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Evaluation of yield and its contributing traits for mung bean (*Vigna radiata* L.) germplasm

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Abstract

The present study was carried out to assess genetic variability, character association and path analysis for seed yield and component characters in 12 genotypes of mungbean grown in a Randomized Block Design with three replications at Organic Research Farm, Kargunawaji, Institute of Agricultural Science, Bundelkhand University, Jhansi (UP), during *Kharif* 2024. Twelve characters were used to record the observations: days to 50% flowering, days to maturity, plant height, number of primary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, protein content, and seed yield per plant. Significant variations between the genotypes for each of the twelve characters under study were found through analysis of variance. Important yield components showed a great deal of variation. Seed yield per plant, number of pods per cluster, number of clusters per plant, number of primary branches, pod length, and number of seeds per pod all showed high phenotypic and genotypic coefficients of variation. Pod length, number of seeds per pod, number of primary branches, number of clusters per plant, and number of pods per cluster. Seed yield per plant showed high heritability and high genetic advancement, followed by days to maturity, number of pods per cluster, days to 50% flowering, number of pods per plant, and pod length.

Keywords: Mungbean (*Vigna radiata* L. Wilczek), genetic variability, heritability, genetic advance, correlation coefficient, path coefficient analysis, seed yield

Introduction

Mung bean, scientifically known as *Vigna radiata* (L.) Wilczek, is a crucial and widely cultivated legume in Asia. It holds significant importance as a nutritious food source and is extensively grown and consumed across India (Datta *et al.*, 2012) [2]. It is believed to have originated in India and remains a prominent pulse crop in the region. Mung bean, a member of the Fabaceae family, is a self-pollinating legume with a somatic chromosome number of $2n=2x=22$. One of India's main pulse crops, mungbean is grown from humid tropical regions to arid and semiarid ones. Bangladesh, China, India, Pakistan, Sri Lanka, Thailand, the Philippines, Myanmar, Indonesia, East Africa, Nepal, and Bhutan are among the countries that grow mungbean. India is where mungbean first appeared, and it later spread to Java, Eastern and Central Africa, and the West Indies. Average productivity of mungbean falls short of its potential due to various factors, including cultivation on marginal and degraded lands with limited rainfall, insufficient use of fertilizers, significant losses from pests and diseases, lack of suitable high-yielding varieties, absence of determinate types of varieties and limited knowledge of improved farming practices among farmers. These constraints contribute to the low productivity of mungbean in India. Another significant challenge is the narrow genetic diversity of the crop, which hinders its ability to achieve higher yield levels. Even though mungbean is a self-pollinating species, there exists considerable genetic variation among mungbean cultivars and their related species (Bisht *et al.*, 2005) [1]. However, this crop's high level of self-pollination reduces natural variability, which limits the selection process's effects. However, the degree of genetic variability in the population determines how well a selection program works in plant breeding. Any effort to improve crops must comprehend the degree of genetic variability and how it is measured for both qualitative and quantitative characteristics of economic significance. As a result, understanding variability, heritability, and genetic advance is critical in efficient breeding,

allowing breeders to select the best genotypes for increased yield (Degefa et al., 2014) [3]. The yield is a complex character formed by the interaction of various yield-contributing characters, each of which has positive or negative associations with yield and with one another. Assessing the magnitude of correlations between various characters and yield would be extremely useful in indirect selection for yield improvement. The current study will examine various aspects of genetic variability, correlation studies, path coefficient analysis, genetic diversity, and selection indices for seed yield and other contributing traits in mungbeans.

Material and Methods

The experimental material consisted of twelve genotypes of mungbean *Vigna radiata* (L.) made available in the Organic Research Farm, Karguan ji, Department of Genetics and Plant Breeding, Institute of Agricultural Science, Bundelkhand University, Jhansi. The experiment was laid out in randomized block design (RBD) with three replications during the *kharif* season 2024-25. Each genotype was planted in a plot of 1.35 m x 1.35 m size, accommodating two rows spaced 45 cm apart. The plant-to-plant spacing of 10 cm was maintained. Non-experimental rows were planted all around the experiment to eliminate the border effects, if any. All the recommended package of practices were adopted to raise a good and healthy crop. The observations were made on five competitive plants chosen at random from each entry, and the average value was used for statistical analysis, with the exception of days to 50% flowering, days, days to maturity, plant height (cm), number of clusters per plant, number of pods per cluster, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), and protein content. Trait association studies used analysis of variance, genetic variances, heritability and genetic advance, correlation analysis, and path coefficient analysis to quantify the interrelationships between different traits and investigate the direct and indirect effects of different traits on yield and quality components, respectively.

Results and Discussion

Mung bean germplasm data analysis was performed to evaluate correlation coefficient, path coefficient analysis, and the direct and indirect effects of various characters on seed yield in Mungbean. Further discussion is provided below.

Correlation coefficients

The genotypic and phenotypic correlation coefficients were estimated for all combinations of the twelve characters under investigation. Table 1 shows the estimated correlation coefficients. There is no tangible test for determining the statistical significance of correlation at the genotypic level, so associations at the phenotypic level are generally considered (Reddy and Sharma 1982, and Dhayal et al., 2003) [4, 5]. The estimates of genotypic correlation coefficients were generally similar in direction but larger in magnitude than their corresponding phenotypic correlation coefficients, indicating a strong association between pairs of characters; however, the values of phenotypic correlation coefficients were reduced with environmental interaction.

Path coefficient analysis

In the current study, twelve characters were chosen to partition their genotypic correlation coefficients with seed yield into direct and indirect effects: days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant, and protein content. The resultant variable was seed yield, and the causal variables were the twelve component characters listed above. Tables 3 and 4 show the genotypic correlation coefficients calculated between seed yield per plant and each of the twelve causal variables, as well as between themselves.

Table 1: Estimates of genotypic correlation coefficient among 12 quantitative traits in twelve mungbean genotypes

Trait	Days to 50% flowering	Days to maturity	Plant height	Primary branches	Clusters/ plant	Pods/ cluster	Pods/ plant	Pod length	Seeds/ pod	100- seed weight	Protein content	Seed yield/ plant
Days to 50% flowering	1 **	0.9143 **	-0.6745 *	-0.2604	-0.4026	-0.3603	0.1114	-0.6039 *	0.3995	0.3311	-0.5826 *	-0.3347
Days to maturity		1 **	-0.6612 *	-0.3126	-0.544	-0.493	0.0398	-0.5364	0.493	0.4724	-0.677*	-0.316
Plant height			1 **	-0.1983	0.0703	0.0103	-0.3428	0.6549*	-0.5384	-0.333	0.5214	-0.0091
Primary branches				1 **	0.9072 **	0.9292 **	0.0411	0.4333	-0.3779	0.2916	0.8629**	1.025 **
Number of clusters/plant					1 **	1.006 **	-0.1501	0.5638	-0.4084	-0.2326	0.7675**	0.757 **
Number of pods/ cluster						1 **	-0.0455	0.4344	-0.2261	-0.2166	0.819**	0.7293 **
Number of pods/ plant							1 **	-0.6372 *	0.4983	0.2751	-0.056	-0.0194
Pod length								1 **	-0.977**	-0.4567	0.7158**	0.6152 *
Number of seeds per pod									1 **	0.413	-0.9034 **	-0.4855
100-seed weight										1 **	-0.7862 **	0.1907
Protein content											1 **	0.7239 **
Seed yield per plant												1 **

Table 2: Estimates of phenotypic correlation coefficient among 12 quantitative traits in twelve mungbean genotypes

Trait	Days to 50% flowering	Days to maturity	Plant height	Primary branches	Clusters/ plant	Pods/ cluster	Pods/ plant	Pod length	Seeds/ pod	100- seed weight	Protein content	Seed yield/ plant
Days to 50% flowering	1 **	0.8028 **	-0.4234*	-0.1903	-0.3076	-0.2826	0.1594	-0.3843 *	0.21	0.1937	-0.3261	-0.269
Days to maturity		1 **	-0.5094**	-0.3009	-0.3916 *	-0.4225 *	0.0902	-0.4675**	0.2136	0.3937 *	-0.4416 **	-0.2551
Plant height			1 **	-0.0779	-0.0012	-0.0827	-0.3063	0.5272**	-0.3078	-0.3896*	0.03	-0.0751
Primary branches				1 **	0.5194 **	0.564 **	-0.043	0.3859 *	-0.0917	0.0936	0.3576**	0.5779 **
Number of clusters/ plant					1 **	0.8812 **	-0.1471	0.4071 *	-0.1559	0.0661	0.5103**	0.6012 **
Number of pods/cluster						1 **	0.0121	0.3023	-0.0229	-0.0306	0.5669**	0.6216 **
Number of pods/plant							1 **	-0.4411**	0.3619 *	0.2161	0.0444	0.0423
Pod length								1 **	-0.4379**	-0.3021	0.492**	0.5061 **
Number of seeds per pod									1 **	0.3066	-0.3546 *	-0.1489
100-seed weight										1 **	-0.1278	0.1888
Protein content											1 **	0.5497 **
Seed yield per plant												1 **

Table 3: Genotypic path analysis of direct and indirect effects of 12 quantitative characters on seed yield in mungbean

Trait	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	100-seed weight	Protein content	Seed yield/plant
Days to 50% flowering	-0.77007	0.79841	0.06185	-0.05381	-0.25804	0.02605	0.03074	-0.02738	-0.18768	0.09184	-0.04655	-0.3347
Days to maturity	-0.70411	0.8732	0.06063	-0.0646	-0.34868	0.03564	0.01098	-0.02432	-0.23161	0.13102	-0.05409	-0.316
Plant height	0.51941	-0.57733	-0.0917	-0.04099	0.04505	-0.00075	-0.09456	0.0297	0.25292	-0.09254	0.04165	-0.0091
Number of primary branches	0.20049	-0.27293	0.01819	0.20669	0.18751	-0.06718	0.01134	0.01965	0.17751	0.08089	0.06893	1.025 **
Number of clusters per plant	0.31004	-0.47505	-0.00645	0.18751	0.64093	-0.07273	-0.04141	0.02557	0.19182	-0.06454	0.06131	0.757 **
Number of pods per cluster	0.27744	-0.43046	-0.00095	0.19206	0.64477	-0.0723	-0.01256	0.0197	0.10623	-0.06008	0.06543	0.7293 **
Number of pods per plant	-0.08581	0.03474	0.03144	0.0085	-0.09622	0.00329	0.27583	-0.02889	-0.23407	0.07631	-0.00447	-0.0194
Pod length	0.46504	-0.46837	-0.06005	0.08956	0.36136	0.3023	-0.17575	0.04535	0.45893	-0.12667	0.05718	0.6152 *
Number of seeds per pod	-0.30767	0.43053	0.04937	-0.07811	-0.26173	0.01635	0.13744	-0.0443	-0.46974	0.11455	-0.07217	-0.4855
100-seed weight	-0.25495	0.41245	0.03059	0.06028	-0.14911	0.01566	0.07588	-0.02071	-0.19399	0.27739	-0.06281	0.1907
Protein content	0.44867	-0.59119	-0.04781	0.17834	0.49192	0.5669	-0.01544	0.03246	0.42438	-0.21809	0.07989	0.7239 **

Table 4: Phenotypic path analysis of direct and indirect effects of 12 quantitative characters on seed yield in mungbean

Trait	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	100-seed weight	Protein content	Seed yield/plant
Days to 50% flowering	-0.22252	0.15842	0.0873	-0.01997	0.04251	-0.14143	0.03637	-0.23875	-0.02045	0.05019	-0.00076	-0.269
Days to maturity	-0.17862	0.19736	0.10503	-0.03161	0.05413	-0.21157	0.02056	-0.29044	-0.02081	0.1018	-0.00103	-0.2551
Plant height	0.09422	-0.10053	-0.20618	-0.00817	0.00017	-0.0414	-0.06989	0.32753	0.02997	-0.10077	0.00007	-0.0751
Number of primary branches	0.0423	-0.05938	0.01604	0.10507	0.05468	0.05929	-0.00449	0.23993	0.00895	0.02363	0.00083	0.5779 **
Number of clusters per plant	0.06843	-0.07728	0.00025	0.05468	-0.13816	-0.1217	-0.03363	0.25273	0.01516	0.01739	0.00119	0.6012 **
Number of pods per	0.06286	-0.0834	0.01705	0.05929	-0.1217	0.50113	0.00596	0.18781	0.00219	-0.00797	0.00132	0.6216 **

cluster												
Number of pods per plant	-0.03547	0.01778	0.06315	-0.00449	0.02037	0.00596	0.22819	-0.27373	-0.03526	0.05588	0.0001	0.0423
Pod length	0.08552	-0.09226	-0.1087	0.04058	-0.05623	0.15134	-0.10054	0.62108	0.04263	-0.18806	0.00115	0.5061 **
Number of seeds per pod	-0.04673	0.04217	0.06346	-0.07811	0.02152	-0.01126	0.08263	0.04263	-0.09738	0.07926	-0.00083	-0.1489
100-seed weight	-0.04315	0.07762	0.08027	0.06028	-0.14911	-0.01542	0.04927	-0.18806	-0.02981	0.25848	-0.0003	0.1888
Protein content	0.07254	-0.08715	-0.00619	0.17834	0.49192	0.28401	0.01013	0.30566	0.03453	-0.03329	0.00233	0.5497 **

Conclusion

The analysis of correlation coefficients revealed that the magnitude of genotypic correlation was greater than the corresponding phenotypic correlation. The number of primary branches, number of pods per cluster, number of clusters per plant, pod length, and protein content all had highly significant and positive correlations with seed yield at both the genotypic and phenotypic levels. At both the genotypic and phenotypic levels, there was a negative and non-significant association between days to 50% flowering, days to maturity, plant height, and number of seeds per pod. The path coefficient analysis revealed that days to maturity, number of clusters per plant, 100-seed weight, and number of pods per plant all had significant direct effects at the genotypic level. Pod length, number of pods per cluster and 100- seed weight at the genotypic level. These characters also exhibited significant and positive association with seed yield per plant.

Future scope

The findings from the correlation analysis and path coefficient analysis provide a foundation for future research and breeding programs aimed at improving crop yield. These identified trait associations and their relationships with yield can be further explored to unravel the underlying genetic mechanisms and physiological processes involved. This could involve investigating specific genes or molecular pathways that influence these traits and yield. Additionally, conducting field trials and genetic studies on diverse germplasm can help validate the observed correlations and explore new trait combinations for yield enhancement.

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