

TO BE OR NOT TO BE THE SAME SPECIES?

Interpreting the significance of colour patterns in the sea slug genus *Nakamigawaia*

Emma S. E. Hellem (1) og Manuel A. E. Malaquias (2)

(1)Faculty of Mathematics and Natural Science, University of Bergen, Norway
(2)Department of Natural History, University Museum of Bergen, University of Bergen, Norway

BACKGROUND, GOALS & METHODS

Nakamigawaia is a small genus of marine sea snails in the family Aglajidae with two described species, *N. spiralis* known from the western Pacific Ocean and *N. felis* restricted to the Caribbean region in the western Atlantic Ocean. These sea slugs are small (approx. 0.5 cm) with a uniform all-black body. They are commonly found in tropical shallow waters in sandy habitats [1].

In 2017, during an expedition carried out by the University Museum of Bergen (UM/UiB) to Taiwan, black specimens of *Nakamigawaia* with white dots scattered over the dorsum were collected. This raised the question whether these white-dotted specimens were conspecific with *N. spiralis* or could be an undescribed species.

The aim of the project is to determine whether the white-dotted colour morph of *Nakamigawaia* found in Taiwan represents a new species or is part of the natural variability of *N. spiralis*.

DNA was extracted from specimens of *Nakamigawaia* from the Caribbean, Taiwan, and Japan. Three gene markers (the mitochondrial COI and 16S rRNA and the nuclear 28S rRNA) were amplified and sequenced. Additional sequences were obtained from GenBank. A Bayesian molecular phylogeny was inferred using the programme MrBayes [2]. Sequences were edited in Geneious [3], alignments performed with Muscle [4], and best fit models of evolution estimated with JModelTest [5]. Uncorrected *p*-distances between and within species and colour morphs were calculated with Mega [6].

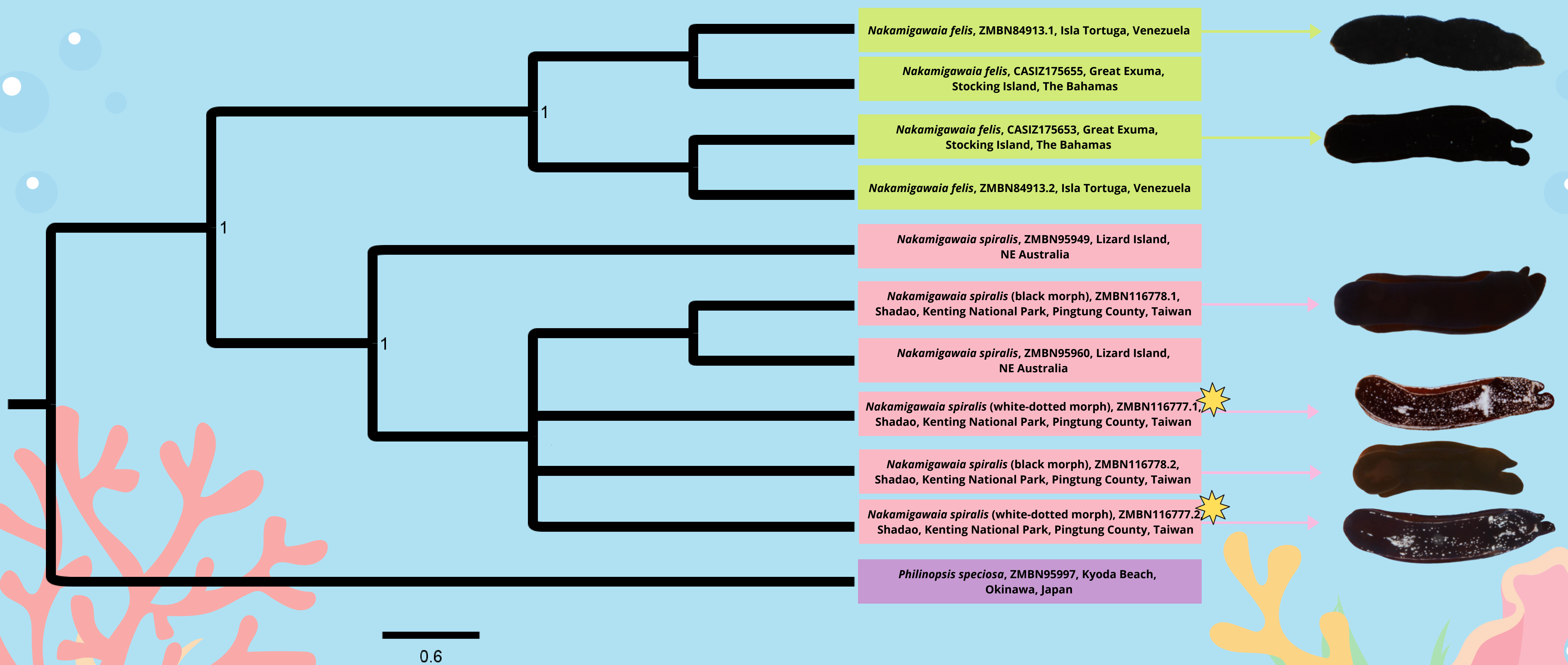


Figure 1: Bayesian molecular phylogeny for the genus *Nakamigawaia* based on the mitochondrial gene marker COI. Figures on nodes refer to posterior probabilities. Yellow stars refer to the white-dotted morph of *Nakamigawaia spiralis*.



Figure 2: *Nakamigawaia spiralis* black morph (Kenting, Taiwan; ZMBN116778).



Figure 3: *Nakamigawaia spiralis* white-dotted morph (Kenting, Taiwan; ZMBN116777).

RESULTS & CONCLUSIONS:

- The COI Bayesian tree shows two well differentiated clades with maximum support; one with all Caribbean specimens (*N. felis*) and the other with western Pacific specimens (*N. spiralis*).
- **No phylogenetic and genetic differentiation was detected between white-dotted and black morphs of *N. spiralis*.**
- The COI uncorrected genetic *p*-distance between white-dotted and black morphs of *N. spiralis* was estimated at 0–0.33%.
- The COI uncorrected genetic *p*-distance between *N. spiralis* and *N. felis* was 19.77–20.10%.
- The genus *Nakamigawaia* includes two species: *N. spiralis* and *N. felis*.
- **The white-dotted and black morphs are part of the natural variability of *N. spiralis*.**

Sources:

[1] Zamora-Silva, A. & Malaquias, MAE. 2018. *Zool. J. Linn. Soc.*, 183: 1–51. [2] Huelsenbeck, J.P. & Ronquist, F. 2001. *Bioinformatics*, 17: 754–755. [3] Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Meintjes, P. & Drummond, A. 2012. *Bioinformatics*, 28: 1647–1649. [4] Edgar, R.C. 2004. *Nucleic Acids Research*, 32: 1792–7. [5] Guindon, S. & Gascuel, O. 2003. *Systematic Biology*, 52: 696–704. [6] Kumar, S., Stecher, G., Li, M., Knyaz, C. & Tamura, K. 2018. *Molecular Biology and Evolution*, 35: 1547–1549.



SCAN ME

