

Abstract

Persian (Common) walnut (*Juglans regia* L.) is a famous fruit tree species valued for its nutritious nuts and high-quality wood. Although walnut is widely distributed and plays an important role in the economy and culture of Pakistan, the genetic diversity and structure of its populations in the country remains poorly understood. Therefore, using 31 nuclear microsatellites, we assessed the genetic diversity and population structure of 12 walnut populations sampled across Pakistan. We also implemented the geostatistical IDW technique in ArcGIS to reveal “hotspots” of genetic diversity. Generally, the studied populations registered relatively low indices of genetic diversity ($N_A = 3.839$, $H_O = 0.558$, $U_{HE} = 0.580$), and eight populations had positive inbreeding coefficient (F_{IS}) values. Low among-population differentiation was indicated by AMOVA, pairwise F_{ST} and D_C . STRUCTURE, PCoA and neighbor joining (NJ) analysis revealed a general lack of clear clustering in the populations except that one population in Upper Dir was clearly genetically distinct from the rest. Furthermore, the Mantel test showed no correlation between the geographic and genetic distance ($r = 0.14$, $p = 0.22$), while barrier analysis suggested three statistically significant genetic barriers. Finally, the spatial interpolation results indicated that populations in Ziarat, Kashmir, Dir, Swat, Chitral, and upper Dir had high intrapopulation genetic diversity, suggesting the need to conserve populations in those areas. The results from this study will be important for future breeding improvement and conservation of walnuts in Pakistan.