

Morphological and Molecular Variation in *Rhinogobius rubromaculatus* (Pisces: Gobiidae) in Taiwan

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Hui-Ling Cheng, Shong Huang, and Sin-Che Lee (2005) Morphological and molecular variation in *Rhinogobius rubromaculatus* (Pisces: Gobiidae) in Taiwan. *Zoological Studies* 44(1): 119-129. A new color type was discovered in the Linbian River of southern Taiwan while investigating morphological and genetic variations of *Rhinogobius rubromaculatus*. The technical approaches we used included allozyme starch gel electrophoresis and partial mitochondrial DNA sequence analysis. Specimens from the Linbian River were characterized by smaller body and egg sizes, and indicated a significant negative correlation with temperature. None of the alleles was fixed among the new color type and *R. rubromaculatus* populations, with an allozyme genetic distance of from 0.001 to 0.078, which greatly differed from those of *R. candidianus* (0.523~0.687) and 2 other undetermined *Rhinogobius* species from the Ryukyus, Japan (0.326~0.464). The complete sequences of the cytochrome b gene, tRNA genes, and the control region of mtDNA revealed substitution differences within *R. rubromaculatus* at 207 base pairs (bp) and among the 3 species at 363 bp. The sequence diversity within the population was from 0.000 to 0.004. Among local populations of *R. rubromaculatus*, the sequence mean distance diversities were from 0.005 to 0.074, which is smaller than that between *R. rubromaculatus* and another *Rhinogobius* species (0.094~0.113). Both markers were congruent in revealing significant differences between samples of *R. rubromaculatus* (global $F_{ST} = 0.404$ for the allozyme and $\Phi_{ST} = 0.986$ for the mitochondrial DNA data). The molecular trees of *R. rubromaculatus* constructed based on both allozyme and mtDNA data revealed a closer relationship between central and southern populations than with a northern population. Discrete phenotypes could have been produced by phenotypic plasticity.
<http://www.sinica.edu.tw/zool/zoolstud/44.1/119.pdf>

Key words: Allozyme, Mitochondrial DNA, Population differentiation, *Rhinogobius rubromaculatus*.

The fluviatile goby, *Rhinogobius rubromaculatus*, from central Taiwan was first nominated in 1996 based on both morphometric and allozymic variations (Lee and Chang 1996). This species is an endemic freshwater fish distributed in tributaries of rivers throughout Taiwan at low and mid-elevations ranging from sea level to 1200 m except on the eastern side of the Central Mountain Range (Chen and Shao, 1996). The fish is generally pale brown with dusky transverse bands, and numerous red spots scattered over the entire body except the anal fin which is uniformly dark brownish. It also possesses the largest egg, higher vertebrae numbers, a shorter snout, and fewer pec-

toral rays among the Taiwanese members of the *Rhinogobius* genus. Nevertheless, little is known about its population structure.

During the course of field trips to extensively collect freshwater gobies throughout the island, a surprising new color type, which externally resembles *R. candidianus* and *R. rubromaculatus*, was obtained from a small river, the Linbian, in southwestern Taiwan. The body size of the Linbian form is the smallest among the *Rhinogobius* species in Taiwan. No other form has red spots scattered over the body. It also differs from 2 fluviatile species, *Rhinogobius* sp. 1 (yellow belly medium-egg type) and *Rhinogobius* sp. 2 (blue

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