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## Study of morphological and molecular characterization of garlic (*Allium sativum* L.)

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**ABSTRACT :** Genotypic and phenotypic co-efficients of variation were high for average weight of clove, yield per plant, cloves per bulb and plant height. Width of clove, plant height and length of leaves, yield per plant, cloves per bulb, average weight of clove exhibited high heritability coupled with high genetic advance as per cent of mean. These characters are governed by additive gene effects. It was also concluded that selection on the basis of these characters will be more useful for the improvement of this crop towards attaining higher yield. Correlation co-efficient studies showed that phenotypic correlation co-efficients are higher than genotypic correlation which indicates the inherent association among the characters dependent of environment influence. Yield per plant had a positive and highly significant correlation with plant height, length of leaves, average weight of clove, equatorial diameter, polar diameter and clove/bulb which implies that these characters were contributing to bulb weight and bulb yield/plant. All the combination of traits should be considered while selecting for high yielding genotypes. Improvement of bulb weight per plant may be achieved by exercising direct selection of plant height, length of leaves, weight of cloves, equatorial diameter of bulb, clove weight, number of cloves per bulb, polar diameter of bulb and clove length as these exhibited significant positive direct effect on bulb weight per plant coupled with high heritability and high genetic advance as per cent of mean. Characters had correlation co-efficient value at par with their direct effect on bulb yield per hectare. In Mahalanobis D<sup>2</sup> analysis, On the basis of Mahalanobis D<sup>2</sup> values, all the 27 genotypes were grouped under study were grouped into six clusters. Cluster III (8), cluster V (6) and cluster VI (6) contained maximum number of genotypes and cluster I (4) and cluster II (2) comprising minimum number of genotypes and cluster IV contained single genotype.

**KEY WORDS :** PCR, SSR, Cluster, EDB, Genotype, Phenotype

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