

# Genomic divergence of *Stellera chamaejasme* through local selection on the Qinghai-Tibet Plateau and adjacent regions

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## Abstract

Understanding how populations diverge and new species arise is a central question in evolutionary biology. ‘Allopatric’ divergence through geographic isolation is considered to be the commonest mechanism generating species biodiversity in mountainous ecosystems. However, the underlying genomic dynamics, especially genomic islands of elevated divergence and genes that are highly diverged as a result of lineage-specific selection, remain poorly understood. *Stellera chamaejasme* is widely distributed on the Qinghai-Tibet Plateau and in adjacent regions, making it a good model with which to explore genomic divergence in mountainous ecosystems. We assembled a high-quality, chromosome-level genome for this species and re-sequenced the genomes of 24 populations across its distributional range. Our population genomic analyses recovered four distinct genetic lineages corresponding to geographic distributions with contrasting environments. However, we revealed that continuous gene flow occurred during the diversification of these four lineages and inter-lineage hybrids, and plastome introgressions were frequently found in regions of contact. The elevated genomic divergences were highly heterogeneous across the genome. The formation of such genomic islands showed neither correlation with rate of gene flow nor relationship to time of divergence. The lineage-specific positively selected genes potentially involved in local adaptation were found both within and outside genomic islands. Our results suggest that genomic divergence in *S. chamaejasme* is likely to have been triggered and further maintained by local selection in addition to geographic isolation.

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