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Estimation of variability, heritability and genetic advance in M₃ generation of natural mutant of dolichos bean

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Abstract

An experiment entitled “Estimation of variability, heritability and genetic advance in M₃ generation of natural mutant of dolichos bean” was carried out at All India Coordinated Research Project on Vegetable Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (MS), which was conducted during the year 2018-19 with an objective to assess the genetic variability in M₃ generation. The estimates of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation for all the characters under study in M₃ generation. High GCV and PCV were observed for vine length, number of racemes per vine, fresh pod width, number of fresh pods per vine, fresh pod yield per vine, fresh pod yield per hectare, fresh seed yield per vine and dry seed yield per vine in M₃ generation indicating the higher magnitude of variability and direct selection of these traits may be advantageous in developing desirable dolichos bean genotype.

The high heritability along with high genetic advance as percent of mean are exhibited by vine length, days to 50 per cent flowering, number of racemes per vine, pod setting per cent, fresh pod length, fresh pod width, number of fresh pods per vine, fresh pod shelling per cent, fresh pod yield per vine, fresh pod yield per hectare, fresh 100 seed weight, fresh seed yield per vine, dry 100 seed weight and dry seed yield per vine in M₃ generation. This indicates presence of additive gene action for the expression of these traits which is fixable for next generation and selection in next population based on this character would be ideal.

Keywords: Dolichos bean, heritability, phenotypic coefficient of variation, genotypic coefficient of variation, genetic advance

Introduction

Dolichos bean (*Lablab purpureus* (L.) Sweet) belongs to the family Fabacea, sub family Faboideae, tribe phaseoleace, sub tribe phaseolineae and the genus Lablab has included several distinct species names but, it is currently regarded as monospecific. Within this genus chromosome number varies, with $2n = 20, 22, 24$ (Philip, 1982) [15]. “Dolichos” is a Greek word meaning “long” and “lablab” is an Arabic or Egyptian name meaning “dull rattle of the seed inside the dry pod” (Chaudhary, 1972) [4]. It is also known as Indian bean and hyacinth bean. The wild forms of lablab are believed to have originated in India and were introduced into Africa from Southeast Asia during the eighty century. Karnataka alone is contributing nearly ninety per cent of both area and production of dolichos bean. The rest area is concentrated in nearby district of Tamil Nadu, Andhra Pradesh and Maharashtra. Maharashtra has a wide range of genetic variability in Dolichos bean with variable plants type (determinate and indeterminate), pod characteristics for shape (small, medium, long *etc.*), and colour (dark green, light green, maroon, red *etc.*).

Variability is the outcome of naturally occurring mutations (Hazra and Som, 1999) [8]. There are large numbers of instances in the past where naturally occurring mutations served important role in cultivar improvement. Green revolution genes in wheat (Norin 10 genes) and rice (Dee-geowoo-gen) are example of natural spontaneous mutations. Genetic improvement of any crop largely depending on the magnitude of several genetic parameters like analysis of variance of each mean value, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2) and genetic advance (GA) on which the breeding methods are formulated for its further improvement.

Dolichos bean being a potential leguminous vegetable crop of India has immense scope for genetic improvement for various qualitative and quantitative characters besides widening the genetic base through mutagenesis. Keeping this in view, the present study was planned, to ascertain the magnitude of genetic variability in M_3 generation for various yield and its attributing traits in dolichos bean var. Phule Gauri.

Materials and Methods

The seeds of thirty-six genotypes (mutants) of variety "Phule Gauri" and one standard check "Phule Gauri" were obtained from All India Coordinated Research Project on Vegetable Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri. Genotypes (mutants) of dolichos bean and one standard check Phule Gauri were grown in a Randomized Block Design with two replications. The sowing of experimental material was done during Kharif-2018. Recommended dose of fertilizers and other cultural package of practices along with bamboo staking were adopted for better crop growth.

The study was carried out with various observations, such as vine length, days to 50 per cent flowering, number of flower buds per raceme, number of racemes per vine, number of nodes per raceme, number of buds per node, pod setting per cent, fresh pod length, fresh pod width, number of fresh pods per vine, fresh pod shelling per cent, days to fresh pod harvest, average weight of fresh pod, fresh pod yield per vine, fresh pod yield (q/ha), fresh 100 seed weight, fresh seed yield per vine, dry 100 seed weight and dry seed yield per vine.

Estimation of genetic variability parameters

Phenotypic and genotypic coefficient of variation

Genotypic and phenotypic coefficients of variability were estimated according to the Burton and Devane (1953) [3] by using the following formulae.

a. Genotypic coefficient of variance (GCV)

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

b. Phenotypic coefficient of variance (PCV)

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where

σ^2_g = Genotypic variance = (Mean sum of squares due to genotypes - Error mean sum of squares) ÷ Replications

σ^2_p = Phenotypic variance = $\sigma^2_g + \sigma^2_e$

σ^2_e = Environmental variance = (Error mean sum of squares) ÷ Replications

\bar{X} = General mean of the character

PCV and GCV were classified as suggested by Siva Subramanian and Menon (1973) [22].

Less than 10% = Low

10-20% = Moderate

More than 20% = High

Heritability (h^2)

Heritability in broad sense for all the characters were computed by the formula as suggested by Lush (1949) [10].

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where

h^2 = Broad sense heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability (h^2 (b)) was categorised as suggested by Robinson *et al.* (1949) [19].

0-30% = Low

31-60% = Medium

61% and above = High

Genetic advance (GA)

This was worked out as per the formula proposed by Johnson *et al.* (1955) [9].

$$GA = k. \sigma^2_p h^2$$

Where,

k = selective differential

σ^2_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

The value of 'k' was taken as 2.06 assuming 5 per cent selection intensity.

Genetic advance as percentage of mean

$$GA \text{ as percentage of mean} = \frac{GA}{\bar{X}} \times 100$$

Where

GA = Expected genetic advance

\bar{X} = Mean of the character

Genetic advance as percentage of mean categorized as suggested by Johnson *et al.* (1955) [9].

<10% = Low

10-20% = Moderate

>20% and above = High

Results and Discussion

Data regarding genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability (h^2) including with genetic advance as per cent of mean of M_3 generation are presented in Table 1.

Phenotypic coefficient of variation and genotypic coefficient of variation

In present study phenotypic coefficient of variation in general were higher than genotypic coefficient of variation for all the traits, but the difference was very low, indicating low environmental effect on the expression of all the traits and is suggestive of the heritable nature of the traits. Similar findings supported by Ramya *et al.* (2014b) [16] in black gram, Reena and Mehta (2014b) [17] in cowpea, Umavathi *et al.* (2015b) [25] in cowpea, More and Borkar (2016c) [13] in french bean, Nepolian *et al.* (2019) [14] in field pea, Shobiya *et al.* (2019) [20] in cluster bean.

High GCV and PCV were observed for vine length, number of racemes per vine, fresh pod width, number of fresh pods

per vine, fresh pod yield per vine, fresh pod yield per hectare, fresh seed yield per vine and dry seed yield per vine indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. These results were similarly hypothesized in other crops by Anbu *et al.* (2010) [1] for seed yield per plant in blackgram, Geeta and Wakode (2011) [7] for plant height, number of pods per plant, and yield per plant in soybean, Devi and Mullainathan (2012) [5] for number of pods per plant and seed yield per plant in black gram, Meshram *et al.* (2013) [12] for number of pods per plant in black gram, Ramya *et al.* (2014b) [16] for number of pods per plant and single plant yield in blackgram, Umavathi *et al.* (2015b) [25] for pods per plant and yield per plant in chickpea, Nepolian *et al.* (2019) [14] for number of pods per plant, plant height and seed yield per plant in field pea.

GCV and PCV estimates were moderate for days to 50 per cent flowering, pod setting per cent, fresh pod length, fresh pod shelling per cent, 100 seed weight and dry 100 seed weight. This implied equal importance of additive and non additive gene action. Similar findings were reported by Ramya *et al.* (2014b) [16] for pod length in blackgram. Low GCV and PCV estimates were recorded for number of buds per raceme, number of nodes per raceme, number of buds per node, days to fresh pod harvest and average weight of fresh pod. These lowest and moderate GCV and PCV estimates for these traits revealed that the extent of response of these traits for selection would be lesser than that of the other traits.

The difference between GCV and PCV was found to be relatively narrow for almost all the characters expect for primary branches, indicating that these traits are less influenced by the environment and indicates a high degree of genetic variability present in these characters and thus a greater scope for effective selection as these characters are less influenced by the environment. Regarding the primary branches, the difference between GCV and PCV was moderately higher which indicates that this trait is much influenced by environment.

Heritability and genetic advance as per cent of mean

Heritability determines the relative amount of heritable proportion of variability and is an important biometrical tool for adopting appropriate breeding procedure. It also acts as a predictive instrument in expressing the reliability of phenotypic value. Therefore, it helps the plant breeder to select a particular character when heritability is high. High heritability was reported for all the characters. The characters having high heritability indicated relative smaller contribution of the environment factors to the phenotype and selection for such characters could be fairly easy due to high additive effect. These results are in agreement with other reports in different crop plants by Reena and Mehta (2014b) [17] for hundred seed weight in cowpea, Umavathi *et al.* (2015b) [25] for days to 50 per cent flowering and number of pods per plant in chickpea, Gaur *et al.* (2018) [6] for pods per plant in

pigeon pea, Shobiya *et al.* (2019) [20] for plant height and number of pods per plant in cluster bean.

Genetic advance is indicative of the expected genetic progress for a particular trait under selection procedure and consequently carries much significance in self pollinated crops. Genetic advance as per cent of mean was estimated to be high for characters vine length, days to 50 per cent flowering, number of racemes per vine, pod setting per cent, fresh pod length, fresh pod width, number of fresh pods per vine, fresh pod shelling per cent, fresh pod yield per vine, fresh pod yield per hectare, fresh 100 seed weight, fresh seed yield per vine, dry 100 seed weight and dry seed yield per vine. This indicates that selection of these traits will be gratifying because they are governed by additive gene action. These results are in agreement with earlier reports on various quantitative traits in different crop plants by Malarvizhi *et al.* (2005) [11] for plant height and days to 50% flowering in cowpea, Shunyu *et al.* (2013) [21] for seed yield per plant, days to 50% flowering, plant height and 100 seed weight in pigeon pea, Gaur *et al.* (2018) [6] for pods per plant, seed yield per plot, and 100 seed weight in pigeon pea.

High heritability estimates along with the high genetic advance as per cent of mean is usually more helpful in predicting gain under selection than heritability alone. The high heritability along with high genetic advance as percent of mean are exhibited by vine length, days to 50 per cent flowering, number of racemes per vine, pod setting per cent, fresh pod length, fresh pod width, number of fresh pods per vine, fresh pod shelling per cent, fresh pod yield per vine, fresh pod yield per hectare, fresh 100 seed weight, fresh seed yield per vine, dry 100 seed weight and dry seed yield per vine reflecting the presence of additive gene action for the expression of these traits which is fixable for next generation and selection in next population based on this character would be ideal.

Similar findings were reported earlier in different crop plants by Renuka Devi and Singh (2006) [5] for 100 grain weight in ricebean, Arulbalachandran *et al.* (2010) [2] for plant height, pods per plant, yield per plant and 100 seed weight in blackgram, Suresh *et al.* (2013) [23] for plant height, number of pods per plant, 100 seed weight and single plant yield in green gram, Ramya *et al.* (2014b) [16] for seed yield per plant in blackgram, More and Borkar (2016c) [13] for number of pods per plant, length of pod, plant height and weight of 100 seeds in french bean, Suresh *et al.* (2017b) [24] for seed yield and 100 seed weight in butter bean, Shobiya *et al.* (2019) [20] for plant height and number of pods per plant in cluster bean.

The traits having high value of heritability coupled with moderate genetic advance as percent of mean *viz.*, number of flower buds per raceme, number of nodes per raceme and days to fresh pod harvest suggested that selection for improvement of these characters may be rewarding. It also indicates greater role of non-additive gene action in their inheritance.

Table 1: Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability (h^2) including with genetic advance as per cent of mean of M_3 generation of dolichos bean

Sr. No.	Characters	GCV (%)	PCV (%)	h^2 (%)	GA as per cent of mean
1.	Vine length (cm)	20.31	21.50	89.30	39.56
2.	Days to 50 per cent flowering	12.43	12.51	98.90	25.47
3.	Number of flower buds per raceme	7.72	8.03	92.50	15.29
4.	Number of racemes per vine	23.66	23.78	99.0	48.51
5.	Number of nodes per raceme	7.93	8.24	92.70	15.73
6.	Number of buds per node	4.58	5.08	81.20	8.49
7.	Pod setting per cent	16.80	17.50	92.10	33.21

8.	Fresh pod length (cm)	13.43	13.54	98.40	27.45
9.	Fresh pod width (cm)	25.64	26.37	94.50	51.35
10.	Number of fresh pods per vine	33.33	33.45	99.20	68.39
11.	Fresh pod shelling per cent	14.16	14.21	99.20	29.05
12.	Days to fresh pod harvest	9.71	9.87	97.00	19.70
13.	Average weight of fresh pod (g)	4.42	4.64	90.80	8.68
14.	Fresh pod yield per vine (g)	35.73	35.87	99.20	73.31
15.	Fresh pod yield per hectare (q)	23.36	23.55	98.40	47.73
16.	Fresh 100 seed weight (g)	14.49	14.50	99.90	29.86
17.	Fresh seed yield per vine (g)	36.09	36.23	99.20	74.04
18.	Dry 100 seed weight (g)	18.73	18.73	99.98	38.57
19.	Dry seed yield per vine (g)	40.02	40.18	99.20	82.12

Conclusions

From the present study, it is evident that the wide range of variability for different traits coupled with high heritability and high genetic advance for important yield traits, hence selection is effective for these traits. This stability of genetic variability should be analyzed next generation for important traits.

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