

# Population Structure and Demographic History of *Davidijordania poecilimon* (Perciformes: Zoarcidae)

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The population structure and demographic history of a zoarcid fish, *Davidijordania poecilimon* (Jordan and Fowler, 1902), around Japan were investigated on the basis of sequence variations in the cytochrome *b* gene of mitochondrial DNA (440 base pairs). Among 44 specimens, 18 haplotypes were recognized. Although some were shared among individuals from different localities in the Sea of Japan or in the Pacific Ocean, no haplotypes were shared between the two regions. The haplotype network showed a rough separation of the Sea of Japan and Pacific population haplotypes, forming a dumbbell-like pattern, each half with a major haplotype. In addition, the pairwise  $\Phi_{ST}$  between the Sea of Japan and Pacific populations of 0.35 was significant according to the permutation test ( $p < 0.01$ ). Such evidence indicates that gene flow between the two populations is restricted by the shallow strait (Tsugaru Strait) between the Sea of Japan and the Pacific Ocean. Mismatch distribution analysis suggests that the Pacific population comprises historically older and larger populations than those in the Sea of Japan.

**Key Words:** Teleostei, Actinopterygii, Sea of Japan, Pacific coast of Japan, *cyt-b*, mismatch distribution analysis.

## Introduction

The Sea of Japan, a marginal semi-enclosed sea in the western North Pacific, is continuous with neighboring waters via relatively narrow shallow straits (*ca.* 150 m depth maximum). Accordingly, sea level regressions during the last glacial period likely resulted in isolation of the Sea of Japan and the fragmentation of many populations of marine organisms (Tyler 2002). In fact, recent molecular and morphological studies have demonstrated that some of the fishes distributed along the Japanese Archipelago have diverged considerably between populations in the Sea of Japan and neighboring waters, such as the Pacific Ocean and/or the Sea of Okhotsk (Katafuchi and Nakabo 2007; Akihito *et al.* 2008; Kodama *et al.* 2008; Kai *et al.* 2011a, b; Kojima *et al.* 2011; Kokita and Nohara 2011; Hirase *et al.* 2012). Interestingly, the pattern of genetic divergence between the Sea of Japan and Pacific populations of coastal shallow-water fishes seems to differ from that of deep-sea fishes. Among coastal shallow-water fishes, for example, the distribution of Sea of Japan and Pacific populations of some goby species seems to

correspond to the routes of the warm Tsushima and Kuroshio Currents, the former occurring along the Sea of Japan coast of Japan and the Pacific coast of northern Honshu Island, and the latter along the Pacific coast of Japan from Kagoshima northward to Chiba (Akihito *et al.* 2008; Kokita and Nohara 2011; Hirase *et al.* 2012) (Fig. 1). In contrast, the distribution of the Sea of Japan and Pacific populations of deep-sea fishes, the zoarcid *Bothrocara hollandi* (Jordan and Hubbs, 1925) and the liparid *Careproctus rastrinus* Gilbert and Burke, 1912, seems to be restricted by the shallow straits (Kodama *et al.* 2008; Kai *et al.* 2011a, b; Kojima *et al.* 2011), apparently due to the fact that both species usually inhabit depths greater than 150 m (Okuyama 2004).

For an understanding of the impact of paleoenvironmental events on fishes of the Sea of Japan, it is necessary to determine common patterns of genetic structure shared by many species. Applications of comparative phylogeographic analyses can test for consistent genealogical splits among different species with overlapping ranges that can be explained by common biogeographic factors (Cutter 2013). As a case study pertinent to fishes of the Sea of Japan and neighboring waters, we investigated the genetic divergence