

Molecular identification of deep-sea blind lobster *Willemoesia forceps* (Crustacea: Decapoda: Polychelidae) from the Central Indian Ridge

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ABSTRACT

The deep-sea blind lobster *Willemoesia forceps* A. Milne-Edwards, 1880 was collected at a water depth of 3433 m and is reported for the first time from the Central Indian Ridge (CIR). The species was identified based on morphological examination and supported by mitochondrial Cytochrome Oxidase Subunit I (mtCOI) gene. The phylogenetic analysis shows that *W. leptodactyla* is sister species of *W. forceps*. Our findings expand the distributional range of the specimen in the southern hemisphere.

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Deep-sea blind lobsters have been classified under the Polychelidae family since all extant taxa possess reduced eyes and live in deep oceanic waters (Ahyong 2009). Interestingly, the deep-sea lobsters are home to the eyeless (blind), claw-footed polychelids, 'living fossils', the long-extinct eryonids. The extant Polychelidae family was most morphologically diverse during the Mesozoic period (Audo et al. 2014). The distribution of *W. forceps* is presently known from the West Indies, the Caribbean Sea, Sargasso Sea, West Africa, eastern Australia (Queensland), Taiwan (Ahyong 2012; Chang et al. 2013, 2014). The CIR is part of a ~65,000 km long global mid-oceanic ridge network that traverses the bottom of the world's oceans. It is a north-south-trending ridge extending from the Rodriguez Triple Junction to the equator at 25°S. Many known hydrothermal vent fields viz., Edmond (Van Dover et al. 2001), Kairei (Hashimoto et al. 2001), Dodo (Nakamura et al. 2012), and Solitaire (Kawagucci et al. 2008, 2016) are located in the vicinity of our study area along the CIR. The studied specimen was collected in January 2017 (Lat: 23°11'15"S; Long: 69°13'18"E, cruise no. MGS 13) during a box core operation. The specimen was identified based on morphological traits (Galil 2000; Chang et al. 2013, 2014). The *Willemoesia forceps* has the lateral margin behind the post-cervical with more than 20 spines with 8–16: 5–8: 39–42. Galil (2000) and Ahyong (2012) also reported a similar range of 14:13–15:27–30 and 14–19:14–15: 29–40, respectively. The specimen has been deposited at the NCPOR sample repository (voucher no.: NCPOR-CIO3433).

The experimental protocols and data analysis methods were followed as described in Periasamy and Ingole (2019). Identified sequence has been deposited in NCBI GenBank (accession No.MG214148). The phylogenetic tree was plotted to visualize similar topologies after comparing mtCOI gene sequences of closely associated polychelids species such as *Polycheles typhlops*, *P. enthrix*, *Stereomastis panglao*, *S. sculpta*, *S. suhmi*, *Pentacheles laevis*, and *Willemoesia leptodactyla* were taken from NCBI website. Out-groups used were *Paramunidas tichas*, *Agononida similis* species. The phylogenetic tree of deep-sea blind lobster *W. forceps* species showed within Polychelidae family was divided into two groups: *P. typhlops*, *P. enthrix*, *S. panglao*, *S. sculpta*, *S. suhmi* consist of the first clades which are sister-group to the remaining genus such as *P. laevis*, *Willemoesia leptodactyla*, and *W. forceps* belong to the second group. The phylogenetics of *Willemoesia*-related Polychelidae and mtCOI phylogenetic reconstruction of the *Willemoesia*-related Polychelidae resulted in two principal group clades, each with a paralogous pair of sequence from CIR. The phylogenetic reconstruction of the mtCOI gene for *Willemoesia* species (Figure 1) showed a clear differentiation between described species and high genetic divergence between *W. forceps* and *W. leptodactyla*. The current distribution of *W. forceps* appears genetically correlated and suggests the species has boundless distribution and has become an independent population. Thus, considering the commercial mining potential of Indian Ocean, any information on the ecology and evolution of deep-sea blind lobster will be utmost importance for the management and conservation of deep-sea biodiversity.

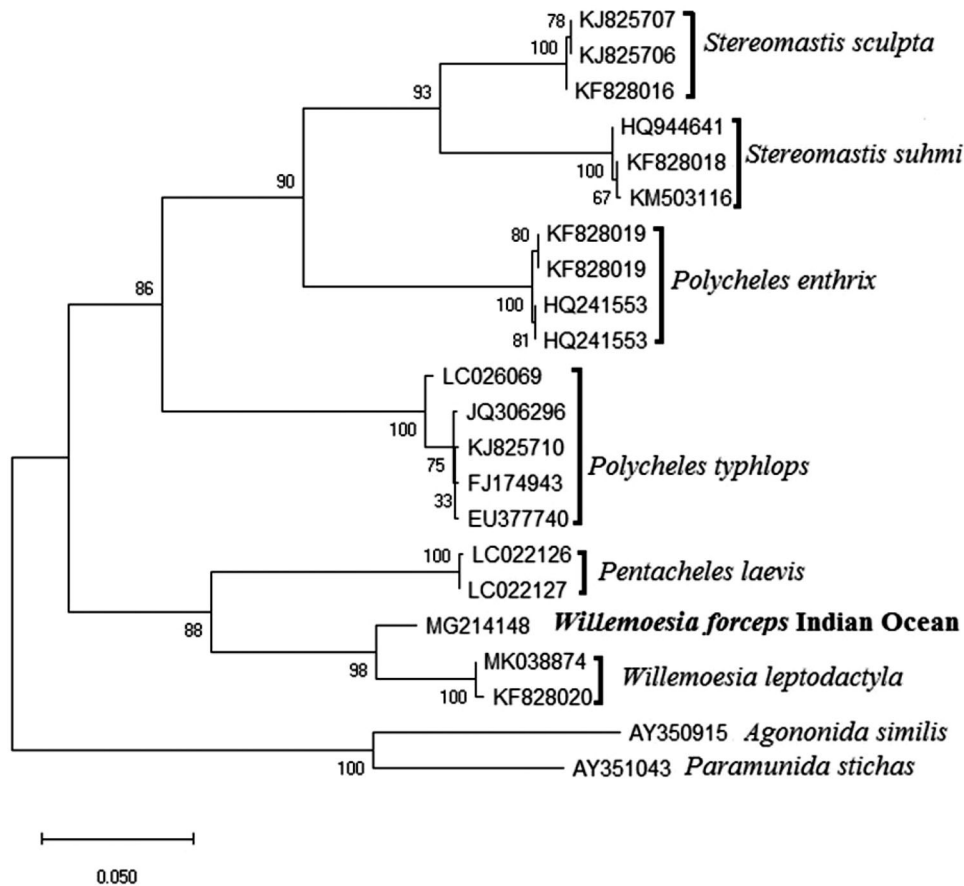


Figure 1. The phylogenetic tree with the highest log likelihood (-3324.94) is shown. The tree is drawn to scale with branch lengths measured in the number of substitutions per site.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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