

Understanding the influence of past and present ecological factors on the population history and genetic divergence of plants is a fundamental question in the fields of ecology and evolutionary biology. Moreover, the extent of range overlap and range disproportion among closely related species offers valuable insights into the significance of geography and ecology in the processes of speciation and adaptation. *Cardamine hirsuta* has been established as a genetic system for comparative studies with *Arabidopsis thaliana* revealing a plethora of differences and resemblances. An open question about these closely related species revolves around whether past climatic events shaped their individual histories in a parallel or divergent fashion. In this study, variation data for the two aforementioned Brassicaceae species was generated using a uniform bioinformatics workflow ensuring reproducibility. Furthermore, the demographic history of *C. hirsuta* was reconstructed with the use of a contemporary ARG-reconstruction method and an approach based on the Site Frequency Spectrum (SFS), allowing for a comparison with the demographic history of *A. thaliana*. The results revealed the existence of two separate genetic ancestry clusters of *C. hirsuta* within Africa, specifically linked to the Eastern and Northern regions of the continent. This was in addition to the four genetic ancestry groups identified in Europe. Other findings indicated that the deepest split event in *C. hirsuta* occurred ~1.1 Mya. This event involved the East African population and a population that has not been sampled, possibly representing the Levant region. European populations, that is, Balkan and Iberia were inferred to have diverged from the ghost population. While in *C. hirsuta*, the North African population showed the most recent divergence and the smallest population size among all *C. hirsuta* populations, the North African population of *A. thaliana* had the earliest divergence and the largest population size. Results based on structural variants (SVs) from *C. hirsuta* confirmed the East African population to be the most diverged and revealed a large number of insertions and deletions fixed in the population.

As *Vitis vinifera* plays a significant role in both the economy and culture, serving as a prominent agricultural crop in Greece, it is noteworthy that there is a lack of recent population genetic studies on essential Greek grapevine cultivars. In this study, we investigated the genetic structure of wild and cultivated grapevines and constructed tree sequences to perform a genealogical analysis of three cultivated and one wild grapevine sampled from Greece. The results revealed the Balkanic origin of an Italian variety as well as the ancient variety Gouais. Lastly, by utilizing the GNN' method developed within the scope of this study, a wide range of opportunities can be pursued to examine accessions from *A. thaliana* and *C. hirsuta* that display ancestry from multiple genetic groups.