

# The role of Pleistocene dispersal in shaping species richness of sky island wintergreens from the Himalaya-Hengduan Mountains

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In addition to topography and climate, biogeographic dispersal has been considered to influence plant diversity in the Himalaya-Hengduan Mountains (HHM), yet, the mode and tempo of sky island dispersal and its influence on species richness has been little explored. Through phylogenetic analysis of *Gaultheria* ser. *Trichophyllae*, a sky island alpine clade within the HHM, we test the hypothesis that dispersal has affected current local species richness. We inferred the dynamics of biogeographic dispersal with correlation tests on direction, distance, occurrence time, and regional species richness. We found that *G. ser. Trichophyllae* originated at the end of the Miocene and mostly dispersed toward higher longitudes (eastward). In particular, shorter intra-regional eastward dispersals and longer inter-regional westward dispersals were most frequently observed. We detected a prevalence of eastward intra-region dispersals in both glacial periods and interglacials. These dispersals may have been facilitated by the reorganization of paleo-drainages and monsoon intensification through time. We suggest that the timing of dispersal corresponding to glacial periods and the prevalence of intra-region dispersal, rather than dispersal frequency, most influenced the pattern of species richness of *G. ser. Trichophyllae*. This study facilitates a more comprehensive understanding of biodiversity in the sky islands within the HHM.

## Haplotype network and phylogenetic relationships • Biogeographic dispersal pattern

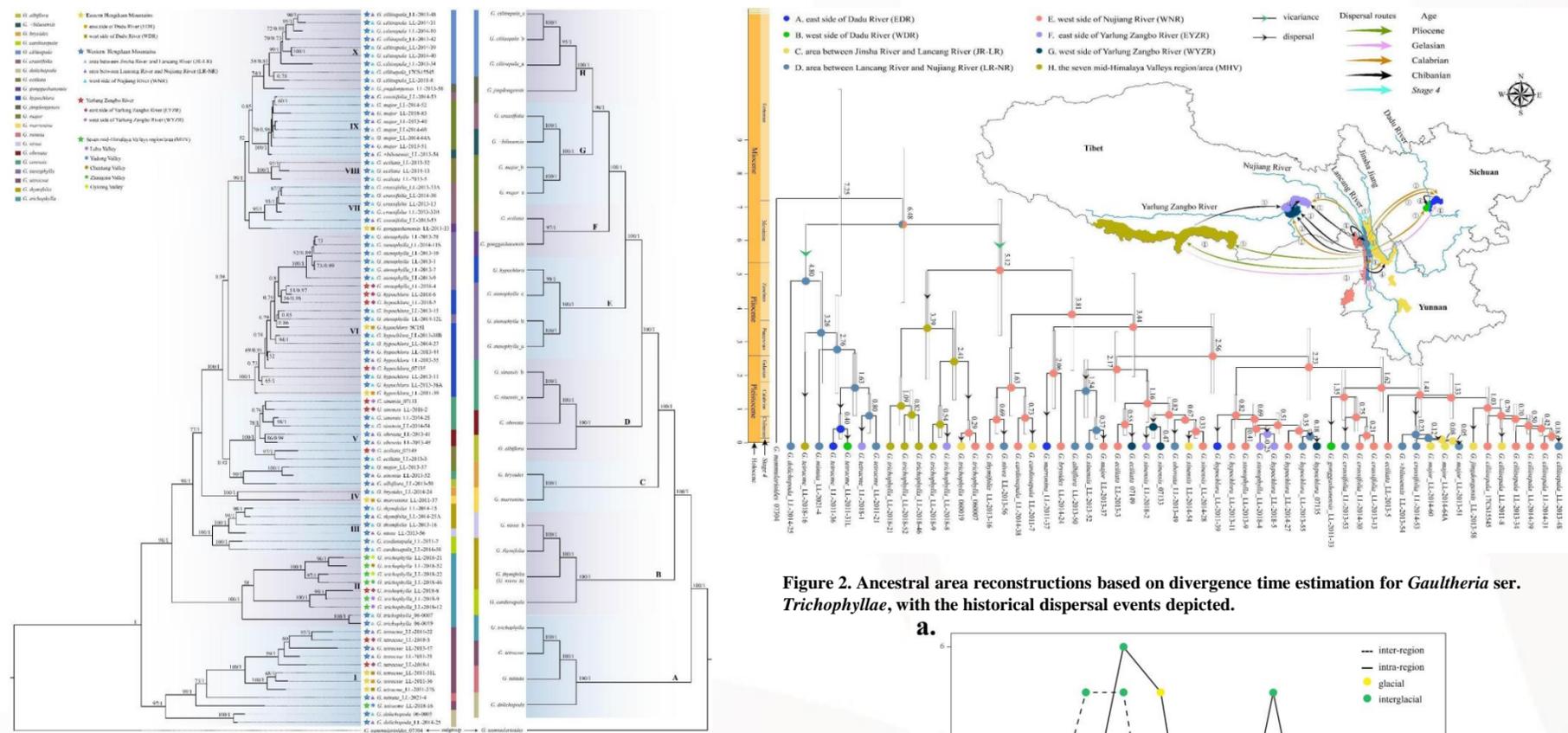


Figure 2. Ancestral area reconstructions based on divergence time estimation for *Gaultheria* ser. *Trichophyllae*, with the historical dispersal events depicted.

Figure 1. Comparison of tree topologies generated in our study (left, shown in a phylogram) and that of Zhang et al. (2017) (right, shown in cladogram). The left majority-rule consensus tree with Bayesian inference of 87 accessions of all 21 species within *Gaultheria* ser. *Trichophyllae* was reconstructed from the combined data of 22 cpDNA genic regions, and nDNA ITS and *PI*.

## Character optimization of elevation, longitude and latitude

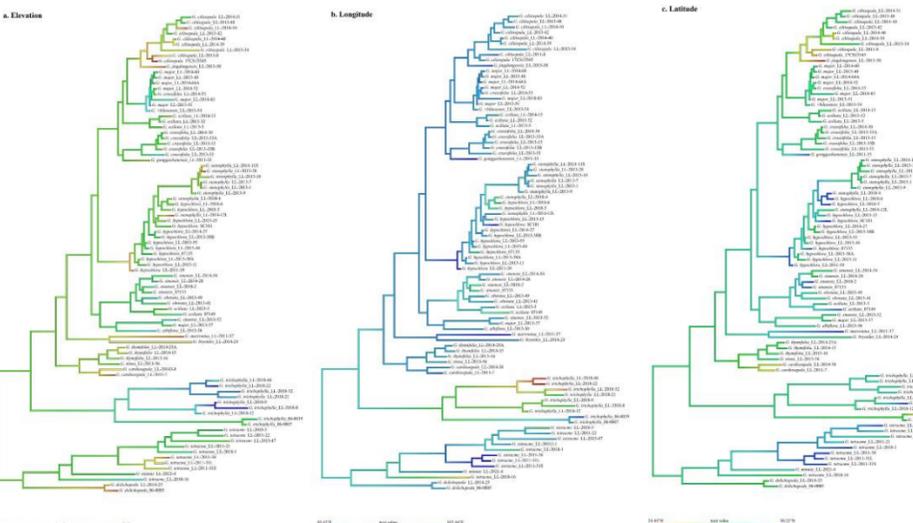


Figure 4 (a-c). Ancestral reconstruction of elevation, longitude and latitude of *Gaultheria* ser. *Trichophyllae*, with trait values optimized on the branches of the Bayesian Inference (BI) tree with R package phytol.

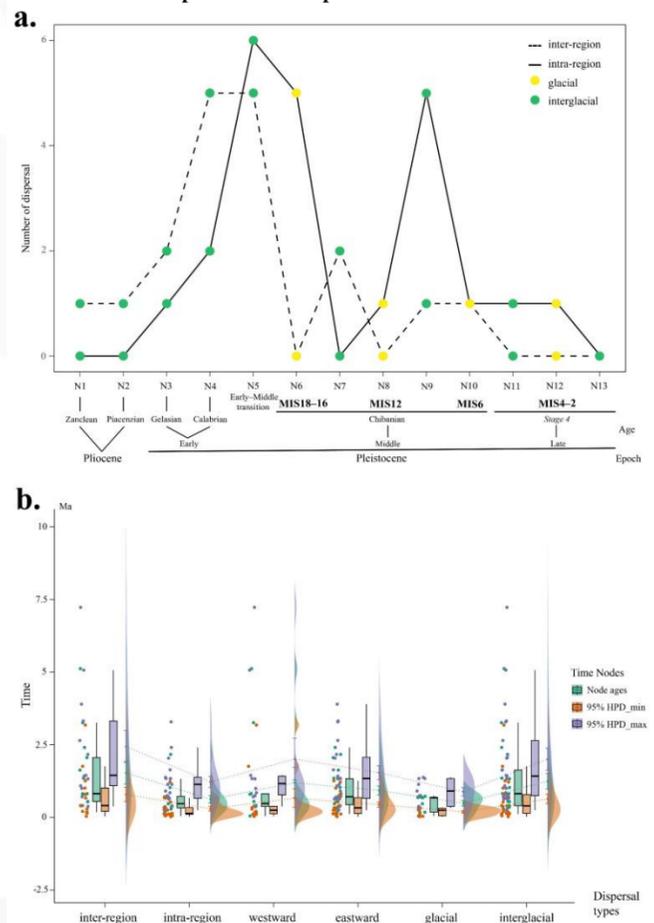


Figure 3. The biogeographic dispersal pattern of *Gaultheria* ser. *Trichophyllae*. Fig (a) the variation trend of the dispersal frequency during the Pliocene and Pleistocene. Fig (b) the six dispersal categories throughout the geological timeline with phylogenetic uncertainty in age estimates considered.



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