



Population structure and demographic history of *Sicyopterus japonicus* (Perciformes; Gobiidae) in Taiwan inferred from mitochondrial control region sequences

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ABSTRACT. The amphidromous goby *Sicyopterus japonicus* is distributed throughout southern Taiwan and Japan. Larvae of this freshwater fish go through a long marine stage. This migratory mode influences population genetic structure. We examined the genetic diversity, population differentiation, and demographic history of *S. japonicus* based on the mitochondrial DNA control region. We

identified 102 haplotypes from 107 *S. japonicus* individuals from 22 populations collected from Taiwan and Islet Lanyu. High mean haplotype diversity ($h = 0.999$) versus low nucleotide diversity ($\theta_{\pi} = 0.008$) was detected across populations. There was low correspondence between clusters identified in the neighbor-joining tree and geographical region, as also indicated by AMOVA and pairwise F_{ST} estimates. Both mismatch distribution analysis and Tajima's D test indicated that *S. japonicus* likely experienced a demographic expansion. Using a Bayesian skyline plot approach, we estimated the time of onset of the expansion of *S. japonicus* at 135 kyr (during the Pleistocene) and the time of stable effective population size at approximately 2.5 kyr (last glacial maximum). Based on these results, we suggest 1) a panmictic population at the oceanic planktonic larval stage, mediated by the Kuroshio current; 2) a long planktonic marine stage and long period of dispersal, which may have permitted efficient tracking of environmental shifts during the Pleistocene; and 3) a stable, constant population size ever since the last glacial maximum.

Key words: *Sicyopterus japonicus*; D-loop; Planktonic larvae; Population structure; Demographic history