

トゲウオ科魚類における種分化の遺伝機構
Genetic mechanisms underlying stickleback speciation

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How are new species formed? To address this question, we are investigating the evolutionary mechanisms underlying reproductive isolation between two stickleback species in Japan, the Japan Sea and Pacific Ocean forms (Fig. 1). These two forms diverged 1.5-2 million years ago by geographical isolation, but are currently found in areas of sympatry, where they are reproductively isolated. We have identified both prezygotic isolating barriers (sexual isolation) and postzygotic isolating barriers (hybrid male sterility) between these sticklebacks. Sexual isolation is partly based on the divergence in male aggressiveness. Hybrid male sterility occurs only in one direction of hybridization. To investigate the genetic architecture of these isolating barriers, we conducted QTL mapping of male courtship behaviors and male sterility. First, we found that a newly evolved sex chromosome harbors genes that contribute to speciation. The Japan Sea form has a neo-sex chromosome system, which was created by a Y chromosome-autosome fusion. The neo-X chromosome has a QTL for the aggressiveness of male courtship behavior that contributes to sexual isolation. Second, we found that the ancestral X chromosome contains QTL for both sexual isolation and hybrid male sterility. Our data suggest that sex chromosome evolution might play an important role in stickleback speciation.

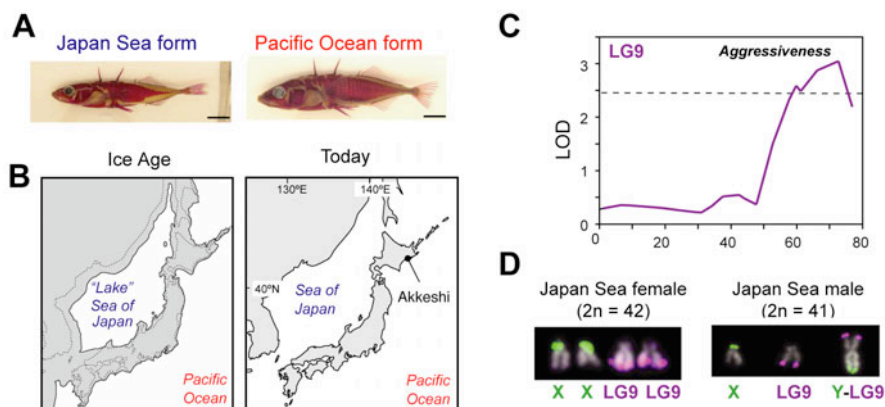


Figure 1. A. Two forms of the Japanese marine sticklebacks. Fish are stained with alizarin red. Scale bar = 1cm. B. Geographical isolation of the Sea of Japan during the ice age. C. Linkage mapping of the aggressiveness of dorsal pricking behavior. D. Fluorescence in situ hybridization of Japan Sea chromosome. In the Japan Sea male, Linkage group (LG) 9 and Y chromosome are fused. Purple = LG9, green = LG19.