transcriptome of *Vulcanolepas fijiensis* (Chan) and *Scalpellum stearnsi* (Pilsbry) remains unexplored. Moreover, few studies have investigated the molecular adaptive characteristics that assist with barnacles’ survival in deep-sea harsh chemosynthetic habitats. Due to the limited prior investigations concerning the transcriptome of barnacles, particularly with regard to the deep-sea adaptation of *V. fijiensis*, our study attempted to address this research gap.

In this study, we collected deep-sea (*V. fijiensis*) and shallow-water (*S. stearnsi*) individuals at Longqi hydrothermal field on the Southwest Indian Ridge and Guangxi Beibu Gulf, respectively. In order to investigate the adaptability of barnacles to the deep-sea environment, the analysis of positive selection pressure was conducted using the comparative transcriptome of these two individuals, as well as the 13 protein-coding genes (PCGs) of mitogenomes from 11 barnacles, including *V. fijiensis*. This research endeavor aimed to not only provide valuable genomic resources for deep-sea barnacles but also establish a foundation for comprehending their genetic strategies and adaptation mechanisms in the deep-sea habitat.”

The corrected sentence appears below:

“While studies on other organisms inhabiting extreme deep-sea environments have identified several potential mechanisms, the transcriptome of them remains unexplored. Moreover, few studies have investigated the molecular adaptive characteristics that assist with barnacles’ survival in deep-sea harsh chemosynthetic habitats. Due to the limited prior investigations concerning the transcriptome of barnacles, particularly with regard to the deep-sea adaptation, our study attempted to address this research gap.

In this study, we collected the deep-sea and shallow-water barnacle individuals at Longqi hydrothermal field on the Southwest Indian Ridge and Guangxi Beibu Gulf, respectively. In order to investigate the adaptability of barnacles to the deep-sea environment, the analysis of positive selection pressure was conducted using the comparative transcriptome of these two individuals, as well as the 13 protein-coding genes (PCGs) of mitogenomes from 11 barnacles. This research endeavor aimed to not only provide valuable genomic resources for deep-sea barnacles but also establish a foundation for comprehending their genetic strategies and adaptation mechanisms in the deep-sea habitat.”

A correction has been made to **Materials and methods, 2.1 Sample collection, DNA and RNA extraction, and sequencing**, paragraph one. This sentence previously stated:

“A variety of manned submarines were used to obtain *V. fijiensis* from a hydrothermal vent Longqi hydrothermal field on the Southwest Indian Ridge (49°64′E, 37°17′S) at a depth of 2,759 m in the Southwest Indian Ocean. *S. stearnsi* were obtained from the Guangxi Beibu Gulf (109°12′E, 21°04′N), depth of about 300 m. In contrast to deep-sea species, the depth of 300m can be considered relatively shallow. Therefore, we provisionally classified *S.*

stearnsi as a shallow species. After collection, they were immediately stored at -80°C.”

The corrected sentence appears below:

“Samples of the deep-sea barnacles from a hydrothermal vent Longqi hydrothermal field on the Southwest Indian Ridge (49°64′E, 37°17′S) at a depth of 2,759 m in the Southwest Indian Ocean collected on board of “Explorer 1” scientific research ship of Institute of Deep-sea Science and Engineering (Chinese Academy of Sciences) by using “Deep-sea Warrior” manned submersible during the winter of 2018, we thank the crew for their help during the cruise. Samples of the shallow-water barnacles were obtained from the Guangxi Beibu Gulf (109° 12 ‘ E, 21° 04 ‘ N), depth of about 300 m. In contrast to deep-sea species, the depth of 300m can be considered relatively shallow. Therefore, we provisionally identified the two barnacle species as the deep water species *Vulcanolepas fijiensis* (Lee et al., 2019) and the shallow water *Scalpellum stearnsi* (Chan et al., 2010). As a result of the Chen et al. Commentary Paper (Chan et al., 2024) we became aware that our initial identification of *V. fijiensis* was incorrect. We have confirmed that the barnacle is actually *Neolepas marisindica* and have revised this paper to include the correct species indentation. After collection, they were immediately stored at -80°C.”

The references for “Lee et al., 2019”, “Chan et al., 2010”, and “Chan et al., 2024” should be:

“Chan, B. K., Prabowo, R. E., Lee, K. S. (2010). North West Pacific deep-sea barnacles (Cirripedia, Thoracica) collected by the Taiwan expeditions, with descriptions of two new species. *Zootaxa* 2405, 1-47. doi: 10.11646/zootaxa.2405.1.1

Chan, B. K., Watanabe, H. K., Chen, C. (2024) Commentary: Comparative omics analysis of a new deep-sea barnacle species (Cirripedia, Scalpellomorpha) and shallow-water barnacle species provides insights into deep-sea adaptation. *Front. Mar. Sci.* 11, 1374419. doi: 10.3389/fmars.2024.1374419

Lee, W. K., Mi Kang, H., Chan, B. K., Ju, S. J., Kim, S. J. (2019). Complete mitochondrial genome of the hydrothermal vent stalked barnacle *Vulcanolepas fijiensis* (Cirripedia, Scalpelliforms, Eolepadidae). *Mitochondrial DNA B.* 4 (2), 2725-2726. doi: 10.1080/23802359.2019.1644564”

In the published article, there was an error in the **Data availability statement**. Our initial identification of *Vulcanolepas fijiensis* was incorrect. We have confirmed that the barnacle mentioned in the name of our deep-sea barnacle species is actually *Neolepas marisindica*. Therefore, the *Neolepas marisindica* and *Scalpellum stearnsi* datasets generated during the current study have been deposited and the statement “The original contributions presented in the study are publicly available. This data can be found here: <https://www.ncbi.nlm.nih.gov/>, BioProject: PRJNA935972.” has been updated. The correct Data Availability statement appears below.

“The *Neolepas marisindica* and *Scalpellum stearnsi* datasets generated during the current study are available in the National Center for Biotechnology Information (NCBI) databases in GenBank repository at the following links: <https://www.ncbi.nlm.nih.gov/nuccore/MZ772032> and <https://www.ncbi.nlm.nih.gov/nuccore/OP345466>.”

In the published article, there was no **Acknowledgments** section. The correct Acknowledgments section appears below.

“We would like to thank the reviewers and Chan et al. for their detailed comments about misidentification. We agree with the commentary paper of Chan et al. and have changed all reference to *Vulcanolepas fijiensis* to *Neolepas marisindica* in our corrected paper. We would also like to thank Professor Haibin Zhang from Institute of Deep-sea Science and Engineering (Chinese Academy of Sciences) for providing the samples and pictures of the deep-sea barnacle.”

Error in Figure

In the published article, there was an error in **Figure 1** as published. The use of photos from the database in **Figure 1** has raised copyright issues. We apologize for the error and have corrected them to photos taken at the time of collection to eliminate copyright and plagiarism issues.

Furthermore, there was an error in the legend for **Figure 1**. Our initial identification of *Vulcanolepas fijiensis* was incorrect. We have confirmed that the barnacle mentioned in the caption of **Figure 1** is actually *Neolepas marisindica*. Therefore, instead of “The mitochondrial genome map of deep-sea barnacle *Vulcanolepas fijiensis* (A) and shallow barnacle *Scalpellum stearnsi* (B)”, the legend should read: “The mitochondrial genome map of deep-sea barnacle *Neolepas marisindica* (A) and shallow barnacle *Scalpellum stearnsi* (B) collected for this study, and photographs in the genome map are from preserved samples that were collected for this study, which were collected by Professor Haibin Zhang and kept in Institute of Deep-sea Science and Engineering (Chinese Academy of Sciences)”. The corrected **Figure 1** and its updated caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Error in Tables

In the published article, there was an error in **Table 2** as published. Our initial identification of “*Vulcanolepas fijiensis*” in the third column of **Table 2** was incorrect and should be “*Neolepas marisindica*” instead. Furthermore, the barnacle mentioned in the legends for **Table 2** is actually “*Neolepas marisindica*”, not “*Vulcanolepas fijiensis*”. The corrected **Table 2** and its updated caption appear below.

In the published article, there was an error in **Table 3** as published. Our initial identification of “*Vulcanolepas fijiensis*” in the first column of **Table 3** was incorrect and should be “*Neolepas marisindica*” instead. The corrected **Table 3** and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Error in Figure/Table Legend

In the published article, there was an error in the legends for Figures 2 – 7 and in the legends for Tables 1, 4, and 5 as published. Our initial identification of *Vulcanolepas fijiensis* was incorrect. We have confirmed that the barnacle mentioned in the legends for Figures 2 – 7 and in the legends for Tables 1, 4, and 5 should be “*Neolepas marisindica*”. The corrected legends appear below.

[TABLE 1 Summary of the mitogenome features of *Neolepas marisindica* and *Scalpellum stearnsi*.]

[FIGURE 2 AT and GC skews in protein-coding genes of the mitochondrial genomes in deep-sea barnacle *Neolepas marisindica* (A) and shallow barnacle *Scalpellum stearnsi* (B). The horizontal and vertical coordinates represent gene name and skew value, respectively; The blue line represents the AT skew and the orange line represents the GC skew.]

[FIGURE 3 The codon usage of the protein-coding genes of the mitochondrial genomes of deep-sea barnacle *Neolepas marisindica* (A) and shallow barnacle *Scalpellum stearnsi* (B). The different colors represent different kinds of codons, and the different columns represent different amino acids.]

[FIGURE 4 Gene Ontology function annotation of the transcriptomes of deep-sea barnacle *Neolepas marisindica* (A) and shallow barnacle *Scalpellum stearnsi* (B). The red terms represent Biological Process, the blue terms represent Cellular Composition, and the green terms represent Molecular Function.]

[FIGURE 5 Classification of the Kyoto Encyclopedia of Genes and Genomes metabolic pathway of the transcriptomes of deep-sea barnacle *Neolepas marisindica* (A) and shallow barnacle *Scalpellum stearnsi* (B). Vertical lines represent five main pathways: red terms denote cellular processes, purple terms denote environmental information processing, blue terms denote genetic information processing, green terms denote metabolism, and yellow terms denote organismal systems.]

[TABLE 4 Results of the selective pressure acting on the protein-coding genes of *Neolepas marisindica*.]

[FIGURE 6 Three-dimensional structural models of the COIII (A) and ND2 (B) genes of deep-sea barnacle *Neolepas marisindica*. The red represents positive selection site; N represents amino terminus and (C) represents carboxy terminus.]

[TABLE 5 Genes that were subject to positive selection pressure in *Neolepas marisindica* and *Scalpellum stearnsi*.]

[FIGURE 7 Enrichment of the Kyoto Encyclopedia of Genes and Genomes metabolic pathway of the positive selection genes in deep-sea barnacle *Vulcanolepas fijiensis* compared with shallow barnacle *Scalpellum stearnsi*. The circle size represents the number of genes, and the color from cool to warm represents the smaller q value.]

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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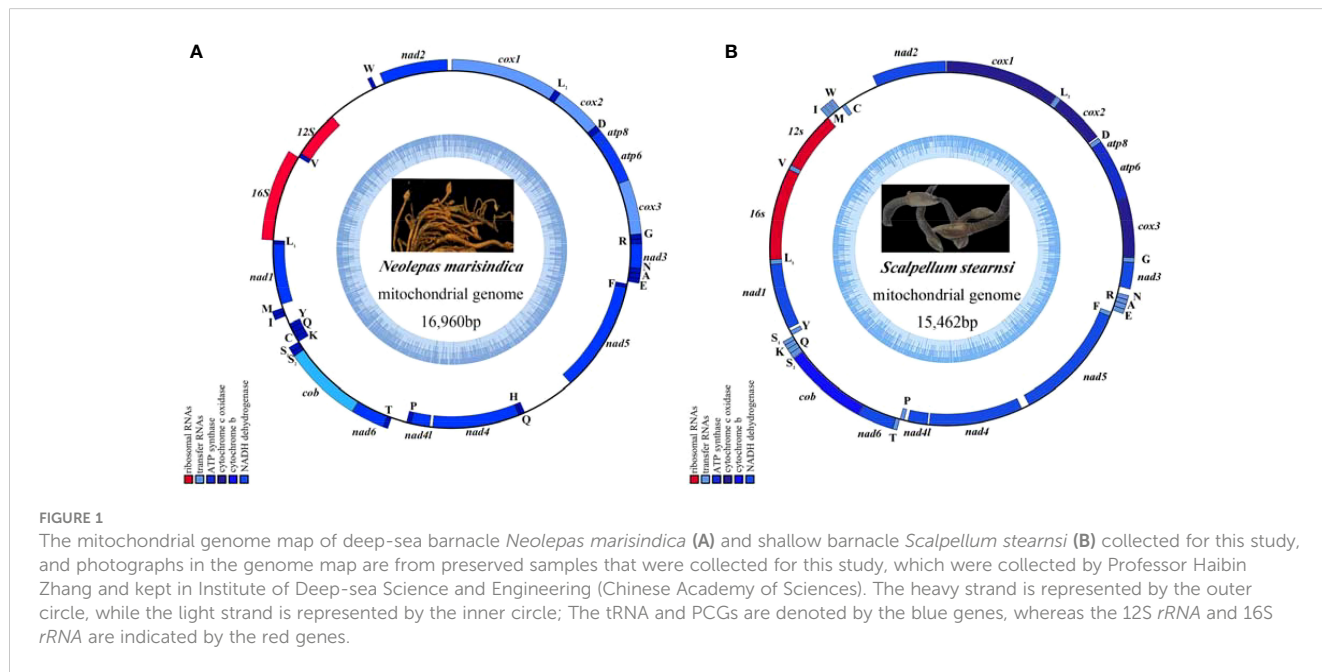


TABLE 2 Transcriptome library basic information of *Scalpellum stearnsi* and *Neolepas marisindica*.

Class	Item	<i>Neolepas marisindica</i>	<i>Scalpellum stearnsi</i>
Assembly	Transcript number (bar)	54,446	99,622
	Unigene number (bar)	53,562	98,686
	Total length of Unigenes (bp)	49,774,143	61,491,550
	N50 length of Unigenes (bp)	1,721	916
	Mean length of Unigenes (bp)	929	623
Annotation	Nr	13,679 (25.53%)	26,304 (26.65%)
	Nt	5,150 (9.61%)	8,036 (8.14%)
	Swiss-Prot	12,019 (22.43%)	19,772 (20.03%)
	KEGG Orthology	6,845 (12.77%)	12,042 (12.2%)
	PFAM	16,685 (31.15%)	26,406 (26.75%)
	GO	16,746 (31.26%)	26,718 (27.07%)
	KOG	7,129 (13.3%)	10,959 (11.1%)
	All Databases	2,422 (4.52%)	2,786 (2.82%)
	At least one database	20,628 (38.51%)	38,666 (39.18%)

TABLE 3 Collection and mitogenome information of the specimens that were used for the positive selection analysis.

Species	Mitochondrial genome size	GenBank accession numbers
<i>Neolepas marisindica</i>	16,960 bp	MZ772032
<i>Conchoderma hunteri</i>	15,202 bp	OL606642
<i>Scalpellum stearnsi</i>	15,462 bp	OP345466
<i>Lepas anserifera</i>	15,653 bp	OP377772
<i>Lepas australis</i>	15,502 bp	NC025295
<i>Lepas anatifera</i>	15,708 bp	NC062431
<i>Capitulum mitella</i>	14,916 bp	AB167462
<i>Arcoscalpellum epeeum</i>	15,593 bp	MH791047
<i>Altiverruca navicula</i>	15,976 bp	NC037244
<i>Glyptelasma annandalei</i>	16,107 bp	NC043898
<i>Ibla cumingi</i>	15,053 bp	NC066682