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Akriti Dutt

Department of Genetic and Plant Breeding, ANDUA and T, Kumarganj, Ayodhya, Uttar Pradesh, India

PK Singh

Department of Genetic and Plant Breeding, ANDUA and T, Kumarganj, Ayodhya, Uttar Pradesh, India

Aditi Dutt

Department of Home Science, CSAUA and T, Kanpur, Uttar Pradesh, India

Mayanker Singh

Department of Crop Physiology, CSAUA and T, Kanpur, Uttar Pradesh, India

Anjali Singh

Department of Genetic and Plant Breeding, ANDUA and T, Kumarganj, Ayodhya, Uttar Pradesh, India

Corresponding Author: Akriti Dutt Department of Genetic and Plant Breeding, ANDUA and T, Kumarganj, Ayodhya, Uttar Pradesh, India

Study of genetic variability heritability and genetic advance for seed yield in mungbean (Vignaradiata (L.) wilczek)

Akriti Dutt, PK Singh, Aditi Dutt, Mayanker Singh and Anjali Singh

Abstract

The study was conducted to estimate the genetic variability, heritability and the expected genetic advance upon selection for all studied characters of F_{1s} hybrids populations. In this we studied about thirteen characters of mungbean crop. The high estimates of genotypic and phenotypic coefficient of variation and high heritability in broad sense along with high genetic advance in percent of mean was recorded for biological yield per plant and seed yield per plant which indicated that these two traits would be ideal traits for improvement through selection in context of present material. Pod Length, Cluster per plant and Pods per cluster recorded moderate PCV and GCV, heritability along with genetic advance. Remaining characters had low to moderate GCV and PCV values or low to moderate heritability to emerge as poor indices of selection. Thus selection for above mentioned traits among these genotypes would be effective in all cases.

Keywords: Genetic variability, heritability, genetic advance and traits

Introduction

The mungbean (*Vignaradiata* (L.) Wilczek) is alternatively known as the green gram, mash or moong. Mungbean is mainly cultivated in India, Pakistan, Bangladesh, Nepal, Sri Lanka, China, Taiwan, Korea, South Asia and South East Asia. It is used as an ingredient in both savory and sweet dishes. Themungbean was domesticated in Persia (Iran), where its progenitor (*Vigna radiata* subspecies sublobata) occurs wild. Mungbean belongs to the legume family and sub family papilionaceae with diploid chromosome number 2n = 22. There are three sub groups of *Vigna radiata*; one is cultivated (*Vigna radiate* subsp. *Radiata*), and two are wild (*Vigna radiate* subsp *sublobata* and *Vigna radiate* subsp. *Glabara*). India has a wide range of genetic diversity of cultivated, as well as of weedy wild types of mungbean, it is considered as the region of its first domestication (Baudoin and Marechal, 1988)^[1].

Mungbean is a rich source of nutrient and is considered a healthy food. It constitutes an important place in vegetarian diets. Mungbean seeds are good source of dietary protein and contain higher levels of folate and iron than most other legumes. It is also a rich source of essential amino acids like isoleucine, leucine, lysine and phenylalanine. The assessment of genetic divergence existing in the germplasm collections is very important for success of hybridization programme leading to development of high yielding varieties of crop plants because optimum magnitude of parental diversity is required for generating superior hybrids for commercial exploitation as well as for isolating transgressive segregants in segregating generations.

Materials and Methods

The present investigation was carried out at The Instruction Farm of Aacharya Narendra Dev University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. The crosses were made during *Zaid*, 2019 and the hybrids along with parental lines and check varieties were evaluated during *Kharif*, 2019. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. All eighty genotypes in a replication will be grown in 4 m. long single row plots following between rows and within rows spacing of 60 cm. and 10 cm, respectively. All the recommended package of practices was adopted to raise a good crop. Observations were recorded on five randomly selected plants from each entry for thirteen traits *viz.*, Days to 50% flowering, Days to maturity, Plant height (cm.), Primary branches per plant, Clusters per plant, Pods per cluster, Pod length (cm.), Pods per plant, Seeds per pod, Seed yield per plant (g.), 100- seed weight (g.), Biological yield per plant (g.) and Harvest index (%). Genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance expressed as percent of mean.

Results and Discussion

The extent of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates (>20%) of phenotypic (PCV) and genotypic (GCV) coefficient of variation were recorded for biological yield per plant (PCV = 33.12%, GCV = 29.62), seed yield per plant (PCV = 32.82%, GCV = 29.78%), plant height (PCV = 26.39%, GCV = 25.88%), primary branches per plant (PCV = 22.13%, GCV = 18.89%), pods per plant (PCV = 21.43%, GCV = 18.38) and seeds per pod (PCV =21.36%, GCV = 20.02%). The moderate estimates (10-20%) of PCV and GCV were recorded for days to 50% flowering, days to maturity, clusters per plant, pod length and pods per clusters. The remaining characters, 100-seed weight and harvest index exhibited low estimates (<10%) of PCV or GCV. The estimates of heritability in broad sense (h²b) and genetic advance in % of mean estimated for thirteen characters have been presented in Table 1. The estimates of broad sense heritability ranged from 32% (harvest index) to 96% (plant height). The high heritability in broad sense (>75%) was recorded for days to 50% flowering, days to maturity, plant height, seeds per pod, 100-seed weight, seed yield per plant and biological yield per plant. Pods per plant, pod length, primary branches per plant, clusters per plant and pods per cluster showed moderate sense heritability (>50% to <75%) while low heritability (<50%) was found for only harvest index. The genetic advance in % of mean was to be very high (>20%) for the characters viz., days to 50% flowering, days to maturity, plant height, primary branches per plant, seeds per pod, pods per plant, biological yield per plant and seed yield per plant. Moderate (>10-20%) estimates of genetic advance in per cent of mean were observed for clusters per plant, pods per cluster, pod length and 100-seed weight. While harvest index (4.70%) showed low genetic advance (<10%). The high estimates of genotypic and phenotypic coefficient of variation and high heritability in broad sense along with high genetic advance in percent of mean was recorded for biological yield per plant and seed yield per plant which indicated that these two traits would be ideal traits for improvement through selection in context of present material. Day to 50% flowering, days to maturity, plant height and seeds per pod heaving high heritability, genetic advance along with PCV and GCV. Pod Length, Cluster per plant and Pods per cluster recorded moderate PCV and GCV, heritability along with genetic advance. Remaining characters had low to moderate GCV and PCV values or low to moderate heritability to emerge as poor indices of selection. The estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in mungbean (Titumeer et al., 2015; Jangra et al., 2015; Pinchhyo et al., 2016).

Conclusion

All the characters recorded high heritability indicating the high influence of genetic components. Traits biological yield per plant and seed yield per plant were governed by additive gene action as they possessed high heritability along with high genetic advance. Pod Length, Cluster per plant and Pods per cluster recorded moderate PCV and GCV, heritability along with genetic advance. Remaining characters had low to moderate GCV and PCV values or low to moderate heritability to emerge as poor indices of selection.

 Table 1: Estimates of coefficient of variation, heritability in broad sense and genetic advance at percent of mean for (13) traits in mungbean

Character	Coefficient of variation (%)		Heritability	Genetic advance
	Phenotipic	Genotipic	broad sense	In (%) of mean
D50F	19.69	18.78	90%	36.91
DM	15.02	14.35	91%	28.25
PH	26.39	25.88	96%	52.30
PB/P	22.13	18.89	72%	33.22
C/P	14.22	11.68	67%	19.78
P/C	11.35	8.07	50%	11.84
PL	12.24	10.46	73%	18.43
P/P	21.43	18.38	73%	32.48
S/P	21.36	20.02	87%	38.64
100-SW	8.71	8.07	85%	15.41
BY/P	33.12	29.62	79%	54.57
HI	7.05	4.01	32%	4.70
SY/P	32.82	29.78	82%	55.67

Traits: D 50% F = Days to 50% flowering, DM = Days to maturity, PH = Plant height(cm), PBTP = Primary branches plant⁻¹, C/P = Cluster plant⁻¹, P/C = Pods cluster⁻¹, PL = Pod length(cm), P/P = Pods Plant⁻¹, S/P = Seeds plant⁻¹, 100-SW = 100-Seed weight(g), BY/P = Biological yield plant⁻¹ (g), HI = Harvest index (%), SY/P = Seed yield plant⁻¹ (g).

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