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Studies on characterization and evaluation of mungbean (*Vigna radiata* L. Wilczak) germplasm's or yield and yield attributing character

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Abstract

The present study on Studies on characterization and evaluation of mungbean (*Vigna radiata* L. Wilczak) germplasm's or yield and yield attributing character was conducted during *Kharif* season of 2024 at Chemical Research Farm, Bundelkhand University, Jhansi, to evaluate 12 mungbean genotypes in Randomized Block Design with three replications. Ten quantitative traits including days to 50% flowering, days to maturity, reproductive phase duration, plant height, branches per plant, clusters per plant, pods per plant, pod length, 100-seed weight, protein content, and seed yield per plant were recorded. Correlation analysis revealed that seed yield per plant had highly significant and positive association with days to 50% flowering, number of seeds per pod, and protein content at both genotypic and phenotypic levels, which is in agreement with earlier reports. Seed yield showed non-significant negative correlation with reproductive phase duration and 100-seed weight. Path coefficient analysis indicated that number of clusters per plant and number of branches per plant had high positive direct effects on seed yield. Additive gene action was observed for seed yield, pods per plant, protein content, and days to maturity as evident from high heritability with high genetic advance. The study concludes that selection based on days to flowering, seeds per pod, clusters per plant, pods per plant, and seed yield per plant would be effective for yield enhancement in mungbean breeding programs.

Keywords: Correlation, path coefficient, heritability, clusters germplasm

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek], also known as green gram or moong, is a legume crop that is widely grown in many parts of the world, particularly in South and Southeast Asia (Pratap *et al.*, 2021) ^[12]. Mungbean belongs to the Fabaceae family in the genus *Vigna* and is a self-pollinating diploid grain legume, $2n = 22$ (Karpechenko, 1927) ^[8]. It is often preferred to other pulse crops because of its better digestibility and lower content of raffinose, stachyose and verbascose, leading to less flatulence (Poehlman, 1991) ^[10]. It is a short-duration crop and can be grown across seasons in varying cropping systems and crop rotations. It can be grown successfully in extreme environments (e.g., high temperatures, low rainfall and poor soils) with few economic inputs (Das *et al.*, 2014) ^[3]. After chickpea and pigeon pea in terms of production and area, mungbean is the third most significant pulse crop in India. The knowledge of genetic variability existing within the different parameters contributing to yield is an important criterion for yield enhancement, but in highly self-pollinated crops like mungbean, natural variation is narrow, resulting in limited scope for selection opportunity. The efficacy of selection depends upon the existence and magnitude of genetic variability for yield and yield-contributing traits in the breeding material (Adewale *et al.*, 2010) ^[2]. For any yield improvement programme, selection of superior parents possessing better heritability and genetic advance for any quantitative trait is an essential prerequisite (Khan *et al.*, 2005) ^[6]. Heritability indicates the relative success of selection (Ortiz and Ng, 2023) ^[9]. Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of the resultant effect of selecting the best individual (Johnson *et al.*, 1955; Singh *et al.*, 2010) ^[5, 14].

Materials and Methods

The experimental material consisted of 12 genotypes of mungbean, which were grown in randomized block design (RBD) with three replications. The experimental material was planted in the field during *Kharif* in the year 2024 at Chemical Research Farm, Narayan Bagh, Institute of Agricultural Science, Bundelkhand University, Jhansi (UP). In the experimental plot, row-to-row spacing was 20-40 cm and plant-to-plant spacing within a row was 5-10 cm. A comprehensive evaluation of 12 mungbean genotypes GJM2011, GJM2012, GJM2013, GJM2015, GJM2017, GJM2018, GJM2019, GJM2020, GJM2021, GJM2026, GJM2032, ANDG1800 revealed significant genetic variability across all traits studied such as Days of flowering, Days to maturity, Reproductive phase duration, Plant height (cm), Number of branches per plant, Number of clusters per plant, Number of pod per plant, Weight of 100 seed (gm), Pod length, Protein content (%), Yield per plant (gm) observations were recorded by selecting randomly five competitive plants from each plot on ten characters were analyzed first by randomized block design to test the significance of difference among the genotypes. Trait association studies were conducted using Analysis of variance, Genetic variances, heritability and genetic advance, Correlation analysis, and path coefficient analysis to quantify the interrelationships between different traits and to investigate the direct and indirect effects of different traits on yield and quality components, respectively.

Results and Discussion

Mung bean germplasm data analysis was done to evaluate correlation coefficient, path coefficient analysis and their direct and indirect effects of various characters on seed yield in Mungbean, and Further discussion are mentioned below:

Correlation Coefficient Analysis

In the present investigation, seed yield per plant had a highly significant and positive correlation with days to 50 per cent flowering, number of seeds per pod, and protein

content at both genotypic and phenotypic levels. Such result also reported by Prasanna *et al.* (2014) ^[11], Sandhiya and Saravanan (2018) ^[13] and Kanavi *et al.* (2019) ^[7] for number of pods per plant. Similar results with Abhisheka and Mogali (2020) ^[1] and Dhunde *et al.* (2021b) ^[4] for number of seeds per pod and number of pods per plant. Seed yield per plant had a non-significant and negative correlation with reproductive phase duration and 100-seed weight. At phenotypic and genotypic levels, these findings are in accordance with Kanavi *et al.* (2019) ^[7]. This indicated that the character seed yield was more influenced by these attributes in mungbean and, therefore, were important for bringing improvement in seed yield. Johnson *et al.* (1955) ^[5] emphasised that these correlated yield attributes can serve as indicator characters for improving seed yield. They have further emphasised that such improvement depends not only on genotypic correlations but phenotypic correlations also play an important role.

Path Coefficient Analysis

In the selection programme, when the interrelationship of a large number of variables with seed yield and among themselves is studied, the situation becomes very complex to understand the actual role of a variable for increasing yield. In such a situation, the information of correlation coefficient coupled with the information on path coefficient greatly helps in identification of suitable characters for giving due weightage during selection. The path coefficient analysis was done for yield and yield attributes to estimate the direct and indirect effects of various characters on seed yield. Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients. To understand these effects, genotypic as well as phenotypic correlation coefficients of different characters with seed yield were partitioned into their direct and indirect effects (Table 2 and Table 3). This facilitates the selection of genotypes on the basis of those traits that will eventually contribute more towards seed yield.

Table 1: Phenotypic (rp) and genotypic (rg) correlation coefficients among twelve characters of mungbean

Characters		DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	PC	SYP
DF	rp	1.000	0.348	-0.011	0.326	0.268	-0.462	0.180	-0.741 **	0.652 *	-0.729 **	0.674 *	0.786 **
	rg	1.000	0.2169	-0.2311	0.1725	0.1435	-0.1668	0.1656	-0.3589 *	0.3797 *	-0.2455	0.3658 *	0.5176 **
DM	rp		1.000	0.232	-0.005	1.072 **	-0.510	0.378	-1.021 **	0.360	0.720 **	0.271	0.335
	rg		1.000	0.2874	-0.1048	0.4644 **	-0.2738	0.3347 *	-0.3443 *	0.3488 *	0.1397	0.2321	0.28
RPD	rp			1.000	0.186	0.375	-1.178 **	0.349	0.220	-0.196	-0.149	0.143	-0.263
	rg			1.000	0.197	0.2499	-0.3004	0.2745	0.1816	-0.0051	-0.228	0.0964	-0.131
PH	rp				1.000	-0.186	-0.071	0.510	0.157	-0.042	-0.089	0.243	0.160
	rg				1.000	-0.0957	0.1557	0.3492 *	0.0576	-0.0409	-0.0468	0.1647	0.1019
NBP	rp					1.000	-0.621 *	0.332	-0.797 **	0.558	0.253	0.488	0.287
	rg					1.000	-0.2914	0.0994	-0.2883	0.3748 *	0.2851	0.2068	0.2105
NCP	rp						1.000	-0.159	0.135	-0.567	0.830 **	-0.700 *	-0.467
	rg						1.000	0.0292	-0.0225	-0.3561 *	0.1358	-0.3898 *	-0.3011
NPP	rp							1.000	-0.084	-0.011	0.342	0.160	0.011
	rg							1.000	-0.2884	-0.0286	0.1344	0.0399	-0.0081
PL	rp								1.000	-0.563	-0.288	-0.461	-0.682 *
	rg								1.000	-0.2999	-0.2687	-0.2299	-0.3464 *
NSP	rp									1.000	-0.093	0.957 **	0.915 **
	rg									1.000	-0.0856	0.8623 **	0.8642 **
100-SW	rp										1.000	-0.195	-0.160
	rg										1.000	-0.1775	-0.1298
PC	rp											1.000	0.884 **
	rg											1.000	0.8368 **

*, ** Significant at 5 % and 1 % levels, respectively

Here: DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL=

Pod length, NSP= Number of seeds per pod, 100-SW= 100-seed weight, PC=Protein content and SYP= Seed yield per plant

Table 2: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 12 genotypes of mungbean

Traits	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	Protein	SYP
DF	0.09889	-0.32528	-0.00033	-0.04408	0.33144	-0.44095	-0.05509	0.47608	-1.37017	0.17661	1.93927	0.786 **
DM	0.03441	-0.93489	0.00689	0.0007	1.32575	-0.48642	-0.11599	0.6555	-0.75663	-0.17428	0.77948	0.335
RPD	-0.00109	-0.21711	0.02965	-0.02516	0.46339	-1.12362	-0.10707	-0.1414	0.4117	0.03617	0.41124	-0.263
PH	0.03228	0.00482	0.00552	-0.13507	-0.22996	-0.068	-0.15658	-0.10091	0.08722	0.02147	0.69898	0.160
NBP	0.02651	-1.00255	0.01111	0.02512	0.23627	-0.59224	-0.10179	0.51175	-1.17117	-0.06117	1.40464	0.287
NCP	-0.0457	0.47656	-0.03491	0.00963	-0.76728	0.95424	0.04884	-0.0864	1.19145	-0.20101	-2.01248	-0.467
NPP	0.01776	-0.35352	0.01035	-0.06895	0.41023	-0.15193	-0.30674	0.05415	0.0226	-0.0829	0.45995	0.011
PL	-0.07329	0.95402	0.00653	-0.02122	-0.98492	0.12835	0.02586	-0.64235	1.1824	0.06973	-1.32722	-0.682 *
NSP	0.06452	-0.33683	-0.00581	0.00561	0.68944	-0.54138	0.0033	0.36166	-0.10007	0.02258	2.75166	0.915 **
100-SW	-0.07213	-0.67292	-0.00443	0.01198	0.31232	0.79218	-0.10503	0.18498	0.19583	-0.24213	-0.56061	-0.160
Protein	0.06666	-0.25331	0.00424	-0.03282	0.60362	-0.66754	-0.04904	0.29635	-2.0087	0.04718	0.08768	0.884 **

*, ** Significant at 5 % and 1 % levels, respectively, Residual effect =0.2616

Here: DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number

of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod, Protein content and 100-SW= 100-seed weight.

Table 3: Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 12 genotypes of mungbean

Traits	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	Protein	SYP
DF	0.12229	0.01605	0.03172	0.01927	-0.01087	0.00562	-0.01031	0.02859	0.20096	0.00612	0.10816	0.5176 **
DM	0.0265	0.07406	-0.03941	-0.01171	0.03511	0.00925	-0.02082	0.02739	0.18471	0.00346	0.06861	0.28
RPD	0.02828	0.02128	-0.13715	0.022	0.01891	0.01014	-0.01707	0.01445	-0.0027	0.00567	0.02847	-0.131
PH	0.02109	-0.00776	-0.027	0.11172	0.00723	-0.00526	-0.02172	0.00458	-0.02165	0.00116	0.04868	0.1019
NBP	0.01758	0.03438	-0.03428	-0.01068	0.07567	0.00983	-0.00618	0.02291	0.19852	0.00711	0.0611	0.2105
NCP	0.02035	-0.02027	0.04115	0.01741	0.02201	-0.03376	-0.00182	0.00182	-0.18868	0.00338	-0.11522	0.3011
NPP	0.02026	0.02478	-0.03764	0.03901	0.00752	-0.00099	-0.06219	0.02294	-0.01519	0.00335	0.01179	0.0081
PL	0.04393	-0.02549	-0.0249	0.00643	0.02178	0.00077	0.01793	0.07956	-0.15866	0.0067	-0.06778	0.3464 *
NSP	0.04641	0.02584	0.0007	-0.00457	0.02836	0.01204	0.00178	0.02384	0.52939	0.00214	0.25489	0.8642 **
100-SW	0.03005	0.01029	0.03123	-0.00521	0.02158	-0.00459	-0.00836	0.0214	-0.04547	0.02488	-0.05229	0.1298
Protein	0.04473	0.01719	-0.01321	0.0184	0.01563	0.01317	-0.00248	0.01824	0.4565	0.00441	0.02955	0.8368 **

*, ** Significant at 5 % and 1 % levels, respectively Residual effect = 0.1562

Here: DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod, Protein content and 100-SW= 100-seed weight

Discussion: The information on the phenotypic and genotypic relationships of seed yield in the mungbean with

its component characters and also among the characters themselves would be very useful to the breeders in developing an appropriate breeding strategy, since seed yield is a complex character and is influenced by a number of traits as well as environmental factors. Hence, selection of genotypes with desirable characters would be greatly enhanced if significant correlations between seed yield and its component characters are established. To improve seed yield by accumulating an optimum combination of yield-

contributing characters in a single genotype, it is essential to know the implications of the interrelationship of various characters. The information on correlation and path coefficient provides an opportunity to know the magnitude and direction of association of yield with its direct and indirect components.

Conclusion

It could be concluded from the present findings that additive gene action was operating for seed yield per plant, number of pods per plant, pod protein content and days to maturity, indicating high heritability coupled with high genetic advance. Study of correlation coefficient showed that days to 50 per cent flowering and number of seeds per pod were the characters that displayed positive and significant association with seed yield per plant, while pod length showed negative and significant association with seed yield per plant. Number of clusters per plant and number of branches per plant displayed a high and positive direct effect on seed yield per plant. Hence, these traits deserve strategic importance while formulating effective breeding strategies with the aim of yield enhancement. A combination of five traits, viz., seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod, was found as the most useful than straight selection for the seed yield alone.

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References

1. Abhisheka LS, Mogali SC. Genetic variability, correlation and path coefficient analysis for yield and yield attributing traits in advanced breeding lines (ABLs) of green gram [*Vigna radiata* (L.) Wilczek] in F6 generation. *Int J Curr Microbiol Appl Sci*. 2020;9(6):314-321.
2. Adewale BD, Okonji C, Oyekanmi AA, Akintobi DAC, Aremu CO. Genotypic variability and stability of some grain yield components of cowpea. *Afr J Agric Res*. 2010;5(9):874-880.
3. Das K, Roychoudhury A. Reactive oxygen species (ROS) and response of antioxidants as ROS-scavengers during environmental stress in plants. *Front Environ Sci*. 2014;2:53.
4. Dhunde BB, Devmore JP, Mahadik SG, Palshetkar MG, Vanve PB, Bhavé SG, *et al*. Correlation and path analysis studies on yield and its components in green gram [*Vigna radiata* (L.) Wilczek]. *Pharma Innov J*. 2021;10(1):727-730.
5. Johnson HW, Robinson HF, Comstock R. Estimates of genetic and environmental variability in soybeans. 1955.
6. Khan MS, Zaidi A, Wani PA, Oves M. Role of plant growth promoting rhizobacteria in the remediation of metal contaminated soils. *Environ Chem Lett*. 2009;7(1):1-19.
7. Kanavi MSP, Rangaiah S, Krishnaprasad BT. Molecular characterisation and genetic diversity analysis through SSR markers in germplasm lines of green gram [*Vigna radiata* (L.) Wilczek]. *Int J Bioresour Stress Manag*. 2019;10(3):298-305.
8. Karpechenko GD. The production of polyploid. *Hereditas*. 1927;9:349.
9. Pereira YFU, Lozano JG, Vega JJ, Valencia AVR, Ortíz NQ. Climate change and spatiotemporal variability of temperature (1980-2020 series) in Tolima, Colombia. 2023.
10. Poehlman ET, Melby CL, Badylak SF. Relation of age and physical exercise status on metabolic rate in younger and older healthy men. *J Gerontol*. 1991;46(2).
11. Prasanna V. Impact of monsoon rainfall on the total foodgrain yield over India. *J Earth Syst Sci*. 2014;123(5):1129-1145.
12. Pratap A, Das A, Kumar S, Gupta S. Current perspectives on introgression breeding in food legumes. *Front Plant Sci*. 2021;11:589189.
13. Saravanan S, Sandhiya V. Genetic variability and correlation studies in greengram (*Vigna radiata* L. Wilczek). *Electron J Plant Breed*. 2018;9(3):1094-1099.
14. Singh B, Singh BP, Cowie AL. Characterisation and evaluation of biochars for their application as a soil amendment. *Soil Res*. 2010;48(7):516-525.