

Incomplete reproductive isolation may promote hybrid zone formation between *Ligularia tongolensis* and *L. cymbulifera*

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Abstract

Natural hybridization is a common key evolutionary process and a long-standing topic in the plant taxon. Hybrid zones, where two closely related species interact, can provide an avenue to insight the process, illuminating the maintenance of the taxon diversity. Incomplete isolation barriers between *Ligularia* species generally form hybrid zones. In this study, we used the double digest restriction-site associated DNA sequencing technology (ddRAD-seq) to examine genetic structure and estimate introgression in four newly discovered hybrid zones between *L. tongolensis* and *L. cymbulifera*. Our results showed high differentiation between parental species, whereas pairwise F_{ST} between parents and their hybrids was low, further corroborating sympatric site form hybrid zones. Moreover, most F1 hybrid individuals were observed within the four hybrid zones implying the presence of substantial barriers to interbreeding. An analysis of genomic clines indicated that a large fraction of loci deviated from a model of neutral introgression in the four hybrid zones, of which most loci exhibited selection favouring *L. cymbulifera* genotypes. Our analysis demonstrated bidirectional but asymmetric introgression appearing in the four hybrid zones. The different habitats among four hybrid zones may affect isolation barriers between both species. Natural hybridization with post-zygotic isolation barriers may significantly contribute to the diversification of *Ligularia* in the HMR.

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