

Sympatric or micro-allopatric speciation in glacial lake? Genomic islands support neither

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Scenery during sampling. Credit: IHB

Speciation is one of the core issues in evolutionary biology. Sympatric

speciation is the evolution of reproductive isolation without geographic barriers in which new species arise from a single ancestral population. However, bidirectional gene flow between species can retard or even reverse the population divergence in the early stages of sympatric speciation, raising doubts about this pattern of speciation.

Gymnocypris eckloni scoliostomus (GS) and *G. eckloni eckloni* (GE), two sister subspecies of *G. eckloni* (Cyprinidae: Schizothoracinae: *Gymnocypris*), are sympatrically distributed in Lake Sunmucu on the Qinghai–Tibet Plateau. Despite their close relationship, these two subspecies show significant differences in morphology, feeding preference and reproductive characteristics. The divergence time between the GS and GE lineages is estimated to be 20–60 Kya. All of these characteristics demonstrate that GS and GE satisfy the biogeographic criteria for sympatric speciation, which is crucial for the theoretical study of sympatric speciation.

Recently, a research group led by Prof. He Shunping from the Institute of Hydrobiology (IHB) of the Chinese Academy of Sciences demonstrated the speciation theory of sympatric speciation. This study was published in the *National Science Review*.

Using [genomic data](#) combined with theoretical simulation, the researchers examined the [genetic diversity](#), phylogeny, [genetic structure](#), population dynamic history, gene flow, genomic island, and selection of the two species. They proposed that sympatric speciation might be a micro-parapatric speciation model.

The researchers then suggested that the geographical scale of speciation should be defined based on gene flow during speciation. For instance, there is no gene flow during allopatric speciation, whereas during sympatric speciation, gene flow should be unimpeded. They identified 54 large genomic islands (≥ 100 kb) of speciation, which accounted for

89.4% of the total length of all genomic islands. Although they clearly indicated speciation with gene flow and rejected micro-allopatric speciation, the genomic islands were too large to support the hypothesis of sympatric speciation.

Theoretical and recent empirical studies suggested that continual gene flow in sympatry should give rise to many small genomic islands (as small as a few kilobases in size). Thus, the observed pattern was consistent with the extensive evidence on parapatric speciation, in which adjacent habitats facilitate divergent selection but also permit [gene flow](#) during speciation.

In addition, these islands harbored divergent genes related to [olfactory receptors](#) and olfaction signals that may play important roles in food selection and assortative mating in fishes.

This study suggests that many, if not most, of the reported cases of sympatric speciation are likely to be micro-parapatric [speciation](#).

More information: Ning Sun et al, Sympatric or micro-allopatric speciation in a glacial lake? Genomic islands support neither, *National Science Review* (2022). [DOI: 10.1093/nsr/nwac291](https://doi.org/10.1093/nsr/nwac291)

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