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Genetic variability and character association for seed yield in Mungbean [*Vigna radiata* (L.) Wilczek

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Abstract

Twenty mungbean (*Vigna radiata* L. Wilczek) genotypes were evaluated for the estimation of genetic variability parameters, Heritability and Genetic advance. The genotypes differed significantly for all characters. Higher GCV and PCV was observed for cluster per plant (31.33%;32.51%) followed by number of primary branches per plant (30.58%;32.95%), number of pods per plant (20.07%; 24.07%), plant height (12.10%; 12.74%), harvest index (11.89%;13.09), seed yield per plant (10.16%; 11.49%), seed per pod (8.33%; 12.44%) High heritability coupled with high expected genetic advance was observed in biological yield (99.00%; 7.59%) indicating the impact of additive gene expression.

Keywords: Greengram, Genetic variability, Heritability, Genetic advance

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is a short duration legume crop belongs to the order Leguminosae and Papilionoideae family. It is a self-pollinating diploid legume with the chromosome number $2n=2x=22$ (Karpechenko, 1925) [7]. Mungbean probably originated in India (De Candole, 1886) [3] or the Indo-Burmese region (Vavilov, 1951) [13]. The primary gene center of diversity for mungbean was suggested to be the central Asian region (Vavilov, 1951) [13] with India as the gene center and probable center of domestication (Smartt, 1985) [15]. In India greengram is cultivated in area of 3.38 million hectares with an average productivity of 4.74 qt / ha and production of 1.61 million tonnes, (IIPR Annual Report 2015-2016). In Uttar Pradesh greengram is cultivated area of 0.72 lakh hectares with an average productivity of 5.5 qt/ ha and production of 0.40 lakh tonnes, (IIPR Annual Report 2015-2016). Mungbean is a major source of protein and minerals for the predominantly vegetarian population of India. Hundred grams of mungbean seeds composed of carbohydrates (62.62 g), sugars (6.60g), dietary fibre (16.3g), vitamin-C (4.8 mg), magnesium (189 mg), phosphorous (367 mg), potassium (1246 mg) and sodium (15 mg). Average protein content in the seeds is around 23% (USDA Nutrient Database). Mungbean is ranks third among pulses after chickpea and pigeon pea in area and production. Mung bean contributes 18.07% of total pulses area and 11.48% of total pulses production in India. Area, production and productivity of mung bean in India is 34.4 lakh ha, 14 lakh tonnes and 406.98 kg/ha respectively. In Uttar Pradesh, it is being cultivated in an area of 0.72 lakh hectare with 0.40 lakh tonnes production and productivity is 555.56 kg/ha (Anonymous, 2012) [1].

Mungbean is predominantly a self-pollinated crop. It is an annual herbaceous, erect or semi-erect, with slight tendency for twining in the upper branches, leaves are trifoliate with basal appendages, stipules minute and leaflets entire ovate. Inflorescence is axillary or terminal raceme with 10-20 flowers crowned on long peduncle, flowers are either light yellowish, olive or live yellow, hermaphrodite, zygomorphic, 5 sepals, 5 petals, 10 stamens in diadelphous (9 +1) condition, single carpelled ovary with hairy style. Immature pods are green and mature pods have iron-grey or live grey or snuff brown color, 4 to 16 cm long, rounded, slender spreading or relaxed with short and moderate pubescence dehisces by both (ventral and dorsal) sutures into two halves contain 9-16 seeds with yellowish cotyledons. (Shil and Bandopadhyay, 2007) [14]. Correlation coefficient analysis is a handy technique, which elaborates the degree and extent of relationship among important plant characters and it provides basic criteria for selection and leads to directional model based on yield and its components in the field experiments. Keeping in view 20 mungbean genotype received from the department to assess genetic variability and correlation

Materials and Methods

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Allahabad (U.P.) during Kharif-2016.

The experimental materials for the present study was obtained from the Rajasthan Agriculture Research Institute, Durgapur, (Rajasthan), and Agricultural Research Station, Badnapur, (Maharashtra). The experiment was conducted in Randomized Block Design with 20 treatments. The treatments were replicated three times. Treatments were randomly arranged in each replication divided into 60 plots. The gross area of experiment was 152.54 m² and cash plot size was 1 x 1 m. The row to row spacing was 30 cm and plant to plant distance was 10 cm. The five competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the crop plant growth. Data were recorded from twelve characters viz., days to 50% flowering, plant height, Number of branches, days to maturity, number of clusters per plant, number of pod per plant, pod length, number of seed per pod, biological yield, 100 seed weight (g), harvest index and seed yield per plant (g). Mean values were computed and data were analysed for analysis of variance as suggested by (Fisher, 1936) [4] and coefficient of variances as well as heritability (inbroad sense), as suggested by Burton and Devane (1953) [2] The estimates of genetic advance were obtained by the formula suggested by Lush (1949) [10] and Johnson *et al.* (1955) [6].

Results and Discussions

The variability exploited in breeding programme is desired from the naturally occurring variants and wild relatives of main crop species as well as from strains and genetic stocks artificially developed by human efforts. Through this study an attempt was made to assess the mean performance of 20 genotypes for 12 quantitative characters.

Coefficient of variation

The estimates of phenotypic coefficient of variation (PCV) were slightly higher than those of genotypic coefficient of variation (GCV) for all the traits studied. In this study, slight differences indicated minimum environmental influence and consequently greater role of factors on the expression of the traits.

Genotypic Coefficient of Variation (GCV)

A wide range of genotypic coefficient of variation (GCV) was observed for all the traits ranged from days to maturity (3.52) to number of cluster per plant (31.33). high magnitude of GCV was recorded for number of cluster per plant (31.33) followed by primary branches per plant (30.58), while moderate GCV were recorded for pod per plant (20.07), plant height (12.10), harvest index (11.89), seed yield per plant (10.16), seed per pod (8.33) showed low genotypic coefficient of variation (GCV). The studies on genotypic coefficient of variation indicated the magnitude of GCV was high in case of number of pods per plant, biological yield per plant indicating the presence of high amount of variation in these traits.

Similar results were reported by registered high genotypic coefficient of variation for number of pods per plant.

Phenotypic Coefficient of Variation (PCV)

Higher magnitude of phenotypic coefficient of variation (PCV) was recorded for number of primary branches per plant (32.95), followed by number of clusters per plant (32.51) and number of pods per plant (24.19). The studies on phenotypic coefficient of variation characters indicated the magnitude of PCV was highest in case of all the characters. The magnitude differences were medium to low in GCV and PCV for days to maturity and seed index suggesting the little role of environment in the expression of these characters. These finding agree with the finding of.

Heritability (h²)

Heritability plays an important role in deciding the suitability and strategy for selection of a character. In the present study heritability (%) ranged from 99.00 to 42.00%. Maximum heritability observed for the biological yield per plant (99.00%) followed by test days to 50% flowering and seed yield per plant (97.00%), number of clusters per plant (93.00%), plant height (90.00%) and primary branches per plant (86.00%). Rahim *et al.* (2010) [11] and Islam *et al.* (1999) [5] also reported high heritability for plant height.

Genetic Advance (GA)

Genetic advance is the improvement in the mean of selected families over the base population (Lush, 1949) [10]. Genetic advance when expressed, as percentage over mean is called genetic gain. Genetic advance value represented for nine yield characters is represented in table 1 and table 2 Genetic advance for all the quantitative characters under study was ranged from 0.21 for seed index to 15.60 for plant height. Plant height (15.60) showed high genetic advance among all the traits, while moderate for biological yield (7.59), number of pod per plant (6.79), days to 50% flowering (6.32), harvest index (4.34) and days to maturity (2.93), number of cluster per plant (2.55), seed yield per plant (1.90) had low estimates of genetic advance.

Genetic advance as per cent of mean

The high expected genetic gain was recorded for number of pods per plant (34.29) followed by number of primary branches per plant (58.47), number of pods per plant (34.29) while moderate for plant height (23.67), harvest index (22.24), seed yield per plants (18.50) showed low genetic gain. Heritability along provides no indication of the amount of genetic improvement that would result from selection of the individual genotypes. Similar results were also reported by recorded high genetic advance for number of pods per plant and seed yield per plant. Also recorded high genetic advance for days to 50% flowering.

Table 1: Analysis of variance for twelve characters of mungbean genotypes

| S. No. | Characters | Mean sum of square | | |
|--------|-----------------------------------|---------------------|--------------------|----------------|
| | | Replication (d.f=2) | Treatment (d.f=19) | Error (d.f=38) |
| 1 | Days to 50% flowering | 0.83 | 560.06** | 11.83 |
| 2 | Plant height | 3.21 | 3755.27** | 263.00 |
| 3 | Number of Primary Branches/ Plant | 0.10 | 6.67** | 0.679 |
| 4 | Number of Clusters/ Plant | 0.17 | 96.77** | 4.80 |
| 5 | Number of Pods/ Plant | 13.65 | 1036.75** | 272.20 |
| 6 | Pod length(cm) | 36.70 | 399.25** | 251.30 |
| 7 | Seeds /pod | 0.012 | 9.68** | 5.86 |
| 8 | Days to maturity | 0.69 | 63.08** | 36.72 |

| | | | | |
|----|------------------|-------|----------|-------|
| 9 | Seed index | 0.018 | 1.49** | 0.68 |
| 10 | Biological yield | 1.34 | 329.13** | 43.52 |
| 11 | Harvest index | 0.29 | 68.05** | 11.57 |
| 12 | Seed yield | 0.008 | 783.75** | 4.97 |

** Significant at 1% level of significance

Table 2: Coefficient of Variation, Heritability and Genetic Advance for 12 yield contributing characters of 20 mungbean genotypes.

| S. No | Parameters Character | σ^2g | σ^2p | Coefficient of variation | | Heritability (h^2) (BS) (%) | Genetic advance 5% | Genetic advance as % of mean 5% |
|-------|------------------------------|-------------|-------------|--------------------------|-------|---------------------------------|--------------------|---------------------------------|
| | | | | GCV | PCV | | | |
| 1 | Days to 50% Flowering | 9.72 | 10.03 | 8.11 | 8.24 | 97 | 6.32 | 16.45 |
| 2 | Plant Height | 63.58 | 70.50 | 12.10 | 12.74 | 90 | 15.60 | 23.67 |
| 3 | Primary Branches/ Plant | 0.11 | 0.13 | 30.58 | 32.95 | 86 | 0.64 | 58.47 |
| 4 | Clusters/ Plant | 1.66 | 1.78 | 31.33 | 32.51 | 93 | 2.55 | 62.21 |
| 5 | Pods/ Plant | 15.80 | 22.96 | 20.07 | 24.19 | 69 | 6.79 | 34.29 |
| 6 | Days to Maturity | 4.80 | 11.41 | 3.52 | 5.43 | 42 | 2.93 | 4.70 |
| 7 | Pod Length | 0.12 | 0.27 | 4.70 | 7.13 | 43 | 0.47 | 6.38 |
| 8 | Seeds/ Pod | 0.78 | 1.75 | 8.33 | 12.44 | 45 | 1.22 | 11.49 |
| 9 | Seed Index (100 Seed Weight) | 0.02 | 0.04 | 4.31 | 5.91 | 53 | 0.21 | 6.47 |
| 10 | Biological Yield | 13.71 | 13.84 | 7.01 | 7.04 | 99 | 7.59 | 14.36 |
| 11 | harvest Index | 5.39 | 6.54 | 11.89 | 13.09 | 82 | 4.34 | 22.24 |
| 12 | Seed Yield/ Plot | 1.09 | 1.40 | 10.16 | 11.49 | 78 | 1.90 | 18.50 |

σ^2g = Genotypic variance, σ^2p = Phenotypic variance, h^2 = Heritability (broad sense), GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation.

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