GENETIC VARIABILITY AND CORRELATION STUDIES AMONG YIELD AND YIELD CONTRIBUTING CHARACTERS OF YARDLONG BEAN (*VIGNA UNGUICULATA* SSP. *SESQUIPEDALIS* L. VERDC.)

Muhammad Shahidul Haque*, Afifa Azad, Nihar Ranjan Saha
and Mohammad Monirul Islam[1]

*Department of Biotechnology, Bangladesh Agricultural University,
Mymensingh-2202, Bangladesh*

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Abstract

Twenty-five genotypes of yardlong bean were planted in the field to determine genotypic variances and correlations among characters related to yield. Analysis of variance revealed a highly significant difference among the genotypes for all traits, indicating the presence of variability. The phenotypic coefficients of variations were found slightly higher than the genotypic coefficients of variations, which suggests that the apparent variation is not only genetic but also influenced by the growing environment. High heritability and a high genetic advance were observed in pod yield per plant, pod weight and the number of pods per plant. Yield/plant was positively and significantly correlated with the number of pods/plant, pod length and the number of seeds/pod. The combination of the high heritability along with high genetic advance provides a clear image of the traits in the selection process reflecting the presence of additive gene action for the expression of these traits and improvement of these characters could be done through selection.

Introduction

Vigna unguiculata ssp. *sesquipedalis* (L.) Verdc. belongs to Fabaceae family, subfamily Faboideae. Being a self-pollinated crop it is widely spread throughout the tropics as a minor vegetable crop. But it is mostly cultivated in India, Bangladesh, as well as Southeast Asia, and Oceania (Pandey and Westphal 1989). Yardlong bean is an excellent source of nutrition as the tender green pods have 3.5 - 5% crude protein as well as they are a good source of vitamin A (941 IU) and C (13 mg), iron (2.5 mg), calcium (80 mg), phosphorus (74 mg) and dietary fibre (2 g) (Singh *et al.* 2001). It provides fixation of nitrogen, acts as ground cover, and improves the soil from plant residues (Singh *et al.* 1997). Yardlong bean is one of the economically important vegetable crops in Bangladesh. This crop occupied approximately 16284 acres in area, and during the year 2017-2018, the production was 25651 m tons (BBS 2019). Although yardlong bean is mainly cultivated in summer in Bangladesh, it may be grown throughout the year in this country's climate. In Bangladesh, no significant research has been done on this crop as yet. BARI, one of the leading agricultural institutes in Bangladesh, has released only one variety named BARI Barbati, and a limited effort has been given in its research (Ullah *et al.* 2011). Yardlong bean is still a relatively minor or orphan legume crop though its importance both as a vegetable and as a legume cannot be over-emphasized.

It is essential to improve the yield components for developing a superior variety. However, the yield is a complex character and is associated with many other inherited contributing traits (Rao *et al.* 1990). Genetic variability is the foundation of any breeding program and is invaluable

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*Author for correspondence: <haquems@bau.edu.bd>. [1]Biotechnology Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh-2202, Bangladesh.

for genetic improvement and conservation of the crop (Lin *et al*. 2007, Clark and Hoy 2006). Generation of information on genetic variability, genotypic coefficient of variation, heritability, and genetic advance of yardlong bean is very valuable for genetic improvement by the breeding program. As the existing variability can be used to enhance the yield level of the cultivars, the evaluation of existing genetic variability in any crop species is a prerequisite for formulating effective breeding strategies (Belaj *et al*. 2002). Heritability gives information on the magnitude of the inheritance of characters from parent to offspring, and genetic advance explains the degree of the gain obtained in character under particular selection pressure (Nwangburuka and Denton 2012, Ogunniyan and Olakojo 2015). High heritability estimates coupled with high genetic advances provide the most suitable condition for selection. Correlation coefficients are generally employed to determine the relation of grain yield and yield components where the genotypic correlation is higher than phenotypic correlation in general (Pavan *et al*. 2011). The objective of this study was to understand the magnitude of genotypic as well as phenotypic variation, heritability and genetic advance along with correlation coefficients of yield contributing traits among the collected accessions/genotypes of yardlong bean in Bangladesh.

Materials and Methods

A total of 25 yardlong bean genotypes were included in this experiment. Sixteen accessions were collected from the Plant Genetic Resources Center (PGRC), Bangladesh Agricultural Research Institute (BARI) and others were collected from farmers and also from the local seed market (Table 1).

The experiment, laid out in RCBD, was replicated thrice. The plot size was 100×50 cm with three rows. At maturity three plants were selected from each replication of each accession and data were recorded for 14 quantitative characters *viz.* plant height, number of branches per plant, days to flowering, days to fruit set, number of pods per plant, pod length, breadth and single pod weight, number of seeds per pod, seed length, seed breadth, 100-seed weight, dry weight of 100-seed, pod yield per plant.

The collected data were ANOVA to test the variations among genotypes. The analysis of variance was calculated using the Statistical Analysis System (SAS) software version 9.2 (SAS 2008). The genotypic and phenotypic coefficient of variation was calculated by Kwon and Torrie (1964) technique. The genetic advance in the percentage of mean was calculated by using Falconer (1989) formula:

$$\text{Genetic Variance (Vg)} = \frac{\text{Genotype Mean Square (GMS)} - \text{Error Mean Square (EMS)}}{\text{Number of Replication (r)}}$$

Environmental variance = Error mean square

Phenotypic variance Vp = Vg + Ve/r

Genotypic, phenotypic and environmental coefficients of variation were calculated as

$$\text{GCV\%} = \sqrt{\frac{\text{Vg}}{\overline{\text{X}}}} \times 100$$

$$\text{PCV\%} = \sqrt{\frac{\text{Vp}}{\overline{\text{X}}}} \times 100$$

where, GCV% = Genotypic coefficient of variation, Vg = Genotypic variance, PCV % = Phenotypic coefficient of variation and Vp = Genotypic variance.

Heritability (H^2) on entry mean basis was calculated as

$$H^2 = \frac{Vp}{Vg}$$

The expected genetic advance for each trait was calculated as

$$GA = K\sqrt{Vp}H^2$$

where, K = 1.40 at 20% selection intensity for the trait, Vp = Phenotypic variance for the trait, H^2 = Broad sense heritability of the trait and genetic advance as a percentage of mean is calculated as,

$$GA\% = \frac{GA}{\overline{X}} \times 100$$

The relationship between morphological and yield contributing characters was studied through analysis of the correlation between them. The correlation coefficient was estimated by the formula suggested by Miller *et al.* (1985).

Table 1. List of yardlong bean genotypes.

Sl. No.	Name of the genotypes	Source
1	Kagornatki	Laal Teer seed
2	Saba	"
3	Lal Benny	"
4	Toki	"
5	Banalata	"
6	1070	"
7	Bari Borboti-1	"
8	BD-1529	BARI
9	BD-1528	"
10	BD-1524	"
11	BD-1517	"
12	BD-1516	"
13	BD-1511	"
14	BD-9830	"
15	BD-9831	"
16	BD-9833	"
17	BD-9852	"
18	BD-10069	"
19	BD-10070	"
20	BD-10082	"
21	BD-10077	"
22	BD-10075	"
23	BD-10074	"
24	Kashikanchon	Satkhira
25	Thai variety	Local Market

Results and Discussion

The analysis of variance showed that significant variation present for all traits (Table 2). It reflected the existence of large variability among tested genotypes, and this variability can be further utilized in the yardlong bean improvement program. Ahsan *et al.* (2015) and Zulfahmi *et al.* (2016) reported significant variations in the analysis of variance for all the traits for local chili pepper genotypes and *Gossypium hirsutum* L. accessions, respectively.

Table 2. Analysis of variance for different quantitative characters in the yardlong bean.

Source of variation	Replication	Genotypes	Error
Plant height	3.43	311.766**	9.794
No. of branch/plant	0.093	2.226**	0.046
Days to flowering	3.64	234.80**	3.112
Days to fruit setting	2.093	249.33**	4.482
No. of pods/plant	1.213	37.50**	0.588
Pod length (cm)	8.843	261.93**	8.524
Pod breadth (m)	0.006	0.124**	0.004
Pod weight (g)	0.016	135.64**	0.443
No. of seed/pod	10.013	30.59**	2.152
Seed length (mm)	0.016	0.159**	0.018
Seed breadth (mm)	0.002	0.017**	0.003
Weight of 100 seeds (g)	2.769	138.97**	0.645
Dry weight of 100 seeds (g)	0.884	25.06**	0.198
Pod yield (g)	192.75	13488.46**	56.05

** = Significant at 1% level of probability.

The estimates of phenotypic variances (Vp), genotypic variances (Vg), phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) are presented in Table 3. Genotypic variance values ranged from 0.005 to 4477.47, while phenotypic variance values ranged from 0.008 to 4533.52. The pod yield per plant exhibited the highest genotypic and phenotypic variances of 4477.47 and 4533.52, respectively. This was followed by the plant height that has genotypic and phenotypic variance value of 100.66 and 110.45, respectively. The lowest genotypic and phenotypic variance was recorded for the traits of seed breadth (Table 3). Zulfahmi *et al.* (2016) found genetic variance values ranging from 0.02 to 8092.05 for fruit diameter and fruit weight per plant. While, phenotypic variances ranged from 0.03 to 8761.17 for fruit diameter and fruit weight per plant, respectively. Ahsan *et al.* (2015) reported that the seed cotton yield per plant exhibited the highest genotypic and phenotypic variance of 752.39 and 753.34, respectively. The lowest genotypic and phenotypic variance were recorded for the traits of boll weight and seed index (0.303 and 0.304 for boll weight and 1.76 and 1.77 for the seed index, respectively.

The genotypic coefficient of variance ranged from 10.23 to 53.55% (Table 3). The highest genotypic coefficient of the variation was observed for the pod yield per plant (53.55%) which was followed by the number of pods per plant (52.61%). Seed breadth showed the lowest genotypic coefficient of the variation (10.23%). Similar aptitude as a genotypic coefficient of variation was observed in a phenotypic coefficient of variation. There was a close correspondence between the genotypic and phenotypic coefficient of variation for all the recorded traits. It also

showed that these characters are influenced less by the environment. As stated by Deshmukh *et al.* (1986), PCV and GCV values greater than 20% are regarded as high and values between 10 and 20% to be medium, whereas values less than 10% are considered low. High PCV and GCV values were recorded for pod yield per plant, dry weight of 100-seed, number of seeds per pod, pod weight, breadth, length, number of pods per plant, days to flowering, and number of branches per plant. High PCV and GCV values indicate that selection can be performed based on these traits to separate more promising genotypes. Traits with moderate PCV and GCV were seed length and breadth, days to fruit setting and plant height. High values of PCV and GCV indicated the existence of substantial variability for such characters and selection might be effective based on these characters. Yadeta *et al.* (2011) reported a similar finding for fruit weight, fruit diameter, fruit per plant, fruit yield per plant. In this study, the PCV was relatively greater than GCV for all traits. It indicates that all traits interacted with the environment to some extent. Makeen *et al.* (2007) also reported a similar result. The similarity of GCV and PCV for almost all the characters indicates the high contribution of the genotypic effect for phenotypic expression of such aspects. A similar result was reported by Yadeta *et al.* (2011) for days to flower and days to maturity. Therefore, the study of GCV and PCV in yardlong bean genotypes exhibited variability for almost all characters (Table 3) indicating the existence of wider genetic variation in Bangladeshi genotypes.

Table 3. Estimation of genetic parameters of 25 yardlong bean genotypes based on different morphological traits related to yield.

Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (GA)	Genetic advance (%)
Plant height (cm)	100.66	110.45	18.21	19.08	91.13	19.73	35.81
No. of branch/plant	0.727	0.773	46.66	48.11	94.05	1.7	93.21
Days to flowering	77.23	80.34	21.43	21.86	96.13	17.75	43.29
Days to fruit setting	81.62	86.1	19.15	19.66	94.79	18.12	38.4
No. of pods/plant	12.3	12.89	52.61	53.86	95.44	7.06	105.88
Pod length (cm)	84.47	92.99	25.27	26.52	90.83	18.04	49.62
Pod breadth (mm)	0.04	0.044	23.92	25.09	90.91	0.39	46.99
Pod weight (gm)	45.07	45.51	51.45	51.7	99.03	13.76	105.46
No. of seeds/pod	9.48	11.63	24.23	26.84	81.5	5.73	45.06
Seed length (mm)	0.047	0.065	15.89	18.69	72.31	0.38	27.84
Seed breadth (mm)	0.005	0.008	10.23	13.11	60.87	0.11	16.44
Weight of 100-seeds (g)	46.11	46.75	31.68	31.9	98.62	13.89	64.81
Dry weight of 100-seeds (g)	8.29	8.49	29.43	29.78	97.67	5.86	59.92
Pod yield (g)	4477.47	4533.52	53.55	53.88	98.76	136.99	109.62

Genetic coefficient of variance together with heritability estimates would give the best picture of the amount of advance to be expected from selection (Burton and Devane 1953). Heritability values help in predicting the expected progress to be achieved through the selection process. In this study, estimates o f heritability in the broad sense ranged from 60.87 to 99.03% (Table 3).

Table 4. Correlation coefficients among different yield components of 25 yardlong bean genotypes.

Characters	No. of branches/ plant	Days to flowering	Days to fruit setting	No. of pods/ plant	Pod length (cm)	Pod breadth (mm)	Pod weight (g)	No. of seeds/ pod	Seed length (mm)	Seed breadth (mm)	Fresh wt. of 100-seed (g)	Dry wt. of 100-seed (g)	Pod yield/ plant (g)
Plant height (inch)	0.178	0.120	0.164	−0.139	0.239	0.003	0.327	0.333	0.415*	0.092	0.440*	0.289	0.114
No. of branch/plant		−0.167	−0.158	0.006	0.006	−0.120	−0.083	−0.076	0.303	0.218	0.300	0.278	0.446*
Days to flowering			0.987**	−0.493*	−0.419*	−0.533**	−0.397*	−0.075	−0.276	−0.180	−0.351	−0.248	−0.435*
Days to fruit setting				−0.490*	−0.420*	−0.547**	−0.385	−0.078	−0.291	−0.200	−0.359	−0.266	−0.439*
No. of pods/plant					0.465*	0.260	0.217	0.417*	0.057	0.134	0.171	0.130	0.605**
Pod length (cm)						0.330	0.744**	0.397*	0.377	0.243	0.399*	0.369	0.493*
Pod breadth (mm)							0.394	−0.024	−0.027	0.131	0.140	−0.019	0.016
Pod weight (g)								0.142	0.376	0.205	0.386	0.305	0.346
No. of seeds/pod									0.067	−0.102	0.146	0.138	0.397*
Seed length (mm)										0.639**	0.836**	0.907**	0.165
Seed breadth (mm)											0.720**	0.560**	0.118
Fresh wt. of 100-seed (g)												0.864**	0.289
Dry wt. of 100 seed (g)													0.193

Highest, heritability was observed in individual pod weight (99.03%) followed by pod yield (98.76%), while the minimum was found in seed breadth (60.87%). Heritability values greater than 80% were very high, values from 60 - 79% were moderately high, values from 40 - 59% were medium and values less than 40% were low, these findings were confirmed by Singh (2001). Accordingly, the estimates of heritability for all the traits were very high except seed length and seed breadth, which were moderate-high. Environmental factors contributed relatively small to the phenotype of highly heritable characters and selection for such characters could be fairly easy due to the high additive effect. Syukur and Rosidah (2014) reported high estimates of broad-sense heritability for plant height, stem diameter, days to flowering, days to first harvest, fruit length, and fruit diameter. For plant height, days to flowering, fruit per plant, fruit length, fruit diameter, fruit weight, canopy diameter, and fruit yield per plant was found by Yadeta *et al.* (2011).

Genetics and environmental factors contribute to variation in a population as genetic variability is the only heritable character from one generation to the next generation, so the heritability alone does not give the idea about expected gain in the next generation. Still, it should be considered in connection with the genetic advance. The characters exhibiting maximum heritability and high genetic advance as a percentage of mean could be used as a powerful tool in the selection process, such attitudes are controlled by the genes and influenced less by the environment (Panes and Sukhatme 1995). Estimates of GA values for all characters are presented in Table 3. The genetic advance as a percentage of means for 14 traits ranged from 16.44 to 109.62% (Table 3). The higher genetic advance as a percentage of mean was recorded by pod yield (109.62%) which was closely followed by the number of pods per plant (105.88%) and pod weight (105.46%). According to Jonhson *et al.* (1955), the value of genetic advance as per cent of the mean is categorized as low (< 10%), moderate (10 - 20%) and high (> 20%). The GAM of seed breadth is classified as moderate, whereas other characters were high (Table 3). High heritability and the high genetic advance were observed in traits *viz.,* pod yield per plant, pod weight and a number of pods per plant. These traits are highly reliable during the selection process of the accessions. High heritability estimates coupled with the high genetic advance are usually more helpful in predicting gain under selection than heritability alone (Jonhson *et al.* 1955). Since, a high heritability does not always indicate a high genetic gain, heritability is recommended to be considered in association with genetic advances to predict the effect of selecting superior crops varieties. High heritability and moderate genetic advance were found in seed breadth, which was confirmed by Muhammad *et al.* (2004), indicating a more significant role of non-additive gene action in their inheritance. The findings of this study are in agreement with those of Ibrahim *et al.* (2001). Yadeta *et al.* (2011) also reported that plant height and days to flowering had high heritability and moderate genetic advance.

The correlation coefficients between all the 14 characters are presented in Table 4. In the present study out of 91 associations 27 were highly significant (considering both 1 and 5% level of significance). Among them 18 associations were positively significant and the rest 9 were negatively significant. Rests of the 64 associations were non-significant. Significant and positive correlations among the characters were suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, 43 relationships were positive and non-significant and 21 relationships were negative and non-significant. The positive and non-significant association referred information of inherent relation among the pairs. While the negative and non-significant association referred to a complex linked of the relation among the pair of combinations (Pavan *et al.* 2011).

From Table 4 it appears that yield/plant was positively and significantly associated with the number of branch/plant, number of pods/plant, pod length and, number of seeds/pod. Pods/plant and seeds/pod contributed maximum positive and direct effect on yield indicating these two traits

should be emphasized while selecting high yielding yardlong bean cultivars. But negative significant association had been found among days to flowering and days to fruit set. Among the yield contributing characters, pod length was significantly correlated with the number of seeds/pod and fresh weight of 100-seed was significantly correlated with pod length, seed length and seed breadth. A similar kind of association was reported earlier by Kamala *et al.* (2007). They found that pod length was significantly correlated with seeds/pod and seed length. Hundred seed weight showed a significant correlation with seed length. The above information revealed that the number of pods/plant and seeds/pod were related to yield/plant mostly through their direct effects and the present findings suggest that these characters should be used as selection index for selecting higher yield in yardlong bean.

It can be concluded from the results of this study that genetic variability within the selected genotypes is very high for yield contributing traits. A high PCV and GCV for the characters indicated that environmental influences on the expression of these traits were minor. Based on the findings in this study, pod yield per plant, pod weight and the number of pods per plant could be useful criteria for selection in the yardlong bean improvement because these characters had a high genotypic coefficient of variation, heritability estimate and genetic advance. Besides pods/plant and seeds/pod had the highest positive and direct effect on yield. Therefore, it is recommended that these characters should be used for the development of high yielding varieties through selection.

Acknowledgements

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