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## **A strange mitogenome sequence in spiny lobster**

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All lobster species of the genus *Panulirus* are commercially very important. A number of genetic studies in *Panulirus* lobster species have investigated evolutionary relationships and population structure (e.g. Bracken-Grissom et al. 2014; Chow et al. 2011). To date, the complete mitochondrial DNA (mtDNA) sequences of 17 *Panulirus* species have been published in peer-reviewed scientific journals (Yamauchi et al. 2002; Li and Cui 2011; Qian et al. 2011; Shen et al. 2013; Kim et al. 2016; Andriyono et al. 2019; Liu and Xia 2021; Baeza et al. 2024; Jeena et al. 2024). For phylogenetic analysis, Chow et al. (2024) and Jeena et al. (2024) did not use the complete mtDNA sequence of *P. penicillatus* (accession number MT533488) reported by Liu and Xia (2021) because the sequences of the COI and 16S rDNA regions of this mitogenome did not match those of *P. penicillatus* reported previously. Jeena et al. (2024) also noted that the control region sequence of MT533488 showed very high similarity to that of *P. inflatus*. Based on adult morphology and geographic distribution, *Panulirus* lobster species were classified into four groups (I to IV) (George and Main 1967), with *P. penicillatus* in group II and *P. inflatus* in group IV. Several molecular phylogenetic analyses strongly supported two divergent groups (I/II and III/IV) in the genus *Panulirus* (Ptacek et al. 2001; Chow et al. 2006; Palero et al. 2009; Bracken-Grissom et al. 2014; Davis et al. 2015; Jeena et al. 2016). In contrast, Liu and Xia's (2021) *P. penicillatus* was placed in group III/IV. We attempted phylogenetic analyses using the COI and 16S rDNA region sequences of MT533488, the previously available *P. penicillatus*, *P. echinatus* as the closest relative of *P. penicillatus* (Ptacek et al. 2001; Chow et al. 2011), *P. inflatus*, *P. japonicus* as a representative of group I/II, and *P. ornatus* as a representative of group III/IV. Since substantial genetic differentiation has been reported among Indian Ocean (IN), Western Pacific (WP), and Eastern Pacific (EP) populations of *P. penicillatus* (Chow et al. 2011; Abdullah et al. 2014; Iacchei et al. 2016), the two most divergent haplotypes were selected from each ocean basin sample. Both trees (Figs. 1 and 2) apparently indicated that MT533488 is not from *P. penicillatus*, and the average nucleotide sequence divergence (K2P distance) between MT533488 and other *P. penicillatus* sequences was 24.8 % in COI and 20.5 % in 16S rDNA. As Jeena et al. (2024) found, we also observed that the control region sequence of MT533488 was highly homologous (98 % identity) to that of *P. inflatus* (accession number OR612314). Moreover, Abdullah et al. (2014) reported partial nucleotide sequences of the control region from 469 *P. penicillatus* individuals collected in the Pacific Ocean, all of which were too divergent from MT533488 to obtain an unambiguous alignment. Thus, the specimen analyzed by Liu and Xia (2021) was not *P. penicillatus* but must be assigned to *P. inflatus*. Liu and Xia (2021) mentioned that the specimen they used was collected in Qionghai, China (19°18'48.37" N, 110°40'20.21" E), but the distribution of *P. inflatus* is restricted to the Pacific coast of central North America (Holthuis 1991). It is possible that the specimen used by Liu and Xia (2021) was imported and purchased at a fish market in China. We believe that the morphology of the specimen stored at the Qionghai Research Base of the population Hainan Academy of Ocean and Fisheries Sciences, China should therefore be re-examined.

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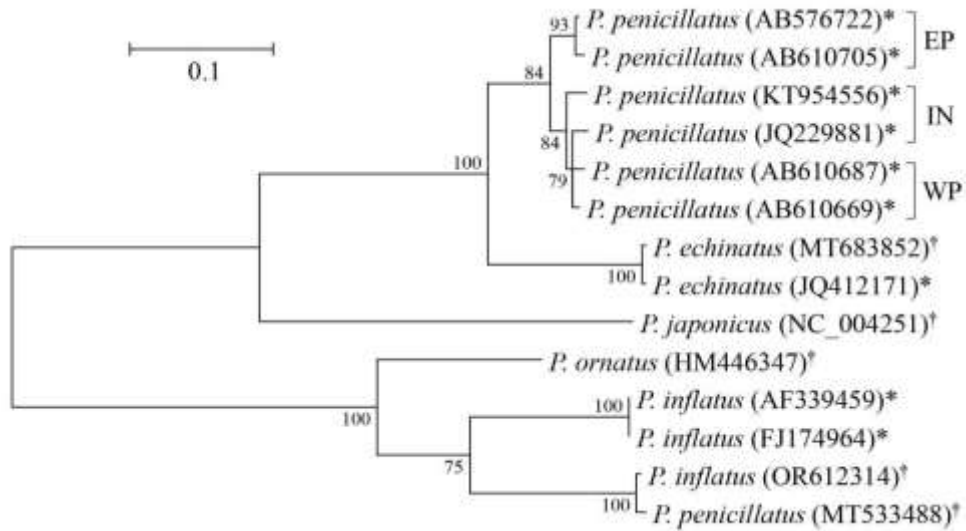


Fig. 1. Maximum likelihood phylogenetic tree of selected spiny lobster species of the genus *Panulirus* based on the HKY+G best-fit model for the mitochondrial COI sequences. Asterisks and daggers indicate partial and entire stretch sequences, respectively. Bootstrap probabilities over 50 % (1,000 replicates) are shown at the node. EP: Eastern Pacific, IN: Indian Ocean, WP: Western Pacific.

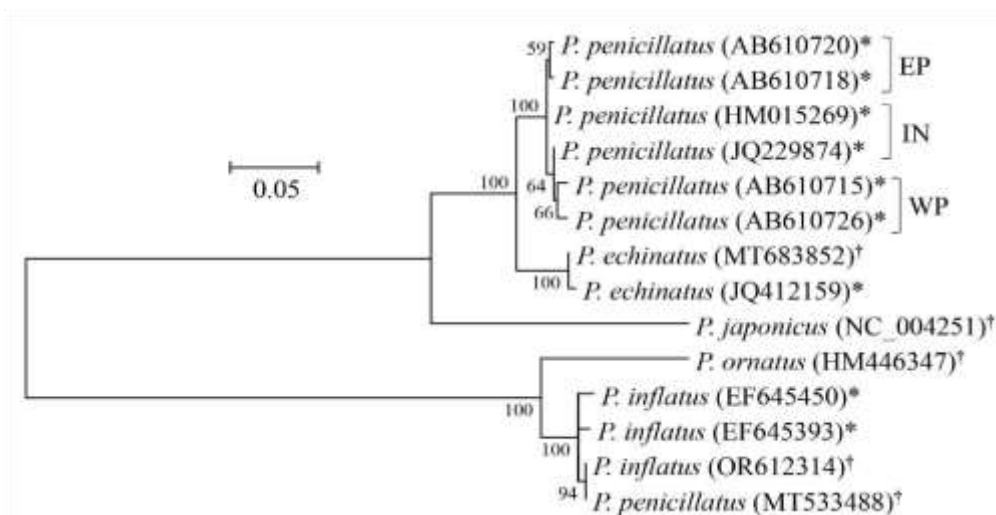


Fig. 2. Maximum likelihood phylogenetic tree of selected spiny lobster species of the genus *Panulirus* based on the HKY+I best-fit model for the mitochondrial 16S rDNA sequences. Asterisks and daggers indicate partial and entire stretch sequences, respectively. Bootstrap probabilities over 50 % (1,000 replicates) are shown at the node. EP: Eastern Pacific, IN: Indian Ocean, WP: Western Pacific.