CHARACTERIZATION OF OKRA GENOTYPES (*Abelmoschus esculentus* (L.) MOENCH) THROUGH PLANT MORPHOLOGY AND SEED QUALITY PARAMETERS

**ABSTRACT**

*Key words*: Characterization, plant, seed, morphology, analysis of variance, variability, heritability, correlation, path analysis, okra

The present investigation was carried out to assess the "Characterization of okra (*Abelmoschus esculentus* (L.) Moench) genotypes through plant morphology and seed quality parameters". The experiment was undertaken at Sagdividi Farm, Department of Seed Science and Technology, Junagadh Agricultural University, Junagadh during summer season 2016. The experiment was conducted on 28 genotypes (Released varieties), advance lines and accessions received from IIVR, Varanasi. The observations viz., stem diameter (cm), number of nodes at first flowering, number of leaves per plant, length of leaf blade (cm), width of leaf blade (cm), flower length (cm), flower diameter (cm), pedicel length (cm), days to 50% flowering, fruit length (cm), fruit diameter (cm), number of fruits per plant, number of branches per plant, plant height (cm), number of seeds per fruit, seed yield per plant (g) and 100-seed weight (g) was analysed by Randomized Block Design (RBD). The observations viz., speed of germination, germination percentage, shoot length (cm), root length (cm), seedling length (cm), seedling fresh weight (mg), seedling dry weight (mg), seedling vigour index, seed moisture content were analysed by Completely Randomized Design (CRD).

Based on the stem colour the genotypes were grouped into green (27 genotypes) and red (1 genotype). On the basis of Intensity of green colour on stem the genotypes were classified into medium intensity of green colour (14 genotypes) and dark intensity of green colour (14 genotypes). On the basis of stem diameter all the genotypes were grouped into large size of stem diameter. On the basis of Number of nodes at first flowering the genotypes were classified into few number of nodes at first flowering (15 genotypes) and medium number of nodes at first flowering (13 genotypes). On the basis of leaf vein colour all the genotypes were grouped into light green leaf vein colour. On the basis of depth of lobbing the genotypes were grouped into deep (7 genotypes), medium (15 genotypes) and shallow (6 genotypes). On the basis of flower petal colour all the genotypes were grouped into cream flower petal colour. On the basis of days to 50% flowering the genotypes were grouped into early days (8 genotypes) and medium days (20 genotypes). On the basis of fruit colour the genotypes were classified into green (27 genotypes) and red (1 genotype). On the basis of fruit diameter all the genotypes were grouped into large size of fruit diameter. On the basis of number of branches all the genotypes were classified into medium...
number of branches. On the basis of plant height all the genotypes were grouped into short plant height. On the basis of seed colour the genotypes were classified into green (13 genotypes) and brown (15 genotypes). On the basis of seed hairiness the genotypes were classified into hair present (1 genotype) and hair absent (27 genotypes).

Twelve genotypes were superior to general mean in speed of germination, seed germination percentage, seedling length, seedling dry weight, seedling vigour index I and seedling vigour index II. In shoot length eleven genotypes were superior to general mean. In root length fourteen genotypes were superior to general mean. In seedling fresh weight thirteen genotypes were superior to general mean. In seed moisture content fourteen genotypes were superior to general mean.

The analyses of variance revealed that mean square due to genotypes were significant for all the characters studied. It indicates the presence of sufficient variability in the material investigated in the present study.

The estimates of genotypic and phenotypic coefficient of variability indicated that the value of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters studied. The GCV and PCV were moderate for seed yield per plant followed by 100 seed weight, fruit length, fruit diameter, number of branches, number of fruits per plant, width of leaf blade, number of leaves per plant, number of nodes at first flowering, and number of seeds per fruit. The low estimates of GCV and PCV were observed for number of branches, number of fruits per plant, number of seeds per fruit, number of leaves per plant, width of leaf blade, days to 50 % flowering, stem diameter, plant height, pedicel length, length of leaf blade, flower length, flower diameter and stem diameter.

High values of heritability were observed for 100 seed weight followed by days to 50 % flowering, fruit length and flower length. Moderate to low values of heritability were observed for fruit diameter, number of seeds per fruit and number of nodes at first flowering.

The high genetic advance expressed as percent of mean found high for 100 seed weight. Moderate genetic advance expressed as percent of mean was reported for fruit length, seed yield per plant, fruit diameter, number of seeds per fruit, number of nodes at first flowering, number of fruits per plant, number of branches, number of leaves per plant. However low genetic advance expressed as percent of mean was reported for days to 50 % flowering, flower length, pedicel length, stem diameter, length of leaf blade, width of leaf blade, plant height, flower diameter.

In general the values of genotypes correlation were higher than phenotypic counter parts in present investigation for the most of the characters. This indicates that though there was a high degree of association between two variables at genotypic level its phenotypic expression was defeated by the influence of environment. Such low amount of phenotypic correlation could result due to the masking or modifying effect of environment on the association of characters.

The correlation of seed yield per plant showed positive and significant at genotypic and phenotypic level with fruit length, number of fruits per plant, plant height and number of seeds per fruit, indicating that the selection based on these traits will help increasing the yield of okra. The correlation of seed vigour index I showed positive and significant at genotypic level with seed germination percentage, shoot length, root length, seedling length, seedling fresh weight, and seedling vigour II.

The genotypic path coefficient analysis revealed that number of fruits per plant followed by number of seeds per fruit and 100-seed weight exhibited high and positive direct effect on seed yield per plant and was found to be the most important yield components. These above characters also had positive indirect effect on each other.