

## Abstract

A thorough and extensive wild germplasm exploration survey was undertaken and 50 high yielding candidate plus trees (CPTs) of *Pongamia pinnata* (L.) Pierre from different locations from a latitudinal and longitudinal spread between 12°41' and 22°E longitude and 77° and 84°40'N latitude covering 11 locations in an area spread of 150,000km<sup>2</sup> were collected for evaluating genetic association and variability in seed and growth characters. There were significant differences observed in seed morphology and oil content as was in plant height, and number of branches in the progeny trial. Plant height and number of branches exhibited much higher values of both phenotypic and genotypic variance than observed in the seed characters. Among seed characters oil content exhibited highest broad sense heritability of more than 93% followed by seed length (90.0%). In contrast seed width showed the second highest genetic advance of 5.64% following the highest genetic advance of 10.15% exhibited by oil content. Hierarchical clustering by Ward's Minimum Variance Cluster Analysis method showed phylogeographic patterns of genetic diversity. K means clustering revealed that trees from different geographic regions were grouped together in a cluster and as were trees from the same geographical area placed in different clusters suggesting that geographical diversity did not go hand in hand with genetic diversity. In addition clustering identified promising accessions with favourable traits for future establishment of orchards. Keywords Biodiesel–Heritability–Genetic advance–Cluster analysis–Tree breeding–Germplasm