Abstract

The accelerating loss of global biodiversity necessitates proactive conservation strategies that integrate genetic diversity with projected climate impacts, especially in biodiversity hotspots such as the Hengduan Mountains. While previous phylogeographic studies in this region primarily relied on a few DNA fragments, plastid phylogeography has seldom been integrated with ecological niche modelling for conservation planning. Here, we combined plastid phylogeography and ecological niche modelling using data from 107 individuals across 14 populations of *Acanthochlamys bracteata*, a vulnerable alpine species and monotypic genus, to identify genetically distinct populations and predict potential climatic refugia. We identified three genetically distinct groups (Groups A to C), all characterised by low nucleotide diversity but high haplotype endemism. Notably, Group C comprised a single population from Luhuo County, Sichuan Province, and represents an independent evolutionarily significant unit due to its pronounced genetic distinctiveness. Most genetic variation occurred among populations, with one population showing relatively high diversity, while three lacked variation. A northward range shift and expansion of suitable habitats are projected under future climatic scenarios. Three climatic refugia were identified, characterized by divergent genetic lineages and numerous private haplotypes, and supported by the persistence of suitable habitat through time. The observed phylogeographic structure is likely driven by both geographical distance and relict persistence. We recommend that conservation efforts should focus on protecting genetically distinct and diverse populations through an integration of *in situ*, *ex situ*, and assisted migration measures. This study advances our understanding of the evolutionary history of *Acanthochlamys bracteata* and could serve as a model for conserving other rare and isolated plants under climate change and human disturbance.