

# **Population structure and genetically based latitudinal phenotypic variation of neon damsel fish (*Pomacentrus coelestis*) in Northwest-Pacific Ocean**

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## **Abstract**

The population genetic structure of neon damsel (*Pomacentrus coelestis*) in Northwest-Pacific Ocean was revealed by 343 bp mitochondrial first hypervariable region. A total of 170 fish were sampled from eight localities that distributed between Taiwan and Japan, and 71 haplotypes were obtained through sequence alignment. High haplotypic diversity with low nucleotide diversity ( $h = 0.956 \pm 0.008$ ,  $\pi = 0.010 \pm 0.006$ ) and the results of mismatch distribution test suggested that a historical population expansion might have occurred among *P. coelestis* populations. Based on the results of UPGMA tree and AMOVA ( $\Phi_{st} = 0.193$ ,  $p < 0.05$ ) analyses, fish populations from the eight sampling localities were divided into 2 groups. One includes populations from localities around mainland Japan, and the other includes those from Okinawa and southern Taiwan. A genetic break was found between mainland Japan and Okinawa that corresponding to the countergradient haplotypic variations found in previous studies. This provides the evidences to link the genetic variations with haplotypic variations of *P. coelestis* populations. Results from this study suggest both the Last Glacial Maximum and present current patterns played an important role on the genetic structure of *P. coelestis* populations.