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Genotypic evaluation and Morpho biochemical characterisation of Mungbean genotypes for yield and quality traits

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Abstract
The present study was carried out to evaluate the extent of variability, heritability, genetic advance and genetic advance as a percentage of mean (GAM) in twelve mungbean (*Vigna radiata* (L.) Wilczek) genotypes for a range of morphological and biochemical traits. Field experiments were conducted during the Kharif seasons of 2013 and 2014 at the Agricultural Farm, Rajoula, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.), using a randomized block design with three replications, while biochemical estimations were performed in the Department of Crop Science, College of Agriculture, MGCGV, Chitrakoot. Observations were recorded on ten randomly selected plants from each genotype, and the data were analysed using IBM SPSS. Across both years, phenotypic coefficients of variation were marginally higher than genotypic coefficients of variation for all traits, suggesting that environmental influence on trait expression was present but relatively small. High estimates of both GCV and PCV for seed yield and number of pods per plant indicated substantial inherent variability and strong prospects for improving these traits through selection. Traits such as seed yield per plant, number of pods per plant, 100-seed weight, number of clusters per plant, pod length, polyphenol content, phytate content, total sugar percentage, fat percentage, methionine content, free amino acids, ash percentage and soluble protein percentage exhibited high heritability coupled with high genetic advance. This combination points towards the predominance of additive gene action and suggests that selection for these characters would be particularly effective in developing superior mungbean genotypes.

Keywords: biochemical characterization, genetic advance, heritability, mungbean, variability, quality traits

Introduction
Mungbean (*Vigna radiata* (L.) Wilczek) is an erect, short-duration grain legume characterized by a limited number of branches and pod clusters concentrated near the upper portion of the plant canopy. Each slender pod typically encloses 8-15 green seeds. As a leguminous crop, mungbean requires minimal nitrogen fertilizer because of its ability to form symbiotic associations with *Rhizobium* species, which biologically fix atmospheric nitrogen. Its short growth cycle of about 75-90 days enables it to fit efficiently into diversified crop rotations while demanding considerably less water than many other summer crops. Owing to these features, mungbean is frequently grown as a cover crop or incorporated as green manure either before or after cereal cultivation, contributing to soil fertility and interrupting pest and disease cycles in cereal-based systems.

Cultivated widely across tropical and subtropical regions of Asia, mungbean is valued for its capacity to adapt to diverse agro-ecological conditions. Globally, the crop holds substantial agricultural and nutritional significance, with an estimated annual production of nearly 6 million tonnes harvested from about 7.3 million hectares (Gayacharan *et al.*, 2023) [1]. India remains the world's largest producer, contributing approximately 41% of global output, followed by Myanmar, Bangladesh, and Pakistan (Schreinemachers *et al.*, 2019) [2]. When intercropped with cereals, mungbean has been shown to markedly improve the productivity of companion crops through enhanced nitrogen input and better resource use efficiency (Rachaputi *et al.*, 2002) [3].

Nutritionally, mungbean is often described as a "nutritional powerhouse." Its seeds contain 24-28% protein and 59-65% carbohydrates on a dry-weight basis, supplying around 3400 kcal kg^{-1}. The relatively small proportions of fat (1-1.5%), fibre (3.5-4.5%), and ash (4.5-5.5%) complement its macronutrient profile. The proteins of mungbean are rich in essential amino acids particularly lysine, which is typically deficient in cereal proteins making mungbean an excellent complement to cereal-based diets (Tsou *et al.*, 1979) [8]. Although sulfur-containing amino acids may be limiting, the overall digestibility and amino acid balance make mungbean a valuable and affordable protein source (Khalil, 2006) [5]. In addition to dry seeds, mungbean pods and sprouts are consumed as vegetables and provide significant levels of vitamins, minerals, and bioactive compounds (Kumar *et al.*, 2011) [11].

Mungbean also holds therapeutic relevance in traditional medicine. It is incorporated in *Sansarjana Karma* after *Panchakarma* therapy and is recommended for managing conditions such as fever, obesity, heat disorders, digestive insufficiency (*agnimandya*), and various skin ailments. Mungbean sprouts are associated with lowering serum cholesterol, alleviating heat-related illnesses, and offering protection against metabolic disorders like diabetes.

Beyond its dietary and medicinal roles, mungbean contributes significantly to soil health through robust nitrogen fixation, facilitated by nodulating *Rhizobia* residing in its root nodules (Ashraf *et al.*, 2003) [4]. This function makes mungbean a strategic component of sustainable agriculture, especially in systems seeking to reduce chemical fertilizer inputs.

From a crop improvement perspective, the assessment of genetic diversity is vital for identifying promising parents, understanding evolutionary relationships, and determining centers of origin (Mohammadi and Prasanna, 2003) [9]. Biochemical, morpho-physiological, and biophysical traits provide crucial insights into the performance of mungbean genotypes, particularly under rainfed and heat-prone environments. Traits such as stomatal conductance which plays a key role in regulating carbon diffusion and photosynthetic efficiency (Wong *et al.*, 1978) [7] are essential indicators of varietal performance under stress.

The variability observed among genotypes in their nutritional composition, isoenzyme activities, and other physiological parameters reflects the crop's extensive genetic base. Studying this variability under rainfed conditions helps identify lines possessing superior nutritional attributes, better stress endurance, and enhanced yield potential. Estimating genetic variability, heritability, genotypic and phenotypic coefficients of variation, and expected genetic advance provides a scientific foundation for selecting elite genotypes capable of contributing to yield improvement and stress resilience.

Materials and Methods

Plant material: The experimental material consisted of twelve mungbean (*Vigna radiata* (L.) Wilczek) genotypes, namely Pratap, K-8541, Pusa-9531, PDM-54, Pant-M5, SML-32, Pant-M1, JM-724, Sona, HUM-6, Pant-M3 and HUM-16, which were collected from the ICAR-Indian Institute of Pulses Research, Kanpur (U.P.). The field experiment was conducted during the Kharif seasons of 2013 and 2014 at the Agriculture Farm, Rajoula, MGCGV, Chitrakoot, Satna (M.P.), following a randomized block design with three replications. Each genotype was sown in four rows of 3 m length, maintaining a spacing of 30 cm between rows and 10 cm between plants within rows. Uniform crop management practices were adopted to ensure optimum growth and productivity. All biochemical estimations were carried out in the Department of Crop Science, College of Agriculture, MGCGV, Chitrakoot, Satna (M.P.).

Data Collection

The assessment of morphological and seed-quality traits was performed on ten randomly selected plants under rainfed conditions. Observations were recorded for number of primary branches per plant, number of clusters per plant, plant height, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, germination percentage, seed viability percentage, specific gravity and seed yield per plant, while days to 50% flowering was recorded on a plot basis.

Biochemical Analysis

Biochemical analyses were performed to determine nitrogen content, crude protein, total free amino acids, total soluble sugars, reducing sugars, non-reducing sugars and methionine content. Nitrogen percentage was estimated by the Micro-Kjeldahl method (AOAC, 1970), which involves digestion, distillation and titration to convert organic nitrogen into ammoniacal form. Crude protein was calculated by multiplying total nitrogen by the factor 6.25. Total free amino acids were estimated following the procedure of Moore and Stein (1948). For this, 0.5 g of powdered seed sample was extracted with 5 ml of 80% ethanol and centrifuged at 5000 rpm for 10 minutes. The extraction was repeated twice, and pooled supernatants were collected. A 0.1 ml aliquot was mixed with 1 ml ninhydrin reagent and the volume was made up to 2 ml with distilled water. The mixture was heated in a boiling water bath for 20 minutes, followed by the addition of 5 ml of diluent solvent. After 15 minutes, the absorbance of the developed purple colour was measured at 570 nm using a Systronics 169 spectrophotometer. Total free amino acids were quantified using a leucine standard curve and expressed as leucine equivalents. All estimations were conducted in triplicate.

Total soluble sugar content was determined using the Anthrone method described by Yemm and Willis (1954). For this estimation, 0.2 g of powdered sample was extracted with 5 ml of 80% hot ethanol, centrifuged and transferred into a 100 ml volumetric flask. The volume was adjusted to 100 ml with distilled water. A 1 ml aliquot was mixed with 10 ml of freshly prepared anthrone reagent under ice-cold conditions and heated in a boiling water bath for exactly 10 minutes. After cooling, the absorbance was recorded at 630 nm against a reagent blank. Quantification was performed using a standard curve.

Reducing sugars were estimated by the DNS method described by Miller (1972). A 0.1 g mungbean sample was extracted with 5 ml of 80% hot ethanol twice, and the pooled supernatant was evaporated over a water bath at 80°C. The residue was dissolved in 10 ml distilled water. To 1 ml of this extract, 3 ml of DNS reagent was added and the solution was heated in a boiling water bath for 5 minutes. While still warm, 1 ml of 40% sodium-potassium tartrate was added. After cooling, absorbance was recorded at 510 nm. Non-reducing sugars were obtained by subtracting

reducing sugars from total sugars. Methionine content was estimated following the procedure of Horn *et al.* (1946). For this, 0.5 g defatted seed powder was hydrolysed with 6 ml of 2N HCl in an autoclave at 15 lb pressure for one hour. Activated charcoal was added to the hydrolysate, heated and filtered. The filtrate was neutralized with 10N NaOH to pH 6.5 and the volume was made up to 50 ml. A 25 ml aliquot was then treated with 3 ml of 10% NaOH and 0.15 ml sodium nitroprusside. After 10 minutes, 1 ml glycine solution was added, followed by the addition of 2 ml orthophosphoric acid after another 10 minutes. The intensity of the resulting red colour was measured at 520 nm against a blank prepared without nitroprusside.

The recorded data were statistically analysed using one-way ANOVA as described by Panse and Sukhatme (1967) [13] with the help of IBM SPSS software. Estimates of heritability were derived following Robinson *et al.* (1949) [17], whereas genetic advance was calculated as per the method of Allard (1960) [15]. The genetic parameter analysis was performed using Windostat Version 9.3.

Results and Discussion

Estimates of Genetic Variability

Genetic variability serves as the foundation of any crop improvement programme, and a thorough assessment of existing variation is essential before formulating a breeding strategy (Haussmann *et al.*, 2004) [12]. The analysis of variance carried out in the present investigation revealed highly significant differences among the genotypes for all the morphological and biochemical traits examined, demonstrating the presence of ample genetic variability within the material under study (Table 1). The existence of substantial variability among mungbean genotypes has also been reported earlier by Muthuswamy *et al.* (2019) [20] and Dhunde *et al.* (2021) [19]. Similar trends were observed by Garg *et al.* (2017) [21], who documented marked differences among mungbean genotypes for characters such as days to flowering, days to maturity, plant height, number of branches, pods per plant, pod length, seeds per pod, 100-seed weight, seed yield, biological yield and harvest index. Significant genotypic variation in traits like seeds per pod, test weight, seed yield per hectare, biomass production and harvest index has also been highlighted in prior studies (Reddy *et al.*, 2011; Dhoot *et al.*, 2017) [22, 23]. Reports on black gram (Rolaniya *et al.*, 2017; Partap *et al.*, 2019) [24, 25] further corroborate the presence of extensive variability within pulse crops. Many of the traits evaluated in the present research have also previously been shown to differ significantly across mungbean genotypes (Rahim *et al.*, 2010; Mondal *et al.*, 2011) [27, 28], reinforcing the reliability of the current findings.

A critical examination of Tables 2 and 3 indicates that the phenotypic and genotypic coefficients of variation were generally close in magnitude for most characters, reflecting minimal environmental influence on their expression. As expected, the phenotypic coefficient of variation (PCV) exceeded the corresponding genotypic coefficient of variation (GCV) for all traits; however, the differences between the two were relatively small. The highest GCV (>20%) was observed for seed yield (26.338%), followed by number of pods per plant (20.316%), indicating that these characters possess a large proportion of heritable genetic variation and are less affected by environmental fluctuations. Mariyappan *et al.* (2022) [31] also reported similar trends in mungbean. The PCV values for these traits were also high, with seed yield (26.749%) and number of pods per plant (20.498%) exceeding the 20% threshold. High estimates of both GCV and PCV suggest that selection for these traits is likely to be effective due to their considerable inherent variability.

The consistently higher PCV values relative to GCV across all traits suggest that environmental factors exerted some influence on trait expression, particularly in morphological parameters. For biochemical traits, the GCV and PCV values generally fell in the moderate range and showed relatively narrow differences, implying a limited role of the environment and a larger contribution of genetic factors to phenotypic expression. While GCV provides an indication of the extent of genetic variability present in a trait, it does not alone determine the proportion of variation that is heritable (Raturi *et al.*, 2015; Pathak *et al.*, 2011; Nandini *et al.*, 2024) [26, 29]. Therefore, further parameters such as heritability and genetic advance were considered to assess the true breeding potential of the traits.

Heritability and Genetic Advance

Heritability estimates are crucial for determining the proportion of total variation that is genetic in origin and can thus be effectively utilized in selection. In the present study, heritability in the broad sense varied widely from 33.6% for number of branches per plant to as high as 99.0% for moisture content. High heritability values were recorded for number of pods per plant (98.2%), seed yield per plant (97.0%), 100-seed weight (95.3%), pod length (90.0%), number of clusters per plant (89.6%), germination percentage (88.6%), viability percentage (86.8%), number of seeds per pod (81.2%) and plant height (66.9%). Moderate heritability was observed for days to 50% flowering (47.8%), specific gravity (46.4%) and number of branches per plant (33.6%). Similar ranges of heritability in mungbean germplasm have been reported by earlier workers (Tabasum *et al.*, 2010; Tyagi and Khan, 2011; Tiwari *et al.*, 2014) [32, 33, 34]. For biochemical parameters, heritability estimates were exceptionally high and ranged from 84% for free amino acids to 99% for soluble protein, ash content, polyphenol content and calorific value, suggesting a strong genetic basis for these characters.

While high heritability provides an indication of the proportion of transmissible genetic variance, heritability alone is not sufficient to predict selection response. Genetic advance expressed as a percentage of mean offers a more informative perspective, as it accounts for both variability and heritability. In the present investigation, high heritability combined with high genetic advance was recorded for seed yield per plant (53.42%), number of pods per plant (41.48%), 100-seed weight (33.55%), number of clusters per plant (29.23%) and pod length (20.53%). This combination suggests that these traits are primarily governed by additive gene action and are therefore amenable to improvement through direct selection, even in early segregating generations. High heritability associated with moderate genetic advance was observed for plant height (15.44%) and moisture percentage (11.83%), indicating that although these traits are heritable, selection may be more effective after a few cycles of recombination.

Among biochemical traits, high heritability coupled with high genetic advance was observed for polyphenol content (31.55%), phytate content (31.37%), total sugar (31.46%),

fat percentage (31.19%), methionine content (30.23%), free amino acids (29.99%), ash content (24.43%) and soluble protein (21.42%). High heritability paired with moderate genetic advance was recorded only for calorific value (16.38%). Traits exhibiting this pattern are likely controlled by additive genetic effects, making selection highly effective. Conversely, traits with high heritability but moderate genetic advance may require delayed selection to allow accumulation of favourable additive alleles.

Conclusion

The results obtained from the present investigation clearly demonstrate that mungbean possesses substantial genetic variability for both morphological and biochemical traits. The narrow difference observed between the phenotypic and genotypic coefficients of variation for most characters indicates that the influence of the environment on trait expression was relatively small, and that genetic factors played a predominant role. Traits such as seed yield per plant and number of pods per plant exhibited high values of both GCV and PCV, accompanied by high heritability estimates and substantial genetic advance. This combination strongly suggests that these traits are largely governed by additive gene action. Consequently, direct selection for these characters is likely to be highly effective and can contribute meaningfully to the development of superior mungbean genotypes in future breeding programmes.

Table 1: Analysis of Variance (Mean Squares) for 24 characters in Mungbean

S. No.	Traits	Source of variation			Treatments	Error
		Replication	Environment	Interaction		
		2	1	2	11	55
1	Days to 50 (%) Flowering	4.29	159.01	1.26	15.85**	2.44
2	Plant Height	55.72	64.03	0.522	172.35**	13.13
3	Number of Primary Branches per Plant	0.001	0.093	0.023	0.795**	0.196
4	Number of Cluster per Plant	0.619	0.031	0.195	5.972**	0.112
5	Number of Pods per Plant	0.025	1.587	0.019	77.66**	0.232
6	Pod Length	0.043	0.030	0.391	3.527**	0.064
7	Number of Seeds per Pod	0.020	0.087	0.045	1.891**	0.070
8	Seed Yield per Plant	0.015	2.010	0.028	19.373**	0.100
8	100- Seed Weight	0.002	0.220	0.004	2.158**	0.017
10	Germination Per cent	0.722	7.347	0.222	66.983**	1.410
11	Viability Per cent	3.722	5.013	4.055	54.347**	1.338
12	Specific Gravity	0.000	0.001	0.000	0.002**	0.000
13	Moisture content	0.010	0.006	0.012	1.778**	0.003
14	Soluble protein	0.069	0.088	0.007	17.125**	0.027
15	Crude Protein content	0.015	0.058	0.020	2.354**	0.056
16	Total Carbohydrate	0.327	0.532	0.083	37.257**	0.104
17	Total soluble sugar	0.006	0.194	0.006	2.055**	0.014
18	Fat	0.002	0.022	0.001	0.244**	0.003
19	Ash	0.003	0.194	0.007	1.077**	0.001
20	Total Free amino acids	0.017	0.144	0.018	0.229**	0.007
21	Phytate	0.002	0.047	0.003	0.387**	0.003
22	Polyphenol	0.251	0.956	0.058	472.32**	0.154
23	Methionine	0.001	0.008	0.002	0.179**	0.001
24	Calorific Value	0.114	0.009	0.221	3985.788**	2.428

Table 2: Genotypic, phenotypic variance, coefficient of variation, heritability (%) in broad sense and genetic advance for 13 morphological quantitative characters of mungbean.

S. No	Characters	Grand mean	Range		GCV	PCV	h^2 (%)	GA 5 %	GV	PV	CV %
			Min.	Max.							
1	Days to flowering	40.042	37.00	41.67	3.733	5.402	0.478	5.32	2.235	4.678	3.90
2	Number of branches/plant	6.069	5.62	6.85	5.204	8.972	0.336	6.22	0.100	0.297	7.31
3	Number of clusters/plant	6.593	4.40	8.17	14.989	15.832	0.896	29.23	0.977	1.089	5.10
4	Plant Height (cm)	56.190	46.45	64.27	9.168	11.210	0.669	15.44	26.536	39.673	6.45
5	Numbers of pod/ plant	17.683	11.77	22.43	20.316	20.498	0.982	41.48	12.906	13.138	2.73
6	Pod length (cm)	7.232	6.46	8.97	10.504	11.072	0.900	20.53	0.577	0.641	3.50
7	Number of seed/Pod	10.791	9.90	11.54	5.105	5.665	0.812	9.48	0.304	0.374	2.46
8	Moisture%	9.426	8.79	10.36	5.771	5.800	0.990	11.83	0.296	0.299	0.58
9	100 seed weight (g)	3.581	2.87	4.90	16.684	17.091	0.953	33.55	0.357	0.374	3.71
10	germination %	92.431	86.00	98.00	3.577	3.800	0.886	6.93	10.929	12.340	1.29
11	Viability%	91.264	85.33	97.17	3.257	3.495	0.868	6.25	8.835	10.173	1.27
12	Specific gravity	1.100	1.07	1.13	1.397	2.050	0.464	1.96	0.000	0.001	1.50
13	Seed yield/Plant (g)	6.805	4.51	11.38	26.338	26.749	0.970	53.42	3.212	3.313	4.67

Table 3: Genotypic, phenotypic variance, coefficient of variation, heritability (%) in broad sense and genetic advance for 11biochemical quantitative characters of mungbean

S. No	Characters	Mean	Range		GCV	PCV	h² (%)	GA 5%	GV	PV	CV %
			Min	Max							
1	Soluble Protein %	16.29	13.35	18.15	10.36	10.41	0.99	21.42	2.85	2.88	1.01
2	Crude Protein %	23.10	22.32	24.40	2.67	2.87	0.87	5.15	0.38	0.44	1.03
3	Carbohydrate %	61.34	56.92	64.48	4.06	4.09	0.98	8.29	6.19	6.30	0.53
4	Total Sugar %	3.74	3.22	4.61	15.59	15.91	0.96	31.46	0.34	0.35	3.17
5	Fat (%)	1.27	1.08	1.63	15.74	16.36	0.92	31.19	0.04	0.04	4.47
6	Ash%	3.55	2.50	3.94	11.92	11.98	0.99	24.43	0.17	0.18	1.20
7	Free Amino Acid %	1.21	0.92	1.57	15.90	17.37	0.84	29.99	0.04	0.04	6.98
8	Phytate mg/ g	16.20	1.22	2.20	15.61	16.00	0.95	31.37	0.06	0.07	3.51
9	Poly Phenol mg/100g	57.85	46.19	73.59	15.30	15.35	0.99	31.55	78.67	78.85	0.68
10	Methinine g/16gN	1.14	0.87	1.55	15.04	15.41	0.95	30.23	0.03	0.03	3.37
11	Calorific Value Kcal/100g	323.49	282.86	357.52	7.96	7.98	0.99	16.38	663.89	666.32	0.48

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