Abstract

Aims

A comprehensive understanding of the genetic variation of walnuts (*Juglans regia* and *J. sigillata*) in the Himalaya and its potential drivers are essential for the conservation and sustainable utilization of these plant genetic resources. In this study, we aimed to uncover the genetic landscape of walnuts and potential drivers in the Himalaya for better utilization, awareness, sustainable management and conservation of the extant genetic resources of walnuts in the vast Himalayan landscape.

Location

The Himalaya biodiversity hotspot.

Methods

A total of 1410 wild or feral walnut trees from 65 populations of *J. regia* and *J. sigillata* across four countries in the Himalaya were collected. The genetic diversity, population structure, hybridization and gene flow were thoroughly investigated based on the chloroplast genome and 31 nuclear microsatellite markers. The patterns and drivers of the walnut genetic landscape were further explored.

Results

We detected three genetic groups of *J. regia* (JR1, JR2, JR3), one of *J. sigillata* (JS) and two hybrid types (JR1 × JS and JR3 × JS) of walnut in the Himalaya, with the western Himalaya identified as the genetic diversity hotspot of *J. regia*. The spatial genetic pattern of the *J. regia* was significantly influenced by geographic and climatic factors. Human-mediated dispersal probably promoted the hybridization and gene introgression between *J. regia* and *J. sigillata*, which reshaped the genetic landscape of walnut populations in the Himalaya.

Main Conclusions

The extant genetic landscape of walnuts in the Himalaya was driven by natural and anthropogenic forces. Regarding conservation, the western and eastern Himalaya are the genetic reservoir of *J. regia* and *J. sigillata*, and hence, pure individuals should be urgently protected from frequent hybridization and introgression. In addition, we propose the utilization of natural hybrid resources coupled with new breeding techniques that combine genomic and phenotypic data.