

Abstract

Background and Aims Afromontane forest ecosystems share a high similarity of plant and animal biodiversity, although they occur mainly on isolated mountain massifs throughout the continent. This resemblance has long provoked questions on former wider distribution of Afromontane forests. In this study *Prunus africana* (one of the character trees of Afromontane forests) is used as a model for understanding the biogeography of this vegetation zone.

Methods Thirty natural populations from nine African countries covering a large part of Afromontane regions were analysed using six nuclear microsatellites. Standard population genetic analysis as well as Bayesian and maximum likelihood models were used to infer genetic diversity, population differentiation, barriers to gene flow, and recent and all migration among populations.

Key Results *Prunus africana* exhibits strong divergence among five main Afromontane regions: West Africa, East Africa west of the Eastern Rift Valley (ERV), East Africa east of the ERV, southern Africa and Madagascar. The strongest divergence was evident between Madagascar and continental Africa. Populations from West Africa showed high similarity with East African populations west of the ERV, whereas populations east of the ERV are closely related to populations of southern Africa, respectively.

Conclusions The observed patterns indicate divergent population history across the continent most likely associated to Pleistocene changes in climatic conditions. The high genetic similarity between populations of West Africa with population of East Africa west of the ERV is in agreement with faunistic and floristic patterns and provides further evidence for a historical migration route. Contrasting estimates of recent and historical gene flow indicate a shift of the main barrier to gene flow from the Lake Victoria basin to the ERV, highlighting the dynamic environmental and evolutionary history of the region.