Background: Previous studies have indicated that several plant species had shown remarkable resistance to Pleistocene climate changes and survived the Last Glacial Maximum in scattered ice-free refugia within the European Alps and peripheral areas nearby. The ‘Expansion–Contraction’ model has been proposed to describe the responses of organisms to Pleistocene climate change. Nevertheless, the timing and extent to which species were affected by Quaternary glaciations remain uncertain.

Aims: To test whether the ‘Expansion–Contraction’ model appropriately describes plant distribution responses to Pleistocene climate change in the Western Alps.

Methods: We employed two Bayesian coalescent-based methods on plastid DNA sequences to infer the demographic histories of *Ranunculus kuepferi*, *R. glacialis*, *Biscutella laevigata*, *Saxifraga oppositifolia*, *Primula allionii*, *P. marginata*, *Silene cordifolia* and *Viola argenteria*.

Results: *R. kuepferi* conformed to the ‘Expansion–Contraction’ model, while other species did not. For example, *P. allionii* showed an alarming population decline during the Middle-Late Pleistocene.

Conclusions: The application of Bayesian coalescent-based methods to plastid DNA data offers useful insights into plant demography as a function of palaeoclimatic events. Our findings favour an idiosyncratic response of plant species in the Western Alps to Pleistocene climate change.