# Variations, heritability and genetic advance studies in bougainvillea genotypes

L. SINGH, Z. RAM, A. SINGH, P. SINGH AND S. VERMA

## SUMMARY

Present investigation was conducted to study the variations, heritability and genetic advance studies in bougainvillea genotype. The considerable amount of genetic variation in genotype was noticed. A high heritability was found coupled with genetic advance. The best heritability was found in length of floral tube and diametre of branch which showed that influence of environment in different characters was less.

Key Words : Bougainvillea, Variations, Heritability, Genetic advance, Genotypes

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**B**ougainvillea is an important shrub belongs to the family Nyctanginanceae. Popularity of this plant as a shrub of climbing nature and its capacity for adoptability in various situations alongwith growing behavior are appreciated (Sindhu, 2001). It is a fast growing plant and has the exhaustive range of different colours (Criley, 1977; Kumar *et al.*, 1998; Khoshoo, 1998). Some of the varieties have a great potential for earning to the nurserymen for meeting out the demands of plants in the season (Jayanti, 2000; Kumar and Prasad, 2001; Swarup, 1993). Mathur (2001), Sindhu (2001) and Singh (1996) reported that it is needful and important to study the performance of existing varieties, hybrids and also to test the new ones for superiority of performance and also identity new colour or hybrids and colour combinations

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Address of the co-authors: L. SINGH AND Z. RAM, Department of Botany, C.P.W.D. (NEW DELHI) INDIA A. SINGH, Department of Botany, Govt. H.S.S. PAWARKHERA (M.P.) INDIA P. SINGH, Department of Botany, A.N.D. College, KANPUR (U.P.) INDIA S. VERMA, Department of Botany, N.B.R.I., LUCKNOW (U.P.) INDIA alongwith desirable floral parameters *i.e.* length of branch, sub-branch, more number and better size of bracts increasing its life on a branch or after removal from it and take in use for vaselife. In fact the knowledge of different varial characteristic and magnitude of genetic variability increase immense nature of planning for efficient breeding work to improve the desired potential of different genotypes.

#### **MATERIALS AND METHODS**

30 genotypes were selected for the present investigations. Experiment was planned in Randomized Block Design with three replications in D.A.V. College, Kanpur during 2006-07 and 2007-08. Observational data were analyzed as per method recommended by Robinson *et al.* (1949).

## **RESULTS AND DISCUSSION**

Results were drawn after data analysis which revealed the significant differences among the genotypes for different component characters. A considerable amount of genetic variation in the genotypes of bougainvillea was noted. A high range of heritability was found to range from 5.90202 to 95.98127 in diameter of thorn and length of branch, respectively. In fact high heritability was found coupled with

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· / ·	Damester of Coral wood	90.97755	19.21006	0.12059	0.05%	0.588//	0.22327	29.978.6		3.39808	22.19093
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the genetic advance. The next best high heritability was found in length of floral tube (93.52921) and diameter of branch (93.25093) (Table 1). This indicated the lesser influence of environment in expression of the different characters. It also indicated the prevalence of the additive gene action in their inheritance hence, it expressed the possibility of the simple action. Present findings are in accordance with the results observed by Mathur and Paswan (1995). In addition to that high heritability and moderate genetic advance was recorded for different characters indicating that the characters were also governed by additive gene action. Further it was marked to understand that high heritability coupled with low genetic advance was observed in certain characters indicating non gene action. Present findings are in conformity with the results reported by Misra et al. (1987) in their studies of variability and correlation in Dathia genotypes. It is evident from the data that genetic advance and GA (wr.mean) were found to range from 0.00674. to 11.09349 and 0.06572 to 0.89456, respectively (Table 1). Similarly cv. (genotype) and cv. (phenotype) were also found with considerable variations.

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