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Study of Genetical Components Determining Vegetative, Flowering and Seed Parameters in Dogflower (*Antirrhinum majus* L.)

Suneeta Singh*; Anil Kumar Saxena
School of Agricultural Sciences, Shri Guru Ram Rai University, Dehradun -248 001, Uttarakhand, India
*Email of Corresponding Author: drsuneetaksaxena@gmail.com

ABSTRACT: ***Field experiment was conducted to elucidate the genetical components for vegetative, flowering and seed characters following Vr-Wr graphical analysis. The study was carried out in half diallel mating system excluding reciprocals involved 10 inbreds and 45 hybrids were developed by crossing inbreds in one direction. The F_1s were evaluated during 2016-17 and 2017-18 for some of the floricultural important traits. Additive and dominant genetic components were found significant for plant height, number of primary branches, leaf area index, days taken to flowering, diameter of spike, length of spike, days taken to seed ripening, number of seeds/pod and weight of seeds/pod in both years except number of leaves/plant. However, the dominant genetic component was more in magnitude as compared to additive genetic component. It indicates that dominant genetic variance was more important than additive genetic variance in determining all the characters except number of leaves/plant.***
Keywords: Dogflower, vegetative, flowering, seed parameters, genetic components

Introduction

Dogflower is one of the important annuals among the flowering plants. Its flowers are not only in demand for winter season flowering plant but now have become popular for cut flower purpose. The magnificent flowers of bunny, penstemon or intermediate shape with bright array of colours arranged on long spike captivate and display a charming beauty. Snapdragon is identified as very profitable crop (Banerjee and Ali, 2016). The export of the cut flower of dogflower is increasing in American and Europian market.

Improvement of ornamental crops through classical breeding techniques provides stability in the characters. But before starting any such kind of improvement programme, it is imperative to have certain information regarding the crop at genic level or gene actions

responsible for particular trait. This helps in deciding the methodology of improvement of any crop. Although, dogflower (*Antirrhinum majus* L.) is a model crop of dicotyledons for their study at genic level, it is still less studied to elucidate the genetic components for floriculturally important traits. However, Malik (1998) found overdominance in some of the characters studied in snapdragon, the inheritance of colour and floret shape of snapdragon was studied by some researchers (Misiha and El-Always, 1992 and Watts, 1998). For post-harvest life, significant additive component was observed in the cut flowers of snapdragon (Martin and Stimart, 2013). Breeding trials in other crops were also conducted to observe the remarkable gene effect i.e. additive gene effect and dominance × dominance gene interaction in marigold (Singh and Swarup, 1999), non additive gene action for several characters in China aster (Raghava, 1984 and Raghava and Negi, 1992). Therefore, the present investigation was carried out in dogflower to attain the basic general information on the type of genetic association between various characters of economic importance and precise knowledge of type of genetic components involved in expression of characters.

Materials and Methods

The experiment was carried out at Horticulture Research Block of School of Agricultural Sciences, Shri Guru Ram Rai University, Dehradun, Uttarakhand during 2016-17 and 2017-18. In the present study ten parental lines of snapdragon were crossed in diallel mating system and reciprocal crosses were excluded (Griffing, 1956). For hybridization, crossing of male and female plants were done. In the succession of crossing the flowers were emasculated around three days before opening of flowers followed by bagging. In early morning and evening, the female part i.e. stigma was pollinated with pollens of desired male flowers. After pollination, flowers were bagged with all details regarding name of parents, date of pollination, etc. Fruits reached to maturity in 45-60 days after pollination and turned brown. Thus, the developed seeds were harvested, dried and stored. Seeds of 10 parents and 45 F_1s were sown in the polyhouse. Seedlings were ready to transplant in about 40 days and transplanted in previously manure and well levelled field at 50 × 50 cm distance. Plot size was kept 2.5 X 2.5 m, thus 25 plants accommodated in each plot. A fertilizer dose of 10:10:10 g/m^2 of NPK was given. The dose of N, P and K was supplied by urea, single super phosphate and muriate of potash, respectively. Fungicides and insecticides were also applied

to prevent wilting and attack of *Helicoverpa armigera*, respectively. All the genotypes were maintained by the application of uniform agrotechniques. The experiment was carried out in randomized block design with three replications. The observations were recorded for growth parameters such as number of leaves/plant, number of primary branches/plant, leaf area index and plant height; for flowering parameters, days taken to flowering, diameter of spike and spike length; while for seed parameters, days taken to seed ripening, number of seeds/pod and weight of seeds/pod. The expected values of main components of genetic variance were estimated for F_1 generation (Hayman, 1954). Based on parental variance (Vr) and parent-offspring co-variance (Wr) relationship in diallel cross progenies, a two-way representation or distribution of parental arrays along a regression line of Wr and Vr was studied (Hayman, 1954).

Results and Discussion

Analysis of genetical components indicated that additive genetic variance (D) was significant for plant height and number of primary branches/plant in both years, while for number of leaves/plant and leaf area index in first year only. Both dominance components (H_1 and H_2) were significant for plant height, number of primary branches/plant and leaf area index in first and second year. However, in first year, both additive and dominance genetic variance equally important in the expression of this character, while in second year dominance component was more important than the additive genetic variance for the expression of plant height. In case of number of leaves/plant, additive component was more important than the dominance genetic variance in year 2016-17. Whereas the mean degree of dominance (it was more than 1 in both years) showed that overdominance governed number of leaves/plant. This contrast may be due to genetics × environment interactions. The dominance genetic variance in number of primary branches and leaf area index in both years was greater than additive genetic variance showed that dominance genetic variance was more important in determination of the above said parameters in comparison to additive genetic variance.

Raghava and Negi (1993) also found non-additive genetic variance for plant height and number of main branches/plant in China aster. Mean degree of dominance $[(H_1/D)^{1/2}]$ (greater than unity) indicated the presence of overdominance for plant height, number of leaves/plant, primary branches/plant and leaf area index. In marigold similar findings have

been observed by Nand Kishore and Raghava (2011), where they indicated the existence of non-additive genetic variance in the control of number of primary branches/plant. Ratio of dominant and recessive alleles $[(4\ DH_1)^{1/2} + F/(4\ DH_1)^{1/2}\text{-}F]$ was more than unity for number of leaves and primary branches/plant and leaf area index consistently over both the years except plant height. Those values were confirmed by positive 'F' values for each of the above mentioned characters and by negative F value for plant height. This indicated the higher proportion of dominant genes for expression of these characters, while proportion of recessive genes was higher for plant height. Similar findings have been reported in other crops i.e. the above findings are in conformity with the results of Swarup *et al*. (1996) in balsam, Reddy *et al*. (1989) in marigold and Aswath and Parthasarathy (1993) in China aster. The estimate of h^2/H_2, measure of number of effective factors/block of dominant genes, was rather low for plant height, number of leaves and primary branches/plant and leaf area index, indicating at least one group of genes responsible for these characters.

In flowering parameters (days taken to flowering, diameter of spike and length of spike) the additive genetic variance (D) and dominance components (H_1 and H_2) were found significant. The dominance genetic variance was more than additive genetic components in both years indicating the importance of dominance genetic variance over additive genetic component in determination of above characters. Non-additive genetic variance was also reported by Raghava and Negi (1993) in China aster. As the non-additive genetic variance is highly significant, so heterosis breeding can be used for improvement of this trait. Mean degree of dominance $[(H_1/D)^{1/2}]$ was noticed to be greater than unity for all flowering characters. Proportion of dominant and recessive alleles $[(4\ DH_1)^{1/2} + F/(4\ DH_1)^{1/2} - F]$ was more than unity for all characters consistently for two years. Those values were confirmed by positive F values for each of the above mentioned characters, indicating higher proportion of dominant genes for expression of these characters. This finding is in conformity with the results of Malik (1998), Swarup *et al*. (1996) in balsam, Singh and Swarup (1971) and Reddy *et al*. (1989) in marigold.

The estimates of additive and dominance component was found to be significant for all the seed parameters (days taken to seed ripening, number of seeds/pod and weight of seed/pod) during both the years. However, the dominance genetic variance for all characters in both years was more than additive genetic variance. This showed that dominance genetic

component was more important in expression of the above said seed parameters. This is in agreement with the findings of Singh and Swarup (1971) who noticed preponderance of both additive and non-additive genetic variances in seed yield.

Graphical analysis of the experimental data recorded in order to get information about allelic constitution of the parents used in the diallel cross. The 1-b Vr/Wr was detected to be non significant for plant height (2016-17), number of leaves/plant (2016-17 and 2017-18), number of primary branches/plant (2016-17 and 2017-18), leaf area index (2016-17), days taken to flowering (2017-18), diameter of spike (2016-17 and 2017-18), length of spike (2017-18), days to seed ripening (2017-18), number of seeds/pod (2016-17 and 2017-18) and weight of seeds/pod (2016-17 and 2017-18), denoting the success of some of the basic assumptions and indicating the absence of non-allelic interaction. After plotting, the graphs of leaf area index (2016-2017) and diameter of spike (2016-17 and 2017-18) were not drawn properly due to negative regression coefficient. Therefore, the reanalysis of data was performed after deleting the parents and their crosses which had high level of variance than the other parents and their crosses. Even after that graphs of leaf area index (2016-17) was again not properly drawn. The Vr-Wr graphical analysis demonstrated that plant height was governed by partial dominance, while number of leaves/plant was under the control of overdominance gene effect and character like number of primary branches/plant was under the control of complete dominance, whereas epistasis was found in leaf area index. For almost all the characters, the parental points were scattered all along the regression line in the Vr-Wr graph. This indicates the genetic diversity among the parents for all the vegetative traits studied. The above findings are in close conformity with the results of Raghava (1984) and Raghava and Negi (1993) in China aster and Song and Bang (2012). In some characters, the results of analysis of genetical components and Vr-Wr graphs varied from each other. This might be due to the fact that both analysis based on different assumptions and it is possible to get different results (Hayman, 1954).

The Vr-Wr graphical analysis showed that Sant-11 was located away from the origin and thus had preponderance of recessive alleles for days taken to flowering. SA-1, showed early flowering was near the origin showing mostly the dominant alleles for this character. This character along with length of spike and diameter of spike were under the control of

partial dominance gene effect. Similar pattern of results have also been reported by Hussein and Misiha (1979) in petunia and Singh and Swarup (1971) in marigold.

The Vr-Wr graphical analysis demonstrated that number of seeds/pod in both years was governed by partial dominance, whereas the days taken to seed ripening and number of seeds/pod and weight of seed/pod was under the control of overdominance. Nand Kishore and Raghava (2011) reported the existence of non-additive gene action in control of seed yield.

From the present investigation it was concluded that the non-additive genetic variance (dominance component) was found pre-dominant in all the characters studied. Thus, these characters can be utilized for the improvement of crop by exploiting heterosis through hybridization. The increased hybrid vigour in leaf area index and number of primary branches/plant would lead to improve the quality of flowers and number of spikes/plant, respectively. On the basis of inbreds' performance, early and late flowering hybrids can be developed.

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Table1: Genetic components of variations and their proportions for growth parameters in snapdragon

Components/ proportions	Plant height (cm)			Number of leaves/plant			Number of primary branches/plant			Leaf area index		
	I Year	II Year	Average	I Year	II Year	Average	I Year	II Year	Average	I Year	II Year	Average
D	264.51**	247.61**	256.06	226099.77**	58384.09	142241.93	155.80**	152.93**	154.37	445.07*	421.65	433.36
SE (±)	45.66	43.33	44.50	68789.90	52410.00	60599.95	30.24	23.23	26.74	217.43	223.10	220.27
F	-72.83	-112.97	-92.90	198950.00	-11883.80	93533.10	190.56**	178.59**	184.58	466.45	392.26	429.36
SE (±)	105.34	99.97	102.66	158719.00	120926.00	139822.50	69.78	53.61	61.70	501.68	514.76	508.22
H_1	251.21**	499.95**	375.58	0.01	0.01	0.01	321.08**	248.21**	284.65	2314.32**	2270.89**	2292.61
SE (±)	97.18	92.22	94.70	146426.00	111560.00	128993.00	64.37	49.46	56.92	462.82	474.89	468.86
H_2	209.04*	343.90**	276.47	786552.00	933685.00	860118.50	218.76**	152.10**	185.43	2006.99**	1988.56**	1997.78
SE (±)	82.59	78.38	80.49	124446.00	941813.30	533129.65	54.71	42.03	48.37	393.35	403.61	398.48
h^2	200.73**	163.68**	182.21	437768.00**	666416.00**	552092.00	104.69**	82.68**	93.69	393.13**	314.57**	353.85
SE (±)	55.29	52.46	53.88	83299.00	63464.30	73381.65	36.62	28.13	32.38	263.29	270.15	266.72
E	15.46	28.13*	21.80	10847.80	10433.90	10640.85	6.81	10.45	8.63	24.58**	20.85	22.72
SE (±)	13.77	13.06	13.42	20740.90	15802.20	18271.55	9.12	7.01	8.07	65.56	67.26	66.41
$(H_1/D)^{1/2}$	0.97	1.42	1.20	2.29	4.24	3.27	1.43	1.27	1.35	2.28	2.32	2.30
$H_2/4H_1$	0.21	0.17	0.19	0.21	0.22	0.22	0.17	0.15	0.16	0.22	0.22	0.22
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$ or KD/KR	0.75	0.72	0.74	1.47	0.95	1.21	2.48	2.69	2.59	1.59	1.50	1.55
h^2/H_2	0.96	0.48	0.65	0.56	0.71	1.18	0.48	0.54	0.51	0.19	0.16	0.17

* Significant at 0.05 level of probability, ** Significant at 0.01 level of probability

Table 2: Genetic components of variations and their proportions for flowering parameters in snapdragon

Components/ proportions	Days taken to flowering			Diameter of spike (mm)			Length of spike (cm)		
	I Year	II Year	Average	I Year	II Year	Average	I Year	II Year	Average
D	109.48**	265.61**	187.55	3.30*	3.28*	3.29	297.84**	338.48**	318.16
SE (±)	14.46	52.66	33.56	1.48	1.49	1.49	52.55	56.37	54.46
F	64.63	251.09*	157.86	2.89	2.86	2.88	272.60*	264.63*	268.62
SE (±)	33.36	121.49	77.43	3.42	3.45	3.44	121.27	130.08	125.68
H_1	168.04**	796.90**	482.47	9.69**	9.69**	9.69	429.84**	527.81**	478.83
SE (±)	30.78	112.08	71.43	3.16	3.18	3.17	111.87	120.00	115.94
H_2	153.72**	641.89**	397.81	8.27**	8.28**	8.28	292.66**	390.01**	341.34
SE (±)	26.16	95.25	60.71	2.68	2.70	2.69	95.08	101.99	98.54
h^2	256.75**	443.42**	350.09	0.12	0.11	0.12	102.92	11.43	57.18
SE (±)	17.50	63.76	40.63	1.80	1.81	1.81	63.65	68.26	65.96
E	15.91**	13.53	14.72	0.12	0.12	0.12	0.97	6.45	3.71
SE (±)	4.36	15.88	10.12	0.45	0.45	0.45	15.85	16.99	16.42
$(H_1/D)^{1/2}$	1.24	1.73	1.49	1.71	1.72	1.72	1.20	1.25	1.23
$(H_2/4H_1)$	0.23	0.20	0.22	0.21	0.21	0.21	0.17	0.18	0.18
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$ or KD/KR	1.62	1.75	1.69	1.69	1.68	1.69	2.23	1.91	2.07
h^2/H_2	1.67	0.69	0.88	0.01	0.01	0.01	0.35	0.03	0.17

* Significant at 0.05 level of probability
** Significant at 0.01 level of probability

Table 3: Genetic components of variations and their proportions for seed parameters in snapdragon

Components/ proportions	Days taken to seed ripening			Number of seeds/pod			Weight of seeds/ pod (mg)		
	I Year	II Year	Average	I Year	II Year	Average	I Year	II Year	Average
D	104.38*	170.97**	137.68	36777.27**	40919.25**	38848.26	669.09**	712.60**	690.85
SE (±)	40.79	51.41	46.10	9052.71	10972.20	10012.46	191.84	156.10	173.97
F	108.65	197.61	153.13	36297.30	43066.60	39681.95	835.07	772.59*	803.83
SE (±)	94.11	118.63	106.37	20887.30	25316.10	23101.70	442.62	360.16	401.39
H_1	273.58**	781.88**	527.73	83073.80**	90293.10**	86683.45	2617.02**	2125.35**	2371.19
SE (±)	86.82	109.44	98.13	19269.50	23355.30	21312.40	408.35	332.27	370.31
H_2	210.52**	626.41**	418.47	63031.50**	68020.00**	65525.75	2172.06**	1791.73**	1981.90
SE (±)	73.79	93.00	83.40	16377.00	19849.40	18113.20	347.05	282.39	314.72
h^2	212.33**	287.09**	249.71	12039.50	14816.20	13427.85	192.26	94.83	143.55
SE (±)	49.39	62.26	55.83	10962.10	13286.04	12124.07	232.30	189.02	210.66
E	12.06	0.97	6.52	1619.71	2092.95	1856.33	52.29	33.87	43.08
SE (±)	12.29	15.50	13.90	2729.50	3308.23	3018.87	57.84	47.06	52.45
$(H_1/D)^{1/2}$	1.62	2.14	1.88	1.50	1.48	1.49	1.98	1.73	1.86
$(H_2/4H_1)$	0.19	0.20	0.20	0.19	0.18	0.19	0.20	0.21	0.21
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$ or KD/KR	1.95	1.74	1.85	1.98	2.09	2.03	1.92	1.92	1.92
h^2/H_2	1.01	0.46	0.60	0.19	0.22	0.20	0.09	0.05	0.07

* Significant at 0.05 level of probability
** Significant at 0.01 level of probability

