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Genetic variability, heritability and genetic advance studies in spine gourd (*Momordica dioica* Roxb.) genotypes

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Abstract

In spine gourds systemic research work to understand the genetic architecture and endeavor in an improvement programme is not known. On the other hand, the information on the genetic variability of the crop has not been exploited to the fullest extent possible and due to this, appreciable improvement has not been made in terms of yield and quality. There is need to improve its yield potential of the crop and make it more acceptable among the indigenous population. Eighteen promising spine gourd genotypes were obtained from various locations of Maharashtra and evaluated during *kharif* season of 2022-23. The experiment was set up in randomized block design replicated thrice with plant spacing of 1 m x 0.9 m. The higher values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for the no. of primary branches plant⁻¹, no. of fruits plant⁻¹, fruit yield plant⁻¹, fruit yield plot⁻¹ and fruit yield ha⁻¹. The highest value of heritability was observed for total soluble solids followed by ascorbic acid, plant height, no. of primary branches plant⁻¹, fruit yield plot⁻¹, fruit yield plant⁻¹, internodal length, fruit yield ha⁻¹ and pedicel length. The higher values of genetic advance at percent of mean were shown for fruit yield ha⁻¹, fruit yield plant⁻¹, fruit yield plot⁻¹ and no. of fruits plant⁻¹. High heritability along with high genetic advance at percent of mean for the fruit yield plant⁻¹, fruit yield plot⁻¹ and fruit yield ha⁻¹. High values of heritability and GA as percent of mean also indicated the additive gene effect regulating the inheritance of such characters therefore, these characters offer plenty of options for selection.

Keywords: Heritability, variability, genetic advance, spine gourd, genotypes

Introduction

Spine gourd (*Momordica dioica* Roxb.) is nutritionally important dioecious, perennial and under exploited vegetable crop. The systemic research work so as to understand the genetic architecture and endeavor in crop improvement programme of spine gourd is looking. Estimation of genetic parameters is needed to be studied for understanding the genetic make up for yield and yield contributing components. Evaluation of germplasm is useful in selection of basic collection and also its future utilization in breeding programmes. The estimation of an amount of heritability reveals the extent to which the crop improvement is possible through selection and relative degree to which a character is hereditated from parents to offsprings. For selection of superior germplasms heritability estimates along with genetic advance are important. The achievement of any breeding programme depends upon the amount of genetic variability for utilization, genetic coefficient of variation, heritability estimates, genetic advance among different traits with the fruit yield. To step improve the yield potential of the crop and make it more acceptable among the population.

Materials and Methods**Experimental site**

The field experiment was set up at Research Farm, Department of Horticulture, Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani. The experimental site was geographically located at latitude: 19°16'0"N and longitude: 76°47'0"E with at an altitude of about 408m from mean sea level. Parbhani district comes under semi-arid climate, with a dry and hot summer, humid monsoon and cold winter.

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Experimental material

Eighteen promising spine gourd genotypes were obtained from various locations of Maharashtra and evaluated in *kharif* season of 2022-23. The source of all the germplasms which were utilized in the study are given in Table 1.

Experimental details and observations recorded

The experiment was set up in randomized block design replicated thrice with plant spacing of 1 m x 0.9 m. To produce a healthy crop, all cultural operations and plant protection techniques were uniformly applied to each treatment. The data were collected on five randomly selected plants from each treatment on seventeen traits *viz.*, plant height (cm), no. of primary branches plant⁻¹, internodal length, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length (cm), fruit diameter (cm), fruit pedicel length (cm), no. of fruits plant⁻¹, ascorbic acid content (mg/100 gm), total soluble solids (TSS), average fruit weight (g), fruit yield plant⁻¹ (g), fruit yield plot⁻¹ (kg), fruit yield ha⁻¹ (q).

Statistical analysis

Standard statistical procedures were used for the estimation of genetic variability, GCV and PCV, heritability (Burton and Devane, 1953) [12] and genetic advance (Allard, 1960) [11], and the data was classified as suggested by PCV and GCV (Cherian, 2000) [13], heritability and genetic advance as percent of mean (Warshamana, 2005) [12]

Table 1: Details of genotypes used under investigation

Sr. No	Genotypes	Source
1.	MDW-1	Mandwa, Dist. Beed
2.	MDW-2	Mandwa, Dist. Beed
3.	MDW-3	Mandwa, Dist. Beed
4.	YLD-1	Yelda, Dist. Beed
5.	YLD-2	Yelda, Dist. Beed
6.	PGK-1	Pimplegaon Gadhe, Dist. Beed
7.	PGK-2	Pimplegaon Gadhe, Dist. Beed
8.	ZDG-1	Zodga, Dist. Washim
9.	ZDG-2	Zodga, Dist. Washim
10.	DHD-1	Dhadgaon, Dist. Nandurbar
11.	DHD-2	Dhadgaon, Dist. Nandurbar
12.	DHD-4	Dhadgaon, Dist. Nandurbar
13.	DHD-5	Dhadgaon, Dist. Nandurbar
14.	KKD-1	Kakardi, Dist. Nandurbar
15.	KKD-3	Kakardi, Dist. Nandurbar
16.	NDB-1	Nandurbar
17.	NDB-2	Nandurbar
18.	NDB-3	Nandurbar

Results

Wide range of variation observed for all characters. Components of variation estimated for all the traits indicated wide range of variability in mean plant height (358.14-177.00 cm), no. of primary branches plant⁻¹ (4.96-2.14), internodal length (4.04-7.02 cm), days to first flowering (37.58-51.06), days to 50% flowering (47.81-62.04), days to first harvest (57.91-87.57), days to last harvest (119.43-147.37), fruit length (3.30-4.79 cm), fruit diameter (2.03-3.21 cm), pedicel length (1.49-2.73 cm), average fruit weight (9.03-19.02 g), no. of fruits plant⁻¹ (19.21-60.89), fruit yield plant⁻¹ (179.75-788.12 g), fruit yield plot⁻¹ (1.94-8.77kg), ascorbic acid (6.85-11.22mg/100 gm), total soluble solids (2.15-3.20%) and fruit yield ha⁻¹ (19.74-93.84q) which indicated that there is more scope for selection

pressure for the improvement of these characters. These findings are in close proximity with the results those of Sukwariya *et al.* (2019) [10] in spine gourd, Som *et al.* (2020) [9] in sponge gourd and Patil *et al.* (2022) [7] in spine gourd.

The phenotypic variance was found more than the genotypic variance for all traits studied. The genotypic variance obtained for various yield, yield attributing traits ranged from 22092.07 to 0.09 and phenotypic variance obtained for various yield, yield attributing traits ranged from 24662.81 to 0.10. The highest GCV was observed in fruit yield ha⁻¹ (38.76) followed by fruit yield plant⁻¹ (37.16), fruit yield plot⁻¹ (36.36), no. of fruits plant⁻¹ (28.13) and no. of primary branches plant⁻¹ (24.82), while the GCV observed in plant height (19.49), average fruit weight (18.11), pedicel length (17.60), internodal length (14.91), ascorbic acid (11.87), total soluble solids (11.64) and fruit diameter (11.36) were moderate. The GCV was low in days to first fruit harvest (9.31) followed by days to first flowering (7.46), fruit length (7.01), days to 50% flowering (6.01) and days to last harvest (4.49). The highest PCV observed was in fruit yield ha⁻¹ (40.50) followed by fruit yield plot⁻¹ (39.55), fruit yield plant⁻¹ (39.27), no. of fruits plant⁻¹ (30.98), no. of primary branches plant⁻¹ (26.37), average fruit weight (24.59) and plant height (20.64), and while the PCV observed in pedicel length (19.41), internodal length (16.40), fruit diameter (15.42) days to fruit harvest (12.75), ascorbic acid (12.35), total soluble solids (12.06), fruit length (12.01) and days to 50% flowering (10.01) were moderate. The PCV was low in followed by days to first flowering (9.82) and days to last harvest (8.04), and those results are in close conformity to the result of Jena *et al.* (2017) [5] in pointed gourd, Sukwariya *et al.* (2019) [10] in spine gourd, Patil *et al.* (2022) [7] in spine gourd and Sagar *et al.* (2024) [8] in bitter gourd.

The genotypes had recorded high heritability value for total soluble solids (93.36), followed by ascorbic acid content (92.31), plant height (89.18), no. of primary branches plant⁻¹ (88.58), fruit yield plot⁻¹ (83.91), fruit yield plant⁻¹ (82.94), internodal length (82.71), fruit yield ha⁻¹ (82.25) and pedicel length (82.18), and while no. of fruits plant⁻¹ (61.43), days to first flowering (57.76), fruit diameter (54.25) and days to first harvest (53.28) were moderate. The low heritability was recorded in days to last harvest (8.47), fruit length (34.05), days to 50% flowering (36.02) and average fruit weight (38.89). Genetic advance ranged observed was fruit length (0.35) to fruit yield plot⁻¹ (289.79). High genetic advance as percent of mean was also recorded for fruit yield ha⁻¹ (76.32), fruit yield plant⁻¹ (72.46), fruit yield plot⁻¹ (68.86) and no. of fruits plant⁻¹ (52.62), and while no. of primary branches plant⁻¹ (48.12), plant height (37.91), pedicel length (32.86), internodal length (27.94) and average fruit weight (27.48) were moderate. The low genetic advance as percent of mean was recorded in ascorbic acid (23.49), total soluble solids (23.17), fruit diameter (17.24), days to first harvest (14.00), days to first flowering (11.68), fruit length (8.43), days to 50% flowering (7.43) and days to last harvest (5.16), and those results are in proximity to findings of Devi and Mariappan (2013) [4] in snake gourd, Jena *et al.* (2017) [5] in pointed gourd, Sukwariya *et al.* (2019) [10] in spine gourd, Patil *et al.* (2022) [7] in spine gourd and Sagar *et al.* (2024) [8] in bitter gourd.

Discussion

For selecting better genotype for character improvement and for selecting the most promising parent for crop

improvement programme genetic variability is most important for any crop. The achievement of any breeding programme relies upon the quantum of genetic variability exists in available germplasms. The results for all the seventeen characters of spine gourd with respect to mean, overall range, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance were represented in Table 2 and Fig. 1.

Studies on genotypic and phenotypic coefficient of variation indicated the level of variability for different traits in spine gourd. PCV and GCV for all the traits under experimentation indicated that environmental factors were affecting the expression of these traits. The traits which expressed high phenotypic and genotypic coefficient of variation are of great economic value and there is offering

more scope for improvement of these traits through selection procedures and was in agreement with the findings of Devi and Mariappan (2013)^[4] in snake gourd, Jena *et al.* (2017)^[5] in pointed gourd, Sukwariya *et al.* (2019)^[10] in spine gourd, Patil *et al.* (2022)^[7] in spine gourd and Mane *et al.* 2024. They reported low or moderate heritability and genetic advance as percent mean adds less scope for selection, as they indicate the role of non-additive genetic effects. The characters having high heritability along with high genetic advance as percent mean is depicts greater role of additive genetic effect and there is offering more scope for future improvement through selection and was in accordance with the findings of Venkatraman *et al.* (2024)^[11] in bottle gourd.

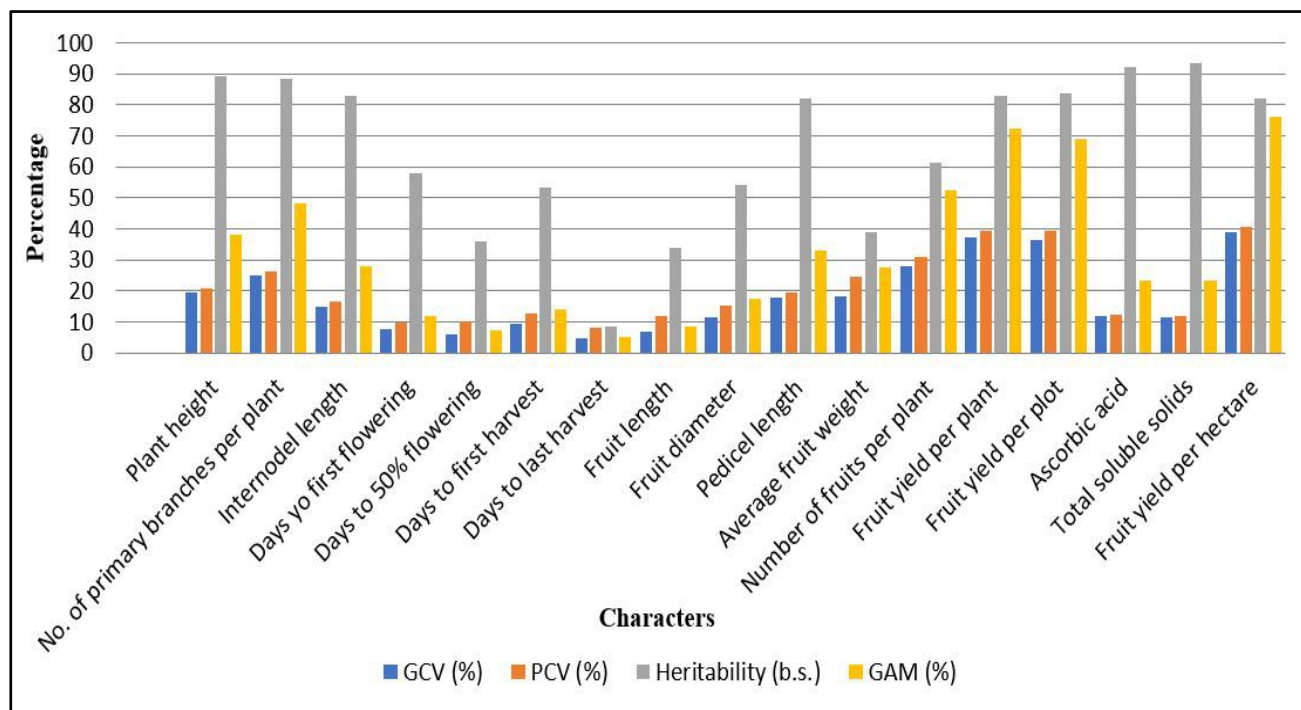


Fig 1: GCV, PCV, Heritability and Genetic Mean Advance of seventeen quantitative traits in spine gourd.

Table 2: Estimates of genetic parameters of variability for yield and attributes in spine gourd

S. No.	Traits	Range		Mean	GV	PV	GCV (%)	PCV (%)	Heritability (b.s.)	GA	GAM (%)
		Min.	Max.								
1	PH	358.14	177.00	218.41	1811.89	2031.75	19.49	20.64	89.18	82.81	37.91
2	NPBPP	4.96	2.14	3.43	0.72	0.82	24.82	26.37	88.58	1.65	48.12
3	IL	7.02	4.04	5.15	0.59	0.71	14.91	16.40	82.71	1.44	27.94
4	DFH	51.06	37.58	45.16	11.36	19.66	7.46	9.82	57.76	5.28	11.68
5	D50%F	62.04	47.81	54.44	10.70	29.70	6.01	10.01	36.02	4.04	7.43
6	DFH	87.57	57.91	71.73	44.59	83.69	9.31	12.75	53.28	10.04	14.00
7	DLH	147.37	119.43	131.09	34.60	111.13	4.49	8.04	08.47	6.76	5.16
8	FL	4.79	3.30	4.20	0.09	0.25	7.01	12.01	34.05	0.35	8.43
9	FD	3.21	2.03	2.61	0.09	0.16	11.36	15.42	54.25	0.45	17.24
10	PL	2.73	1.49	2.00	0.12	0.15	17.60	19.41	82.18	0.66	32.86
11	AFW	19.02	9.03	12.46	5.09	9.39	18.11	24.59	38.89	3.42	27.48
12	NFPP	60.89	19.21	32.68	84.53	102.53	28.13	30.98	61.43	17.20	52.62
13	FYPP	788.12	179.75	399.95	22092.07	24662.81	37.16	39.27	82.94	289.79	72.46
14	FYPP	8.77	1.94	4.07	2.19	2.59	36.36	39.55	83.91	2.80	68.86
15	AA	11.22	6.85	9.72	1.33	1.44	11.87	12.35	92.31	2.28	23.49
16	TSS	3.20	2.15	2.58	0.09	0.10	11.64	12.05	93.36	0.60	23.17
17	FYPH	93.84	19.74	46.08	319.01	349.15	38.76	40.55	82.25	35.17	76.32

PH- Plant height (cm), NPBPP- No. of primary branches plant⁻¹, IL- Internodal length (cm), DFF- Days to first flowering, D50%F- Days to 50% flowering, DFH- Days to first harvest, DLH- Days to last harvest, FL- Fruit length (cm), FD- Fruit diameter (cm), PL- Pedicel length (cm), AFW- Average fruit weight (g), NFPP- No. of fruit plant⁻¹, FYPP- Fruit yield plant⁻¹ (g), FYPH- Fruit yield plot⁻¹ (kg), AA- Ascorbic acid (mg/100 g), TSS- Total soluble solids (%) and FYPH- Fruit yield ha⁻¹

Conclusion

The traits which reveal high phenotypic and genotypic coefficient of variations are of economic value and provide scope for improvement of these traits through selection process. High values of heritability and GA as percent of mean also indicated the additive gene effect regulating the inheritance of such characters therefore, these characters offer plenty of options for selection.

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