

Morphometric trait variability of autochthonous Walnut (*Juglans regia* L.) in north-western Himalayan region

Rafiq Ahmad Shah

Central Agricultural University, India

Abstract

The assessment of variability is the first step of crop improvement and selection of superior clones which depends on the extent of genetic variability present within the gene pool. Therefore the present study was undertaken to study the genetic variability of autochthonous walnut and to analyze the degree of association between different nut traits through correlation and path analysis. The correlation matrix was subjected to PCA to quantify and to find out major contributing traits and genotypes towards genetic diversity. Nut weight being an important trait showed positive correlation with nut width ($r = 0.540$), nut thickness ($r = 0.518$), kernel weight ($r = 0.765$) and kernel percent which is other important trait also showed positive correlation with kernel weight ($r = 0.582$) and negative correlation with shell per cent ($r = -0.969$) and shell thickness ($r = -0.890$). Kernel weight had maximum (0.947, 0.898) direct effect at phenotypic and genotypic respectively, on nut weight and maximum positive indirect effects on nut weight was exhibited by kernel per cent (0.696) via kernel weight. Kernel weight, kernel percent, Shell per cent and Shell thickness were the most contributing traits in the PC1, whereas nut weight was the principal trait of PC2. Among genotypes, JWSG-43 and JWSD-29 were most contributing (%) to PC1 and PC2. Based on quality of representation on factor map kernel percent > shell percent > kernel weight > shell thickness and nut weight were the major important contributing traits and among genotypes JWSD-18 and JWSG-43 were the most prominent contributing genotypes. This research helps to identify the relative amount of variability in nut traits and genotypes, detect and reveal the most important traits and genotype which explain the variability in the dataset. Furthermore, robust identification of important traits in this study can help to reduce the costs and time associated with phenotyping of all nut and kernel traits of each genotype and will help breeder in precise selection of promising genotypes based on objective of walnut breeding program.

Received: June 6, 2022; **Accepted:** June 11, 2022; **Published:** June 21, 2022

Biography

Rafiq Ahmad Shah has completed his/her phd at the age of 30 years from SKUAST-Jammu, India. He is working as Junior Research Fellow under DBT funded walnut Project. He has over 14 publications that have

been cited in national and international journals, and his publication H-index is 1 and has been a life member of different reputed Journals and societies.