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## Estimates of Genetic and Environmental Variability in *Mung (Phaseolus aureus Roxb.)*

by

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Collection of widely divergent germplasms is considered as the source of genetic material and is useful in altering the course of further development. If the genetic variability is lacking, it can be assembled primarily from the primary centres of the origin of a crop. The variability can also be created through the use of various mutagens to some extent. The breeder can draw the material for his use from these gene pools for manipulation of the desired plant type. Seventy-five indigenous and exotic lines that appeared to differ in some quantitative characters contributing towards yield were selected from a collection of 400 strains made at the Punjab Agricultural University to estimate the presence of variability in *mung*. The observed variability was partitioned into its heritable (genetic) and non-heritable (environmental) components. The range, co-efficient of genetic variability and expected genetic advance were also determined. The knowledge of these genetic parameters

which is lacking in *mung* would be of immense help in deciding the future course of breeding work.

**Materials and Methods:** The material was grown in a randomised block design with three replications during 1967 at Ludhiana. The plot size was a single row of four metres length and the spacing between and within rows were 60 cm and 15 cm respectively. Observations were recorded on eight characters including days of flower, days to mature, bunches per plant, pods per plant, pod length, seeds per pod, 100-seed weight and seed yield per plant. The mean value of five plants, selected at random in each replication for each character, were used for statistical analysis.

**Statistical analysis:** a) *Co-efficient of genetic variability (C.G.V.):* It was calculated by the formula suggested by Burton (1952).

$$\text{C.G.V.} = \frac{\text{Genotypic standard deviation}}{\text{Mean of particular character under study}} \times 100$$

b) *Heritability and genetic advance:* These estimates were calculated by the formula described by Allard (1960).

$$\text{Heritability} = \frac{6_G^2}{6_G^2 + 6_E^2}$$

Where,  $6_G^2$  is genetic variance and  $6_E^2$  is environmental variance.

$$\text{Expected Genetic Advance (G.A.)} = H \times 6_p \times K$$

$$\text{G.A. as per cent of mean} = \frac{\text{G.A.}}{\bar{X}} \times 100$$

Where,  $6_p$  is the phenotypic standard deviation,  $K$  is the selection differential ( $K=2.06$  at 5% intensity of selection) and  $\bar{X}$  is the general mean of the character in the population.

**Results:** The analysis of variance indicated significant differences among the varieties in respect of all the characters under study. The range, mean and phenotypic and genotypic variances are shown in Table 1. All the characters exhibited wide range of phenotypic variation. However, bunch number, pod number, 100-seed weight and seed yield showed greater range as compared to other characters. The genotypic variance in respect of days to flower, days to mature and 100-seed weight were higher than error variance, while for other traits it was lower.

The estimates of co-efficient of genetic variability, heritability in broad sense (genetic variability) and expected genetic advance are also presented in Table 1. The co-efficient of genetic variability ranged from 23.29% for bunches

TABLE 1. Range, mean and phenotypic and genotypic variance and estimates of coefficient of genetic variability, heritability and genetic advance in mung for different characters

Character (Unit)	Range	Mean	Phenotypic variance	Genotypic variance	Coefficient of genetic variation	Heritability %	Genetic advance	GA in percentage of mean
Days to flower (days)	56-88	72.1 ± 2.10	37.91	24.68	6.89	65.10	8.25	11.44
Days to mature (days)	81-119	99.2 ± 0.23	39.31	24.14	4.95	61.41	7.88	7.94
Bunches per plant (No.)	16.6-70.4	34.69 ± 6.00	173.26	65.25	23.29	37.76	10.30	29.69
Pods per plant (No.)	38.1-145.1	68.6 ± 12.96	729.25	225.51	21.90	30.92	17.24	25.13
Pod length (cm)	4.78-6.77	5.88 ± 0.23	0.24	0.08	4.76	33.33	0.33	5.61
Seeds per pod (No.)	7.7-11.4	9.44 ± 0.51	1.28	0.39	6.57	30.47	0.70	7.41
100-seed weight (gm)	1.45-3.64	2.17 ± 0.05	0.18	0.16	18.43	88.89	0.77	35.48
Seed yield per plant (gm)	5.56-22.35	11.03 ± 2.32	22.29	6.13	22.48	27.50	2.71	24.66

per plant to 4.76% for pod length and it was high for pod number, 100-seed weight and seed yield whereas for other characters it was relatively low

The heritability value was highest for 100-grain weight (88.89%) and lowest for seed yield (27.50%). It was also high for days to flower and days to mature but comparatively low for other characters. The expected genetic advance in percentage of mean showed a wide range from 5.61 for pod length to 35.48 for 100-seed weight. High values were observed for 100-seed weight, High values were observed for 100-seed weight, bunch number, pod number and seed yield.

**Discussion:** The study exhibited the presence of wide range of phenotypic variation for most of the characters. The characters which showed wide range had also high coefficient of genetic variation. The heritable component of variation which is also called genetic variability or heritability in broad sense was the highest for 100-seed weight and was followed in order by days to flower and days to mature. It indicates that these characters are least influenced by environmental factors. High heritability for 100-seed weight has also been reported by Bhargava *et al.* (1966) in *mung* and Johnson *et al.* (1955) in soybean. Estimate of heritability for days to flower and days to mature were also high and are in agreement with those observed by Sikka and Jain (1958) in wheat and Shukla and Singh (1967) in jute. Lowest heritability for seed yield indicated that this character is highly influenced by environment. Similar results in other self-pollinated crops were reported by Sikka and Jain (1958) in wheat and Johnson *et al.* (1955) in soybean.

Johnson *et al.* (1955) while working on soybean suggested that heritability estimate alongwith genetic gain is normally more helpful in predicting gain under selection than heritability estimates alone. In the present study high heritability for 100-grain weight was accompanied by high genetic advance indicating that most likely the heritability is due to additive gene effects and mass selection for such trait should be practiced. Genetic advance was also observed to be high for pod number, bunch number and seed yield but these characters had low heritability estimates.

It was interesting to note that the characters which had wider range and high coefficient of genetic variation had also high genetic advance. On the other hand, it was observed that high heritability estimate does not necessarily mean an increased genetic advance which has also been reported by Johnson *et al.* (1955) in soybean and Swarup and Chaugale (1962) in sorghum. It therefore suggests the importance of genetic coefficient of variation, the selection differential measured in terms of phenotypic standard deviation and the square root of the heritability ratio which are the factors responsible for expected genetic advance.

**Summary:** Genetic and environmental variability in *mung* were studied in a collection of 75 indigenous and exotic strains. Wide range of genotypic and phenotypic variability was observed in the population. It was concluded that the selection based on 100-seed weight, which has highest genetic variability and very high genetic advance, would be the most effective. It is suggested that the improvement in characters, like bunch number, pod number and seed yield, which had a wide range, high coefficient of genetic variation and high genetic advance could be possible by selection programme. A close association between estimates of coefficient of genetic variation and genetic advance was observed whereas high genetic variability does not necessarily mean high genetic advance.

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