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SURPRISING PERFORMANCE OF GENOTYPES OBSERVED UNDER RAINFED CONDITION DURING STUDY OF GENETIC VARIABILITY, CORRELATION, PATH AND D² ANALYSIS IN MUNGBEAN (*VIGNA RADIATA* L. WILCZEK)

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ABSTRACT

Among all the environment stresses, drought causes the greatest losses in global agricultural production. About 80 percent area under pulses is rainfed in India. Rainfed regions of the country supports about 40% of human and 2/3rd of livestock population (DPD, 2025). Therefore, it holds promise for future food security because of the saturation of productivity in the green revolution regions. Deficit of sufficient genetic variability for high yield potential is one of the lacking factors for breakthrough in green gram production (Ramanujam, 1977).

The present investigation was carried out at the department of Genetics and Plant Breeding, College of Agriculture, Navsari Agricultural University, Bharuch campus during *Kharif*-2021 to identify trait specific genotypes best suited to rainfed condition and to develop mung bean improvement strategies through study of genetic variability, heritability, Genetic advance % of mean, genotypic and phenotypic correlation coefficients, path analysis, D^2 analysis studied for Seed yield and its 11 component traits.

CO 7 (COGG 912), though it is recommended for South Indian states with about 8.0 q/ha yield (DPD; 2025), surprisingly it performed best under rainfed condition at Bharuch location of Gujarat as it recorded highest seed yield/plant (14 q/ha) as well as highest no. of pods/plant (28.07), highest no. of clusters/plant (11.20) and highest no. of pods/cluster (7.73) also. CO 6 (COGG 902), released for all seasons in Tamil Nadu due to about 10.0 q/ha productivity (DPD; 2025), and TARM 2, recommended for *Rabi* cultivation in Eastern Vidarbha region due to 10-12 q/ha productivity (PDKV; 2025) *i.e.* both are not recommended for Gujarat though both ranked second and third respectively for seed yield/plant (both with 13.42 q/ha). HUM-1 (Malviya Jyoti), recommended for summer cultivation in Gujarat, Maharastra, Madhya Pradesh, Tamil Nadu and Karnataka (DPD; 2025) but in present investigation in *Kharif* season too, it yielded 12.95q/ha which was much more than its recommended yield (8-9 q/ha). Performance of TARM 18, released for Vidarbha region, (PDKV; 2025) was also amazing because in Gujarat condition also it was earliest to mature (72.67 days) and had tallest plant height (49.27 cm) and had heaviest 100-seed weight (3.58 g) as well. K 851, GM 4; both released and recommended for Gujarat state for both *Kharif* and Summer (KVK; 2023); but neither of it ranked first for seed yield or its any yield components (except for branches/plant by K 851). All the genotypes displayed wide range of variation in their mean performance with respect to all the traits evaluated. High heritability along with high to moderate genetic advance as % of mean were observed for seed yield per plant, branches per plant, clusters per plant and pods per plant. Highest genotypic correlation was found between pods/plant and clusters/plant followed by seeds/pod and plant height. Path analysis revealed that 100-seed weight followed by seeds/pod and days to 50% flowering had highest positive direct effect on seed yield per plant. Protein content followed by pod length (cm) and branches per plant contributed the most in overall genetic divergence in the experimental material.

Keywords: Rainfed, Genetic variability, Genetic advance, Correlation, Path analysis, Genetic divergence, Intra and Inter cluster distance.

Introduction

Among all the environment stresses, drought causes the greatest losses in global agricultural production. About 80 percent area under pulses is rainfed in India. Rainfed regions of the country supports about 40% of human and 2/3rd of livestock population (DPD, 2025). Therefore, it holds promise for future food security because of the saturation of productivity in the green revolution regions. Despite large strides made in improving productivity, a great number of poor families in Africa and Asia still face poverty, hunger, food insecurity and malnutrition where rainfed agriculture is the main agricultural activity. Mungbean [*Vigna radiata* (L.) Wilczek] is the third most important legume crop grown in India after chickpea and pigeon pea. It is also known as moong, moong bean, green bean, green gram and golden gram. Area, production and productivity of *Kharif* mungbean in India is about 31.74 lakh ha; 11.54 lakh tonnes and 364 kg/ha respectively (DIPL; 2023-24), while in Gujarat, it is about 55220 hectares, 33610 kg and 608.72 kg/ha respectively (DoA; GOG; 2024-25). Green gram has a rich nutritional profile, its 100g of mature grain contains, 1.2g of fat, 62.6g of carbohydrate, 16.3g dietary fiber and 347 kilocalories of energy (Majhi *et al.* 2020). It is a good source of minerals (calcium, iron, zinc, potassium and phosphorus) and vitamins (Folates, Vitamin K) and dietary fibers. Along with this, it is a staple source of plant-based protein in India completing a balanced human diet. It's average protein content is nearly 24 *per cent* which is rich in lysine, an essential amino acid for humans (Ramakrishnan *et al.,* 2018). Because of constant exploding population and increasing urbanization and constant decreasing cultivable land together with uncertainty of environments now food security in developing world is becoming serious issue. Scientist capture and store diversity in the form of germplasm or its part either *in vivo* or *in vitro* or both. To mitigate the challenge of food security at nation and global level under scenario of changing climatic conditions, scarcity of water resources, increasing population and urbanization, changing consumer demand/preference etc conservation and evaluation of genetic resources over diverse environments/locations require priority. Therefore, success of any breeding programme depends on the presence of genetic variability which forms the solid foundation of any crop improvement programme because response to selection is directly proportional to the variability exists. Overall seed yield per plant in mungbean is governed by multiple yield components, making it a quantitatively inherited trait. Therefore, plant breeders must understand the direction and size of correlations between different traits in order to attain the goal of enhancement in crop productivity. Exploring the link between yield and its components is crucial for understanding degree and direction of correlations which ultimately helps in selection. Traits that are positively correlated with yield are considered effective because selection for such traits would result in the simultaneous improvement in yield, the ultimate goal (Mahalakshmi *et al.*, 2005). The correlation coefficient may be confounded with indirect effect due to frequent association inherited in trait inter-relationship. The applicability of correlation can be more visibly understood by path analysis, which permits the partitioning of correlation into direct and indirect effects, thus would serve a valuable tool in breeding programmes (Dewey and Lu, 1959; Gomes and Lopes, 2005). In light of this, the current study planned to identify genotypes best suited to rainfed condition and to develop mungbean improvement strategies through study of genetic variability, correlation, path coefficient and D^2analysis. Seed yield and its 11 component traits were measured and GCV, PCV, H%, Genetic advance % of mean, genotypic and phenotypic correlation coefficients, path analysis, D^2 analysis were carried out.

Materials and Methods

Investigation was carried out under rainfed condition during *Kharif*-2021-22 at the College Farm (22.56^{O} N, 72.95^{o}E and MSL 15.64 m), College of Agriculture, Navsari Agricultural University, Bharuch campus, Gujarat, on eighteen mungbean genotypes planted in Randomized Block Design (RBD) with three replications. Important weather parameters as well as physio-chemical properties of experimental site is given in Table 1 & 2 respectively. Each genotype was presented by a row of fifteen plants, spaced at 45 cm x 15 cm apart. Healthy crop was raised by timely adoption of all recommended packages of practices. The observations were recorded for 12 most important traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), seeds per pod, 100-seed weight (g), seed yield per plant (g), crude protein content (%). In each replication, five plants per genotype were randomly selected and tagged to record observations and average value calculated for further analysis. However, the data on days to 50% flowering and days to maturity were recorded on a whole plot basis. The formulae utilized to estimate the genetic parameters are cited in Table 3 and their categorization is presented in Table 4.

Table 1 : Weather parameters during crop duration

Month	**Standard Week**	**Temperature (^oC)**		**Relative Humidity (%)**		**BSSH**	**Rainfall (mm)**	**Rainy Days**
		Max.	**Min.**	**Max.**	**Min.**			
August, 2021	33	33.9	26.3	81.0	60.4	4.5	22.4	1
	34	30.9	25.5	87.3	70.9	3.6	50.6	3
	35	31.9	25.8	91.0	70.3	4.8	33.0	3
September, 2021	36	31.3	25.6	90.3	73.7	1.9	69.8	7
	37	30.5	25.1	94.1	81.1	3.0	67.0	6
	38	29.9	25.0	89.1	81.6	2.1	95.8	6
	39	30.2	24.7	89.1	78.6	1.6	264.8	7
October, 2021	40	32.9	25.5	81.3	67.1	5.6	7.0	1
	41	34.7	5.9	85.6	64.4	4.9	8.4	1
	42	34.7	223	76.3	35.1	8.6	0.0	0
	43	34.7	20.7	72.4	37.3	8.9	0.0	0
	44	34.4	18.4	60.9	28.3	8.6	0.0	0
November, 2021	45	33.1	17.6	60.0	29.3	8.2	0.0	0
	46	32.7	18.5	60.0	42.6	7.2	0.0	0
	47	34.1	20.7	74.9	53.0	6.3	13.6	1
	48	32.1	16.9	72.7	52.6	7.0	37.6	1

Table 2 : Physio-chemical properties of soil

Soil characteristics	**Soil depth (0-15 cm)**	**Soil characteristics**	**Soil depth (0-15 cm)**
Mechanical analysis of soil		**Chemical analysis of soil**	
Coarse sand (%)	12.30	P^H2.5	7.32
Fine sand (%)	24.87	EC2.5 (dS/m)	0.40
Silt (%)	23.12	Organic carbon (%)	0.43
Clay (%)	39.48	CEC (cmol $(P^+)kg^{-1}$)	51.3
Textural class	Clay loam		
Physical analysis of soil		**Available macronutrient**	
Bulk density (g/cm^3)	1.33	N	287.6 kg/ha
		P_2O5	41.17 kg/ha
		K_2O	358.96 kg/ha

Table 3 : Estimates of genetic variability

Sr. No.	**Variability Estimates**	**Equation**	**Reference**
1.	Genotypic variance (σ^2e)	$\sigma^2 g = \frac{MSSt - MSSe}{\bar{X}} \times 100$	Lush (1940)
2.	Environmental variance (σ^2e)	$(\sigma^2e) = MSS(e)$	Lush (1940)
3.	Phenotypic variance (σ^2e)	$(\sigma^2e) = \sigma^2g + \sigma^2e$	Lush (1940)
4.	Genotypic Coefficient of Variation (GCV)	$GCV\% = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$	Burton (1952); Johnson *et al.* (1955a)
5.	Phenotypic Coefficient of Variation (PCV)	$PCV\% = \frac{\sqrt{\sigma^2_P}}{\bar{X}} \times 100$	Burton (1952); Johnson *et al.* (1955a)

6.	Heritability (h^2bs) (%)	$h^2(bs)\% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$	Lush (1940)
7.	Genetic advance (GA)	$GA = h^2(b) \times k \times \sigma_p$	Johnson *et al.* (1955b)
8.	Genetic Advance as per cent of Mean (GAM) (%)	$G.A.\ \text{as \% of mean} = \frac{G.A.}{\bar{X}} \times 100$	Johnson *et al.*(1955b)

Table 4 : Categorization of genetic estimates

Sr. No.	Estimates	Categories			References
		Low	Medium	High	
1.	GCV & PCV (%)	<10	10-20	>20	Sivasubramanian and Madhavamenon (1973)
2.	Heritability (h^2 bs) (%)	<30	30-60	>60	Johnson *et al* (1955b)
3.	GAM (%)	<10	10-20	>20	Johnson *et al* (1955b)

Genotypic correlation coefficient (r_g) and phenotypic correlation coefficient (r_p) were calculated using the procedure expounded by Miller *et al.* (1958). Path coefficient analysis was carried out as per the method suggested by Wright (1921) and Dewey and Lu (1959). Degree of correlations and direct effects were considered as follow.

Degree	Negligible	Low	Medium	High	Very High
Range	<0.100	0.100 to 0.249	0.250 to 0.500	0.501 to 0.749	> 0.750

The study of genetic divergence among genotypes was performed by employing Mahalanobis's D^2 statistics based on Tochers clustering method described by Rao (1952). Ranking (contribution) of individual traits towards total divergence was also calculated using formula [X=N*100/M] where X = *Per cent* contribution of trait, N = Number of genotype contributions where the trait ranked first and M = All possible combinations of the genotypes concerned.

Results and Discussion

India witnessed Green Revolution in wheat & rice but it also led to great coverage of very limited cultivars (boom) which simultaneously unconsciously germinated the problem of genetic erosion and extinction of adaptive genes (loss of land races). As per Freeman and Herron, 1998, genetic variability is not only prerequisite for initiating an effective and successful environment/location specific breeding programme but it is the soul of any population and species to survive over evolutionary periods of time through changing environments. It also provides opportunity to crop specialists to develop superior genotypes that includes both farmers and plant breeders' preferred traits like high productivity, earliness, bold seed, biotic-abiotic stress tolerance, high protein/oil, absence of anti-nutritional factors etc (Govindraj *et al.,* 2015).

Surprising performance of genotypes was observed because CO 7 (COGG 912), released for South Zone of country (DPD; 2025); though it found promising as it registered highest seed yield (9.45 g/pl i.e. 14.00 q/ha) as well as highest no. of clusters/plant (11.20), pods/cluster (7.73) and pods per plant (28.07) also in outside of its area of recommendation (Table 5). Traits related to early maturity are most desirable in unpredictable growing environments in general and rainfed condition in particular. This study segregated the genotypes for earliness also and depicted that TARM 18, recommended for general cultivation in *Kharif* season in Vidarbha (PDKV; 2025), was promising for earliness as it was earliest to flower (33.67) and earliest to mature as well (72.67) in Gujarat. For protein content, TARM 2, though released for *Rabi* season for eastern Vidarbha region (PDKV; 2025); recorded highest protein content (24.64%) and moreover it also ranked second for seed yield/plant (Table 5) in Gujarat *i.e.* outside of its recommended area and season as well. It was amazing that for seed yield/plant, all the top ranking three genotypes *viz*; CO 7 (COGG 912), CO 6 (COGG 902) and TARM 2 are released cultivars recommended for South zone, Tamil Nadu and eastern Vidarbha region respectively of the country but they performed best in rainfed condition in Gujarat also *i.e.* out of its recommended zone also. Except GM-4 and BPMR 145, it is observed that all other genotypes recorded higher seed yield than its recommended average seed yield while yield of Pant 4, PM-2, Virat, TARM-18, AKM 8802 nearly same as its recommended average seed yield. So, for further confirmation, their performance need thoroughly evaluation.

Under rainfed growing environment, the present investigation had given chance of selection of desirable types as it is evident from variation in the performance of genotypes for traits evaluated (Table 6). Seed yield/plant ranged from 5.96 g/plant (i.e. 8.83 q/ha) for to 9.45 g/plant (i.e. 14.00 q/ha) for with general mean of 7.77 g/plant (i.e. 11.60 q/ha). Days to maturity is very important trait that fits the crop for multiple cropping system. It ranged between 72.67 days (TARM 18) to 82.67 days (Pusa 1501) with mean maturity days of 78.11. India is predominantly vegetarian country so pulses are main source of protein for most of civilian of the country. General mean for Crude Protein Content across all the genotypes was 22.21 % with lowest content observed in CO 6 (20.16%) while highest protein content was recorded by TARM 2 (24.64%) [Fig. 1 & Table 6].

The traits *viz.,* Seed yield/plant, clusters/plant and branches/plant exhibited both moderate PCV as well as GCV (Table 7). Moderate value of GCV indicates the diverse performance of genotypes in rainfed condition and selection would be fruitful for further improvement of traits. Similar results for moderate PCV and GCV were reported by Narsimhulu *et al.* (2013), Jagdhane *et al.* (2017), and Marawar *et al.* (2020). Very negligible difference between PCV and GCV values observed for crude protein content, branches/plant and pod length thus suggesting environment has negligible role in the expression of these three traits (Table 7).

Low value of GCV was observed in Days to 50% flowering and days to maturity. It emphasized prevalence of non-additive gene action in the heredity of these traits. Hybridization in bi-parental fashion should be practiced for further elevating these traits. Earlier Prassanna *et al.* (2013), Salman and Anuradha (2020) and Singh *et al.* (2021) revealed low estimate of GCV for days to 50 % flowering and days to maturity.

Estimates of heritability provide very important information to breeders in assessing the heritable proportion of variation. When heritability of a trait is high (>60%), selection responds well for further developing superior genotype/s because of smaller contribution of the environment to the phenotype; but when heritability of a trait is low (<30%), selection may be misleading due to hiding effect of environment. In the investigation, it was amazing that neither of trait manifested low heritability. Four traits *viz;* branches per plant (78.32%), protein content (71.36%), seed yield per plant (62.36%) and 100-seed weight (61.19%) manifested high heritability (Table 7). Rest of all the traits recorded moderate heritability. Similar results were also observed earlier by Prassanna *et al.* (2013), Salman and Anuradha (2020) and Singh *et al.* (2021). To measure the extent of genetic improvement achieved in the selected population over the base population for the trait concerned genetic advance was also calculated. Heritability estimates alone do not provide complete information on the amount of genetic progress and Johnson *et al.* (1955a) demonstrated that heritability and genetic advance jointly would be more useful for the reliable conclusion of selecting the best genotype. Therefore, genetic advance as a percentage of mean (GAM) was calculated in order to check the relative merits of different traits in mung bean improvement programme/s. Seed yield/plant, branches/plant and 100-seed weight manifested moderate to high genetic advance % of mean together with high heritability (Table 7). This clears the picture that these traits are dominated by fixable genetic variance (additive gene action) so in the present investigation selection method of breeding can be rewarding for generating superior genotypes which will be adapted/suited to rainfed condition. Earlier parallel output was reported by Salman and Anuradha (2020) and Singh *et al.* (2021). Clusters/plant, Plant height, pods/cluster and pods/plant possessed moderate heritability as well as moderate genetic advance as % of mean (Table 7). Similar findings were earlier observed by Pandey *et al.* (2007) and Singh *et al.* (2021). Moderate genetic advance indicates involvement of both fixable (additive) as well as non-fixable (non additive) gene action in the expression of these traits. Under such condition, biparental mating will be ideal strategy to utilize both fixable (additive) and non-fixable (non additive) genetic behavior.

As per Grafius, 1978; there may not be genes for yield *per se* but rather for the various components, the multiplicative interactions among them result into the artifact of yield. Pulses crops in general and mungbean in particular; yield is resultant product of summation of its component's traits like no. of branches/plant, no. of pods/plant, no. of seeds/pod, 100-seed weight, pod length etc. These components are mostly polygenic in nature so yield has more complex type of inheritance. This creates more challenge in rainfed condition because of uncertainty of enough moisture. So, for increasing seed yield, it is necessary to know the amount of genetic association among participating component traits as well as between individual component trait with seed yield. Total 66 correlations obtained each at genotypic and phenotypic levels. Among it, 30 correlations found significant and desirable while 3 correlations were significant and undesirable (Table 8). For days to 50% flowering and days to maturity negative correlation was desirable as they impart earliness and for rest of traits positive correlation taken as desirable. In mungbean there is no question of logging, so positive correlation was considered as desirable. Highest genetic correlation was found between clusters/plant x Pods/plant (0.925) followed by plant height x seeds/pod (0.897) and clusters/plant x seeds/pod (0.770). Seed yield is the most economic important traits and for that pods/plant (0.758) followed by clusters/plant (0.678) and seeds/pod (0.606) had highest positive and significant genotypic correlation. Positive association among components and between component and seed yield were earlier experienced by Asari *et al.* (2019), Agbeleye *et al.* (2021), Dash *et al.* (2021), Joshi *et al.* (2021) and Kumar *et al*. (2021).

Many times, strong genotypic correlation between seed yield and its components observed is due to association *via* other component traits. Under such circumstances value of genotypic correlation is not giving true information of direct association of component trait with seed yield/plant. Path coefficient analysis gives information about cause-and-effect situations so it provides more realistic pictures of interrelationships among seed yield and its components. It is carried out to partition the genotypic and phenotypic correlation coefficients of seed yield with its contributing traits into direct and indirect effects by taking seed yield as a dependent variable and other components as independent variables (Table 9). Through path analysis, it was clear that 100-seed weight (0.877) had highest direct association with seed yield/plant followed by seeds/pod (0.752) and days to 50% flowering (0.551). Asari *et al.* (2019) for days to 50% flowering.; Joshi *et al.* (2021) for 100-seed weight and days 50% flowering while Dash *et al.* (2021) for seeds/pod reported similar findings. It is surprising that direct association of important yield components *viz*; plant height (-0.381), pods/plant (-0.213) and pods/cluster (-0.192) with seed yield/plant was negative though all these three traits had significant and desirable genotypic correlation with seed yield/plant (Table 7). This indicates the usefulness of study of path analysis. Comparable outcomes were revealed by Parihar *et al*. (2018) for plant height and pods/plant; Asari *et al.* (2019) for pods/plant; Joshi *et al.* (2021) for plant height and protein content; Singh *et al.* (2021) for pods/cluster, pods/plant and protein content.

Not only study of variability but generating broad spectrum of variability that possess transgressive segregants is the heart of crop improvement programme. For developing high heterotic hybrids, first it is necessary to quantify the degree of divergence between different genotypes by study of genetic diversity analysis and then selecting parents with maximum genetic distance. Mahalanobis (1936) defined the distance between two populations as D^2 which was obtained by Tochers method. Contribution of individual traits towards divergence was estimated according to the method described by Singh and Chandhary (1985). Result revealed that all the genotypes grouped into four different non-overlapping clusters (Table 10). Grouping of the genotypes into different clusters was done by using Ward's minimum variance method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should be at least on an average show a smaller D^2 value among themselves than those belonging to different clusters. Highest intra cluster distance was found for Cluster I (7.10) which comprises of 11 genotypes (Table 11) followed by Cluster II (6.88) which had 5 genotypes. Cluster III & IV are mono genotypic and hence their intra cluster distance was 0.0 but it was surprising that the highest inter cluster distance was recorded between Cluster III and Cluster IV (13.32), both with single genotypes, followed by Cluster I and IV (10.94) and Cluster II and IV (10.27).

The *Per cent* contribution of twelve traits towards total divergence was also analyzed and shown in Table 12. Among all the traits, crude protein content contributed the maximum (33.33 %) to the diversity by taking first rank with 51 times out of 153 combinations, followed by Pod length (20.92% with 32 times first rank) and branches/plant (11.76 % with 18 times first rank). Days to 50 per cent flowering had no contribution towards genetic divergence.

It was interesting that, for every trait, cluster mean values were not same but different from each other except for clusters/plant for Cluster I & IV. This indicated that diverse performance of genotypes resulted into diversity among cluster means. Cluster IV was best for traits *viz*; days to 50% flowering, days to maturity, Plant height, branches per plant, pod length and 100-seed weight (Table 12). Genotypes of Cluster I reported most dwarf plant while highest crude protein content was manifested by cluster II. Cluster III (that comprise of only COGG 912/CO7) was best for seed yield/plant, clusters/plant, pods/cluster, pods/plant and seeds/pod. It was very surprising that top three genotypes for seed yield/plant, clusters/plant, pods/plant, seeds/pod and days to maturity comes from different clusters (Table 13). This type of distribution is best to improve trait/s because it can facilitate the hybridization between top performing genotypes that simultaneously possess high diversity also so it can be helpful in the production of high heterotic hybrids that have high potential for generating transgressive segregants in segregating generation/s.

Conclusion

CO 7 (COGG 912), with highest seed yield, highest no. of pods/plant, highest no. of pods/cluster and highest no. of clusters/plant and TARM 18, with earliest to mature and also had heaviest 100-seed weight (Table 6), emerged as most promising genotypes under rainfed situation. Surprisingly both these varieties are not released for Gujarat. So their promising performance need to be tested thoroughly over locations and seasons. Amazingly these genotypes are also among Cluster III & IV having maximum inter cluster distance (Table 10 & 11). So not only selection but crossing between CO 7 and TARM 18 may yield better transgressive segregants that may be adapted better to rainfed condition. Moreover traits *viz*; Pods/plant, pods/cluster, cluster/plant, pod length are equally under control of additive and non-additive gene actions so to develop early varieties (as it is prerequisite for rainfed agriculture) with high seed yield and high and desirable mean values for important yield components, crossing of CO-7 X TARM-2, CO 7 X Kopergaon, Kopergaon X K851 and CO 7 X K851 will be most rewarding as each participating genotype in hybridization had highest mean value for seed yield or its components *viz;* CO 7 best for high seed yield (9.45 g/pl.), pods/plant (28.07), clusters/plant (11.20) and pods/cluster (7.73); Kopergaon had longest pod (8.05 cm) while K 851 registered highest no. of branches/plant (6.60). Moreover, they also fall into clusters with wider inter-cluster distance (Table 10 & 11) so they may provide best scope to obtained transgressive segregants. Biparental mating will be best strategic option to utilize both additive and non-additive gene actions and it may generate promising genotype/s adapted to rainfed situation through transgressive segregation. 100-seed weight (0.877) had highest direct association with seed yield/plant followed by seeds/pod (0.752) and days to 50% flowering (0.551). It is surprising that direct association of important yield components *viz*; plant height (-0.381), pods/plant (-0.213) and pods/cluster (-0.192) with seed yield/plant was negative though all these three traits had significant and desirable (positive) genotypic correlation with seed yield/plant. Crude protein content contributed the maximum (33.33 %) to the diversity followed by Pod length (20.92 %) and branches/plant (11.76 %).

Table 5: Surprising performance of genotypes for different traits

Sr. No.	Genotypes	Seed Yield (q/ha)	Recommended area of Genotype/ Variety	Recommended average seed yield (q/ha)	Reference	Remarks (Performance during study)
1	CO 7 (COGG 912)	14.00	Kharif cultivation in South Zone of India	8.0	DPD; 2025 https://masujournal.org/	Highest seed yield/plant as well as no. of clusters/plant, pods/cluster, pods/plant
2	CO 6 (COGG 902)	13.42	Suitable for all season cultivation in Tamil Nadu	10.0	DPD; 2025	Second highest for seed yield
3	TARM 2	13.42	Rabi cultivation in Eastern Vidarbha region	10-12	PDKV; 2025	Highest protein content, Highest seeds/pod, Second highest for seed yield, Late to flower
4	HUM 1 (Malviya Jyoti)	12.95	Summer cultivation in Gujarat, Maharashtra, Madhya Pradesh, Tamil Nadu & Karnataka	8-9	DPD; 2025	-
5	Pant 4 (UPM-92-1)	12.77	Eastern UP and North-East plains zone (Assam, Bihar & West Bengal) of the country	12-15	https://www.gbpuat.res.in/ DPD; 2025	-
6	Vaibhav (PHULE M-9339)	12.65	Suitable for Kharif planting in all the districts of Maharashtra	10-12 (Average) 12-14 (Potential)	https://mpkv.ac.in/ Uploads/	-
7	K 851	12.37	Well adapted to whole Northern India & Summer all over India	10-12	https://idl-bnc-idrc.dspacedirect.org/ https://kvk.icar.gov.in	Highest no. of branches/plant

8	Virat (IPM 205-7)	12.21	Summer cultivation in Punjab, Haryana, Uttar Pradesh, Karnataka, Tamil Nadu, Madhya Pradesh, Gujarat	13-15	https://iipr.icar.gov.in/ https://seednet.gov.in	-
9	TARM-18	11.57	*Kharif* cultivation in Vidarbha region	10-12	PDKV; 2025	Earliest to flower as well as mature, highest test weight, Tallest plant height
10	AKM 8803	11.57	*Kharif* cultivation in Vidarbha region	9-10	PDKV; 2025	-
11	OUM 11-5 (Kamadeva)	11.47	*Kharif* cultivation in South Zone	7.0	DPD; 2025	-
12	PM 2	11.26	Uttar Pradesh and plains of Uttara Khand for *Kharif* and *Zaid* (specially suitable for late sowing in *Kharif*)	10-12	https://www.gbpuat.res.in	-
13	RMG 62	10.71	Rajasthan	7.0	http://farmer.gov.in	Most dwarf plant
14	Kopergaon	10.53	Suitable for Summer in Madhya Pradesh & Maharashtra	5-6	https://idl-bnc-idrc.dspacedirect.org http://farmer.gov.in	Highest pod length
15	Pusa 1501	10.19	-	-	-	Longest to mature
16	AKM 8802 (PKV Moong)	10.01	Kharif cultivation in Vidarbha region	10-11	PDKV; 2025	-
17	GM 4	8.84	Summer & Kharif in Gujarat, Rajasthan	12-13	https://kvk.icar.gov.in https://www.dpd.gov.in/	-
18	BPMR 145	8.83	All season cultivation in Maharashtra	12-14	https://www.vnmkv.ac.in/ http://farmer.gov.in/image default/ https://www.appjpds.org/	-

Table 6: Mean value of seed yield and its components in mung bean

Ranking for SYP	**Genotypes**	**SYP (g)**	**SYP (q/ha)**	**DF**	**DM**	**PH (cm)**	**BP**	**CP**	**PC**	**PP**	**PL (cm)**	**SP**	**TW (g)**	**CPC (%)**
1	CO 7	**9.45**	**14.00**	36.67	78.67	42.45	5.60	**11.20**	**7.73**	**28.07**	7.49	14.27	2.83	23.30
2	CO 6	9.06	13.42	36.00	77.67	43.06	5.33	10.67	6.47	26.47	7.27	14.43	3.40	20.16
3	TARM 2	9.06	13.42	37.67	77.33	44.67	4.73	9.80	7.13	26.13	7.41	**14.60**	3.41	**24.64**
4	HUM 1	8.74	12.95	37.00	74.33	46.75	4.93	9.80	7.07	27.03	7.55	14.07	3.35	23.19
5	Pant 4	8.62	12.77	34.00	79.00	43.30	5.13	9.80	6.80	22.87	7.51	14.27	3.28	21.74
6	Vaibhav	8.54	12.65	34.33	78.33	39.52	5.60	10.07	6.47	26.27	7.87	12.33	3.36	20.72
7	K 851	8.35	12.37	36.00	80.00	42.71	**6.60**	9.87	6.73	25.70	7.22	13.53	3.36	21.84
8	Virat	8.24	12.21	34.00	75.67	36.45	4.67	9.27	6.53	24.93	7.50	12.87	3.38	21.47
9	TARM 18	7.81	11.57	**33.67**	**72.67**	**49.27**	5.93	9.73	5.67	23.27	7.98	13.07	**3.58**	22.91
10	AKM 8803	7.81	11.57	35.67	79.33	38.25	5.87	9.07	7.33	27.27	7.39	13.07	3.01	21.68
11	OUM 11-5	7.74	11.47	35.33	77.33	38.38	4.93	11.13	6.80	24.67	7.83	14.20	3.34	24.38
12	PM 2	7.60	11.26	34.00	82.00	40.60	5.60	9.67	6.60	25.60	7.98	13.27	3.33	21.19
13	RMG 62	7.23	10.71	36.00	75.00	**34.70**	5.07	9.60	6.27	25.93	6.84	12.53	3.26	21.90
14	Kopergaon	7.11	10.53	35.33	79.67	34.81	5.60	9.00	7.47	24.87	**8.05**	12.73	3.35	21.63
15	Pusa 1501	6.88	10.19	36.33	82.67	39.78	6.13	9.93	5.47	21.33	7.50	13.80	2.66	22.79
16	AKM 8802	6.76	10.02	34.67	79.67	39.52	4.73	7.33	6.13	20.47	6.75	11.13	3.01	22.75
17	GM 4	5.97	8.84	35.33	79.33	45.15	4.47	6.27	6.20	18.20	7.26	12.67	3.30	22.59
18	BPMR 145	5.96	8.83	35.33	77.33	40.46	4.93	10.07	6.87	26.00	7.46	14.07	2.47	20.86
	CV%	9.31	9.31	3.15	3.03	8.12	5.46	9.29	8.32	8.18	4.24	6.53	6.61	3.25
	Minimum	5.96 (BPMR	8.83 (BPMR	33.67 (TARM18)	72.67 (TARM	34.70 (RMG	4.47 (GM	6.27 (GM	5.47 (Pusa	18.20 (GM-	6.75 (AKM	11.13 (AKM	2.47 (BPMR	20.16 (CO 6)

		145)	145)		18)	62)	4)	4)	1501)	4)	8802)	8802)	145)
	Maximum	9.45 (CO 7)	14.00 (CO 7)	37.67 (TARM 2)	82.67 (Pusa 1501)	49.27 (TARM 18)	6.60 (K851)	11.20 (CO 7)	7.73 (CO 7)	28.07 (CO 7)	8.05 (Koper-gaon)	14.60 (TARM 2)	3.58 (TARM 18)	24.64 (TARM 2)
	Mean	7.77	11.60	35.41	78.11	41.10	5.33	9.57	6.65	24.73	7.49	13.38	3.20	22.21

SYP = Seed Yield/Plant (g); DF = Dayes to 50% Flowering; DM = Days to Maturity; PH = Plant Height (cm);
BP = No. of Branches/Plant; CP = No. of Clusters/Plant; PC = No. of Pods/Cluster PP = No. of Pods/Plant
PL = Pod Length (cm); SP = No. of Seeds/Pod; TW = 100-Seed Weight (g); CPC = Crude Protein Content

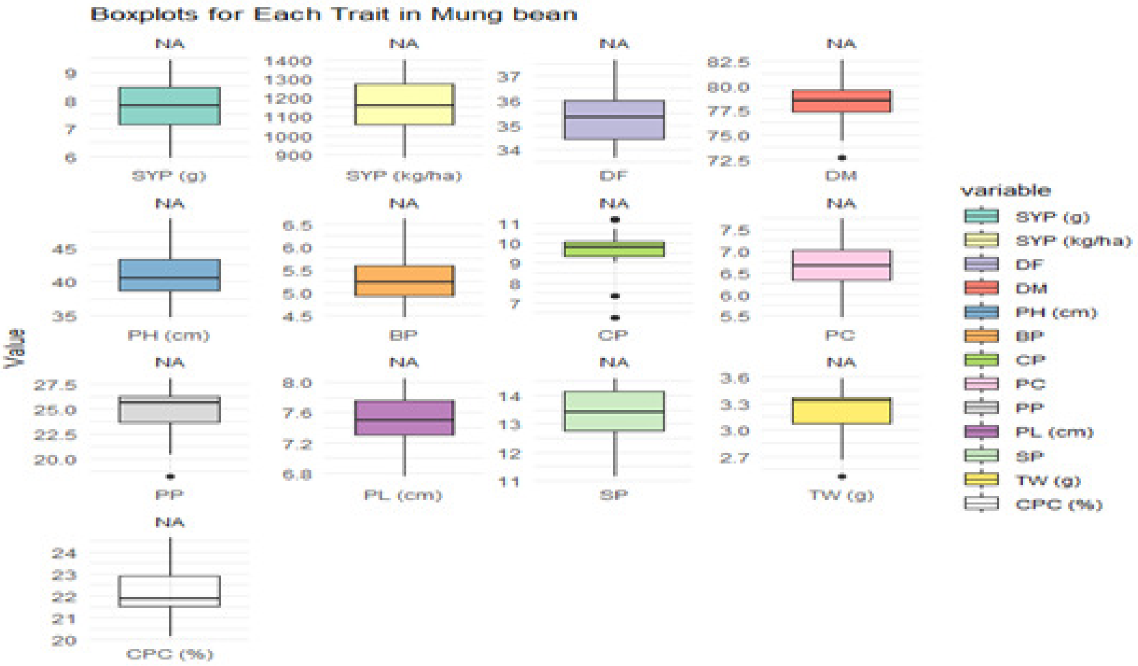

Fig.1: Mean values for seed yield and its components using boxplot technique in mungbean

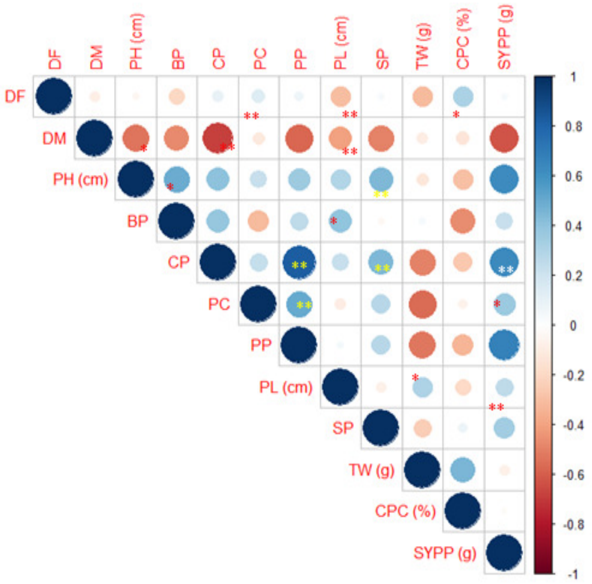

Fig. 2: Status of genotypic correlations among seed yield and its components in mumg bean

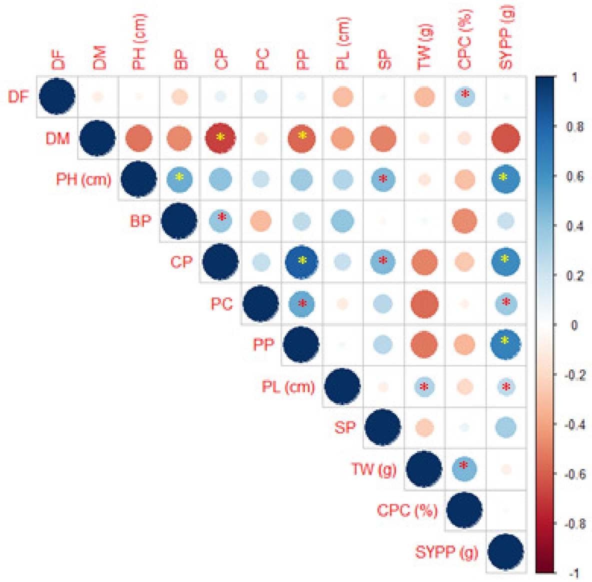

Fig. 3: Status of phenotypic correlations among seed yield and its components in mumg bean

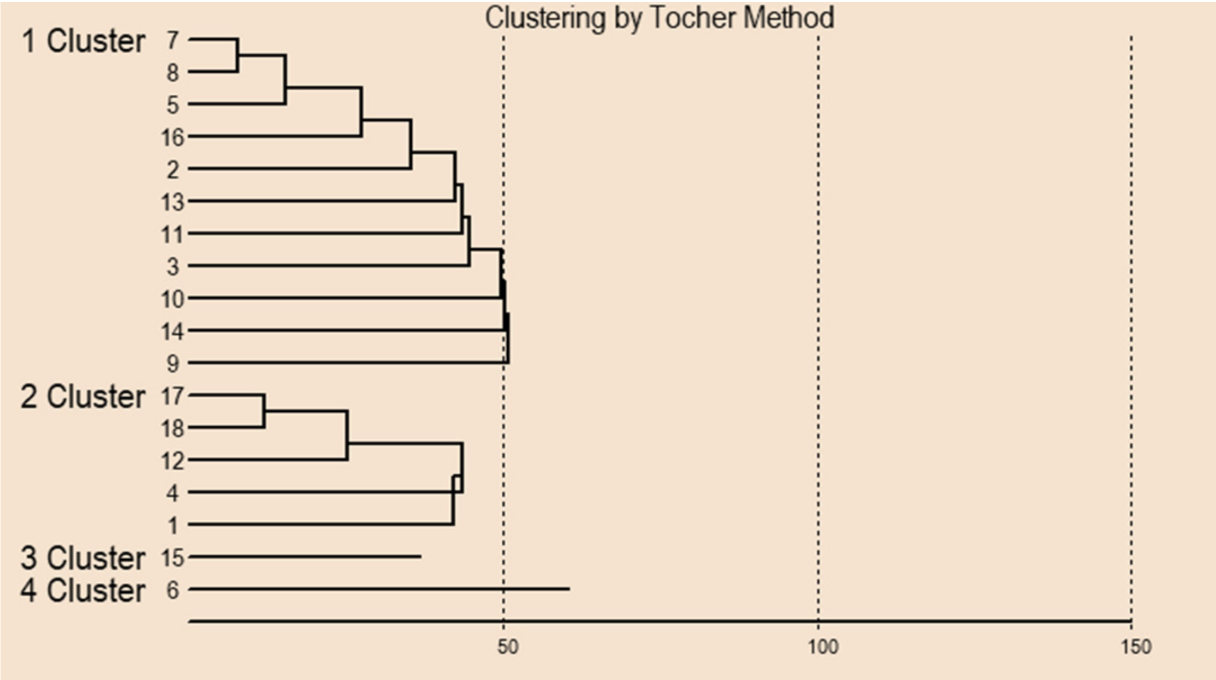

Fig. 4: Cluster diagram of mungbean genotypes by Tocher's method

Fig 4. Genotype No. :

1. GM-4	2. K-851	3. BPMR-145	4. AKM-8802	5. Kopergaon	6. TARM-18	7. PM-2
8. Vaibhav	9. RMG-2	10. Virat	11. Pant-4	12. OUM 11-5	13. Pusa-1501	14. CO-6
15. CO-7	16. AKM-8803	17. TARM-2	18. HUM-1			

Table 7 : Range, mean along with components of variance and heritability for twelve traits in mungbean

Sr. No.	Traits	Range		Mean	GCV (%)	PCV (%)	Heritability Broad Sense (%)	Genetic Advance	Genetic Advance (% of mean)
		Minimum	Maximum						
1.	Days to 50% flowering	33.67 (TARM18)	37.67 (TARM 2)	35.41	2.64	4.11	41.35	1.24	3.50
2.	Days to maturity	72.67 (TARM 18)	82.67 (Pusa 1501)	78.11	2.74	4.09	45.01	2.96	3.79
3.	Plant height (cm)	34.70 (RMG 62)	49.27 (TARM 18)	41.10	8.41	11.68	51.76	5.12	12.46
4.	Branches per plant	4.47 (GM 4)	6.60 (K851)	5.33	10.38	11.73	78.32	1.01	18.93
5.	Clusters per plant	6.27 (GM 4)	11.20 (CO 7)	9.57	11.14	14.50	58.98	1.69	17.62
6.	Pods per cluster	5.47 (Pusa 1501)	7.73 (CO 7)	6.65	7.42	11.15	44.34	0.68	10.18
7.	Pods per plant	18.20 (GM-4)	28.07 (CO 7)	24.73	9.29	12.38	56.34	3.35	14.37
8.	Pod length (cm)	6.75 (AKM 8802)	8.05 (Kopergaon)	7.49	4.14	5.93	48.81	0.45	5.96
9.	Seeds per pod	11.13 (AKM 8802)	14.60 (TARM 2)	13.38	5.71	8.67	43.32	1.04	7.74
10.	100-seed weight (g)	2.47 (BPMR 145)	3.58 (TARM 18)	3.20	8.30	10.61	61.19	0.43	13.38
11.	Seed yield per plant (g)	5.96 (BPMR 145)	9.45 (CO 7)	7.83	11.98	15.18	62.36	1.53	19.50
12.	Crude protein content (%)	20.16 (CO 6)	24.64 (TARM 2)	22.21	5.12	6.06	71.36	1.98	8.91

Table 8 : Genotypic and phenotypic correlations of seed yield per plant with its components in mung bean

Traits		**Days to 50% flowering**	*Days to maturity*	**Plant height (cm)**	**Branches /plant**	**Clusters /plant**	**Pods/ cluster**	**Pods /plant**	**Pod length (cm)**	**Seeds /pod**	**100-seed weight (g)**	**Crude protein content (%)**
Seed yield/plant (g)	r_g	0.295	-0.253	0.463	0.201	0.678 **	0.572*	0.758**	0.303	0.606**	0.161	0.245
	r_p	0.181	-0.184	0.501**	0.192	0.458**	0.328 *	0.493 **	0.272 *	0.257	0.179	0.202
Days to 50% flowering	r_g	1	-0.381	0.214	-0.042	0.273	0.620**	0.465	-0.631**	0.310	-0.189	0.585*
	r_p	1	-0.019	0.138	0.024	0.161	0.152	0.120	-0.002	0.092	-0.094	0.291 *
Days to maturity	r_g		1	-0.475 *	-0.378	-0.641**	0.291	-0.423	-0.611 **	-0.371	-0.151	-0.328
	r_p		1	-0.195	-0.212	-0.337 *	0.004	-0.292 *	-0.159	-0.215	-0.090	-0.117
Plant height (cm)	r_g			1	0.547*	0.462	0.411	0.268	0.387	0.897 **	-0.012	0.065
	r_p			1	0.363 **	0.242	0.251	0.216	0.256	0.346*	0.065	-0.019
Branches/plant	r_g				1	0.430	-0.034	0.356	0.506 *	0.143	0.173	-0.259
	r_p				1	0.277*	-0.103	0.187	0.257	0.027	0.110	-0.151
Clusters/plant	r_g					1	0.428	**0.925****	0.453	0.770**	-0.107	0.033
	r_p					1	0.136	0.598**	0.258	0.334*	-0.227	0.018
Pods/cluster	r_g						1	0.657**	0.185	0.219	-0.442	0.044
	r_p						1	0.386**	0.127	0.222	-0.218	0.118
Pods/plant	r_g							1	0.321	0.236	-0.355	-0.143
	r_p							1	0.070	0.149	-0.171	-0.087
Pod length (cm)	r_g								1	0.031	0.536*	0.032
	r_p								1	0.044	0.279*	0.009
Seeds/pod	r_g									1	-0.174	0.178
	r_p									1	-0.021	0.163
100-seed weight	r_g										1	0.451
	r_p										1	0.361**
Crude protein content	r_g											1
	r_p											1

** Significant at 1% level; * Significant at 5% level

Table 9 : Direct and Indirect effects of twelve causal variables on seed yield per plant in mung bean

Traits	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Branches per plant**	**Clusters per plant**	**Pods per cluster**	**Pods per plant**	**Pod length (cm)**	**Seeds per pod**	**100 seed weight (g)**	**Crude protein content (%)**	**Seed yield per plant (g)**
Days to 50% flowering	**0.551**	-0.032	0.049	-0.023	0.151	0.342	0.264	-0.357	0.383	-0.172	0.323	0.350**
Days to maturity	-0.001	**0.025**	-0.009	0.011	-0.006	0.004	-0.008	-0.001	-0.003	-0.012	-0.007	-0.282*
Plant height (cm)	-0.033	0.147	**-0.381**	-0.001	-0.029	0.129	0.077	-0.039	-0.020	-0.115	-0.137	0.345*
Branches per plant	-0.002	0.025	0.001	**0.061**	0.026	-0.002	0.020	0.021	0.008	-0.004	-0.016	0.217^{NS}
Clusters per plant	0.051	-0.044	0.014	0.080	**0.186**	0.079	0.165	0.086	0.161	-0.003	0.006	0.714**
Pods per cluster	-0.119	-0.034	0.065	0.006	-0.082	**-0.192**	-0.149	-0.034	-0.100	0.021	-0.008	0.492**
Pods per plant	-0.102	0.068	0.043	-0.070	-0.189	-0.166	**-0.213**	-0.069	-0.126	-0.006	0.041	0.728**
Pod length (cm)	-0.046	-0.003	0.007	0.025	0.033	0.013	0.023	**0.072**	0.015	0.019	-0.002	0.082^{NS}
Seeds per pod	0.521	-0.098	0.411	0.104	0.650	0.393	0.443	0.157	**0.752**	-0.143	0.212	0.621**
100-seed weight (g)	-0.273	-0.424	0.265	-0.061	-0.014	-0.094	0.026	0.239	-0.166	**0.877**	0.039	0.429**
Protein content (%)	-0.195	0.089	-0.119	0.086	-0.011	-0.015	0.065	0.008	-0.094	-0.015	**-0.333**	0.117^{NS}

Bold figures indicates Direct effects ** Significant at 1% level * Significant at 5% level; Residual effect= 0. 469

Table 10: Distribution of genotypes of mung bean in different Clusters as per the Tocher's method

Cluster	**No. of genotypes**	**Genotypes included**
I	11	PM 2, Vaibhav, Kopergaon, AKM 8802, K 851, PUSA 1501, PANT 4, BPMR 145, Virat, CO 6, RMG 62
II	5	TARM 2, HUM 1, OUM 11-5, AKM 8802, GM 4
III	1	CO 7
IV	1	TARM 18

Table 11 : Intra and inter-cluster distances amongst different genotypes in mung bean

Cluster	I	II	III	IV
I	**7.10**	9.72	7.95	10.94
II	9.72	**6.88**	9.38	10.27
III	7.95	9.38	**0.00**	13.32
IV	10.94	10.27	13.32	**0.00**

Table 12 : Cluster mean and independent trait contribution towards total divergence

Sr. No.	Traits	Times ranked first	Contribution of traits (%)	Mean of Cluster			
				I	II	III	IV
1	Days to 50% flowering	0	0.00 %	35.18	36.00	36.67	33.67
2	Days to maturity	1	0.65 %	78.79	77.60	78.67	72.67
3	Plant height (cm)	3	1.96 %	39.42	42.89	42.45	49.27
4	Branches per plant	18	11.76 %	5.50	4.76	5.60	5.93
5	Clusters per plant	2	1.31 %	9.73	8.87	11.20	9.73
6	Pods per cluster	14	9.15 %	6.64	6.67	7.73	5.67
7	Pods per plant	2	1.31 %	25.20	23.30	28.07	23.27
8	Pod length (cm)	32	20.92 %	7.51	7.36	7.49	7.98
9	Seeds per pod	9	5.88 %	13.35	13.33	14.27	13.07
10	Seed yield per plant (g)	6	3.92%	7.76	7.65	9.45	7.81
11	100 – seed weight	15	9.80 %	3.17	3.28	2.83	3.58
12	Protein content (%)	51	33.33 %	21.45	23.51	23.30	22.91

Table 13 : Gene action, degree and direction of correlation and direct effect on seed yield and top three genotypes for each traits

Sr. No.	Traits	Gene action	Correlation with Seed yield/Plant	Direction & Degree of direct effect on SYP	Significant and desirable correlation with other traits	Top three Genotypes & (Cluster No.)
1.	Days to 50% flowering	Non additive	Moderate Significant, Undesirable	Undesirable, High	PL, TW	TARM 18 (IV), PM 2 (I), Virat (I), PM 4 (I)
2.	Days to maturity	Non additive	Moderate, Significant, Desirable,	Desirable, Negligible	TW, PH, PP, SYP	TARM 18 (IV), HUM 1 (II), RMG 62 (I)
3.	Plant height (cm)	Both Additive & Non Additive	Moderate, Significant, Desirable	Undesirable, Moderate	SP, DM, CPC, SYP, TW	TARM 18 (IV), HUM 1 (II), GM 4 (II)
4.	Branches/ Plant	Additive	Moderate, Non-significant, Desirable	Desirable, Negligible	CP, PP, PL	K 851 (I), Pusa 1501 (I), TARM 18 (IV)
5.	Clusters/ Plant	Both Additive & Non Additive	High, Significant, Desirable	Desirable, Low	PP, SP, SYP, PL, BP, PC	CO 7 (III), OUM 11-5 (II), CO 6 (I)
6.	Pods/ Cluster	Both Additive & Non Additive	Moderate, Significant, Desirable	Undesirable, Low	PP, SP, SYP, CP	CO 7 (III), Kopergaon (I), AKM 8803 (I)
7.	Pods/Plant	Both Additive & Non Additive	High, Significant, Desirable	Undesirable, Low	CP, PC, SYP, SP, BP, PL, DM	CO 7 (III), AKM 8803 (I), HUM 1 (II)
8.	Pod length (cm)	Non additive	Negligible, onsignificant, Desirable	Desirable, Negligible	CP, BP, PP	Kopergaon (I), TARM 18 (IV), PM 2 (I)
9.	Seeds/Pod	Non additive	High, Significant, Desirable	Desirable, Very High	CP, SYP, PP, PH, PC, CPC	TARM 2 (II), CO 6 (I), CO 7 (III), PM 4 (I)
10.	100-seed weight (g)	Additive	Moderate, Significant, Desirable	Desirable, Very High	SYP, PH	TARM 18 (IV), TARM 2 (II), CO 6 (I)
11.	Seed yield/ Plant (g)	Additive	-	-	PP, CP, SP, PC, TW, PH, DM	CO 7 (III), CO 6 (I) TARM 2 (II)
12.	Crude Protein Content (%)	Both Additive & Non Additive	Desirable, Non-significant, Low	Undesirable, Moderate	PH, SP	TARM 2 (II), OUM 11-5 (II), CO 7 (III)

Conflict of interest

The authors do not have any direct or indirect intense for conflict of interest.

Author contributions

K.N. Chaudhari and R. K. Kalaria conceived and designed the experiment. H.D. Pandya, K.P. Kapadia, K.G. Baria and Naresh Chaudhary collected the data. H.D. Pandya, K.G. Baria and K.P. Kapadia performed the analysis. K. N. Chaudhari wrote the research article and P.G. Bagadiya, Kush Jani prepared diagramme.

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References

Agbeleye, O. A., Akinyosoye, S. T. and Adetumbi, J. A. (2021). Correlation, path coefficient and principal component analysis of yield components in mungbean [*Vigna radiata* (L.) Wilcezk] accessions. *Trop. Agric.*, ***97*** (4).

*Allard, R. W. (1960). *"Principles Pl. Breed.,"* John Wiley and Sons. Inc., New York. Pp: 85-95.

Asari, T., Patel, B. N., Patel, R., Patil, G. B. and Solanki, C. (2019). Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mungbean [*Vigna radiata* (L.) Wilczek]. *Ind. J. Chem. Stud.,***7**(4):383-387.

Datanet India Private Limited. (2023-24). India Stat focused on facts. DOI: https://indiastat.com.

Department of Agriculture, Government of Gujarat (2024-25). Area, production, productivity of agricultural crops in Gujarat. DOI: https://dag.gujarat.gov.in/

*Burton, G. W. and Dewane, E. H. (1953). Estimating heritability in tall Fasciae (*Fescuta arundinacea* L.) from replicated clonal material. *Agron. J.*, **45**: 478-481.

Dash, Sasmita., D.L., Tripathy, S.K. and Dash, M. (2021). Assessment of genetic variation and heritability for morpho-agronomic traits in mungbean germplasm under cold stress. *Biological Forum – An Int. J.*, **13** (3): 163-167.

*Dewey, J. R. and Lu, K.H. (1959). A correlation and path coefficient analysis of component of crested wheat seed production. *Agron. J.*, **51**: 515-518.

Directorate of Pulses Development. (2025). Ministry of Agriculture and Farmers Welfare. Government of India. DOI: www.dpd.gov.in/Final%20Reterospect%20&%20Prospects%20%202018.pdf

Freeman, S. and Herron, J.C. (1998). Evolutionary Analysis, Upper Saddle River, NJ, USA: Prentice-Hall.

Gomes, R.L.F and Lopes, A.C.A. (2005). Correlations and path analysis in peanut. *Crop Breeding and applied Biotechnology,* **5**(1):105-110.

Govindraj, M, Vetriventhan M. and Srinivasan M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. In: *Genetics in Genomics Era*. Special issue published by *Genet Res Int*. pp, 1-14.

Grafius, J.E. (1978). Multiple characters and correlated response. *Crop Sci*., 18: 931-34

http://farmer.gov.in/imagedefault/pestanddiseasescrops pulses.pdf

https://idl-bnc-idrc.dspacedirect.org/items/38b69ca3-6bae-4fd2-b620-1ad9de605112

https://iipr.icar.gov.in/cimprovment/

https://kvk.icar.gov.in/API/Content/PPupload/k0447_5.pdf

https://masujournal.org/store_file/archive/93-7-12-253-255.pdf

https://mpkv.ac.in/Uploads/Research/07%20-%20Pulses_20230828121422.pdf

https://seednet.gov.in/SeedGO/2016/3540_(E).pdf

https://www.appjpds.org/abstract-details.php?volume=1&issue=1&abstractId=5

https://www.gbpuat.res.in/uploads/aicrp/6%20AICRP%20-%20MULLaRP.pdf

https://www.vnmkv.ac.in/Content/Home/pdf/folder/KVKBadnapur/%E0%A4%AE%E0%A5%81%E0%A4%97_%E0%A4%B2%E0%A4%BE%E0%A4%97%E0%A4%B5%E0%A4%A1_%E0%A4%A4%E0%A4%82%E0%A4%A4%E0%A5%8D%E0%A4%B0%E0%A4%9C%E0%A5%8D%E0%A4%9E%E0%A4%BE%E0%A4%A8_1.pdf

Jagdhane, N. M., Suresh, B. G., Ram, B. J. and Yadav, P. (2017). Genetic variability and character association for seed yield in Mungbean [*Vigna radiata* (L.) Wilczek]. *J. Pharmacog. and Phytochem.,* **6** (4):1388-1390.

Joshi, D. P., Parmar, L. D. and Patel, R. S. P. (2021). Estimation of variability, correlation and path coefficient in mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield and its attributing characters. *The Pharma Innov. J,* **10** (11): 1734-1740

*Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955a). Estimate of genetic and environmental variability in soybeans. *Agronomy Journal*, **47** (7):314-318.

*Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955b). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.,* **47**(7): 477-483.

Kumar, P. P., Lavanya, G. R., Sanadya, S. K., Priyatham, K., Kazipyo, C. S. and Suresh, B. G. (2021). Mean performance and correlation analysis for seed yield and components traits in mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Int. J. Curr. Microbiol. App. Sci.*, **11**: 1479-1486.

Krishi Vigyan Kendra. (2023). Green gram. DOI: https://kvk.icar.gov.in/API/Content/PPupload/k0447_5.pdf

Lush, J. L. (1940). Inter-size correlation regression of offspring on dairy as a method of estimating heritability of characters. *Proceedings American Society of Animal Production*, **33**:293-301.

Mahalakshmi, P., Manivannan, N. and Muralidharan, V. (2005). Variability and correlation studies in groundnut *(Arachis hypogaea* L.*). Legume Research,* **28**(3):194-197.

*Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proceedings of the National Institute of Sciences of India **2**:49–55.

*Majhi, P.K., Mogali, S.C. and Abhisheka, L.S. (2020). Genetic variability, heritability, genetic advance and correlation studies for seed yield and yield components in early segregating lines (F_3) of green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Chem. Stud.*, **8**(4): 1283-1288.

Marawar, M. W., Wagh, A. K. and Ujjainkar, V. V. (2020). Correlation and path analysis studies in mungbean. *Ind. J. Agric. Res.*, **6** (6): 395-399.

*Miller, P. A., J. C. Williams (Jr.), H. F. Robinson and R. E. Comstock. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agron. J.*, **50**: 126-31.

Narasimhulu, R., Naidu, N. V., Shanthi, P., Rajarajeswari, V. & Reddy, K. H. P. (2013). Genetic variability and association studies for yield attributes in mungbean (*Vigna radiata* L. Wilczek). *Ind. J. Pl. Sci.*, **2** (3): 82-86.

Pandey, M. K., Srivastava N. and Kole, C. R. (2007). Selection strategy for augmentation of seed yield in mungbean [*Vigna radiata* (L.) Wilczek]. *Leg. Res.,* **30** (4): 243-249.

Parihar, R., Agrawal, A. P., Sharma, D. J. and Minz, M. G. (2018). Character association and path analysis studies on seed yield and its yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. *J. Pharmacogn. and Phytochem.*, **7** (1): 2148-2150.

PDKV. (2025). Dr. Punjabrao deshmukh Krushi Vidyapeeth, Akola. DOI: https://www.pdkv.ac.in/pdf/Technology_-inventory-VARIET.pdf

Prasanna, B. L., Rao, P. J. M., Murthy, K. G. K. and Prakash, K. K. (2013). Genetic variability, correlation and path coefficient analysis in mungbean. *Environ. Ecol.* **31**: 1782-88.

Ramakrishnan, C.D., Savithramma, D.L. and Vijayabharathi, A. (2018). Studies on genetic variability, correlation and path analysis for yield and yield related traits in green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. and App. Sci.*, **7**(3):2753-2761.

Ramanujam S. (1977). Biometrical basis for yield improvement in mungbean. In: *Proceeding of the 1st International Mungbean Symposium. AVRDC, Taiwan. Pp: 210-220.*

* Rao, C. R. (1952). Advanced statistical methods in biometric research.

Salman, M. A. S. and Anuradha, C. (2020). Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. *Leg. Res., An Int. J.*, **1:**5.

Singh, R. K. and Chaudhari B. D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi.

Singh, S. P., Chauhan, M. P., Nath, S., Singh, V. K., Tiwari, A., Singh, P. and Rai, V. R. (2021). Estimation of genetic variability, heritability and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek] in summer season underlate sown condition. *The Pharma Innov. J.,* **10** (6): 1241-1243.

Sivasubramanian, S and Madhavamenon, P. 1973. Genetic analysis of quantitative characters in rice through diallel crosses. *Madras Agricultural Journal*, **60**:1097-1098.

* Wright, S. (1921). Correlation and causation. *J. Agric. Res.,* **20**: 557-585.

* Oiginal not seen