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Variability, heritability and genetic advance in sweet gourd (*Cucurbita moschata* Duch. Ex. Poir.)

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Abstract

Variability, heritability and genetic advance in 81 genotypes of sweet gourd (*Cucurbita moschata* Duch. Ex. Poir.) collected from different regions of Bangladesh were studied. Significant variations among all the studied characters were noted in sweet gourd under study. There were also considerable differences between genotypic and phenotypic coefficient of variation for almost all characters, which demonstrated considerable influence of environment for the expression of traits. Among the studied characters, GCV and PCV were high for the traits, namely, female flowers per plant, number of fruits per plant, yield per plant, total male flower per plant and seeds per fruit. All the characters showed considerably higher heritability, ranging from 41.46 to 98.37%. Among the studied characters, the genetic advance (as % of mean) was high for the traits, namely, female flowers per plant, yield per plant, number of fruits per plant and total male flowers per plant. High heritability coupled with high genetic advance was observed in total male and female flowers per plant, number of fruits and yield per plant, which indicated that these characters were less influenced by environment confirming additive gene action, and therefore, selection of these characters would be more effective for yield improvement of sweet gourd.

Keywords: Variability, Heritability, Genetic advance and Sweet gourd

Introduction

Sweet gourd is one of the popular cucurbitaceous vegetables in Bangladesh. It has the highest storability among all the cucurbits. Due to its good storage quality, nutritional status, reasonable market price and year round availability, it has a great demand in Bangladesh. The average yield of sweet gourd in the country was 7.49 t/ha, which was far below the normal yield level of other countries. The yield of sweet gourd ranged from 42 to 60 t/ha in Netherlands, France and Spain, 14.17 to 20.34 t/ha in USA, China and Sri Lanka, and 9.72 to 10.41 t/ha in Pakistan and India (FAO, 2003). Research reports on the development of sweet gourd variety in Bangladesh are scanty, and until now there has been no released variety of sweet gourds in the country. Lack of improved variety is one of the main constraints for its production.

An understanding of the nature and magnitude of variability among the available genetic stock of a crop is of prime importance to the breeder. A good knowledge of genetic wealth might also help in identifying desirable genotypes for improvement of the crop. Because of its high cross-pollination, any genetically pure strain is hardly available. Among the available cultivated varieties of this crop, a wide range of genetic variability exists, which could be exploited for its improvement (Rashid, 1993). A breeder needs high variability among the population to evolve improved varieties through selection, either from the existing genotypes or from the segregants of crosses. Hence, the genetic information on yield and yield contributing characters needs to be assessed properly for the improvement of this crop.

Expression of different plant characters is controlled by genetic and environmental factors. It is often difficult to estimate the proportion of heritable and environmental variation. The progress of breeding is conditioned by the magnitude, nature and interaction of genotypic and environmental variations in the plant characters. So, the study of such parameters is necessary for a successful breeding programme. The study on sweet gourd would provide valuable information on nature of variation of different characters which would be useful in selecting plants with desirable characters in order to develop new varieties.

Materials and Methods

Eighty one genotypes of sweet gourd were grown in Alpha Lattice Square Design in 3 replications during the period from mid November, 2002 to last of May, 2003 at the experimental farm of "Collection, Evaluation.......Vegetables and Fruits of Bangladesh (CVFB)" project, Dept. of Horticulture, BAU, Mymensingh. The places from where the sweet gourd germplasm were collected are shown in Table 1. The experimental site was a medium high land, soil was silty loam in texture belonging to the Old Brahmaputra Flood Plain Alluvial Tract. The experimental area was under the sub-tropical climatic zone and characterized by heavy rainfall, high temperature, high humidity and relatively long days during the Kharif season (April to September) and scanty rainfall, low humidity, low temperature, and short days during Rabi season (October to March). After final land preparation, pits of 50×50×30 cm were prepared in each block. The seeds were sown in the well prepared pits. There were two pits in each replication and three plants in each pit and pits were spaced 2m apart, while beds were spaced with 2.5m apart. Manures and fertilizers were applied in the experimental field as per dose recommended by BARC (1997). Normal recommended cultural practices were adopted during experimentation. Three plants from each replication, selected at random, provided the material for the evaluation. Data were recorded on yield and different yield contributing characters. TSS was recorded with help of hand refractometer. According to Singh and Chaudhury (1985), genotypic and phenotypic coefficient of variation was calculated of all the quantitative characters. Heritability in broad sense was estimated according to Johnson *et al.* (1955). Genetic advance in per cent of mean was calculated according to the method given by Comstock and Robinson (1952).

Table 1. List and source of collection of 81 sweet gourd germplasm

Accession	Place of collection	Accession	Place of collection	Accession	Place of collecton
CM 001	Jamalpur	CM 042	Mymensingh	CM 080	Pabna
CM 002	Jamalpur	CM 043	Panchagarh	CM 081	Pabna
CM 004	Jamalpur	CM 044	Panchagarh	CM 084	Mymensingh
CM 006	Tangail	CM 045	Pabna	CM 085	Mymensingh
CM 007	Jamalpur	CM 046	Pabna	CM 087	Mymensingh
CM 008	Jamalpur	CM 047	Pabna	CM 088	Gazipur
CM 009	Jamalpur	CM 049	Tangail	CM 089	Mymensingh
CM 014	Jamalpur	CM 050	Tangail	CM 091	Rajshahi
CM 018	Mymensingh	CM 051	Tangail	CM 092	Rajshahi
CM 019	Mymensingh	CM 052	Tangail	CM 093	Rajshahi
CM 020	Mymensingh	CM 056	Tangail	CM 097	Gaibandha
CM 022	Mymensingh	CM 057	Tangail	CM 099	Gaibandha
CM 023	Mymensingh	CM 059	Tangail	CM 100	Gaibandha
CM 024	Mymensingh	CM 061	Pabna	CM 106	Comilla
CM 025	Mymensingh	CM 062	Pabna	CM 109	Comilla
CM 026	Mymensingh	CM 063	Pabna	CM 110	Comilla
CM 027	Mymensingh	CM 064	Pabna	CM 112	Chittagong
CM 029	Pabna	CM 066	Pabna	CM 114	Chittagong
CM 030	Pabna	CM 067	Pabna	CM 115	Chittagong
CM 031	Pabna	CM 069	Pabna	CM 117	Chittagong
CM 032	Pabna	CM 070	Pabna	CM 118	Chittagong
CM 033	Pabna	CM 071	Pabna	CM 119	Chittagong
CM 034	Pabna	CM 072	Pabna	CM 120	Chittagong
CM 035	Pabna	CM 073	Pabna	CM 122	Natore
CM 036	Pabna	CM 074	Pabna	CM 123	Natore
CM 038	Pabna	CM 077	Pabna	CM 128	Dinajpur
CM 041	Mymensingh	CM 078	Pabna	CM 129	Dinajpur

Results and Discussion

Vegetative characters: Wide range of variation was noticed among the vegetative characters of the studied accessions of sweet gourd (Table 2). In all the cases, there were considerable differences between genotypic and phenotypic coefficients of variation for almost all vegetative characters which demonstrated considerable influence of environment for the expression of these vegetative traits. Considerably high degrees of GCV and PCV were exhibited by number of primary branches per plant while other characters exhibited comparatively low GCV and PCV (Table 2). These moderate and low values of GCV and PCV indicated low genetic divergence with the accessions for vegetative characters where effects would provide practically little chance for plant selection. Mohanty (2000) also revealed similar findings in pumpkin where he recorded 24.64 and 21.66% PCV for the traits of vine length and primary branches per plant, respectively. High heritability was observed in case of petiole length followed by vine length at harvest and primary branches per plant. The rest of the characters showed moderate heritability. Similar results were also reported by Lakshmi *et al.* (2002) where they observed 89.07% heritability in case of vine length of pumpkin. The genetic advances (as percentage of mean) for all the vegetative characters were considerably low, which in turn suggested the limited scope for improvement through selection. Genetic advance along with heritability was, however, considerably high for primary branches per plant indicating possibilities of selection towards desired direction. The present findings are in contradictory with the results reported by Mohanty (2002) where he observed considerably lowest percentage of heritability for the characters of primary branches per plant (50.40%) and vine length (24.10%) of pumpkin.

Table 2. Estimates of genetic parameters for different vegetative characters of 81 sweet gourd accessions

Traits	Range	Mean squares	GCV	PCV	h^2b (%)	GA in % means (5%)
Vine length at harvest (m)	10.68-5.4	4.43**	14.26	15.42	85.71	27.20
Leaf length (cm)	26.69-14.33	14.81**	9.03	11.87	57.79	14.14
Leaf breadth (cm)	31.69-18.75	20.62**	8.96	10.65	70.77	15.53
No. of lobes/leaf	7.60-5.40	0.48**	5.25	6.92	57.14	8.17
Petiole length (cm)	37.23-12.05	50.85**	13.78	13.93	97.83	28.08
Internode length (cm)	20.37-11.53	11.45**	9.48	11.56	67.34	16.02
Primary branches/ plant	38.67-10.5	100.73**	24.61	26.66	85.17	46.78

** Significant at 1% level of probability

GCV : Genotypic co-efficient of variation
PCV : Phenotypic co-efficient of variation
h^2b: Heritability in broad sense
GA : Genetic advance

Flower characters: It was observed that there were significant variations among 81 accessions of sweet gourd considering different flower characters (Table 3). Estimates of genotypic and phenotypic coefficients of variation were fairly high for female and male flowers per plant. The high GCV can be exploited by appropriate selection in the improvement programme. Very low differences between GCV and PCV were recorded for almost all the flower characters except female flower per plant and therefore, these characters were least influenced by the environment. In the present study, heritability estimates were high for all the flower characters. High heritability estimates together with high genetic advance were recorded in male and female flowers per plant and nodes for first male flowering demonstrating that both these were simply inherited characters governed by a few major genes with additive gene effects, and selection of these characters would be more effective for yield improvement. Arora *et al.* (1983) and Srivastava and Srivastava (1976) also found high heritability as well as high genetic advance for sex ratio and female flowers per plant in sponge gourd and bitter gourd, respectively which were in the line with the present findings. The heritability was high but genetic advance was low for node order of first female flower opening and anthesis of first male and female flower which might be attributed to the non additive gene action. Lakshmi *et al.* (2002) reported similar findings.

Table 3. Estimates of genetic parameters for different flower characters of 81 sweet gourd accessions

Traits	Range	Mean squares	GCV	PCV	h^2b (%)	GA in % means (5%)
Anthesis of 1st male flower (days)	71.66-54.00	39.17**	4.50	4.68	92.52	8.92
Anthesis of 1st female flower(days)	70.00-54.33	27.54**	4.26	4.55	87.81	8.22
Nodes for 1st male flowering	15.33-3.33	14.19**	25.62	26.56	93.00	50.88
Node for 1st female flowering	28.89-13.67	25.60**	13.11	13.60	92.90	26.05
Total male flowers per plant	157.00-21.00	1699.64**	34.45	34.77	98.37	70.46
Total female flowers per plant	8.00-1.00	6.83**	53.98	57.80	87.34	103.93

** Significant at 1% level of probability

GCV : Genotypic co-efficient of variation
PCV : Phenotypic co-efficient of variation
h^2b: Heritability in broad sense
GA : Genetic advance

Fruit characters: Comparatively higher degree of GCV and PCV were recorded for number of fruits per plant and yield per plant with narrow difference between GCV and PCV confirming least environmental effects on these traits and this offers better scope for selection (Table 4). The present results were in the close conformity with the findings of Lakshmi *et al.* (2002) where they reported highest GCV (43.20%) and PCV (47.95%) for yield per plant of pumpkin. In the present study, moderate GCV and PCV were observed in case of cavity length and weight of placenta with highest difference between GCV and PCV. This suggests selection for these characters would not be effective. Rest of the fruit characters showed lowest GCV and PCV. Higher heritability was found in case of fruit length and diameter, peduncle length, number of fruits per plant and yield per plant, while rest of fruit characters showed moderate heritability. High heritability coupled with high genetic advance was observed in number of fruits per plant and yield per plant, which indicated that these characters were less influenced by environment. High heritability value along with high value of genetic advance would be most effective condition for selection (Doijode and Sulladmath, 1986). Such condition arises due to action of additive genes (Johnson *et al.* 1955 and Panse, 1957). Therefore, effective selection could be made for these traits. High heritability estimates with high genetic advance for yield per plant was also reported in pumpkin by Saha *et al.* (1992), and Rana *et al.* (1986) and their findings were in the same trend with the present study.

Table 4. Estimates of genetic parameters for different fruit characters of 81 sweet gourd accessions

Traits	Range	Mean squares	GCV	PCV	h^2b (%)	GA in % means (5%)
Fruit length(cm)	48.26-24.34	50.77**	10.74	11.99	80.24	19.81
Fruit diameter (cm)	26.05-13.47	19.39**	11.71	12.94	81.80	21.81
Peduncle length(cm)	19.05-5.81	20.92**	21.44	22.00	94.45	42.90
Flesh thickness (cm)	4.60-2.35	0.83**	11.85	18.40	41.46	15.72
Cavity length (cm)	28.00-7.10	59.02**	24.14	32.77	54.29	36.65
Cavity breadth (cm)	17.52-7.82	13.17**	14.53	19.22	57.20	22.64
Weight of placenta (g)	735.25-119.97	46778.68**	25.30	32.87	59.23	40.11
% brix (TSS)	13.30-7.20	5.71**	12.98	15.59	69.37	22.28
% dry matter	11.23-3.72	6.27**	19.10	24.73	59.60	30.38
Number of fruits/plant	5.33-1.00	2.95**	46.21	49.60	87.13	88.75
Yield per plant (kg)	16.62-2.30	39.68**	46.11	46.65	97.73	93.91

** Significant at 1% level of probability

GCV : Genotypic co-efficient of variation
PCV : Phenotypic co-efficient of variation
h^2b: Heritability in broad sense
GA : Genetic advance

Seed characters: High GCV and PCV were recorded for number of seeds per fruit followed by weight of 100 seeds which showed the maximum amount variability among the accessions for these traits, and this offered better scope for selection (Table 5). Bindu *et al.* (2000) also observed high GCV and PCV for 100 seed weight of pumpkin. Whereas, lowest GCV and PCV was observed for seed length and breadth which indicated low genetic variability and very limited scope for improvement through selection of these traits. Doijode and Sulladmath (1986) observed considerable values of GCV and PCV for seeds per fruit (14.50 and 18.90%). The GCV and PCV for 100 seed weight were very close to each other showing less environmental influence on this trait. On the other hand, there was considerable difference between GCV and PCV values for number of seeds per fruit indicating that this character was

Table 5. Estimates of genetic parameters for different seed characters of 81 sweet gourd accessions

Traits	Range	Mean squares	GCV	PCV	h^2b (%)	GA in % means (5%)
No. of seeds/fruit	646.33-46.67	45639.95**	32.14	41.20	60.84	51.64
Seed length (cm)	1.81-1.17	0.042**	6.56	7.60	73.33	11.58
Seed breadth (cm)	1.43-0.66	0.037**	10.74	13.12	69.23	18.41
Weight of 100 seeds	20.63-7.76	15.65**	16.41	17.91	83.95	30.96

** Significant at 1% level of probability

GCV : Genotypic co-efficient of variation
PCV : Phenotypic co-efficient of variation
h^2b: Heritability in broad sense
GA : Genetic advance

somehow affected by environment. All the seed characters showed considerably higher heritability. High heritability coupled with high genetic advance was recorded for 100 seed weight and number of seeds per fruit. This fact could be explained as the action of additive genes what was reported by Panse (1957). Doijode and Sulladmath (1986) reported high heritability along with considerable genetic advance for seeds per fruit. Tyagi (1972) found moderate heritability and considerable genetic advance for 100 seed weight in bottle gourd. Bindu *et al.* (2000) reported high heritability and high genetic advance for 100 seed weight indicating that this trait was governed by additive gene action and was considered as reliable indicator for selection. Seed length and breadth showed moderate heritability, but genetic advance was, however, low for both the traits indicating the non additive genetic control of these characters and limited scope for improvement through selection.

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