

Genome-wide RAD sequencing data suggest predominant role of vicariance in Sino-Japanese disjunction of the monotypic genus *Conandron* (Gesneriaceae)

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Abstract

Disjunct distribution is a key issue in biogeography and ecology, but it is often difficult to determine relative roles of dispersal vs. vicariance in disjunctions. *Conandron ramondioides* (Gesneriaceae) is a tertiary relict monotypic species distributed disjunctively in mainland China, Taiwan Island and Japan, where is a key region for understanding evolution and diversification of modern angiosperms. Population phylogenetic and phylogeographic structures of a comprehensive sampling of *C. ramondioides* by ddRAD sequencing were assessed, combined ABC modeling and SDM to infer the effects of multiple glaciation periods and to survey climatic niche differences by checking putative population divergence models and demographic scenarios. We found a very high degree of genetic differentiation among mainland China, Taiwan Island and Japan, with very limited gene flow between regions and a clear Isolation by Distance pattern. Mainland China and Japan clades diverged first from a widespread ancestral population in middle Miocene, followed by a later divergence between mainland China and Taiwan Island clades at early Pliocene. Three current groups have survived in various glacial refugia during LGM, and experienced contraction and/or bottlenecks since their divergence during Quaternary glacial cycles, with strong niche divergence between mainland China + Japan and Taiwan Island ranges. Overall, we verified a predominant role of vicariance in the current disjunction of monotypic genus *Conandron*. The sharp phylogenetic separation, ecological niche divergences among these three groups and the great number of private alleles in all populations sampled indicate a considerable time of independent evolution, and suggests the need of a taxonomic survey to detect potentially overlooked taxa.

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