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Full Length Research Paper

Character association and path analysis in hip rose (Rosa sp.) genotypes collected from North Western Himalayan region of Kashmir

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Thirty six genotypes of hip rose (Rosa sp.) collected from different areas of Kashmir valley and studied for nine polygenic characters. These revealed higher PCV than corresponding genotypic coefficient of variation (GCV) for plant height, fruit yield, fruit weight, fruit diameter, fruit length, pulp content, pulp to seed ratio, TSS and number of seeds. High heritability accompanied by moderate to high genetic gain and GCV were observed for plant height and yield which could be improved by selection in early generations. Fruit diameter (74.2%), fruit length (80.4%), fruit weight (79.9%) exhibited high heritability coupled with moderate GCV and low genetic gain which needs selection over several successive generations following hybridization for their edification. Genotypic correlations were of higher magnitude to the corresponding phenotypic ones, thereby establishing strong inherent relationship among the characters studied. The phenotypic and genotypic associations of fruit diameter was significantly positive with fruit weight (r = 0.337, 0.418), fruit pulp weight (r = 0.429, 0.507), number of seeds per fruit (r = 0.259, 0.0.406) and plant height (r = 384, 0.417). However, fruit length were significantly linked with fruit weight, pulp weight and fruit flesh ratio. Overall path analysis indicated that highest positive direct effect was showed by average fruit weight (6.694) followed by fruit flesh ratio (3.103), number of seeds per fruit (1.201), plant height (0.993), and fruit length (0.426); however, fruit diameter (-0.327), pulp weight (-8.319) and TSS (-0.529) showed negative direct effects on total hips yield which should be considered simultaneously for amenability in rose hips yield in Rosa species.

Key words: Character association, Rosa sp., path analysis, North Western Himalayan, Kashmir.

INTRODUCTION

The rose hips are the fruits of the rose plant that typically is red-to-orange in color but ranges from dark purple to black in some species. Rose hips are used for herbal tea, jam, jelly, syrup, soup, beverages, pies, bread, wine, and marmalade. The fruit of the wild rose, the rose hip, is an excellent source of total phenolics (Hvattum, 2002), vitamin C (Sen and Gunes, 1996), carotenoids (Hornero-Mendez and Minquez-Mosquera, 2000), sugars (Uggla et al., 2005) and mineral elements (Szentmihalyi et al., 2002). The fruits are commonly used to make jam, marmalade, fruit juice, etc. (Uggla and Nybom, 1999); while the dried fruits and roots are excellent for making tea (Sen and Gunes,1996). The North Western Himalayan region is one of the richest reservoirs of rose species in the world. In India, ten species are reported to be growing truly wild, mostly in the Himalayan region (Kaul et al., 1999). Species endemic to Himalayas are Rosa brunonii Lindl., Rosa gigantean Collett.,

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R. involucrate, Rosa longicuspis Bertol., Rosa leschenaultiana Wight and Arnott., R. macrocarpa, Rosa macroghylla Lindl., R. moschata, R. sericea and R. Recent exploration conducted in North webbiana. Western Himalayan region also confirmed the existence of 16 naturalized wild Rosa sp. species include, Rosa multiflora, Rosa brunonii, Rosa moschata, Rosa Rosa beggeriana, Rosa chinensis, gallica, Rosa laevigata, Rosa x alba, Rosa x fortuniana, Rosa fortida, Rosa banksiae, Rosa macrophnylla, Rosa sericea, Rosa wichuraiana, Rosa x borboniana and Rosa 'Hybrida (Dhananjaya et al., 2009). These species are annually produces hips in thousand of tones, which generally go unutilized due to lack of high yielding cultivars for commercial cultivation and fruit processing. The Kashmir region alone had the large number of native population which is capable to produce good yield of better quality hips. This natural population is generated by natural seed propagation resulted into diverse variability. Information on the performance rose hip genotypes and extent of genetic variation for different quantitative and qualitative characters in temperate agro-climatic situation is lacking.

Since, Rosa sp. is well acclimatized in Jammu and Kashmir and these regions have many strains which need 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 variations in the plant characters. It then becomes necessary to partition the observed variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genetic coefficient 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 plants with desirable characters to develop new varieties. But information on these aspects in Rosa sp. is meager in the country.

Therefore, there is a need to estimate the genetic variability in Rosa sp through biometrical procedures which may be useful to develop some selection criteria in the improvement program of rose hips. The knowledge of association of plant characters as determined by the correlation coefficient is helpful for selection of desirable characters under breeding program. Thus. а measurements of correlation coefficient between characters are a matter of considerable importance in selection indices and also permit the prediction of correlated response (Lerner, 1958). The estimate of path co-efficient analysis is important for better understanding of the crop. It gives specific measure on the direct and indirect effect of each component character upon fruit yield. Therefore, present study undertaken to estimate the extent of genotypic and phenotypic variability, heritability and genetic advance, correlation coefficient among the selected characters and direct and indirect effects of component characters on yield of hip rose.

MATERIALS AND METHODS

In present study, thirty six hip rose genotypes (Table 1) were collected based on morphological differences from different sites of Kashmir valley. Sampling was made by transect method, where 10 permanent quadrants (5 m^2 each) were laid along the straight transect line, each separated by 20 m.

The data were recorded during summer (September) seasons of the year. Morphological features as fruit characteristics, tree height and quality attributes has been recorded. Twenty fruits of each cultivar were individually analyzed for physical characteristics. Fruits were weighted in the air on a sartorius balance. The length and diameter of the fruit was measured with a digital vernier caliper. The measurement of fruit length was made on the polar axis, that is, between the apex and the end of stem. The maximum width of the fruit, as measured in the direction perpendicular to the polar axis, is defined as the diameter. After measuring the whole fruit size, the seeds were manually separated from the fruits, and total seeds and pulp weight per fruit were measured as above. The measurements of the plants height were made using measuring tape. Total soluble solids (TSS) were determined using digital refractometer (AOAC, 1984).

To compare the variations among traits, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed according to Allard (1960) and Burton (1953).

 $PCV = \sqrt{\frac{Vp}{X} \times 100}$ $GCV = \sqrt{\frac{Vg}{X} \times 100}$

Where X is the grand mean for each of the traits measured.

The heritability in broad sense and expected genetic advance were computed according to Johnson et al. (1955). Correlation and path-coefficient analysis were estimated by the association of characters and cause effect relationship studied for yield and component characters. Association of different characters under the study was analyzed by the working out genotypic and phenotypic degree of correlation and simple correlation coefficient for all the possible parts of character combination by the method of Hayes et al. (1955) and Al-Jibouri et al. (1958).

Genotypic correlation
$$r_G = \frac{COV_G (A, B)}{\sqrt{V_G(A)V_G(B)}}$$

where r_G = genotypic correlation coefficient, $COV_G(A,B) = (Mg-Me)/r$ genetic covariance between variables A and B, $V_G(A)=(Mg-Me)/r$ genotypic variance for variable A, $V_G(B) = (Mg-Me)/r$ genotypic variance for variable B, Mg and Me = mean squares of treatments (genotypes) and error, respectively, r = number of replications.

$$\label{eq:phenotypic correlation r_p = } \frac{COV_{P}\left(A,B\right)}{\sqrt{V_{P}(A)V_{G}(B)}}$$

Where r_P = phenotypic correlation coefficient, $COV_P(A,B)$ = phenotypic covariance between variable A and B = $COV_G(A,B)$ + $V_e(A,B)$, $V_P(A) = V_G(A)+V_e(A)$ phenotypic variance for variable A, $V_P(B) = V_G(B)+V_e(B)$ phenotypic variance for variable B, $V_e = Me/r$ error variance, r = number of replications.

In order to find a clear picture of the inter-relationship between fruit yield and other components, path analysis splits the correlation coefficient into the measure of the direct and indirect effect of each contributing characters towards yield at genotypic level, was done following (Dewey and Lu, 1959). After calculating the direct and indirect effect of different characters, the residual effect was calculated using the formula suggested by Singh and Choudhury (1985).

S/N	Genotype	Species	S/N	Genotype	Species
1	RH-OAF-1	Rosa canina	19	RH-OAF-19	Rosa canina
2	RH-OAF-2	Rosa canina	20	RH-OAF-20	Rosa canina
3	RH-OAF-3	Rosa canina	21	RH-OAF-21	Rosa canina
4	RH-OAF-4	Rosa canina	22	RH-1	Rosa canina
5	RH-OAF-5	Rosa canina	23	RH-2	Rosa canina
6	RH-OAF-6	Rosa canina	24	RH-3	Rosa canina
7	RH-OAF-7	Rosa canina	25	RH-4	Rosa canina
8	RH-OAF-8	Rosa canina	26	RH-5	Rosa canina
9	RH-OAF-9	Rosa canina	27	RH-6	Rosa canina
10	RH-OAF-10	Rosa canina	28	RH-7	Rosa canina
11	RH-OAF-11	Rosa canina	29	RH-8	Rosa canina
12	RH-OAF-12	Rosa canina	30	RH-9	Rosa canina
13	RH-OAF-13	Rosa canina	31	RH-10	Rosa canina
14	RH-OAF-14	Rosa canina	32	RH-11	Rosa canina
15	RH-OAF-15	Rosa canina	33	RH-12	Rosa canina
16	RH-OAF-16	Rosa canina	34	RH-PH-1	Rosa canina
17	RH-OAF-17	Rosa canina	35	RH-PH-2	Rosa canina
18	RH-OAF-18	Rosa canina	36	RH-PH-3	Rosa canina

Table 1. List of hip rose genotyped used in studied.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all the characters studied. The extent of variability in respect of range, mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance is given in Table 2. Maximum variability was recorded for the fruit to flesh ratio and number of seeds per fruit. Nanohar et al. (1986) also reported high variability in fruit and pulp stone ratio in ber. Since in breeding program, variability among the population is a pre-requisite, high variability observed in respect of the traits under study implies that there is scope for making effective improvement of these traits (Singh and Jalikop, 1986). Phenotypic coefficient of variation was more than genotypic coefficient of variation for all the characters; this implies the greater influence of environment in the expression of these characters. Comparatively higher phenotypic component of variance than the genotypic component and the extent of latter component showed that quantitative characters of rose hips are mostly hereditary in nature. Similar findings also obtained by (Attri et al., 1999) during study of wild mango germplasm of Andman and Nicobar Island. Maximum PCV and GCV estimated for the characters as plant height (47.01 and 45.48) followed by yield per plant (42.08 and 39.53). Burton and Devane (1953) suggested that genotypic coefficient of variation along with heritability estimates would give better idea about the efficiency of selection. The heritability was highest for plant height (93.61%), followed by yield per plant (88.27%), fruit length (80.48%), fruit weight (79.93%), pulp weight (78.92%), fruit diameter (74.23%), TSS (49.61%), fruit flesh ratio (46.06%) and number of seeds per fruit (45.09%). Which indicate that these characters were less influenced by environment demonstrating either these were simply inherited characters 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 (Johnson et al., 1955; Panse and Sukhatme, 1957). Similar results also reported by Islam et al., 2010 in ber.

Therefore, it is always better that both the genetic parameters should be considered together. Genetic advance percent of mean exhibited maximum value for yield per plant followed by plant height.

The major causes underlying association are either due to pleiotropic gene action or linkage or both. The phenotypic correlation includes genotypic and environmental effects, which provides information about total association between the observable characters. The phenotypic correlations were normally of genetic and environmental interaction which provided information about the association between the two characters. Genotypic correlation provided a measure of genetic association between the characters and normally used in selection, while environmental as well as genetic architecture of a genotype plays a major role in achieving higher yield combined with better quality. The genotypic and phenotypic correlation for fruit (hip) yield and its component in Rosa sp. are presented in Table 3 and only significant correlations are discussed here (Figure 1). The findings clearly indicated that genotypic correlations were of higher magnitude to the corresponding phenotypic

Characters	Range	Mean ± SEm	PCV	GCV	Heritability % (broad sense)	Genetic advance	GA% of mean
Fruit diameter (mm)	8.08 - 14.89	11.29 ± 0.56	17.05	14.69	74.23	2.94	26.02
Fruit length (mm)	11.69 - 24.85	16.47 ± 0.68	16.12	14.46	80.48	4.40	26.70
Fruit weight (g)	0.46 - 2.20	1.47 ± 0.11	29.43	26.31	79.93	0.69	47.04
Pulp weight (g)	0.26 - 1.30	0.88 ± 0.07	31.34	27.84	78.92	0.42	47.79
No. of seeds per fruits	12.60 - 37.00	23.96 ± 2.42	24.33	16.34	45.09	5.40	22.53
Plant height (m)	2.45 - 9.00	4.28 ± 0.29	47.01	45.48	93.61	3.92	91.61
TSS°B	29.9 - 39.60	36.88 ± 1.07	7.11	5.01	49.61	2.65	7.183
Fruit flesh ratio	44.04 - 89.37	60.12 ± 4.33	17.00	11.53	46.06	9.68	16.09
Yield/bush (kg)	0.75 - 7.50	3.05 ± 0.32	42.08	39.53	88.27	2.88	94.49

Table 2. Estimate of genetic parameters for some economic characters in thirty six Rosa sp. genotypes.

ones, thereby establishing strong inherent relationship among the characters studied. The phenotypic and genotypic associations of fruit diameter was significantly positive with fruit weight, fruit pulp weight, number of seeds per fruit and plant height, however, fruit length were significantly associated with fruit weight and pulp weight and fruit flesh ratio. Fruit weight is strongly associated with pulp weight and number of seeds per fruits. Pulp weight was closely associated with number of seeds per fruits and fruit flesh ratio. Plant height had positive and significant correlation with number of seeds per fruit and yield per plant at phenotypic and genotypic levels. Similar findings were also reported by Madry et al. (2000) in black currents and Misra et al. (1998a), Kandalkar et al. (1993) and Kumar et al. (2011) in Withania somnifera berries.

Path coefficient analysis is an important tool for partitioning the correlation coefficients into the direct and indirect effects of independent variables on a dependent variable. With the inclusion of more variables in correlation study, their indirect association becomes more complex. Two characters may show correlation, just because they are correlated with a common third one. In such circumstances, path coefficient analysis provides an effective means of a critical examination of specific forces action to produce a given correlation and measure the relative importance of each factor. In this analysis, fruit yield was taken as dependent variable and the rest of the characters were considered as independable variables. The path coefficient analysis which splits total correlation coefficient of different characters into direct and indirect effects on fruit yield per plant in such a manner that the sum of direct and indirect effects is equal to total genotypic correlation.

The data indicated (Table 4) that highest positive direct effect exhibited by average fruit weight (6.69), fruit flesh ratio (3.10), number of seeds per fruit (1.20), plant height (0.992) and fruit length (0.426). However, highest negative direct effect was showed by fruit diameter (-0.326), TSS (-0.529) followed by fruit pulp weight (-8.312) on total hip yield per plant. Fruit diameter showed positive indirect effect on fruit length, fruit weight, number of seeds, plant height, TSS, fruit flesh ratio and yield. However, negative fruit length exhibited positive indirect effect on fruit weight, TSS, fruit flesh and negative indirect effect on fruit

diameter, pulp weight and yield/ bush. Fruit showed positive indirect effect on fruit length, number of seeds per fruit, plant height, TSS and vield/bush, however, negative indirect effect recorded for fruit diameter, pulp weight and fruit flesh ratio. Pulp weight showed positive indirect effect on fruit length, fruit weight, number of seeds per fruit, plant height, TSS, fruit flesh ratio and yield. However, negative indirect effect recorded on fruit diameter, number of seeds per fruit exhibited positive indirect effect on fruit weight, plant height and yield per bush whereas, negative indirect effect on fruit diameter, fruit length, pulp weight, TSS and fruit flesh ratio, plant height showed positive indirect effect on fruit weight, number of seeds per fruit, fruit flesh ratio and vield, but negative indirect effect on fruit diameter, fruit length, pulp weight and TSS showed positive indirect effect on fruit diameter, pulp weight, number of seeds per fruit, plant height and yield and negative indirect effect on fruit length, fruit weight and fruit flesh ratio. Fruit flesh ratio was exhibited positive indirect effect on fruit length, plant height, TSS, fruit flesh ratio, however, on fruit diameters, fruit weight, pulp weight, number of seeds per fruits and yield negative indirect

Character	Fruit diameter (mm)	Fruit length (mm)	Fruit weight (g)	Pulp weight (g)	No. of seeds per fruits	Plant height (m)	T SS° B	Fruit flesh ratio	Yield/ bush (kg)
Fruit diameter (mm)	G1.000 P1.000	0.251 0.231	0.418* 0.337*	0.507** 0.429**	0.406* 0.259	0.417* 0.384*	-0.315 -0.227	0.293 0.247	0.400 0.316
Fruit length (mm)		G1.000 P1.000	0.514** 0.489**	0.628** 0.572**	-0.041 -0.099	-0.065 -0.054	-0.043 -0.048	0.452** 0.361*	-0.131 -0.104
Fruit weight (g)			G1.000 P1.000	0.926** 0.881**	0.759** 0.497**	0.347 0.315	-0.007 0.016	-0.047 -0.125	0.181 0.178
Pulp wt. (g)				G1.000 P1.000	0.646** 0.394*	0.341 0.303	-0.083 -0.034	0.324* 0.337	0.151 0.168
No. of seeds per fruits					G1.000 P1.000	0.479** 0.399**	0.112 -0.015	-0.280 -0.134	0.305 0.212
Plant height (m)						G1.000 P1.000	0.205 0.151	0.061 0.034	0.944** 0.892**
TSS°B							G1.000 P1.000	-0.101 -0.063	0.219 0.160
Fruit flesh ratio								G1.000 P1.000	-0.040 0.018
Yield/kg per bush									G1.000 P1.000

Table 3. Genotypic and phenotypic correlation among important characters in thirty six Rosa sp. genotypes

*significant at p < 0.05, **significant at p < 0.01.

Table 4. Direct (bold) and indirect effects of different yield attributes on fruit yield of Rosa sp. genotypes.

Characters	Fruit diameter (mm)	Fruit length (mm)	Fruit weight (g)	Pulp weight (g)	No. of seeds per fruits	Plant height (m)	TSS (⁰Brix)	Fruit flesh ratio	Genotypic correlation with fruit yield (kg/plant)
Fruit diameter (mm)	-0.327	0.107	2.803	-4.224	0.488	0.474	0.167	0.912	0.400
Fruit length (mm)	-0.082	0.426	3.445	-5.230	-0.049	-0.065	0.023	1.401	-0.131
Fruit weight (g)	-0.137	0.219	6.694	-7.708	0.912	0.344	0.004	-0.148	0.182
Pulp weight (g)	-0.166	0.268	6.202	-8.319	0.776	0.339	0.044	1.007	0.151
No. of seeds per fruits	-0.133	-0.018	5.084	-5.376	1.201	0.476	-0.059	-0.870	0.305
Plant height (m)	-0.156	-0.028	2.323	-2.845	0.576	0.993	-0.109	0.190	0.944
TSS°B	0.103	-0.018	-0.053	0.695	0.135	0.204	-0.529	-0.513	0.219
Fruit flesh ratio	-0.097	0.192	-0.319	-2.699	-0.337	0.061	0.054	3.103	-0.041

Residual effect: 0.40.

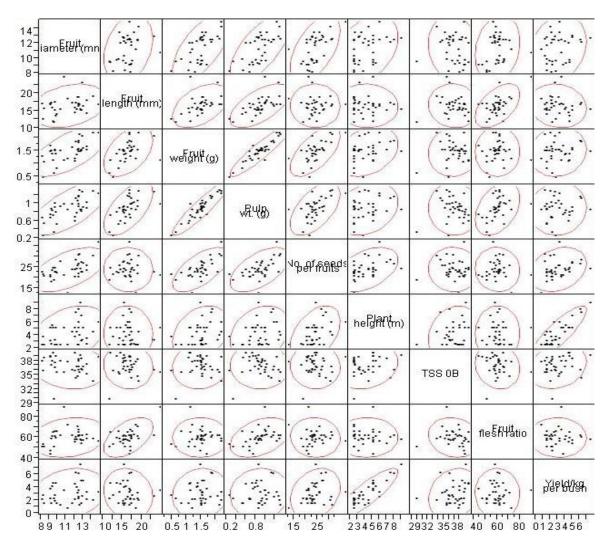


Figure 1. Scatter plot matrix of closely associated traits in thirty six Rosa sp. genotypes.

effect was recorded.

In present investigation the maximum PCV and GCV estimated for the characters as plant height followed by yield per plant; heritability was estimated highest for plant height, followed by yield per plant, fruit length, fruit weight, pulp weight, fruit diameter, TSS, fruit flesh ratio and number of seeds per fruit. Average fruit weight, fruit flesh ratio, number of seeds per fruit, plant height, TSS and fruit length and fruit diameter showed high positive and direct effect had significant positive correlation with fruit yield per plant. Therefore, plant height and average fruit weight should be considered in selection criteria for increasing fruit yield per bush and more emphasis should be given to selecting genotypes with higher fruit weight. Overall, the path analysis confined that direct effect of average fruit weight, fruit flesh ratio, number of seeds per fruit, plant height and fruit length and negative direct effect of fruit diameter, TSS and pulp weight should be considered simultaneously for amenability in fruit yield of hip rose selections. The unexplained variation in genotypic path coefficient was 0.400. It predicted that 60% variation at genotypic level had been determined and further indicated that some more factors need to be considered in this study contributed to hip yield per bush. Thus, few more traits may be considered while selecting the genotypes for high fruit (hip) yield.

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