

ABSTRACT

The present study was carried out to investigate the genetic diversity of 145 genotypes/accessions of pea (*Pisum sativum* L.) at phenotypic level with morphological traits, both qualitative and quantitative. Out of 145 accessions, 82 were evaluated at molecular level using SDS-PAGE technique. Thirty-three morpho-physiological traits were recorded for the whole set of *Pisum* germplasm. Data regarding quantitative traits were analyzed by descriptive statistics and the association among various traits was estimated by correlation analysis. Descriptive statistics of quantitative traits revealed that considerable extent of diversity exists in the present set of *Pisum sativum* germplasm.

Quantitative traits showed significant variance for chlorophyll content, fresh pod width, fresh pod thickness, dry pod width, dry pod thickness, number of pods per plant, 100-seed weight, biomass, grain yield and harvest index. Among qualitative traits high degree of diversity was observed in dry seed color and hilum color. Spots on dry seed testa showed low degree of diversity. To estimate diversity at molecular level SDS-PAGE technique was used. SDS-PAGE results showed comparatively significant variations in major bands, although significant variations in minor bands were there. Variations were there in density of some common bands. The electrophoretic banding profile of seed proteins provides a powerful tool for estimating diversity existing in the

genotypes. Moreover, this technique is hardly affected by experimental conditions.

Selection of genotypes was made on the basis of best performance. Five genotypes 10473, 10603, 10607, 10644 and 11114 displayed high grain yield and have maximum harvest index. To confirm the yield potential, these accessions are suggested to be tested under a wide range of agro-ecological conditions and should be exploited in breeding high yielding cultivars in pea.

Genetic diversity revealed by qualitative, quantitative and molecular traits suggested that the significant variations were there in the genotypes. These variations can be used further for producing high yielding hybrids. Moreover, they are helpful in maintaining gene pool of a particular species and desirable traits. Breeding program primarily depends upon genetically diverse genotypes with high yield potential.