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Study on genetic variability and heritability in bitter gourd (*Momordica charantia*) under Allahabad agro-climatic condition

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Abstract

This chapter contains the details of the materials used and the methods adopted in the present study entitled “Study on Genetic variability and heritability of Bitter gourd [*Momordica charantia*] Under Allahabad Agro-climatic Condition” was carried out on genetic variability, and heritability in bitter gourd during 2017-2018 at the Horticulture Research Farm, Department Of Horticulture, SHUATS, Allahabad in randomized block design with eighteen genotypes of bitter gourd in three replications. Eighteen genotypes of bitter gourd were accessed concerning the variability GCV and PCV, heritability and genetic advance for eighteen quantitative and qualitative characters. The mean sum of squares due to the genotypes were significant for all the characters studied. Estimates of PCV were higher than their corresponding GCV however good correspondence was observed between GCV and PCV for all characters. The study on genotypic and phenotypic coefficient of variation revealed that the magnitude of GCV and PCV highest for fruit weight (34.92 & 34.71). The heritability estimate were found to be high (>60) for almost all characters. Genetic advance was highest for Average fruit weight (g) (39.76). Genetic advance as percent of mean was highest for Average fruit weight (g) (39.76).

Keywords: GCV and PCV, heritability, genetic advance, bitter gourd and *Momordica charantia*

Introduction

Bitter gourd (*Momordica charantia* L.) is known by different name such as Balsam pear or bitter cucumber in English, Karela in hindi, Gujarati, Punjabi and also called as bitter melon, it is a tropical and subtropical crop belonging to the family Cucurbitaceae which has 90 genera and 750 species (Ram, 2005) [3]. It is grown up to an elevation of 1600-1700 m above mean sea level. The center of origin of this crop is India, with a secondary center of diversity in China and South East Asia.

Optimum temperature requirement for the crop growth is 24-27°C (Salunkhe and Kadam, 2005) [4]. In India bitter gourd is grown in wild and cultivated form covering an area of 26,004 ha with an annual production of 1,62,196 MT (Anonymous, 2011a) [1]. Major bitter gourd growing states are Karnataka, Maharashtra, Gujarat, Rajasthan, Punjab and Tamil Nadu. However, total area occupied by cucurbits in Himachal Pradesh is 2,456 ha with an annual production of 63,122 MT (Anonymous, 2011b) [2]. Bitter gourd is found abundantly in various pockets of Kangra district followed by Una and Hamirpur. The crop is grown during rainy season and fruits get lucrative returns in the market of Punjab, Jammu and Kashmir and New Delhi. Thus, bitter gourd being an important vegetable crop requires a thorough knowledge regarding the amount of genetic variability existing for various characters is necessary to initiate any crop improvement programme. Greater the variability in the available germplasm, better will be the chances for selecting superior genotypes. In bitter gourd too, fruits vary in shape, size, colour, maturity and taste. Improvement in any crop depends upon magnitude of genetic variability and extent to which desired characters are heritable.

Materials and Methods

The present investigation entitled “study on genetic variability, heritability, character association and genetic divergence in Bitter gourd (*Momordica charantia*)” was conducted in randomized block design with 18 genotypes of bitter gourd in three replications. The characters studied were viz., quantitative and qualitative characters.

The experiment was laid out at Vegetable Research Farm, Department of Horticulture, Allahabad School of Agriculture, SHUATS Allahabad. The mean data of each character was subjected to statistical analysis for variance and test the significance of each character as per the procedure of Panse and Sukhatme (1967) [8]. Genotypic and phenotypic correlation coefficients were calculated by standard procedures (Johnson *et al.*, 1955; Hanson *et al.*, 1956) [6, 7]. Heritability (h^2 broad sense) and Genetic advance method by Robinson *et al.* (1949) [10] Genetic advance as percentage over mean method by Johnson *et al.* (1955) [6].

Results and Discussion

The mean sum of squares values for all the eighteen characters. The mean sum of squares due to the genotypes were significant for all the characters studied, suggesting the existence of high genetic variability among the genotypes for all the traits.

Genetic variability

The information on the nature of extent of genetic variability is very important for selection of desirable traits for crop improvement programme. The knowledge of genotypic and phenotypic coefficient of variation is being useful in designing selection criteria for variable population. The studies on GCV and PCV indicated that the presence of high amount of variation and role of the environment on the expression of these characters. The magnitude of PCV was higher than GCV for all the characters which may due to higher degree of interaction of genotypes with the environment. The simple measure of variability like mean, phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in broad sense and genetic advance as percent of mean are presented in Table 1. All the eighteen characters under study exhibited high variability as evident from the estimates of mean, coefficients of variation, heritability and genetic advance. The genotypic coefficient variance value were categorized as low (0-10%), moderate (10-20%) and high (20% and above) given by Sivasubramanian and Madhavamenon (1973) [11]. Wide range of genotypic coefficient of variation (GCV) was observed for the characters ranging from average fruit weight (g) (34.71) to number of days to first picking (1.95). Higher magnitude of genotypic coefficient of variance (GCV) was recorded for Specific gravity, Number of seeds per fruit and Number of marketable fruit per vine. While moderate estimates were observed for Number of branches per plant, Average fruit length, Average fruit width, Fruit yield per plant (kg) and Total marketable fruit yield per hectare (q) low estimates of genotypic coefficient of variance was observed for Seed germination %, Days to first female flower appearance, Days to first male flower appearance, Node no.to which 1st female flower appear, Node no. to which 1st male flower appear, Number of days to first picking, Harvest duration (days), Ascorbic acid [mg/100g] and Total soluble solids.

Wide range of phenotypic coefficient of variation (PCV) was observed for the characters ranging from average fruit weight (g) (34.92) to number of days to first picking (3.04). Higher magnitude of phenotypic coefficient of variance (PCV) was recorded for Average fruit weight (g), umber of seeds per fruit, Total marketable fruit yield per hectare (q), Specific gravity and Number of marketable fruit per vine. While moderate estimates were observed for Seed germination %, Number of branches per plant, Node no.to which 1st male flower appear, Average fruit length, Average fruit width and Fruit yield per plant (kg). Low estimates of phenotypic

coefficient of variance was observed for Days to first female flower appearance, Days to first male flower appearance, Node no.to which 1st female flower appear, Number of days to first picking, Harvest duration (days), Ascorbic acid [mg/100g] and Total soluble solids.

Heritability and genetic advance

Heritability and genetic advance were regarded as important selection parameters. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. According to Lush (1949) [5] heritability in broad sense is the ratio of total genotypic variance to phenotypic variance, expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Burton (1952) [12] suggested that genetic variation along with heritability estimates would give a better idea about the efficiency of selection. Heritability is a measure of the extent of phenotypic variation caused by the action of genes. For making effective improvement in the character for which selection is practiced, heritability has been adopted by large number of workers as a reliable indicator. Johnson *et al.* (1955) [6] suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement though selection in genetic advance generation. Therefore it should be heritability along with high genetic advance will be valuable in the selection programme.

The estimates of heritability from present investigation are presented in (Table 1). The heritability was categorized as low (0-30%), moderate (30- 60%) and high (60% and above) as given by Robinson *et al.* (1949) [10]. In the present investigation, the heritability estimate were found to be high (>60) for almost all the characters *viz* high for Number of branches per plant, Days to first female flower appearance, Node no.to which 1st female flower appear, Number of marketable fruit per vine, Harvest duration (days), Average fruit length, Average fruit width, Average fruit weight (g), Fruit yield per plant (kg), Number of seeds per fruit, Specific gravity, Ascorbic acid [mg/100g] and Total soluble solids. The estimate of moderate heritability (>30 to <60) for Days to first male flower appearance, Number of days to first picking and Total marketable fruit yield per hectare (q) and Seed germination % and Node no.to which 1st male flower appear low heritability (<30%) not found.

The estimation of genetic advance for all the characters are presented in (Table 1). Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and $\geq 20\%$) as given by Johnson *et al.* (1955) [6] and Falconer and Mackay (1996) [9]. Genetic advance as percent of mean was highest for Average fruit weight (g) (39.76). And moderate genetic advance as percent of mean was recorded for number of branches per plant (10.81). While as lowest genetic advance percent of mean was observed in Seed germination %, Days to first female flower appearance, Days to first male flower appearance, Node no.to which 1st male flower appear, Node no.to which 1st female flower appear, Number of days to first picking, Number of marketable fruit per vine, Harvest duration (days), Average fruit length, Average fruit width, Fruit yield per plant (kg), Number of seeds per fruit, Total marketable fruit yield per hectare (q), Specific gravity, Ascorbic acid [mg/100g], and Total soluble solids.

Table 1: Estimation of genetic variability, GCV, PCV, Heritability, Genetic advance and Genetic Advance as percent of mean for 18 characters in Bitter gourd genotypes

Sl. No.	Character	Phenotypic variance	Genotypic variance	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability in broad sense (h^2b)	Genetic Advance	Genetic Advance as % of mean
1	Seed germination %	157.95	25.87	13.99	5.66	16	4.24	6.05
2	Number of branches per plant	53.47	38.40	19.17	16.25	72	10.81	36.36
3	Days to first female flower appearance	16.61	14.53	9.12	8.53	87	7.34	21.06
4	Days to first male flower appearance	1.40	0.61	3.25	2.15	44	1.06	3.76
5	Node no.to which 1 st male flower appear	1.27	0.33	11.28	5.77	26	0.60	7.79
6	Node no.to which 1 st female flower appear	1.29	0.96	6.56	5.67	75	1.74	12.92
7	Number of days to first picking	3.21	1.32	3.04	1.95	41	1.51	3.30
8	Number of marketable fruit per vine	6.18	4.21	25.53	21.08	68	3.49	45.94
9	Harvest duration (days)	2.73	2.25	4.44	4.03	82	2.80	9.66
10	Average fruit length	10.05	9.42	19.72	19.09	94	6.11	48.77
11	Average fruit width	2.38	2.17	14.01	13.38	91	2.90	33.75
12	Average fruit weight (g)	381.41	376.97	34.92	34.71	99	39.76	91.11
13	Fruit yield per plant (kg)	0.10	0.07	17.69	14.63	68	0.43	31.94
14	Number of seeds per fruit	15.39	14.75	26.53	25.98	96	7.74	67.14
15	Total marketable fruit yield per hectare (q)	0.38	0.18	20.08	13.85	48	0.60	25.22
16	Specific gravity	0.31	0.28	27.80	26.46	91	1.04	66.49
17	Ascorbic acid [mg/100g]	0.05	0.03	4.81	3.88	65	0.29	8.25
18	Total soluble solids.	0.10	0.08	7.48	6.79	83	0.52	16.29

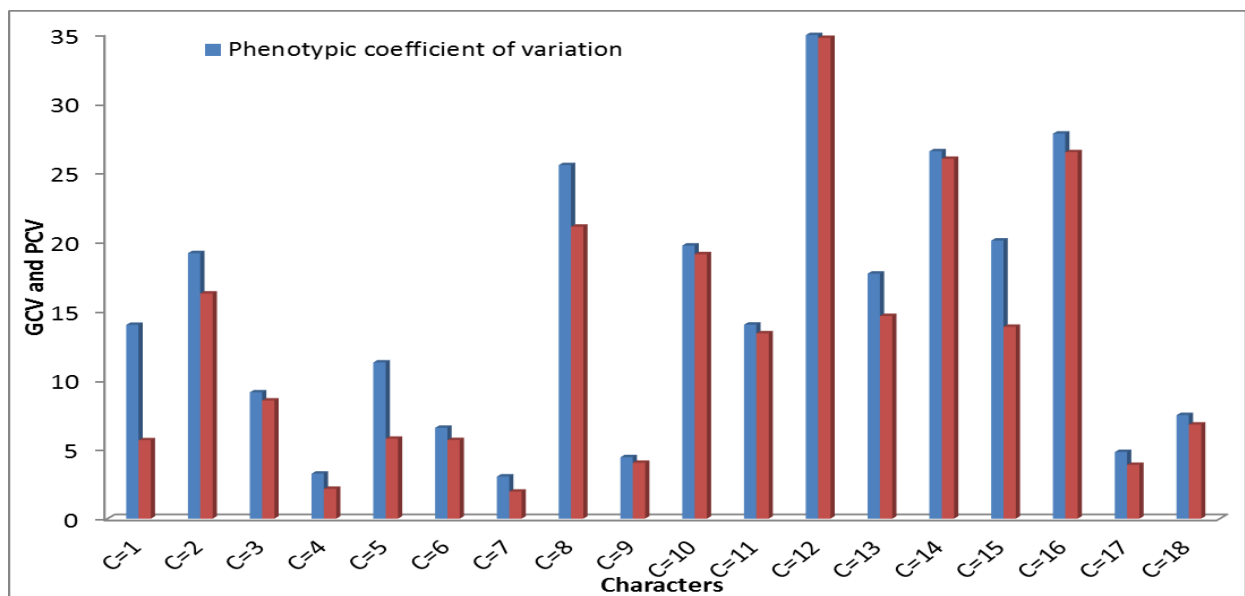


Fig 1: Estimation of genetic variability, GCV and PCV for 18 characters in Bitter gourd genotypes

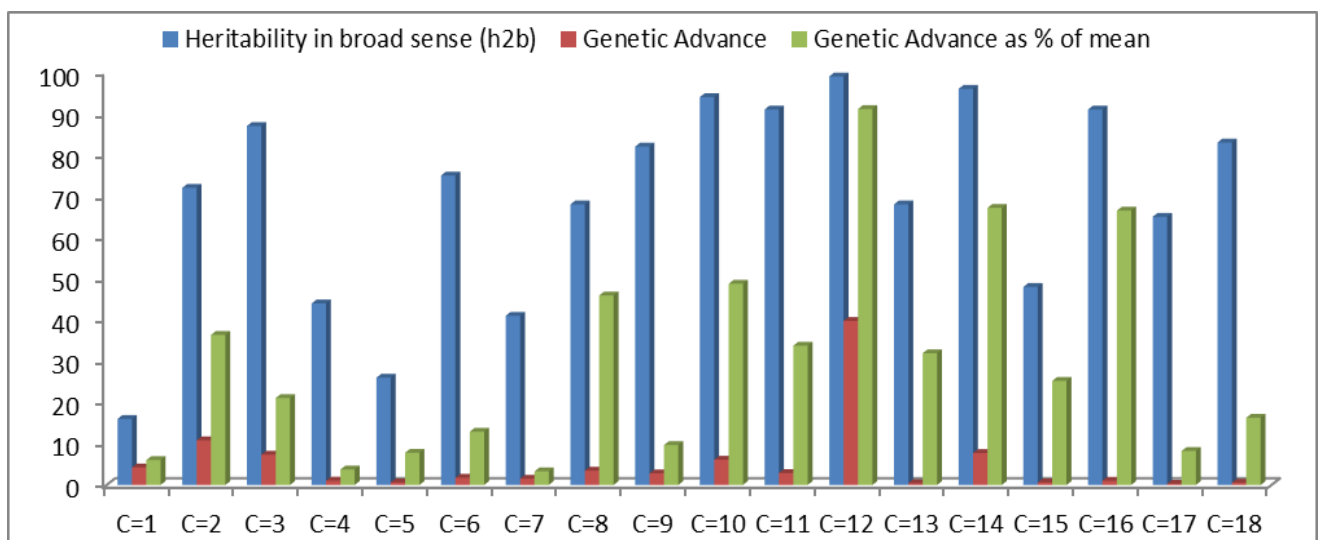


Fig 2: Estimation of heritability in broad sense (h^2b), Genetic advance and Genetic advance as % mean for 18 characters in Bitter gourd genotypes

Conclusion

On the basis of mean performance of eighteen genotypes of bitter gourd, KT-5(2.24 kg) and Kalayanpur baramasi (2.23kg) was found superior in terms of fruit yield /plant (kg). On the basis of Analysis of variance significant difference was recorded for all the quantitative and qualitative traits indicating presence of large amount of variability in the genotypes. The highest genotypic and phenotypic coefficient of variation for fruit weight (34.92 & 34.71) indicating the presence of high amount of variation and role of environment on the expression of these traits. The highest heritability estimate was observed for characters like number of branches per plant, Days to first female flower appearance, Node no. to which 1st female flower appear, harvest duration (days), Average fruit length, Average fruit width, Average fruit weight (g), Fruit yield per plant (kg), Number of seeds per fruit, Specific gravity. The highest estimation of genetic advance was observed in Average fruit weight (g) (39.76).

Genotypic correlation coefficient analysis revealed that fruit yield per plant (kg) showed positive significant association with Germination (%), Node no. to which 1st female flower appear, Harvest duration (days), Average fruit weight (g) and TSS. Phenotypic correlation coefficient analysis revealed that fruit yield per plant(kg) showed positive non-significant association with Germination (%), Node no. to which 1st male flower and 1st female flower appear, Number of marketable fruit per vine, Average fruit length, width and weight(g), Number of seeds per fruit, TSS and Harvest duration (days).

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