GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS OF FRUIT YIELD IN SPINE GOURD (*Momordica dioica* Roxb.)

Vivek Kumar Sandilya[1], R.E. Ekka[1], S.K. Sinha[1] and J.K. Tiwari[1,2]*

[1]Section of Genetics and Plant Breeding, [2]AICRN on Potential Crops, Raj Mohini Devi Collage of Agriculture and Research Station, Indra Gandhi Krishi Vishwavidyalaya, Ambikapur - 497 001, Chhattisgarh (India)
*e-mail: tiwarijk5@gmail.com

ABSTRACT

The present study was conducted on 31 genotypes of spine gourd (*Momordica dioica* Roxb.) to estimate genetic variability, correlation and path coefficient analysis. The high estimates of PCV for the number of stem plant^{-1} (21.47) and moderate GCV and PCV observed for most of the traits which indicated the presence of adequate genetic variation among the genotypes. High heritability estimates coupled with high genetic advance for the number of fruits plant^{-1} and fruit yield confirmed that these traits are under the control of additive gene action. Fruit yield showed significant positive association with days to first flowering, number of stems plant^{-1}, fruit weight and number of fruits plant^{-1}. The higher association of number of fruits plant^{-1}, number of stem plant^{-1}, days to first flowering, fruit weight, fruit diameter and ovary diameter may be attributed to their direct effect on fruit yield. The study showed that the selection of traits with high positive significant association and high positive direct effect on fruit yield can help in improving yield. The similarity coefficient ranged from 0.33 to 0.94. In pair-wise comparison, the maximum similarity was obtained between genotype with a similarity index of 0.32 to 0.50, whereas genotype showed least similarity with other genotypes.

Keywords: Cluster analysis, correlation, fruit yield, heritability, path analysis, variability.

INTRODUCTION

Spine gourd (*Momordica dioica* Roxb.) belongs to the family Cucurbitaceae and has chromosome number (2n) = 28 This is climbing creeper generally found throughout India, Pakistan, Bangladesh, Himalayas to Ceylon and reported up to an altitude of 1500 m in Assam and Garo hills of Meghalaya (Ram *et al*., 2004). The fruits, young twigs and leaves of this crop are used as vegetable or cooked as a vegetable (Bandyopadhyay and Mukherjee, 2009). Among cucurbitaceous crops, spine gourd is a highly nutritious and potential vegetable containing high amount of protein and minerals/vitamins. The edible fruit has 84.1% moisture and 7.7, 3.1, 3.1, 3.0 and 1.1 g 100 g^{-1} carbohydrate, protein, fat, fiber and minerals, respectively (Kushwaha *et al.,* 2005).Apart from its nutritive value, spine gourd root contains aliphatic compounds (Ali and Shrivastva, 1998) and the plant parts are used in traditional medicines(Joseph and Antony, 2008). This potential crop is grown by tribal people of Chhattisgarh (India) under homestead garden and as a popular vegetable has high demand in market because of nutritional and medicinal value, high keeping quality, ability to withstand long-distance transportation, high market price and good export potential (Bhagat *et al*., 2017).

Spine gourd cultivation has a number of constraints including low fruit yield, low rate of tuber production (10-20 tuberous pieces per year), low seed germination, non-availability of improved varieties, difficulties in seed propagation and unpredictable sex ratio in seedling progeny (Ali *et al.*, 1991). The correlation studies provide relative information on the nature and extent of relationship between various traits and help in improving the yield. Correlation studies between yield and other traits are of interest to the breeders in planning hybridization programmes and evaluating the individual plants in segregating population. The wide genetic variability in available genotypes provides ample opportunities for crop improvement through effective selection of desirable traits. The characters having high genetic coefficient of variation indicate high potential for effective selection (Ram *et al.*, 2004) Path analysis further unravels the cause of such association by determining the direct and indirect contributions. There is need to improve yield potential of spine gourd and make it more acceptable among its consumers. Therefore, the present study was aimed to assess the genetic association between fruit yield and yield contributing traits as a basis for selection.

MATERIALS AND METHODS

The experiment material comprised of 31 different genotypes which included twenty one F_1 hybrids [AJSG-1 x IK-1 (G_{11}), AJSG-1 x CK-2 (G_{12}), AJSG-1 x AJSG-2 (G_{13}), RMDSG-3 x IK-1 (G_{14}), RMDSG-3 x CK-2 (G_{15}), RMDSG-3 x AJSG-2 (G_{16}), RMDSG-4 x IK-1 (G_{17}), RMDSG-4 x CK-2 (G_{18}), RMDSG-4 x AJSG-2 (G_{19}), AMBIKA13-5 x IK-1 (G_{20}), AMBIKA13-5 x CK-2 (G_{21}), AMBIKA13-5 x AJSG-2 (G_{22}), AMBIKA13-6 x IK-1 (G_{23}), AMBIKA13-6 x CK-2 (G_{24}), AMBIKA13-6 x AJSG-2 (G_{25}), NDM-2 x IK-1 (G_{26}), NDM-2 x CK-2 (G_{27}), NDM-2 x AJSG-2 (G_{28}), NDM-5 x IK-1 (G_{29}), NDM-5 x CK-2 (G_{30}) and NDM-5 x AJSG-2 (G_{31})], seven lines [AJSG-1 (G_1), RMDSG-3 (G_2), RMDSG-4 (G_3), MBIKA13-5 (G_4), AMBIKA13-6 (G_5), NDM-2 (G_6) and NDM-5 (G_7)], three testers [IK-1 (G_8), CK-2 (G_9) and AJSG-2 (G_{10})]. The lines and their hybrids were procured from Research-cum-Institutional Farm, Raj Mohini Devi College of Agriculture & Research Station, Ambikapur Chhattisgarh (India). The experiment was conducted during *kharif* 2016-17 and 2017-18. The experiment was conducted in a randomized block design with two replications. Plants were planted in field at ratio of 8:1 (female: male). All the recommended agronomic practices and plant protection measures were adopted for raising a healthy crop (Bhagat *et al.*, 2017). Data were recorded for the number of first flowering node, numbe of stem plant^{-1}, fruit length, ovary length, ovary diameter, fruit diameter, average fruit weight number of fruits plant^{-1} and fruit yield (kg ha^{-1}).The data was analyzed with the help of SPAR 2.0 (Ahuja *et al.*, 2008). Similarity matrix was generated using the SimQual programme NTSYSpc software version 2.02 (Rohlf, 1998).

RESULTS AND DISCUSSION

The information on the nature and extent of genetic variability present in a population for desirable characters is essential for crop improvement. The knowledge of genotypic and phenotypic coefficient of variation is useful in designing selection criteria from variable population. In general, it was noted that the phenotypic coefficient of variation (PCV) in studied genotypes was higher than genotypic coefficient of variation (GCV). There were significant differences among all the 31 genotypes studied (Table 1). The number of fruits plant^{-1} showed higher phenotypic (112.60) and genotypic (109.33) variances with high PCV (15.53%) and GCV (15.30%). Estimates of PCV and GCV for fruit traits indicated a narrow range of genetic variability among the genotypes for fruit length and ovary diameter; moderate genetic variability for fruit diameter, and wide variability for the number of fruits

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Table 1: Estimates of genetic parameters of variability for yield and attributes in spine gourd

Characters	General mean	Range		Variance		PCV (%)	GCV (%)	h^2 (%)	Genetic advance	GA as % of mean
		Min	Max	Phenotypic	Genotypic					
Days to 1st flowering	50.31	45.00	56.90	22.37	13.25	7.24	4.04	81	14.28	28.29
No. of 1st flowering node	13.02	9.70	15.80	6.36	4.23	15.81	11.13	50	6.68	51.31
No. of stem plant^{-1}	9.33	5.65	12.90	4.64	4.00	21.47	19.67	84	8.02	86.05
Fruit length (cm)	4.38	3.55	5.58	0.56	0.43	15.12	12.63	70	0.08	18.43
Ovary length (cm)	1.85	1.40	2.44	0.45	0.13	19.95	17.45	76	0.70	38.08
Ovary diameter (cm)	0.65	0.52	0.82	0.01	0.01	11.28	6.80	36	0.01	1.00
Fruit diameter (cm)	3.94	3.60	4.51	0.20	0.15	10.06	8.06	64	0.26	6.69
Single fruit weight (g)	16.92	14.60	19.50	2.17	1.82	7.98	7.16	80	3.58	21.14
No. of fruits plant^{-1}	67.33	50.50	79.50	112.60	109.33	15.53	15.30	97	22.50	33.41
Fruit yield (q ha^{-1})	57.01	36.87	70.77	106.70	102.30	17.75	17.37	96	21.10	37.02

plant^{-1}. The fruit yield plot^{-1} showed higher phenotypic (106.72) and genotypic (102.38) variances with high PCV (17.75%) and GCV (17.37%). The PCV and GCV values for this trait suggested the presence of high degree of genetic variability among the genotypes for days to first flowering, number of first flowering node, number of fruits plant^{-1}, and moderate genetic variability for fruit yield plot^{-1} indicating that these traits possess better potential for further gain and improvement through selection. Very low phenotypic (0.01) and genotypic (0.01) variances with low PCV (11.28%) and GCV (6.80%) were found for ovary diameter. Ovary length recorded very low phenotypic (0.45) and genotypic (0.13) variances with high PCV (19.95%) and GCV (17.45%). GCV helps to measure the range of genetic variability in characters and provides measure to compare the genetic variability present in various quantitative characters. The high estimates of PCV for number of stems was observed for most of the traits which indicated the presence of adequate genetic variation among the genotypes and suitability of these attributes for further improvement by selection.

High heritability estimates coupled with high genetic advance for the number of fruits plant^{-1} (97%) and fruit yield (96%) confirmed that these traits are under the control of additive gene action, and phenotypic selection for their improvement will be effective. Genetic coefficients of variation along with heritability gives clear picture of the amount of advance to be expected from a selection. The character which exhibited high heritability indicated the presence of additive gene action and such character could be fixed by resorting to selection (Panse, 1957). According to Johnson *et al.* (1955), the heritability estimates could not be a lone guideline for improvement work, since high heritability does not mean high expected genetic gain.

The correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables (Galton, 1888). The phenotypic and genotypic correlation coefficients for fruit yield and its component in spine gourd are presented in Table 2. The number of fruits plant^{-1} showed significantly positive correlation with fruit yield plant^{-1} at phenotypic and genotypic levels, and it also positively correlated with single fruit weight at genotypic level. Number of stem plant^{-1} exhibited significant positive correlation with days to first flowering at genotypic levels. Number of fruit plant^{-1} showed positive and significant correlation with the number of stem plant^{-1} at both genotypic and phenotypic level. Fruit yield showed positive and significant correlation with the number of stem plant^{-1}, single fruit weight and number of fruit plant^{-1} at both genotypic and phenotypic levels. The findings clearly indicated that genotypic correlations were of higher magnitude in comparison to the corresponding phenotypic values, thereby established strong inherent relationship among the characters studied. The low phenotypic valves might be due to the appreciable interaction of genotypes with the environments. Similar associations were also reported by Bhagat *et al.* (2018) who found positive and highly significant correlation of fruit yield with fruit weight, ovary diameter, number of stem plant^{-1} and fruit diameter.

Table 2: Estimation of genotypic (G) and phenotypic (P) correlation coefficient among various characters in spine gourd

Characters		Days to 1st flowering	No. of 1st flowering node	No. of stem plant-1	Fruit length (cm)	Ovary length (cm)	Ovary diameter (cm)	Fruit diameter (cm)	Single fruit weight (g)	No. of fruits plant-1	Fruit yield (q ha-1)
Days to 1st flowering	(G)	1.00	-0.55**	0.89**	0.14	-0.72**	0.12	0.43*	0.41*	0.12	0.128
	(P)	1.00	-0.42*	0.51**	0.10	-0.35	0.17	0.10	0.18	0.62**	0.617**
1st flowering node (No.)	(G)		1.00	-0.42*	-0.05	0.45*	-0.18	-0.01	-0.40*	-0.25	-0.363*
	(P)		1.00	-0.31	0.07	0.20	-0.03	0.04	-0.32	-0.19	-0.293
No. of stem plant-1	(G)			1.00	-0.10	-0.14	0.10	0.22	0.32	0.79**	0.831**
	(P)			1.00	-0.06	-0.11	0.20	0.15	0.24	0.70**	0.724**
Fruit length (cm)	(G)				1.00	-0.27	-0.64**	-0.27	-0.01	0.01	-0.023
	(P)				1.00	-0.20	-0.30	-0.10	-0.01	0.04	0.001
Ovary length (cm)	(G)					1.00	0.06	-0.25	0.05	-0.31	-0.248
	(P)					1.00	-0.01	-0.18	0.05	-0.27	-0.210
Ovary diameter (cm)	(G)						1.00	0.22	0.64**	0.13	0.401*
	(P)						1.00	0.03	0.20	0.09	0.182
Fruit diameter (cm)	(G)							1.00	0.19	0.35	0.387*
	(P)							1.00	0.24	0.26	0.336
Single fruit weight (g)	(G)								1.00	0.13	0.502**
	(P)								1.00	0.09	0.509**
No. of fruit plant-1	(G)									1.00	0.919**
	(P)									1.00	0.899**

*Significant at 5% level, ** Significant at 1% level of significance

Fruit yield showed significant positive association with days to first flowering, number of stems plant-1, single fruit weight and number of fruits plant-1. These traits also showed significant positive correlation with fruit yield at genotypic level indicating little effect of environment on the expression of such traits. Hence, improving days to first flowering, number of stems plant-1, single fruit weight and number of fruits plant-1 is expected to improve fruit yield. The number of first flowering node was significant negatively correlated with fruit yield indicating that the improvement of this trait shall reduce the fruit yield.

Table 3: Path analysis coefficient of fruit yield versus component character in spine gourd

Character	Days to 1st flowering	No. of 1st flowering node	No. of stem plant-1	Fruit length (cm)	Ovary length (cm)	Ovary diameter (cm)	Fruit diameter (cm)	Single fruit weight (g)	No. of fruit plant-1	PCC* fruit yield (q ha-1)
Days to 1st flowering	-0.270	0.149	-0.239	-0.038	0.193	-0.033	-0.115	-0.110	-0.302	0.617
No. of 1st flowering node	0.021	-0.039	0.016	0.001	-0.017	0.007	0.000	0.015	0.009	-0.293
No. of stem plant-1	0.475	-0.223	0.535	-0.054	-0.072	0.055	0.120	0.172	0.423	0.724
Fruit length (cm)	0.081	-0.027	-0.058	0.573	-0.157	-0.369	-0.157	0.003	0.008	0.001
Ovary length (cm)	-0.015	0.009	0.003	-0.006	0.021	0.001	-0.005	0.001	-0.006	-0.210
Ovary diameter (cm)	0.087	-0.127	0.073	-0.458	0.041	0.710	0.155	0.454	0.090	0.182
Fruit diameter (cm)	0.083	0.000	0.043	-0.053	-0.048	0.042	0.193	0.037	0.067	0.336
Single fruit weight (g)	-0.060	0.058	-0.047	0.000	-0.007	-0.094	-0.028	-0.147	-0.018	0.509
No. of fruit plant-1	0.725	-0.163	0.512	0.010	-0.202	0.082	0.225	0.081	0.646	0.899

Bold figures are direct effects, *PCC stands for phenotypic correlation coefficient; Residual effect: 0.1269

Path analysis, carried out to estimate the direct and indirect contribution of various component characters for recommending a reliable selection criterion, revealed higher positive association of ovary diameter (0.71 cm) followed by the number of fruits plant[-1] (0.646), fruit length (0.573 cm), number of stem plant[-1] (0.535), fruit diameter (0.193 cm) and ovary length (0.021 cm) [Table 3]. The higher association of the number of fruits plant[-1], number of stems plant[-1], days to first flowering, single fruit weight, fruit diameter and ovary diameter may be attributed to their direct effect on fruit yield. Thus, that selection of traits with high positive significant association and high positive direct effect on fruit yield may help in improving yield. Similar results were reported by Aliya *et al.* (2014) for days to first female flower appearance in spine gourd, Bharathi *et al.* (2005) in sweet gourd, Bhave *et al.* (2003) in teasle gourd and Dey *et al.* (2005) for fruit weight in spine gourd.

UPGMA cluster analysis was performed using SM similarity coefficient matrices calculated from qualitative data to generate a dendrogram for 31 genotypes (Fig. 1). The genotypes were grouped into two major clusters. The similarity coefficient ranged from 0.33 to 0.94. In pair-wise comparison, the maximum similarity was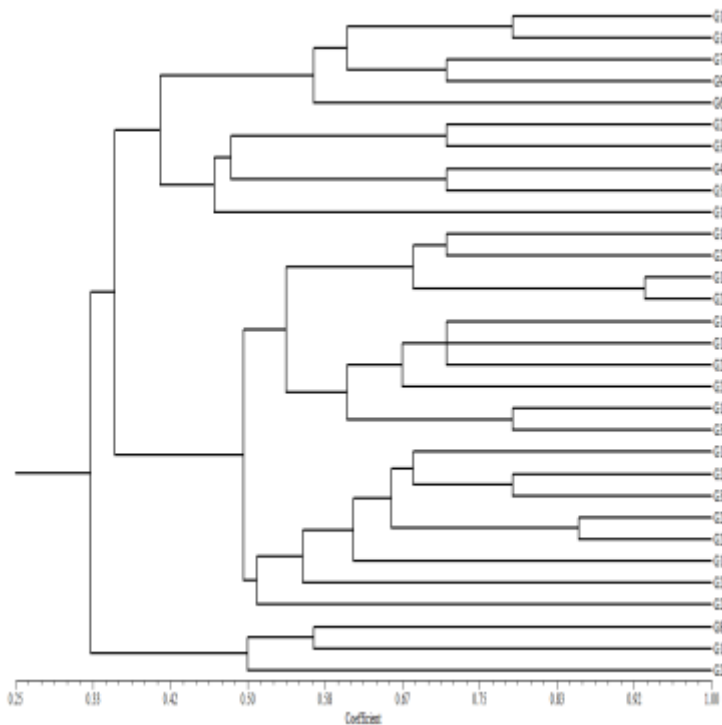 obtained between genotypes with similarity index of 0.32 to 0.50, whereas genotypes showed least similarity with other genotypes (similarity index 0.94). Cluster I consisted of genotypes having 33% similarity whereas, Cluster II consisted of genotypes having 35% similarity among them. Cluster I again partitioned into two sub-clusters in which one sub-cluster had genotypes and crosses with 50% similarity, whereas another sub-cluster had genotypes with 58% similarity. The II cluster consisted of two sub-clusters with 35% similarity and again divided into two sub-clusters having 50 and 40% similarity and another sub-divided with 50 to 72% similarity. The basic objective of genotype characterization is to test the occurrence of traits that helps in identifying a particular genotype.

Fig. 1: Dendrogram of spine gourd genotype based on qualitative characters

The characters that may be used to distinguish genotype should have the ability of precise description and recognition, and this is considered important only when they are not subjected to environmental influences. The dendrogram generated from similarity or genetic distance matrices provided information on an overall pattern of variation and degree of relatedness among genotypes.

Conclusion: The genetic architecture of fruit yield is the resultant of various interactions among selected traits. Based on correlation and path analysis studies, it may concluded that the number of first flowering node, ovary length, single fruit weight, number of fruit plant[-1] and fruit yield plant[-1] being easily observable should be given prime importance during the selection of genotypes to improve the genetic yield potential of spine gourd.

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