

Diversity and taxonomy of *Mnestiidae* in the Pacific Ocean

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The problematic background of *Mnestia*

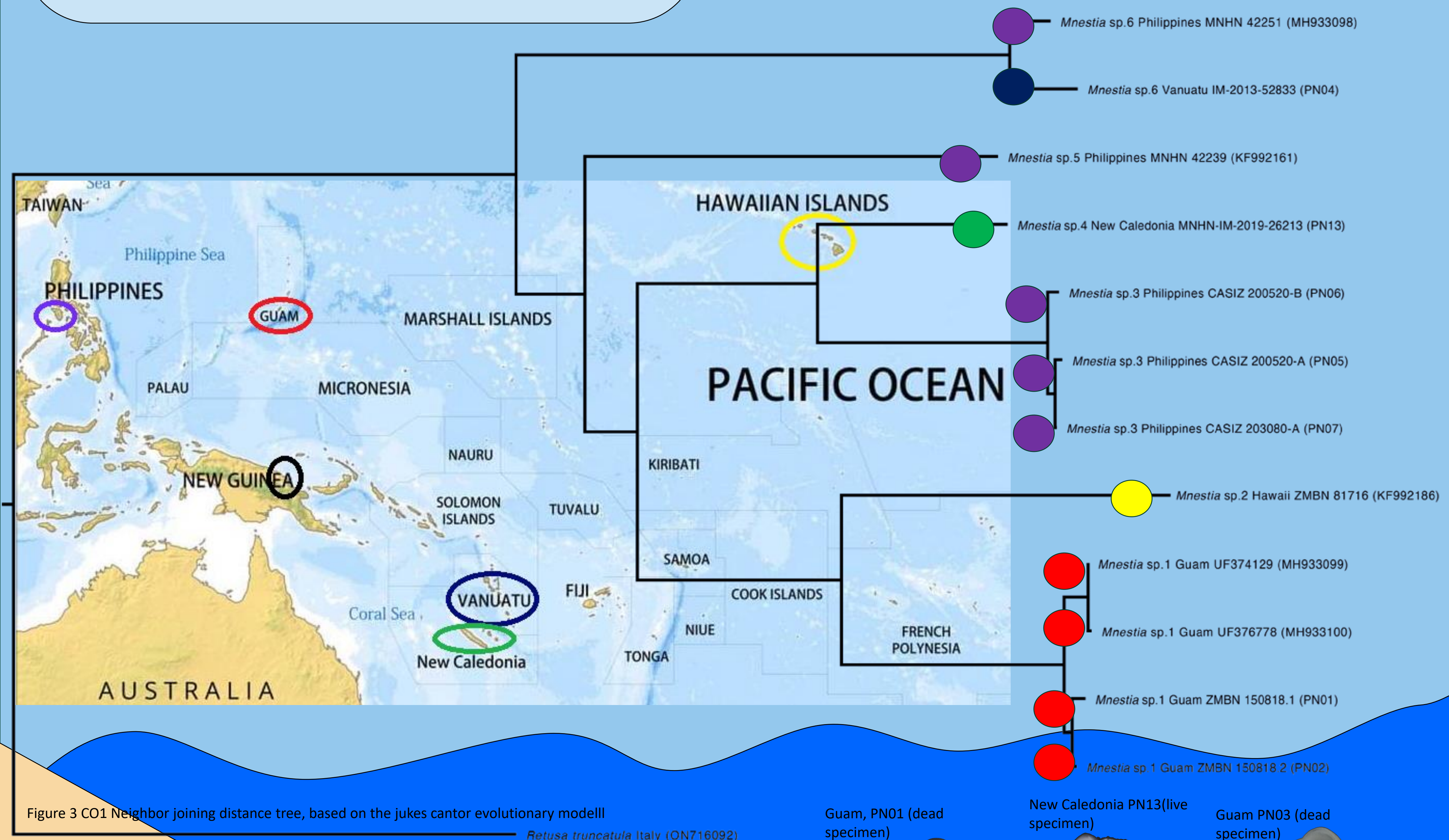
Mnestiidae is a family of bubble snails in the class **Gastropoda** and order **Cephalaspidea** with 3 genera and 10 nominal species, located in the **West Pacific and Red Sea**. They inhabit shallow subtidal waters often associated with sand and filamentous green algae.

The **validity of the 3 genera and 10 species that are considered valid, are questionable** because of the vague and elusive language used in the original description, these have no accompanying figures, creating a difficult and challenging taxonomy.

The goal of this project is to **explore** the **geographical diversity** of species in the family **Mnestiidae** using COI gene, shell characteristics and anatomical differences within a phylogenetic framework, and discuss the **validity** of the current species and **genera**.

Method

- 1. Photos** were taken of 12 of the specimens chosen for DNA sequencing, the photos were taken using **stereo microscopy**.
- 2. DNA was extracted** from specimens from Guam, Vanuatu, New Caledonia, the Philippines and Hawaii.
- The barcoding mitochondrial **COI gene** was **amplified** and sequenced using PCR for 9 specimens. 2 additional sequences were obtained from GenBank.
- 4. The sequences were edited** in the programme Geneious, and the alignment performed with Muscle, A distance Neighbour-Joining molecular phylogeny was inferred in Geneious.



Preliminary results

Using the **COI gene** and a **preliminary phylogenetic analysis** at least 12 species can be found in the West Pacific Ocean

The **taksonomy of the *Mnestia* family has become clearer**, as much of the background literature refers to synonym names that have been **confirmed to not** be a part of the *Mnestia* family. An example of this is *Mnestia arachis* which currently is considered a valid species, however we have been able to place it in the Cylichna family.

According to the neighbor joining distance tree, based on the evolutionary model, and the amount of valid species on WoRMS there is a possibility that a new species can be identified, however to be sure a more thorough analysis has to be made, as well as sequences for other coding genes to have any certainty.



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