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HYDRAZINE INDUCED POLYGENIC MUTANTS IN FIELD BEAN (*DOLICHOS LABLAB* L. var. *LIGNOSUS*)

M.K. WAHABUDDIN* AND J.K. BHALLA

Department of Botany,
Osmania University, Hyderabad-500 007, India

Abstract

Six Hydrazine induced polygenic mutants in field bean were isolated from M_2 generation and their breeding behaviour was studied in M_3 generation by estimating genetic parameters for quantitative characters. High heritability values were observed for plant height followed by number of primary branches per plant. High values of genotypic co-efficient of variation exhibited by the traits, plant height, pod yield, number of seeds per plant indicate that these traits can be exploited for further improvement of crop.

Introduction

The significance of micromutations in evolution was first stressed by Baur (1924) and later by Stubbe & Von Wettstein (1941). Field bean a self pollinated crop and because of its adaptability to adverse conditions, provides opportunities for exploitation of micromutations and of increasing genetic variability in quantitative characters. Six polygenic mutants were selected from M_2 generation based upon statistical data and their breeding behaviour studied in M_3 generation are presented in this report.

Materials and Methods

Seeds of field bean (*Dolichos lablab* L. var. *lignosus*) Ws (white seeded cultivar) soaked for 4 h were treated with various concentations of Hydrazine for 4 h. Plants were grown and their subsequent progenies screened for mutants in M_2 and M_3 generations. In M_1 generation two groups of Macrovariants and Normal plants were made during harvest. The plants with drastic changes in the morphology were considered as macrovariants and screened separately to establish macromutants.

Ten normal plants from each treatment were selected and plant progeny rows were grown for polygenic traits in M_2 generation. Based upon the statistical data of M_2 generation, 6 mutant types for polygenic traits were selected and their M_3 population was grown separately in plant progeny rows to evaluate the breeding behaviour of genetic parameters of different yield contributing characters. Fifty plants were selected randomly

*Present Address: Nawab Shah Alam Khan Research Centre, Anwarul-uloom College, New Mallapally, Hyderabad-500 001, India.

Table 1. Estimation of mean values ($\bar{X}$) and standard error of mean ($SE_{\bar{X}}$) of eight quantitative characters in different M_3 mutants of bean.

S. No.	Mutant/ number	Mutant/ treatment/ origin	Plant height (cm.)	No. of primary branches/ plant	No. of fertile branches/ plant	Pods/plant	Pod yield/ plant (gm.)	Seeds/plant	Seed yield/ plant (gm.)	100 seed wt. (gm.)
1.	Ws	Ws – (control)	80.83 ± 1.25	5.27 ± 0.15	4.22 ± 0.34	35.43 ± 1.43	25.73 ± 1.12	104.32 ± 2.14	14.32 ± 0.60	13.45 ± 0.12
2.	Ws-WB-35	0.0125% HZ/4h	78.11 ± 0.44 **	6.83 ± 0.85 **	4.67 ± 0.86 **	40.23 ± 2.45 **	28.43 ± 0.56 **	112.14 ± 1.45 **	16.44 ± 1.33 **	15.23 ± 0.18 **
3.	Ws-WB-66	0.05% HZ/4h	73.28 ± 1.25 **	7.43 ± 0.28 **	3.89 ± 0.95 **	43.44 ± 2.11 **	30.14 ± 1.33 *	121.21 ± 2.35 **	18.35 ± 0.81 **	16.85 ± 0.13 **
4.	Ws-WB-128	0.0025% HZ/4h	81.23 ± 2.25 **	6.55 ± 0.86 **	5.38 ± 1.23 **	48.45 ± 2.45 **	32.13 ± 0.56 **	128.25 ± 1.66 **	19.43 ± 0.61 *	17.39 ± 0.65 *
5.	Ws-WB-232	0.0125% HZ/4h	69.44 ± 1.23 **	6.43 ± 1.45 **	5.13 ± 0.38 **	41.26 ± 1.78 **	26.26 ± 0.48 **	105.14 ± 2.68 **	13.41 ± 2.14 **	12.83 ± 1.33
6.	Ws-WB-255	0.0125% HZ/4h	78.29 ± 0.88	5.82 ± 0.52	3.45 ± 0.28	39.44 ± 1.54	23.48 ± 0.83	95.21 ± 1.83	12.41 ± 1.33	13.21 ± 1.45

*, ** Significant at 5% and 1% level, respectively.

Ws = White seeded cultivar

WB = Wahabuddin, Bhalla

from each mutant population for the recording the plant height, number of branches, number of fertile branches, number of pods per plant, number of seeds per plant, pod yield per plant, seed yield per plant and 100 seed weight.

Analysis of variance and correlation was carried out according to the method suggested by Steel & Torrie (1960). Phenotypic and Genotypic co-efficient of variation and heritability were estimated according to Singh & Chowdhry (1979). The expected genetic advance was estimated by the formula given by Johnson *et al.* (1955) and Lush (1949).

Results and Discussion

Significant mean values ($P > 0.01$) were observed for different characters such as, number of primary branches, number of fertile branches, pods per plant and yield per plant, almost in all mutant types (Table 1). The results presented in Table 2 reveal that the heritability was highest for plant height (96.55). The high genotypic coefficient of variation exhibited by plant height (15.06), pod yield (18.15), number of seeds (13.76) indicate that these characters are genotypically predominant. The high values of genotypic correlation indicate a strong inherent association and would be more useful for assessing the variability (Allard, 1970). Burton (1952) suggested that genotypic co-efficient of variation together with high heritability values would give a clear picture to the extent that the genetic advance be expected by selection. Johnson *et al.* (1955) further suggested that the heritability estimate together with genetic advance be more useful in predicting the resultant effect for selection of the best individuals. The lowest

Table 2. Estimate of phenotypic and genotypic co-efficient of variation, broad-sense heritability (h^2) and expected genetic advance (Gs) of eight quantitative characters of bean.

Characters	P.C.V.	G.C.V.	h^2	Gs (% of $\bar{X}$)
Plant height (cm.)	15.33	15.06	96.55	30.48
No. of primary branches/plant	18.14	14.78	66.42	24.81
No. of fertile branches/plant	21.55	6.36	8.69	3.66
Pods/plant	15.89	6.22	15.32	5.00
Pod yield/plant (gm.)	22.89	18.15	62.92	29.66
No. seeds/plant	16.72	13.76	67.81	23.24
Seed yield/plant (gm.)	13.04	3.92	9.03	2.41
100 seed wt. (gm.)	13.68	4.42	10.44	2.92

P.C.V. = Phenotypic Co-efficient of Variation
G.C.V = Genotypic Co-efficient of Variation.

genetic advance value observed was for seed yield (2.41) and highest for plant height (30.48). Srivastava & Das, (1973) suggested that, heritable variation can be estimated with more accuracy when heritability in conjunction with genetic advance is studied. The results indicate that selection for agronomically important characters, like pod yield, number of seeds per plant can be made in early generations, which reveal high degree of phenotypic and genotypic variation along with high heritability values. It further provides an evidence on the Hydrazine induced genetic variability, which could be effectively exploited for improving the yield and attributes of the crop.

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