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Genetic variability and diversity studies in snapdragon (*Antirrhinum majus*) under tarai conditions of Uttarakhand*

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Snapdragon (*Antirrhinum majus* L.) belongs to family Scrophulariaceae and is one of the principal cut-flower crops grown in many part of the world. It is also used as bedding plant, in rockeries, herbaceous borders and as a potted plant. A detailed study of nature and extent of variability and heritability in relation to their contribution towards yield is pre-requisite for an efficient plant breeding programme. Heritability estimates give a measure of transmission of characters from one generation to other, as consistency in the performance of the selection depends on the heritable portion of the variability, thus enabling the plant breeder in isolating the elite selection in the crop. Nature and magnitude of genetic divergence in a population is essential for selecting diverse parents which upon hybridization leads to greater opportunity for crossing over which release by breaking up the predominantly repulsion phase linkages. Earlier geographic diversity was considered to be an index of genetic diversity. However, genetic diversity of parents is not necessarily associated with geographic diversity or place of origin (Yadava *et al*. 2011). Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures such as D^2 statistics and cluster analysis. These procedures characterize genetic divergence using criteria of similarity or dissimilarity based on aggregate effect of a number of economically important characters. Therefore, the present study was undertaken to determine the magnitude of variability in the population and to identify genotypically diverse and economically desirable genotypes for utilization in a breeding programme aimed at improving yield and quality.

Thirtyfive genotypes were evaluated at Model Floriculture Centre, G B P U A & T, Pantnagar, during 2008–10. Seedlings were transplanted at a spacing of 50 cm × 50 cm in open field conditions during second week of September. The experiment was laid out in randomized block design (RBD) with three replications. All the recommended cultural operations were carried out to grow a successful crop. Observations were recorded on five randomly selected plants from each genotype in each replication for different morphological characters. Phenotypic and genotypic coefficients of variation were calculated as per formula described by Burton (1952). Heritability, in broad sense, was calculated according to formula suggested by Allard (1960). To determine the genetic diversity, Mahalanobis (1919) D^2 analysis was done.

Analysis of variance revealed significant variation among the genotypes for most of the characters studied (Table 1). Results revealed maximum value for range in number of leaves/plant (75.13–1853.93) and minimum in petiole length (0.32–1.08). General mean was highest for number of leaves/plant (822.47) and minimum for petiole length (0.62). Estimates of phenotypic coefficient of variation (PCV) were slightly higher than genotypic coefficient of variation (GCV) for all the characters under consideration, indicating the apparent variation is not only due to genotypes, but also due to influence of the environment in the expression of the genotypes. Higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for number of secondary branches/plant (76.02 and 75.93), number of leaves/plant (72.77 and 72.73) and number of spike/plant (70.37 and 70.10) respectively. High value of PCV and GCV indicates that the genotypes exhibit much variation among themselves with respect to these characters. Lowest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was recorded for days taken to flowering (8.75 and 8.53). Low

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*Short note

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Table 1 Estimates of range, mean, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for different characters in snapdragon (pooled over two years)

Character	Range	General mean ± SE	P C V	G C V	E C V	Heritability (h^2) %	Genetic advance	Genetic advance as per cent of mean
Plant height (cm)	28.93–94.34	61.80±1.31	28.94	28.70	3.69	98.37	36.25	58.66
Plant spread (cm)	21.98–46.65	31.47±1.15	20.21	19.19	6.34	90.15	11.81	37.53
Number of primary branches/plant	5.75–62.85	26.35±0.82	54.72	54.45	5.44	99.00	29.41	111.61
Number of secondary branches/plant	19.32–347.38	78.23±1.89	76.02	75.93	4.19	99.84	170.58	218.05
Number of leaves/plant	75.13–1853.93	822.47±11.47	72.77	72.73	2.41	99.88	1232.01	149.79
Internodal length (cm)	1.13–3.56	1.89±0.06	38.18	37.74	5.78	97.70	1.45	76.72
Days taken to bud initiation	94.79–131.28	116.54±1.30	9.01	8.80	1.94	95.36	20.63	17.70
Days taken to flowering	104.45–144.20	128.59±1.42	8.75	8.53	1.92	95.18	22.06	17.16
Duration of flowering	48.75–83.03	68.59±1.18	11.27	10.87	2.98	92.99	14.81	21.59
Spike length (cm)	21.27–82.96	52.56±1.00	33.54	33.37	3.32	99.01	35.96	68.42
Rachis length (cm)	6.35–56.09	25.80±0.78	50.55	50.27	5.24	98.92	26.58	103.02
Weight of spike (g)	15.82–33.02	24.60±0.88	18.63	17.55	6.24	88.77	83.83	340.77
Floret diameter (cm)	2.32–4.27	3.00±0.03	20.02	19.93	1.89	99.10	12.30	410.00
Number of florets/spike	8.43–35.08	17.85±0.90	35.63	34.39	9.33	93.13	12.20	68.35
Number of spike/plant	3.48–78.44	21.61±0.77	70.37	70.10	6.19	99.24	31.09	143.87
Vase life (days)	7.85–11.95	9.43±0.32	10.38	8.52	5.93	67.35	1.35	14.32
Water uptake (ml)	21.08–51.45	34.56±1.67	21.40	19.68	8.40	84.56	12.88	37.27
Number of open florets/spike	4.84–28.16	14.00±1.46	40.91	36.68	18.11	80.39	9.48	67.71
Per cent opening of florets	48.51–93.19	70.86±3.59	15.29	12.50	8.79	66.91	14.93	21.07
Days to seed ripening	123.95–164.32	143.72±2.35	8.97	8.51	2.84	89.96	23.90	16.63
Number of pods/spike	7.03–35.19	17.05±1.10	37.63	35.93	11.19	91.15	12.05	70.67
Number of seeds/pod	143.83–549.23	315.54±9.81	38.11	37.72	5.38	98.00	242.78	76.94
Weight of seeds/pod (mg)	10.73–60.72	29.26±1.99	42.10	40.42	11.77	92.17	23.39	79.94
1000 seed weight (mg)	61.80–113.70	86.30±1.48	15.02	14.72	2.98	96.04	25.64	29.71
Leaf area (cm^2)	1.47–6.14	3.18±0.24	38.84	36.41	13.52	87.87	2.23	70.13
Petiole length (cm)	0.32–1.08	0.62±0.01	40.53	40.19	5.26	98.31	0.51	82.26
Diameter of spike (mm)	4.33–12.03	9.48±0.06	16.46	16.42	1.19	99.46	3.19	33.65
Weight of seeds/plant (g)	1.90–13.17	6.76±0.17	49.19	48.98	4.58	99.13	6.79	100.44

P C V, phenotypic coefficient of variation; G C V, genotypic coefficient of variation; E C V, environmental coefficient of variation

value of PCV and GCV indicates that the genotypes do not exhibit much variation among themselves with respect to these characters. Similar results were reported by Namita *et al*. (2008) and Punetha *et al*. (2011).

High estimates of heritability were obtained for all the characters studied except per cent opening of florets and vase life (Kavitha and Anburani 2010). Maximum heritability value was recorded in number of leaves/plant (99.88 %) and minimum in per cent opening of florets. High heritability estimates for these traits indicates less influence of environment in their expression. So there is a good scope for the improvement of these traits through direct selection. Highest value of genetic advance was observed for number of leaves/plant (1232.01). However, lowest value of genetic advance was observed for petiole length (0.51). High heritability with high genetic advance as per cent of mean was noticed for floret diameter followed by weight of spike and number of secondary branches/plant. The characters having high heritability with high genetic advance as per cent of mean appeared to be controlled by additive gene action and selection for such characters will be very effective. The results are in conformity with the findings of Singh and Singh (2007), Baskaran *et al*. (2009) and Karuppaiah and Kumar (2011). However, high heritability with lowest genetic advance as per cent of mean was observed for vase-life (14.32). The characters having high heritability with low genetic advance as per cent of mean appeared to be controlled by non-additive gene action and selection for such characters may not be effective (Singh and Singh 2007).

Thirtyfive genotypes were grouped into five clusters under Torcher's method of D^2 analysis. Among the five clusters, the maximum inter-cluster distance (D^2 values) was

Table 2. Average intra- and inter-cluster D^2 values among five clusters in snapdragon

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**2.372**	5.213	5.092	7.489	3.728
Cluster II		**2.729**	8.418	4.205	3.881
Cluster III			**2.438**	9.660	5.711
Cluster IV				**2.311**	5.245
Cluster V					**2.444**

* Figures in bold represent intra-cluster D^2 values

observed between cluster III and IV, followed by II and III (Table 2). Parental lines from these three distant clusters (II, III and IV) may be used in a hybridization programme which is likely to produce wide variability and transgressive segregations with high heterotic effect. The small inter-cluster distance was observed between cluster I and V. The lines belonging to these clusters were relatively closer to each other in comparison to lines grouped in other clusters. Maximum intra-cluster distance was recorded in cluster II, followed by cluster V and cluster III. The lines belonging to these clusters (II, V, III) were relatively more diverse than those in other clusters. Hence, it is suggested that inter-mating between the genotypes included in diverse clusters may give high heterotic response and thus better segregants (Nimbal Kar *et al.* 2006).

Thus, it may be concluded that the traits like floret diameter, number of primary and secondary branches/plant, number of spike/plant, rachis length and weight of seeds/plant, which exhibited high heritability coupled with high genetic advance as per cent of mean can be relied upon for effective selection and crop improvement. The studies also indicated that the geographic and genetic diversity are not necessarily related. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity. Hence, inter-mating between genotypes included in these diverse clusters may give high heterotic response and thus better segregants. This will provide an opportunity to select better recombinants for various characters and thereby creating large variability for these characters in the future generations.

SUMMARY

Field experiment was conducted for two consecutive years to evaluate snapdragon genotypes for genetic variability, heritability and genetic advance. Analysis of results revealed highest range of variation for number of leaves/plant. General mean was highest for number of leaves/plant and lowest for petiole length. Phenotypic and genotypic coefficient of variation was recorded maximum for number of secondary branches/plant and minimum for days taken to flowering. Genetic advance was observed maximum for number of leaves/plant and minimum for petiole length. High heritability with high genetic advance as per cent of mean was noticed for floret diameter. On the basis of D^2 values, thirtyfive genotypes were grouped into five clusters. Maximum inter-cluster distance was observed between cluster III and IV, followed by II and III.

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