

DETAILS

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Phylogeography and paleoclimatic range dynamics explain variable outcomes to contact across a species' range

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Abstract

Replicability of divergence after contact is a poorly characterized process, particularly in the contexts of phylogeography and postglacial range dynamics within species. Using contact zones located at the leading-, mid- and rear-edges of a species' range, we examined variation in outcomes to contact between divergent lineages of *Campanula americana*. We investigated whether contact zones vary in quantity and directionality of gene flow, how phylogeographic structure differs between contact zones, and how historic range dynamics may affect outcomes to contact. We found that all contact zones formed at similar times via primary contact yet detected significant admixture in only the rear-edge (RE) contact zone. In the northern leading-edge contact zone and the mid-range Virginia contact zone, gene flow was minimal and asymmetric. In the southern RE contact zone, gene flow was strong and symmetric. Asymmetric admixture in the leading-edge and Virginia contact zones matches the directionality of a known cosmopolitan cytonuclear incompatibility between lineages of *C. americana*. Our results emphasize the dependence of speciation processes on phylogeographic structure, evolutionary history and range dynamics.

KEYWORDS
contact zones, phylogeography, range dynamics, speciation

1 | INTRODUCTION

Species often exhibit complex patterns of phylogeographic structure and intraspecific patterns of reproductive isolation across their respective ranges (Barnard-Kubow et al., 2017; Mandeville et al., 2015; Sianta et al., 2024; Van Riemsdijk et al., 2023). For example, in *Catostomus* spp., reproductive isolation was found to vary strongly among geographically isolated rivers (Mandeville et al., 2015). Similarly, other studies examining contact zones between divergent species of *Scaphiopus* (Giesen et al., 2022), intertidal mussels

reproductive isolation among closely related species. Yet, the phylogeographic contexts that presage the development of intraspecific genetic divergence is often ignored in the speciation literature (but see: Hewitt, 1996, 2000), leaving broad gaps in our understanding of how range dynamics inform both intraspecific patterns of phylogeographic divergence and broader processes of interspecific speciation (Cutter, 2015).

After the last glacial maximum, species' ranges expanded from southern refugia northward to occupy newly available habitat (Schröter, 2007). As ranges expanded, populations near

