



Research Paper

MORPHOLOGICAL CHARACTERIZATION AS INDICES FOR YIELD AND YIELD COMPONENTS SELECTION IN COMMON BEAN (*Phaseolus vulgaris* L.) IN J&K

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Abstract

The present study was conducted at the Sher e Kashmir University of Agricultural Science and Technology, Srinagar, during the 2014 growing season and were evaluated ten genotypes: WB-494, SR1, WB-939, WB-399, WB-640, WB-375, WB-967, WB-359, WB-335 & WB-933. The aims of this work were to estimate the variance components, heritability, phenotypic and genotypic coefficients, phenotypic and genotypic correlation coefficient and genetic divergence, for seed yield and its components (pods number per plant, seeds number per pod, 100-seed weight, seed yield per ha) and expected genetic advance as indices for yield selection in common bean. The highest proportion of genetic variance presented a number of 100-seed weight. Amongst the yield characters, a very small difference between GCV% and PCV% was observed for the character 100-seed weight and yield per ha in all genotypes. Large difference between GCV% and PCV% was observed for the number of seed per pod and number of pods per plant. High heritability coupled with high genetic advance were observed for 100-seed weight and yield per ha. Low heritability coupled with low genetic advance were observed for number of pods per plant and number of seeds per pod.

Key words: common bean, morphological characterization, yield and yield components.

INTRODUCTION

For determining improvement of a crop, yield is the principal factor. Seed yield in common bean (*Phaseolus vulgaris* L.) is a quantitative character and is influenced by a number of yield contributing traits. Yield as well as on other yield components should be used in the selection of desirable types. For efficient utilization of the genetic stock in crop improvement program of this crop, information on mutual association between yield and yield components is necessary. Seed yield in common beans is a complex trait with three components: number of pods per plant, number of seeds per pod, and mean seed weight [7]. Heritability, or the degree of genetic control associated to some interest trait, is one of the most important parameters within the breeding context. Heritability indicates how much of the phenotypic variability has a genetic origin, and gives objective information for the genetic selection [5]. It is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability, for any planned breeding programs aimed to improve grain yield potentials of crops. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for

example, is used to indicate the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. The present study was undertaken to estimate the variance components, heritability for seed yield and its components and expected genetic advance.

MATERIAL AND METHODS

This research work was carried out at Sher e Kashmir University of Agricultural Science Technology Shalimar, Kashmir during the 2014 growing season. 10 common bean genotypes were grown under natural conditions. The genotypes for crosses were selected based on variability for growth habit and flower color (Table1). The experimental design was random blocks, in three replications. Each single row was 4 m long, spaced 65 cm apart and with 6 cm between plants within row. It represented single plant selection. Number of pods per plant, number of seeds per pod, 100-seeds weight and seed yield per plant were determined.

Statistical analysis

Phenotypic variance (VP), genotypic variance (VG) were determined by formulas proposed by Brewbaker (Brewbaker, 1964). Broad sense heritability (Hbs) was calculated using the formula proposed by Mahmud and Kramer (Mahmud and Kramer, 1951). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PGV) were estimated by the formula suggested by Burton (Burton, 1952). The genetic advance (GA) was calculated according to Allard's (Allard, 1960).

RESULTS AND DISCUSSION

Coefficients of variation

The comparison of characters as regards to the extent of genetic variation could be better judged by the estimation of genotypic coefficient of variation (GCV) in relation to their respective phenotypic coefficient of variation (PCV). Amongst the yield characters very small difference between GCV and PCV was observed for the character like 100 seed weight and yield per ha (Table 3). It indicates that the observed variations for the trait were mostly due to genetic factors. On the other hand, large difference between GCV and PCV was observed for the characters pod number per plant and number of seeds per pod plant. This indicated the role of environmental influence over this characters (Table 3). In this experiment, high GCV was observed in character like seed yield per hectare. The high GCV for this trait indicated further selection could improve the genotypes.

Heritability and genetic advance

Johnson et al. (Johnson *et al.*, 1955) reported that effectiveness of selection depends not only on heritability but also on genetic advance. Estimates of heritability (broad sense) was low (<10%) for no. of pods plant⁻¹ and no. of seeds pod⁻¹ and it was high (>60%) for 100 seed weight, yield (q ha⁻¹). The estimate revealed that the expected genetic gain was high (30%) for 100 seed weight, yield (q ha⁻¹). Whereas, it was low (<20%) no. of pods plant⁻¹ and no. of seeds plant⁻¹. Similar results were reported by Asifa et al. (Asifa *et al.*, 2005), indicating that these traits are mainly controlled by additive type of genes. However, high heritability coupled with high genetic advance was observed for 100-seeds weight (Table 3). Thus this character is controlled by non-additive genes (dominance and epistasis). Our results agreed with those of Singh and Singh (Singh and Singh, 1995). Therefore, judicious application of pure line selection may be effective for improving the characters with moderate or high heritability and with low genetic advance

Table 1: 10 common bean genotypes used for studying genetic variability, heritability and expected genetic gain.

Pedigree	Flower colour	Growth habit
WB-494	White	Bush type
SR-1	White	Bush type
WB-939	Pink	Pole type
WB-399	White	Bush type
WB-640	Pink	Bush type
WB-375	White	Pole type
WB-967	White	Bush type
WB-359	White	Pole type
WB-335	Whitish yellow	Pole type
WB-933	White	Bush type

Table 2: Estimates to genotypic and phenotypic coefficients of variation (GCV - %, PGV - %)

Genetic parameter	Traits			
	No of pods plant ⁻¹	No of seed pod ⁻¹	100 seed wt.	Yield ha ⁻¹
PCV	15.05	10.45	24.18	23.98
GCV	2.42	3.14	23.28	23.86
RD%	83.92	69.95	3.72	0.50

RD %: Relative difference between PCV% and GCV% = $[100 (PCV - GCV)] / PCV$

Table 3: Estimates of heritability in broad sense (H-bs), genetic advance (GA) and genetic advance express as percentage (GA%)

Genetic parameters	No. pods per plant	No. seeds per pod	100-seeds weight (g)	Seed yield per ha
H-bs	0.02	0.090	0.92	0.99
GA	0.04	0.07	17.84	2.21
GA%	0.80	1.94	46.17	48.92

CONCLUSIONS

1. The genetic parameters discussed here are based on the moderate heritability and high genetic advance shown by the different characters, especially, pod number per plant and seed number per pod, it could conclude that the determinant genetic effects of the phenotypic expression of these characters are fundamentally of the additive type. For this reason, a high response should be achievable after several selection cycles.
2. Seed yield can be improved by selecting ideotypes having more number of pods per plant coupled with number of seeds per pod.

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