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## A strange mitogenome sequence in spiny lobster

Seinen Chow<sup>1\*</sup>, Philippe Borsa<sup>2</sup>

<sup>1</sup>Aquos Institute, 3-2153-79 Motohachioji, Hachioji, Tokyo193-0826, Japan. <sup>2</sup>Institut de recherche pour le développement - UMR 250 S, Nouméa, New Caledonia and Montpellier, France.

\*Corresponding author, e-mail: kaiyoeel@yahoo.co.jp

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**Abstract** - Lobsters of the genus *Panulirus* are commercially important. A number of genetic studies in *Panulirus* spp. have investigated evolutionary relationships and population structure. To date, the complete mitochondrial DNA (mtDNA) sequences of 17 *Panulirus* species have been published. Based on *COI* and *16S rDNA* phylogenies, it appears that one of these complete mtDNA sequences, labelled “*P. penicillatus*” [H. Liu and G. Xia, *Mitoch. DNA Pt. B*, 6 (2021) 148–150; GENBANK accession no. MT533488], should be assigned to *P. inflatus*.

**Keywords** - *Panulirus inflatus*; *P. penicillatus*; mitogenome; *COI*; 16S rDNA; control region

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.

## References

- Abdullah, M. F., Chow, S., Sakai, M., Cheng, J-H., Imai, H. (2014). Genetic diversity and population structure of pronghorn spiny lobster *Panulirus penicillatus* in the Pacific Region 1. *Pac. Sci.* 68:197–211.
- Andriyono, S., Alam, M. J., Pramono, H., Abdillah, A. A., Kim, H. W. (2019). Next-generation sequencing yields the complete mitochondrial genome of mud spiny lobster, *Panulirus polyphagus* (Crustacea: Decapoda) from Madura water. *IOP Conf. Ser. Earth Environ. Sci.* 348: 012020.

- Baeza, J. A., Baker, A., Childress, M., Pirro, S. (2024). Nuclear and mitochondrial genome datasets for spiny lobster genus *Panulirus* (Decapoda: Achelata: Palinuridae). Data Brief 55: 110588.
- Bracken-Grissom, H. D., Ahyong, S. T., Wilkinson, R. D., Feldmann, R. M., Schweitzer, C. E., Breinholt, J. W., Bendall, M., Palero, F., Chan, T. Y., Felder, D. L., Robles, R., Chu, K. H., Tsang, L. M., Kim, D., Martin, J. W., Crandall, K. A. (2014). The emergence of lobsters: phylogenetic relationships, morphological evolution and divergence time comparisons of an ancient group (Decapoda: Achelata, Astacidea, Glypheidea, Polychelida). Syst. Biol. 63: 457–479.
- Chow, S., Suzuki, N., Imai, H., Yoshimura, T. (2006). Molecular species identification of spiny lobster phyllosoma larvae of the genus *Panulirus* from the northwestern Pacific. Mar. Biotech. 8: 260–267.
- Chow, S., Jeffs, A., Miyake, Y., Konishi, K., Okazaki, M., Suzuki, N., Abdullah, M. F., Imai, H., Wakabayasi, T., Sakai, M. (2011). Genetic isolation between the western and eastern Pacific populations of pronghorn spiny lobster *Panulirus penicillatus*. PLoS One 6: e29280.
- Chow, S., Yasuike, M., Yanagimoto, T. (2024). Reevaluation of nuclear mitochondrial pseudogenes (NUMTs) and heteroplasmy in the Japanese spiny lobster *Panulirus japonicus*. Crust. Res. 53: 27–36.
- Davis, K. E., Hesketh, T. H., Delmer, C., Willis, M. A. (2015). Towards a supertree of arthropoda: a species-level supertree of the spiny, slipper and coral lobsters (Decapoda: Achelata). PLoS One 10: e0140110.
- George, R. W., Main, A. R. (1967). The evolution of spiny lobsters (Palinuridae): a study of evolution in the marine environment. Evolution 21: 803–20.
- Holthuis, L. B. (1991). FAO Fisheries Synopsis FAO species catalogue. Vol. 13. Marine Lobsters of the World. FAO, Rome.
- Iacchei, M., Gaither, M. R., Bowen, B. W., Toonen, R. J. (2016). Testing dispersal limits in the sea: range-wide phylogeography of the pronghorn spiny lobster *Panulirus penicillatus*. J. Biogeogr. 43: 1032–1044.
- Jeena, N. S., Gopalakrishnan, A., Radhakrishnan, E. V., Kizhakudan, J. K., Basheer, V. S., Asokan, P. K., Jena, J. xK. x (2016). xMolecular xphylogeny xof commercially important lobster species from Indian coast inferred from mitochondrial and nuclear DNA sequences, Mitochondrial DNA Part A 27: 2700–2709.
- Jeena, N. S., Rahuman, S., Sebastian, W., Kumar, R., Sajeela, K. A., Kizhakudan, J. K., Menon, K. K., Roul, S. K., Gopalakrishnan, A., Radhakrishnan, E. V. (2024). Mitogenomic recognition of incognito lineages in the mud spiny lobster *Panulirus polyphagus* (Herbst, 1793): A tale of unique genetic structuring and diversification. Int. J. Biol. Macromol. 277: 134327
- Kim, G., Yoon, T-H., Park, W. G., Park, J. Y., Kang, JH., Park, H., Kim, H. W. (2016). Complete mitochondrial genome of Australian spiny lobster, *Panulirus cygnus* (George, 1962) (Crustacea: Decapoda: Palinuridae) from coast of Australia. Mitochondrial DNA A DNA Mapp. Seq. Anal. 27: 4576–4577.
- Liu, Y., Cui, Z. (2011). Complete mitochondrial genome of the Chinese spiny lobster *Panulirus stimpsoni* (Crustacea: Decapoda): genome characterization and phylogenetic considerations. Mol. Biol. Rep. 38: 403–410.
- Liu, H., Xia, G. (2021). The complete mitochondrial genome of pronghorn spiny lobster *Panulirus penicillatus* (Olivier, 1791). Mitochondrial DNA Part B 6: 148–150.
- Palero, F., Crandall, K. A., Abelló, P., Macpherson, E., Pascual, M. (2009). Phylogenetic relationships between spiny, slipper and coral lobsters (Crustacea, Decapoda, Achelata). Mol. Phylogenet. Evol. 50: 152–162.
- Ptacek, M. B., Sarver, S. K., Childress, M. J., Herrnkind, W. F. (2001). Molecular phylogeny of the spiny lobster genus *Panulirus* (Decapoda: Palinuridae). Mar. Freshw. Res. 52: 1037–1047.
- Qian, G., Zhao, Q., Wang, A., Zhu, L., Sun, H. (2011). Two new decapod (Crustacea: Malacostraca) complete mitochondrial genomes: bearing on the phylogenetic relationships within the Decapoda. Zool. J. Linnean Soc. 162: 471–481.
- Shen, H., Braband, A., Scholtz, G. (2013). Mitogenomic analysis of decapod crustacean phylogeny corroborates traditional views on their relationships. Mol. Phylogenet. Evol. 66: 776–789.
- Yamauchi, M. M., Miya, M. U., Nishida, M. (2002). Complete mitochondrial DNA sequence of the Japanese spiny lobster, *Panulirus japonicus* (Crustacea: Decapoda). Gene 295: 89–96.

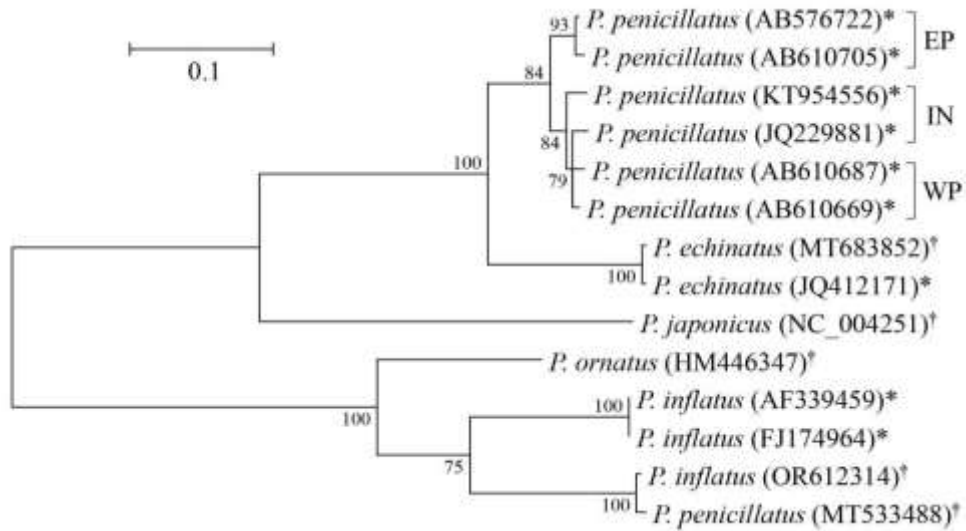


Fig. 1. Maximum likelihood phylogenetic tree of selected spiny lobster species of the genus *Panulirus* based on the HKY+G best-fit model for the mitochondrial COI sequences. Asterisks and daggers indicate partial and entire stretch sequences, respectively. Bootstrap probabilities over 50 % (1,000 replicates)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

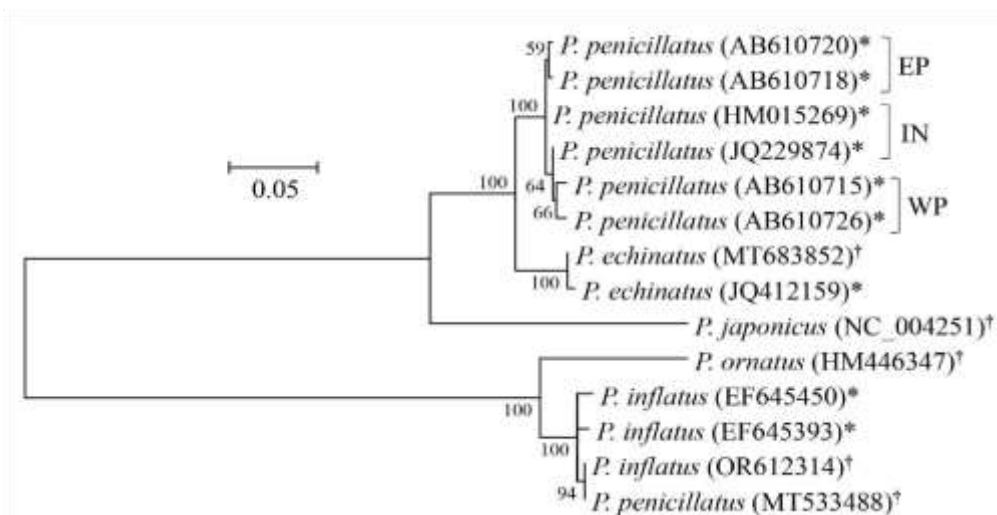


Fig. 2. Maximum likelihood phylogenetic tree of selected spiny lobster species of the genus *Panulirus* based on the HKY+I best-fit model for the mitochondrial 16S rDNA sequences. Asterisks and daggers indicate partial and entire stretch sequences, respectively. Bootstrap probabilities over 50 % (1,000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