

STUDIES ON VARIABILITY FOR VARIOUS QUANTITATIVE TRAITS IN ROSE (*Rosa* spp.)

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ABSTRACT

Twenty nine genotypes of roses collected from different places and maintained in Horticulture section were evaluated in RBD replicated twice in 2015, with the objective to estimate GCV, PCV, heritability and genetic advance. Observations recorded on plant height, primary branches plant⁻¹, secondary branches plant⁻¹, canopy diameter, stem girth, bud length, bud width, diameter of flower, days taken to anthesis, stalk length, thorn density, fresh weight of flower, flower yield plant⁻¹, flower yield plot⁻¹ were used in this study for computing genetical analysis. The maximum mean was observed for plant height (86.62 cm) followed by flower yield plot⁻¹ (83.61), canopy diameter (74.32 cm), flower yield plant⁻¹ (20.24), stalk length (14.83) and thorn density (14.75). Similarly, the maximum range was recorded by flower yield plot⁻¹ (106.08) followed by canopy diameter (86.40), plant height (68.50), thorn density (56.96), stalk length (28.00) and flower yield plant⁻¹ (23.63). The PCV and GCV estimated from corresponding variances, exhibited the values from low to high category. High GCV and PCV were exhibited for thorn density (77.32% and 78.09%), stalk length (65.39% and 77.24%), flower yield plant⁻¹ (31.99% and 35.86%), flower yield plot⁻¹ (30.98% and 34.73%), canopy diameter (22.87% and 24.24%) and fresh weight of flower (23.73% and 27.66%). High estimates of heritability were established by thorn density (98.05%), canopy diameter (89%), stem girth (83.44%), plant height (83.06%), flower yield plant⁻¹ and flower yield plot⁻¹ (79.58%), fresh weight of flower (73.56%) and stalk length (71.67%). Moderate estimate of heritability were observed for bud length (58.37), days taken to anthesis (55.73%), number of secondary branches plant⁻¹ (55.03%) and number of primary branches plant⁻¹ (46.22%). Genetic advance as percentage of mean value were high for thorn density (157.72%), stalk length (114.04%), flower yield plant⁻¹ (58.78%), flower yield plot⁻¹ (56.93%), canopy diameter (44.44%), fresh weight of flower (41.92%), stem girth (36.02%), plant height (33.39%), bud length (27.39%), number of secondary branches plant⁻¹ (24.83%) and moderate for number of primary branches plant⁻¹ (13.26%) and days taken to anthesis (10.83%). Stalk length, canopy diameter, stem girth and plant height were identified for primary selection based on high GCV, PCV, high heritability along with high genetic advance. Considering these characters, the five genotypes Kiss of fire, Peter F, Centenary, Double delight and Veternas honor were identified for further purification and multiplication.

(Key words: Rose, variability, heritability, genetic advance)

INTRODUCTION

Rose have gained the title of worlds favorite flower in part due to their vast diversity in plant habitat and floral characteristics (Cairns, 2001). Among the flowers, rose (*Rosa* spp.) is one of the nature's most beautiful creations and is universally acclaimed as the Queen of flowers. They have been breed and selected to secure a number of niches including flowering landscape shrubs, formal garden specimens, cut flowers, blooming potted plates and sources of perfume and vitamin C (Zlesak, 2006). Despite the large number of cultivated rose varieties, only a few of them exhibit the marked fragrance in world. A very peculiar aspect of rose production is to get the cut flower which generally deals with the floricultural business.

A huge quantum of variability exists in this crop

with respect to growth habit, flowering behaviors etc. In spite of such variability, very few are having desirable characters in terms of yield and quantity. Different regions where rose is cultivated have many strains which needs to be identified, compared, selected and further improved for commercial utilization of rose hips for fresh consumption, processing and pharmaceutical purpose. The progress of breeding is conditioned by the magnitude, nature and interaction of genotypic and environmental variation in the plant characters. Then it becomes necessary to partition the observed variability into its heritable components with the help of suitable genetic parameters such as genetic coefficient of variation, heritability estimates and genetic advance etc. This will provide valuable information on the mode of inheritance of different characters, which would be useful in selecting varieties. But information on these aspects in *Rosa* sp. is meager in the country. Therefore,

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there is a need to estimate the genetic variability in *Rosa* sp. through biometrical procedures which may be useful to develop some selection.

MATERIALS AND METHODS

This experiment was undertaken during the season of 2015-2016 at farm of Horticulture section, College of Agriculture, Nagpur. The experimental material consisted of 29 rose genotypes collected and maintained by Horticulture Section. The 29 rose genotypes were planted in 4.5 m x 4.5 m plot of flat bed with a spacing 0.9 m x 0.9 m in randomized block design with two replications and maintained by Horticulture Section. The plants were time to time supplemented with nutrient mixture along with RDF (recommended dose of fertilizer) for the proper growth and development of flower bud. Irrigation was given to the rose plants at proper interval. Weeding, earthing up, plant protection, irrigation, etc. were adopted as and when found essential. Pruning in rose was done twice in a year, first pruning done in 1st fort night of June and second in 1st fort night of October. Generally moderate pruning was done with the help of sharp shear. Half dose of N and full dose of P and K were provided after pruning for proper growth and development of plants. Data were recorded on five competitive plants for fourteen characters like plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, canopy diameter, stem girth, bud length, bud width, diameter of flower, days taken to anthesis, stalk length, thorn density, fresh weight of flower, flower yield plant⁻¹, flower yield plot⁻¹. The data recorded were subjected to various statistical and biometrical analysis *viz.*, Analysis of variance (Panse and Sukhatme, 1954), estimation of genotypic and phenotypic coefficient of variation (Burton and Devane, 1953), estimation of heritability in broad sense (Hanson *et al.*, 1956) and estimation of genetic advance (GA) (Robinson *et al.*, 1949).

RESULTS AND DISCUSSION

The analysis of variance for experimental design (Table 1) revealed that the mean squares due to genotypes were highly significant for all the characters studied except for bud width and diameter of flower. This indicates that the rose genotypes had substantial genetic variability among themselves for flower yield and most of the yield components except for bud width and diameter of flower which allows the further estimation of different parameters for the twelve traits. Similar to this result wide variability for flower yield plant⁻¹ and yield contributing characters were also observed by Sezari and Ahmet (2004), Susek *et al.* (2005) Babaei *et al.* (2008), Verma *et al.* (2008), Zeinali *et al.* (2009) and Atram *et al.* (2015) in rose.

Mean and range for different characters

The mean, maximum, minimum and range values for 14 different traits were measured in 29 genotypes of roses and are presented in table 2.. In this study plant height ranged from 43.40 cm to 111.90 cm, number of primary

branches plant⁻¹ ranged from 2.40 to 4.00, number of secondary branches plant⁻¹ ranged from 9.25 to 19.11, canopy diameter ranged from 34.80 cm to 121.20 cm, stem girth ranged from 1.36 cm to 3.58 cm, bud length ranged from 2.24 cm to 5.02 cm, days taken to anthesis ranged from 2.20 days to 3.40 days, stalk length ranged from 1.00 cm to 29.00 cm, thorn density ranged from 2.98 to 59.95, fresh weight of flower ranged from 3.28 g to 12.39 g, flower yield plant⁻¹ ranged from 6.45 to 30.08 and flower yield plot⁻¹ ranged from 28.98 to 135.06.

The maximum mean was observed for plant height (86.62 cm) followed by flower yield plot⁻¹ (83.61), canopy diameter (74.32 cm), flower yield plant⁻¹ (20.24), stalk length (14.83) and thorn density (14.75). Similarly, the maximum range was recorded by flower yield plot⁻¹ (106.08) followed by canopy diameter (86.40), plant height (68.50), thorn density (56.96), stalk length (28.00) and flower yield plant⁻¹ (23.63). This indicated the presence of considerable amount of genetic variation in rose genotypes. These results revealed that characters like flower yield plot⁻¹, canopy diameter, plant height, thorn density, stalk length and flower yield plant⁻¹ showing maximum mean and range can be considered as traits for selecting superior genotypes. Such high proportion of mean and range values for flower yield plot⁻¹, canopy diameter, plant height, thorn density, stalk length etc. were also reported by Verma *et al.* (2008) and Zeinali *et al.* (2009) in rose. Higher extent of variation reflecting in high range could be attributed to difference in the genetic composition of the rose genotypes collected from different places. This might be due to genetic characteristic and/or acclimatization to the environment from where collected.

Estimates of genetic variability parameters

Results in table 2 indicated a considerable range of variation with respect to phenotypic and genotypic coefficient of variation. The study revealed that estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding values of genotypic coefficient of variation (GCV) for all the fourteen characters under consideration indicating that, the apparent variation was not only due to genotypes but also due to the influence of environment in the expression of genotypes. The results were in agreement with the results of Verma *et al.* (2008), Zeinali *et al.* (2009) and Verma *et al.* (2013) in rose who also reported higher values of PCV than their respective GCV due to the influence of environment. The PCV and GCV were estimated from the corresponding variances and were used for the assessment of variability among the characters studied. Genotypic coefficient of variation exhibited the values from low to high category. High GCV was exhibited for thorn density (77.32%), stalk length (65.39%), flower yield plant⁻¹ (31.99%), flower yield plot⁻¹ (30.98%), fresh weight of flower (23.73%) and canopy diameter (22.87%). Moderate GCV was noticed for stem girth (19.14%), bud length (17.50%), plant height (17.78%) and number of secondary branches plant⁻¹ (16.25%). Low GCV was

observed for primary branches plant⁻¹ (9.47%) and days taken to anthesis (7.04%). Similarly phenotypic coefficient of variation was also observed to be low to high for different characters. High PCV was exhibited for thorn density (78.09%), stalk length (77.24%), flower yield plant⁻¹ (35.86%), flower yield plot⁻¹ (34.73%), fresh weight of flower (27.66%), canopy diameter (24.24%), bud length (22.91%), number of secondary branches plant⁻¹ (21.91%) and stem girth (20.96%). Moderate PCV was noticed for plant height (19.51%) and number of primary branches plant⁻¹ (13.93%) and low PCV was observed for days taken to anthesis (9.44%).

Amongst all the characters studied, the highest GCV and PCV were recorded for thorn density, stalk length, flower yield plant⁻¹, flower yield plot⁻¹, fresh weight of flower and canopy diameter indicating high variation in these characters, predicting greater scope for improvement of these six characters. Similarly, high variability has been reported by Susek *et al.* (2005), Verma *et al.* (2008), Zeinali *et al.* (2009) and Verma *et al.* (2013) for flower yield plant⁻¹, number of flowers plant⁻¹ and thorn density etc.

Estimates of heritability, genetic advance and response to selection as percentage of mean

The estimates of heritability in broad sense give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite selection in the crop. Heritability and genetic advance increase the efficiency of the selection in a breeding programme by assessing the influence of environmental factors and additive gene action. The estimates of heritability in broad sense specifying the heritable portion of total variation, helps in identification of the appropriate characters for selection.

Data regarding the heritability estimated for the 14 characters using 29 genotypes of rose collected from different places are presented in table 2. High estimates of heritability were recorded for thorn density (98.05%), canopy diameter (89.00%), stem girth (83.44%), plant height (83.06%), flower yield plant⁻¹ and flower yield plot⁻¹ (79.58%), fresh weight of flower (73.56%) and stalk length (71.67%) reflecting the importance of these traits in selection programme. This indicated that these characters were less governed by a few major genes or additive gene effect even, if they were under polygenic control and therefore, selection of these characters would be more effective for yield improvement. Moderate estimate of heritability were observed for bud length (58.37%), days taken to anthesis (55.73%), number of secondary branches plant⁻¹ (55.03%) and number of primary branches plant⁻¹ (46.22%). In accordance to these results Babaei *et al.* (2008) reported high heritability for flower weight (89%), number of petals (88%), number of stamens (82%) and thorn density (86%) in rose. Zeinali *et al.* (2009) recorded high heritability for flower yield plant⁻¹ (57.7%), fresh weight of flower (63.6%), bud length (60.4%), number of petals flower⁻¹ (74.1%), length of

receptacle (70.7%) and width of receptacle (82.6%) in rose. Gitonga *et al.* (2014) also documented that, in rose traits of days to bending, plant height and plant vigour had heritabilities of 80%, 82 % and 73%, respectively. Number of petals flower⁻¹ had the highest observed heritabilities in all the environments with a range of 0.88 to 0.99. The traits stem length, prickles on the stem, prickles on the petiole also had high broad sense heritabilities with a range from 0.84 to 0.93.

Genetic advance as percentage of mean value were high for thorn density (157.72%), stalk length (114.04%), flower yield plant⁻¹ (58.78%), flower yield plot⁻¹ (56.93%), canopy diameter (44.44%), fresh weight of flower (41.92%), stem girth (36.02%), plant height (33.39%), bud length (27.55%) and number of secondary branches plant⁻¹ (24.83%) and moderate for number of primary branches plant⁻¹ (13.26%) and days taken to anthesis (10.83%). Similar to these results high genetic advance as percentage of mean were also reported in rose by Verma *et al.* (2008) for thorn density (203%), length of shoot after one month of sprouting (75.46%), number of flowers plant⁻¹ (62.43%), length of shoot after 15 days of bud sprouting (55.94%), days taken to bud sprouting (44.76%), total shelf life (40.25%), plant height at second flower flush (39.60%) and number of flowers at first flower flush (38.10%). Length of flower bud (25.32%) and diameter of flower (30.11%). Verma *et al.* (2013) also reported maximum genetic advance per cent of mean for yield plant⁻¹ followed by plant height.

Since, heritability estimates are influenced by environment, genetic material and also other factors hence their utility will be restricted. Thus, heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955). Heritable variation can be determined with greater accuracy when heritability along with genetic advance is studied. High heritability with high genetic advance tells that, the character is governed by additive gene action, for that simple selection is advocated. In the present study, thorn density, canopy diameter, stem girth, plant height, flower yield plant⁻¹, flower yield plot⁻¹, fresh weight of flower and stalk length showed the high heritability along with high genetic advance. Estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High heritability along with high genetic gain indicated in these characters was due to considerable additive gene effects. Thus, selection on the basis of these characters would be more effective for further breeding programs. In accordance to this result Verma *et al.* (2008) and Babaei *et al.* (2008) also reported that characters namely, thorn density, plant spread and number of flowers plant⁻¹ showed high heritability accompanied with high genetic advance indicated that most likely the heritability is due to additive gene effect and selection may be effective.

Per se performance for different characters

The *per se* performance for 14 characters over 29

Table 1. Analysis of variance for various traits in rose

Sources of Variation	df	Mean sum of squares													
		Plant height (cm)	No. of pri. branches plant ⁻¹	No. of sec. branches plant ⁻¹	Canopy diameter (cm)	Stem girth (cm)	Bud length (cm)	Bud width (cm)	Diameter of flower (cm)	Days taken to anthesis (days)	Stalk length (cm)	Thorn density (No.)	Fresh weight of flower (g)	Flower yield plant ⁻¹ (No.)	Flower yield plot ⁻¹ (No.)
Replications	1	96.47	0.43	15.33	12.94	0.13	1.11	0.12	0.85	0.001	118.90	2.60	4.88	25.11	401.83
Genotypes	28	522.98**	0.33*	13.04**	613.29**	0.41**	1.05**	0.19	1.30	0.12**	225.19**	262.63**	8.47**	94.63**	1514.08**
Error	28	48.39	0.12	3.78	35.68	0.04	0.28	0.16	1.06	0.03	37.16	2.59	1.29	10.76	172.17

* Significant at 5 % level

** Significant at 1 % level

Table 2. Estimates of mean, range, GCV, PCV, heritability and genetic advance for different traits in rose genotypes

Str.No.	Characters	Mean	Min.	Max.	Range	GCV (%)	PCV (%)	Heritability (%)	G.A.	GA (% of mean)
1	Plant height (cm)	86.62	43.40	111.90	68.50	17.78	19.51	83.06	28.92	33.39
2	No. of primary branches plant ⁻¹	3.41	2.40	4.00	1.60	9.47	13.93	46.22	0.45	13.26
3	No. of secondary branches plant ⁻¹	13.24	9.25	19.11	9.86	16.25	21.91	55.03	3.29	24.83
4	Canopy diameter (cm)	74.32	34.80	121.20	86.40	22.87	24.24	89.00	33.03	44.44
5	Stem girth (cm)	2.27	1.36	3.58	2.22	19.14	20.96	83.44	0.82	36.02
6	Bud length (cm)	3.55	2.24	5.02	2.78	17.50	22.91	58.37	0.98	27.55
7	Bud width (cm)	2.68	1.97	3.49	1.52	4.20	15.65	7.21	0.06	2.32
8	Diameter of flower (cm)	8.16	7.08	10.43	3.35	4.22	13.33	10.04	0.22	2.76
9	Days taken to anthesis (days)	2.88	2.20	3.40	1.20	7.04	9.44	55.73	0.31	10.83
10	Stalk length (cm)	14.83	1.00	29.00	28.00	65.39	77.24	71.67	16.91	114.04
11	Thorn density (No.)	14.75	2.98	59.95	56.96	77.32	78.09	98.05	23.26	157.72
12	Fresh weight of flower (g)	7.99	3.28	12.39	9.11	23.73	27.66	73.56	3.35	41.92
13	Flower yield plant ⁻¹ (No.)	20.24	6.45	30.08	23.63	31.99	35.86	79.58	11.90	58.78
14	Flower yield plot ⁻¹ (No.)	83.61	28.98	135.06	106.08	30.98	34.73	79.58	47.60	56.93

Table 3. Mean performance of 29 rose genotypes for different traits

Sr. No.	Varieties	Plant height (cm)	No. of pri. branches Plant ⁻¹	No. of sec. branches plant ⁻¹	Canopy diameter (cm)	Stem girth (cm)	Bud length (cm)	Bud width (cm)	Diam-eter of flower (cm)	Days taken to an-th-esis	Stalk length (cm)	Thorn density (No.)	Fresh wt. of flower (g)	Flower yield plant ⁻¹ (No.)	Flower yield plot ⁻¹ (No.)
1	Ace of heart	73.60	3.20	12.07	66.00	1.84	3.01	2.52	7.71	2.30	32.69	15.08	7.39	17.12	68.50
2	Forever	93.90	3.60	15.08	80.90	2.32	4.02	2.86	8.65	2.50	42.25	20.62	9.39	23.03	92.15
3	Queen elizabeth	99.30	3.60	15.57	85.00	2.55	4.32	2.92	8.85	2.80	45.27	19.11	9.54	25.75	103.02
4	Centenary	104.40	3.80	17.23	95.90	2.77	4.62	3.15	9.20	2.20	55.33	7.24	10.36	31.18	124.75
5	Doude Delight	103.80	3.80	16.82	93.40	2.73	4.52	3.14	9.05	2.60	54.09	5.73	10.06	29.17	116.70
6	Kiss of fire	111.90	3.90	19.81	116.40	3.61	4.98	3.25	10.48	3.00	65.39	13.07	12.07	33.76	135.05
7	Peter F.	111.00	3.80	17.40	98.40	2.84	4.72	3.17	9.71	3.10	59.77	9.85	11.06	32.19	128.77
8	Vermas honor	103.20	3.80	16.09	93.40	2.61	4.52	3.12	8.95	3.00	52.31	11.06	9.84	29.17	116.70
9	Gold Medallion	91.60	3.40	14.08	76.80	2.16	3.82	2.72	8.25	2.80	39.23	7.04	8.84	21.12	84.51
10	Wall street	78.90	3.20	12.57	66.60	2.03	3.21	2.57	7.85	3.20	34.20	10.55	8.04	18.10	72.43
11	Bridges Dream	95.70	3.60	15.39	81.50	2.51	4.32	2.92	8.75	3.00	45.26	8.04	9.45	24.14	96.58
12	Just Joey	102.70	3.70	16.02	92.40	2.60	4.47	3.05	8.95	2.90	48.70	6.03	9.75	27.16	108.65
13	Paradise	93.90	3.60	15.29	81.50	2.38	4.02	2.92	8.75	2.80	44.26	3.54	9.45	23.13	92.50
14	Black Lady	93.30	3.50	14.08	80.40	2.25	3.93	2.76	8.29	3.10	42.05	8.61	9.15	22.12	88.53
15	Wild Fire	89.90	3.30	13.58	75.60	2.14	3.68	2.72	8.25	3.00	38.23	11.06	8.84	20.11	80.48
16	Toro	101.40	3.60	15.69	85.40	2.56	4.42	3.02	8.86	3.30	48.29	6.50	9.75	26.15	104.62
17	Whisper	87.80	3.30	13.07	75.40	2.08	3.61	2.67	8.19	2.90	38.29	12.07	8.55	20.11	80.48
18	Landora	75.90	3.20	12.07	66.20	1.96	3.01	2.52	7.85	2.80	33.19	11.06	7.84	18.10	72.43
19	Gladiator	79.10	3.20	12.57	69.90	2.03	3.41	2.62	7.95	3.10	34.75	3.34	8.14	19.01	76.05
20	Sugandha	92.40	3.50	14.08	79.40	2.23	3.82	2.76	8.26	3.00	40.01	25.50	8.95	21.42	85.71
21	Chardoni	67.30	2.80	10.56	50.50	1.81	2.84	2.38	7.45	3.00	29.17	17.63	5.13	13.08	52.35
22	Kum kum	87.00	3.30	13.07	74.50	2.06	3.57	2.62	7.95	2.80	38.09	27.26	8.44	19.91	79.68
23	Taj mahal	70.10	2.80	10.76	57.20	1.82	2.86	2.41	7.55	3.00	30.18	30.57	5.33	14.58	58.34
24	Dr. M. S. Randhawa	65.70	2.70	10.05	49.50	1.79	2.71	2.38	7.32	2.80	25.88	59.95	4.70	8.84	35.41
25	Bonnint	43.40	2.40	9.05	38.10	1.29	2.51	2.10	6.76	3.00	22.25	30.58	3.68	7.24	28.97
26	Birendranath	64.80	2.50	10.03	45.40	1.74	2.61	2.21	7.14	2.80	25.14	11.28	4.43	7.94	31.79
27	Whimala	72.90	3.10	11.96	60.80	1.84	2.91	2.43	7.61	2.90	31.18	16.09	6.73	17.09	68.41
28	Sun Bright	86.60	3.20	12.68	73.70	2.05	3.45	2.62	7.95	2.90	35.21	14.08	8.34	19.11	76.46
29	Maronia	71.00	2.90	11.86	58.70	1.82	2.91	2.41	7.57	2.80	30.83	11.06	6.43	16.09	64.38
	SE ±(m)	4.92	0.35	1.94	4.22	0.14	0.37	0.29	0.73	0.13	4.31	1.14	0.80	2.32	9.28
	CD (5%)	14.25	0.71	3.98	12.23	0.40	1.08	-	-	0.37	12.48	3.30	2.33	6.72	26.87

genotypes are presented in table 3. The genotype Kiss of Fire ranked first for 12 characters viz., plant height (111.90 cm), number of primary branches plant⁻¹ (3.90), number of secondary branches plant⁻¹ (19.81), canopy diameter (116.40 cm), stem girth (3.61 cm), bud length (4.98 cm), bud width (3.25 cm), diameter of flower (10.48 cm), stalk length (65.39 cm), fresh weight of flower (12.07 g), flower yield plant⁻¹ (33.76) and flower yield plot⁻¹ (135.05) and was significantly superior over other genotypes.

This was followed by the genotype Peter F, Centenary, Double delight and Veternas honor which were at par with Kiss of fire and significantly superior over other genotypes for 10 characters i.e. plant height (111.00, 104.40, 103.80 and 103.20 cm respectively), number of primary branches plant⁻¹ (3.80), number of secondary branches plant⁻¹ (17.40, 17.23, 16.82, 16.09, respectively), bud length (4.72, 4.62, 4.52, 4.52 cm, respectively), bud width (3.17, 3.15, 3.14, 3.12, cm, respectively), diameter of flower (9.71, 9.20, 9.05, 8.95 cm, respectively), stalk length (59.77, 55.33, 54.09, 52.31 cm respectively), fresh weight of flower (11.06, 10.36, 10.06, 9.84 g, respectively), flower yield plant⁻¹ (32.19, 31.18, 29.17, 29.17, respectively) and flower yield plot⁻¹ (128.77, 124.75, 116.70, 116.70 respectively). The same four genotypes Peter F, Centenary, Double delight and Veternas honor were at par with each other and next to Kiss of fire but significantly superior over other genotypes for canopy diameter (98.40, 95.90, 93.40, 93.40 cm, respectively) and stem girth (2.84, 2.77, 2.73, 2.61 cm, respectively).

From the various aspects of genetic parameters (GCV, PCV, heritability and genetic advance expressed as percentage of mean), studied in this experiment, four characters i.e., stalk length, canopy diameter, stem girth and plant height were identified for primary selection as they had high GCV, PCV, high heritability along with genetic advance. Considering these characters, the five genotypes Kiss of Fire, Peter F, Centenary, Double delight and Veternas honor which showed significantly superior mean were identified for further purification and multiplication.

REFERENCES

- Atram, V. R., D. M. Panchabhai and S. R. Patil, 2015. Evaluation of hybrid tea rose varieties for Nagpur condition based on morphological, yield and yield contributing parameters.. J. Soils and Crops, **25**(2): 300-305.
- Babaei, A., S. R. Tabaei-Aghdaei, M. R. Naghavi, M. Khosh-Khui, R. Omidbaigi and M. H. Assareh, 2008. *Rosa damascena* (rosaceae) characters and their heritability analysis in Iran IRAN, J. BOT. **14** (1): 75-80.
- Burton, G. W. and E. M. Devane, 1953. Estimating heritability in tall fescue (*Festuca circumclinaceae*) from replicated clonal-material. Agron. J. **45**: 478-481.
- Carins, T. 2001. The geography and history of the rose. American Rose Annual. pp.18-29.
- Gitonga, V. W., C. F. Bocoiran, K. Verlinden, O. Dolstra, R. G. Visser, C. Maliepaard and F. A. Krens, 2014. Genetic variation, heritability and genotype by environment interaction of morphological traits in a tetraploid rose population. BMC Genetics, **15**:146.
- Hanson, G. H., H. F. Robinson and R. E. Comstock, 1956, Biometrical studies of yield in segregating populations of Korean Lespedza. Agron.J. **48**: 268-272.
- Johanson, H.W., H.F. Robinson and H.S. Comstock, 1955. Estimation of genetic and environmental variability in soyabean, Agron. J. **47** :314-318.
- Pansee, V. G. and P. V. Sukhatme, 1954. Statistical method for agriculture worker. I.C.A.R. publications, New Delhi. 2nd edn. pp. 63-66.
- Robinson, H. F., R. E. Comstock and V. H. Harvey, 1949. Estimates of studies on yield in segregating populations. Agron. J. **41**:268-272.
- Sezari, E. and E. Ahmet, 2004. Fruit characteristics of native rose hip (*Rosa* spp.) selections from the Erzurum province of Turkey. New Zealand J. Crop and Hort. Sci. **32**:51-53.
- Susek, A., A. Lvancic, A. C. Lemoine, J. P. Guillemin, J. Caneill, M. Sisko, F. Janzekovic and L. Praprotnik, 2005. Variability of Christmas Rose populations and its potential use in genetic breeding. Acta Biologica Oracoviensia Series Botanica, **47** (12): 129-135.
- Verma, M. K., S. Lal, N. Ahmed and P. A. Sagoo, 2013. Character association and path analysis in hip rose (*Rosa* spp.) genotypes collected from North Western Himalayan region of Kashmir. Afr. J. Agric. Res. **8**(39):4949-4955.
- Verma, S., S. Kumar and D. Singh, 2008. Studies on variability for various quantitative traits in rose (*Rosa* spp.). J. Ornamental Hort. **11**(1):62-65.
- Zeinali, H., S. R. T. Aghdaei and A. Arzani, 2009. A study of morphological variations and their relationship with flower yield and yield components in *Rosa damascene*. J. Agric. Sci. Technol. **11**:439-448.
- Zlesak, D. C. 2006. Rose. In N. O. Anderson (ed.), Flower Breeding and Genetics. Springer the Netherlands: pp. 698-738.

Rec. on 15.05.2016 & Acc. on 30.05.2016