



Principal component analysis for assessing phenotypic parameters in brassica rapa var. Brown sarson

Asmat Ara¹, Rehana Mohi ud din², Uzma Mehraj³

^{1,3}Division of Genetics & Plant Breeding (India)

²Division of Agronomy (India)

Sher-e-Kashmir University of Agricultural Sciences & Technology of
kashmir, Faculty of Agriculture, Sopore

ABSTRACT

Principal component analysis (PCA) is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The principal component analysis (PCA), one of Multivariate Analysis methods elucidates among a set of the traits which ones are decisive in genotypic differentiation and selection. The present study was undertaken in rabi 2013-14 at three locations. The collection comprising of 10 genotypes including two checks namely SS-1 and Farmer's variety was studied using factor analysis. Ten quantitative traits related to seed yield namely days to flowering, days to maturity, plant height, primary branches plant⁻¹, length of main raceme (cm), number of siliquae on main raceme, number of siliqua plant⁻¹, number of seeds siliqua⁻¹, 1000-seed weight and seed yield plant⁻¹. Analysis of variance revealed that there were significant differences between checks and accessions, between accessions and between checks for all the traits. It indicated presence of substantial amount of variation among the test entries. The factor analysis was based on Pearson correlation matrix and Euclidean distances. Total variance explained by the first principal component was 67.03% and the variation explained by the second component with 10.6%. Latent roots (Eigen values) are between 6.703 for the first PC and 1.06 for the second PC. Plant height and 1000-seed weight were the important traits in the first principal component. Primary branches per plant and number of siliqua on main raceme were the important traits in second principal component.

Key Words : Genotype, Trait, Variation