



Glacial retreat and treeline shifts drive plant biodiversity in Hengduan Mountains (Southwest China) as revealed by sedimentary ancient DNA and modelling

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The Hengduan Mountains in southwest China are considered to be a biodiversity hotspot. However, the magnitude of changes in millennial-scale diversity and its driving forces are unknown. We inferred plant diversity from sedimentary ancient DNA records (sedaDNA) retrieved from Lake Naleng in Hengduan Mountains using trnl *g/h* DNA barcoding. Results were compared to estimated plant diversity, derived from modelled glacier and treeline changes, combined with modern plant diversity observations. During the time period 17.7 - 14.6 ka the catchment was largely covered by glaciers. Plant species richness is low due to the reduced habitat area available for alpine plants. Pronounced increase in alpine species richness starting at 14.5 ka was synchronous with glacier retreat due to a sharp increase in temperature, which allowed species to move upward and colonize new areas at higher altitude. A remarkably decrease in alpine plant species diversity occurred during the early Holocene temperature-related climate optimum. In contrast to alpine plants diversity, Pinaceae and Ericaceae, which presently are more common in the forest zone at lower altitudes, showed a high diversity during this period. Forest decline at 4.4 ka was accompanied by temporally increased alpine plant diversity. Overall, our results suggest that the plant diversity changes in millennial-scale in Hengduan Mountains were mainly caused by habitat changes (area effect), which we relate to climate-driven glacial dynamics and treeline shifts. To our knowledge this represents the first palaeodata-based proof of the importance of the area effect on plant diversity change. This implies that alpine area loss in the course of global warming will entail a loss of alpine plant diversity.