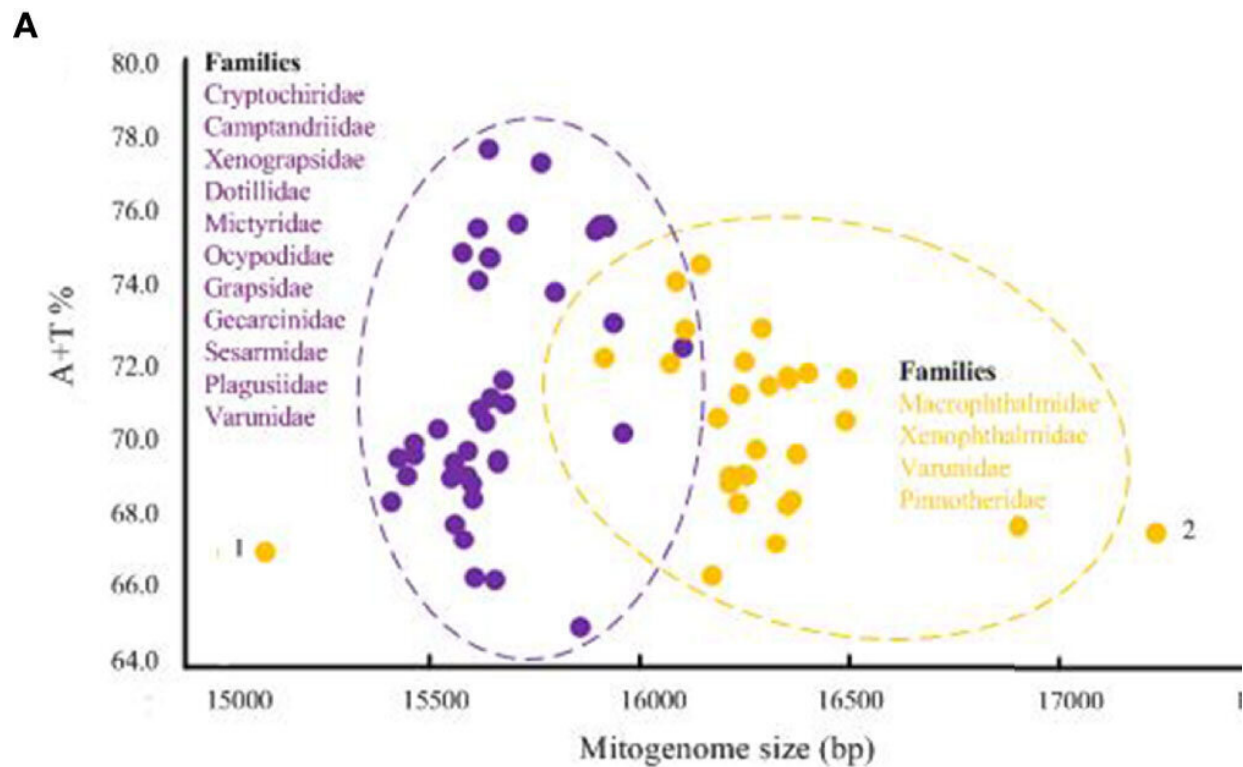


# Study reveals evolution of crab group Thoracotremata

May 13 2022, by Li Yuan



(A) Genome size versus A+T content of the thoracotreme mitogenomes. The yellow dots represented the families Macrophthalmidae, Xenophthalmidae, Varunidae, and Pinnotheridae. The purple dots represented the families Cryptochiridae, Camptandriidae, Xenograpsidae, Dotillidae, Mictyridae, Ocypodidae, Grapsidae, Gecarcinidae, Sesarmidae, Plagusiidae, and Varunidae. The yellow dots 1 (15,107 bp) and 2 (17,226 bp) represented *Chasmagnathus convexus* from Varunidae and *Macrophthalmus pacificus* from Macrophthalmidae, respectively, which were the outliers. (B) AT-skew versus

GC-skew in the thoracotreme mitogenomes. Ocypodoidea, Grapsoidea, Cryptochiroidea, and Pinnotheroidea were represented by blue, red, yellow, and green dots, respectively. Credit: *Frontiers in Marine Science* (2022). DOI: 10.3389/fmars.2022.848203

Thoracotremata (Brachyura, Decapoda) is the most derived crab group, encompassing 1,248 extant species. It currently comprises four superfamilies: Grapsoidea MacLeay, Ocypodoidea Rafinesque, Cryptochiroidea Paulson and Pinnotheroidea De Haan.

As one of the most diverse crab groups with diversified lifestyles, the phylogenetic relationships of Thoracotremata are unclear.

Recently, a research team led by Prof. Sha Zhongli from the Institute of Oceanology of the Chinese Academy of Sciences (IOCAS) has revealed the evolution of mitochondrial gene order (MGO) among thoracotremes, and provided new insights into the internal phylogenetic relationships of Thoracotremata.

The study was published in *Frontiers in Marine Science* on April 14.

The researchers obtained twelve new mitogenomes from the four thoracotreme superfamilies, which enhanced the taxonomic coverage of Thoracotremata mitogenomic data. They also identified nine distinct patterns of MGO among thoracotreme mitogenomes, among which four MGOs were newly found.

The symbiotic groups, the cryptochiroid and pinnotheroid crabs, display variable MGOs, providing evidence for possible correlations of rearranged MGOs to the adaptation to specialized lifestyles.

The expanded Thoracotremata mitochondrial phylogenetic relationships were resolved for the first time. The Pinnotheroidea formed the basal monophyletic clade. Cryptochiroidea grouped with an ocypodoid lineage (Dotillidae/Xenophthalmidae/Camptandriidae) located at a more evolved position, indicating that commensalism may have evolved independently multiple times within Thoracotremata.

Moreover, the macrophthalmid crab *Tritodynamia horvathi* from Ocyphodoidea was more closely related to the varunid crab *Asthenognathus inaequipes* from Grapsoidea, which supports the inclusion of *Tritodynamia* in the family Varunidae.

"The [phylogeny](#) of Thoracotremata and the phylogenetic position of Cryptochiroidea and Pinnotheroidea within Thoracotremata were first estimated using mitogenomic data by inclusion of representatives of all available thoracotreme superfamilies. This study also provides a novel insight towards understanding the internal phylogenetic relationships of the thoracotreme superfamilies," said Dr. Sun Shao'e, first author of the study.

"The phylogenetic relationship based on mitogenomes was of great value to the studies of biodiversity, origin and evolution, as well as biogeography in Thoracotremata," said Prof. Sha.

**More information:** Shao'e Sun et al, Mitogenomes Provide Insights Into the Evolution of Thoracotremata (Brachyura: Eubrachyura), *Frontiers in Marine Science* (2022). [DOI: 10.3389/fmars.2022.848203](https://doi.org/10.3389/fmars.2022.848203)

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