Research Paper

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Studies on genetic variability and its importance in brinjal (*Solanum melongena* **L.**) **KARIBASAVA NAIK**, G.B. SREENIVASULU, S.J. PRASHANTH, R.P. JAYAPRAKASHNARAYAN, M.B.

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ABSTRACT

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KARIBASAVA NAIK Department of Olericulture, K.R.C. College of Horticulture, Arabhavi, BELGAUM (KARNATAKA) INDIA The experiment was conducted in 2005 at Olericulture Unit, Kittur Rani Channma College of Horticulture, Arabhavi, Gokak, Belgaum, Karnataka during *Kharif* season of 2004-05 to evaluate 61 genotypes using randomized block design. The observations on 24 characters were recorded. Genotypic and phenotypic variance were high for plant height, plant spread from east to west at 60 days after transplanting (DAT), number of fruits per plant, yield per plot and yield per hectare. High values of genetic advance over mean (GAM) coupled with high estimates of heritability was observed for characters fruit length, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per plot, yield, per hectare and fruit length-diameter ratio. This indicates additive component is predominant and hence direct selection would be more effective in improving these traits.

Key words : Genetic variability, Brinjal, Genotypes, Heritability

Genetic variability is essentially the first step of plant breeding for crop improvement and exploitation of variability is of great importance and is a prerequisite for the effective screening of superior genotypes. The progress in breeding for the economic characters that are mostly polygenically controlled and hence environmentally influenced is determined by the magnitude and nature of their genetic variability. Hence, it is essential to partition the overall variability into its heritable and nonheritable components with the help of genetic parameters like genetic coefficient of variation, heritability and genetic advance. With this aim, brinjal genotypes of diverse geographic and genetic origin assembled in the germplasm were evaluated for yield and other characters.

MATERIALS AND METHODS

Sixty-one genotypes were tested in a Randomized Block Design in two replications at Olericulture Unit, Kittur Rani Channamma College of Horticulture, Arabhavi, Gokak, Belgaum, Karnataka during *Kharif* season of 2004-05. Recommended cultural practices were adopted to obtain good phenotypic expression of the quantitative characters. Observations were recorded on five randomly selected plants in each treatment. Statistical analysis was done according to the methods of Panse and Sukhatme (1967), Burton and Devane (1953) for genotypic coefficient of variation, Falconer (1981) for heritability in broad sense and Robinson *et al.* (1949) for genetic advance.

RESULTS AND DISCUSSION

The Variances due to treatments (genotypes) was highly significant for all characters except plant spread east to west at 90 DAT, plant spreads form north to south at 60 and 90 DAT, early yield per plant and per cent fruit and shoot borer infestation, suggesting the presence of high genetic variability among the genotypes assessed.

The data for range, general mean, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance are presented in Table 2. A wide range of variation for different characters was observed. Phenotypic coefficient of variation was minimum for days to first fruit maturity (2.94) and maximum for total yield per plant (35.20). Similarly, genotypic coefficient of variation was minimum for days to first fruit maturity for days to first fruit maturity (2.64) and maximum for days to first fruit maturity (2.64) and maximum for days to first fruit maturity (2.64) and maximum for days to first fruit of variation were higher than genotypic coefficient of variation indicating that the genotypic influence is lessened under the influence of the given environment.

The estimated of heritability (broad sense) for most of the characters were moderate to high showing that the genotypes under study have a great scope for the selection based on these characters. The heritability estimates were highest for total sugar (98.33) followed by number of fruits per cluster (97.64), fruit length (96.94) number of primary branches at 90 DAT (96.59) and plant spread from east to west at 60 DAT (95.38). Genetic