Bacillus cereus: An Eco-Friendly Alternative for Inducing Salinity Tolerance and Augmenting Plant Growth in *Vigna radiata* L.

Pulivathi Jeeshitha, Sam A. Masih, Ann Maxton

ABSTRACT

The biggest global obstacle to agricultural productivity and food security is crop stress exposure. Osmotic stressors such as salinity cause a plant's outer roots to experience elevated osmotic pressure, which lowers the plant's ability to absorb water. Rhizospheric microorganisms used in seed priming improve soil fertility and restore agro-ecological equilibrium. During current study mung bean (*Vigna radiata* L.), a significant legume crop's genotypes were treated with isolated rhizospheric *Bacillus cereus* against salinity stress to study genetic variability. Among the selected genotypes, IC- 119604, IC- 22456, IC- 282079, and IC- 38995 were discovered to be high seed yielders. The variables with the highest PCV and GCV were the biological yield. Seed yield recorded highest positive significant correlation with harvest index followed by number of pods per cluster, number of clusters per plant, and biological yield. The critical estimation of path coefficient analysis direct effects indicates that the number of primary branches had the highest direct and positive effect on seed yield followed by harvest index at phenotypic and genotypic levels respectively. At both phenotypic and genotypic levels, seed yield is indirectly influenced by days to 50% and 100% flowering, maturity, plant height, and harvest index. Based on mean performance, seed bio priming of *Bacillus cereus* and *Bacillus cereus* with NaCl for the genotypes IC- 119604, IC- 22456 and IC- 282079 will be best for salinity tolerance.

Keywords Mung bean, *Bacillus cereus,* Salinity, Bio-priming, Corelation, Path analysis.

Pulivathi Jeeshitha[1], Sam A. Masih[2], Ann Maxton[3]*

[3]Assistant Professor
[1,3]Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj 211007, India

[2] Assistant Professor (Senior Grade)
[2]Molecular and Cellular Engineering, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj 211007, India

Email: ann.maxton@shiats.edu.in
*Corresponding author

INTRODUCTION

Mung bean (*Vigna radiata* L.) is a significant legume crop within the Fabaceae family, Papilionaceae subfamily, with a diploid chromosome count of $2n = 2x = 22$, native to India, also thrives in tropical and subtropical regions worldwide. Proteins (26%), carbs (62%), fiber (1.4%), vitamins, and minerals including calcium and phosphorus are all abundant in it. The production of mung beans is grown on 7.3 million hectares worldwide, with an average yield of 721 kg/ha. Together, India and Myanmar account for 30% of the world's 5.3 million tons of output. 10% of pulse production and 16% of the land used for pulse cultivation are made up mostly of mung beans. With

46% of the land and 45% of the production going to mung bean agriculture, Rajasthan emerges as the major contributor (Anon *et al.* 2023).

Global food security is at risk because anthropogenic factors and accelerating climate change constantly worsen the negative consequences of these pressures on crop yield. Another key abiotic stressor that hinders plant development and growth worldwide is salinity. Defence priming sensitises and prepares the plant for future abiotic stress, displaying faster and more efficient defence responses. Compared to conventional breeding techniques or genetic alterations, the application of Plant Growth-Promoting Rhizobacteria (PGPR) offers a viable and economical approach to resolving this issue (Mayak *et al.* 2004).

PGPR formulations are being employed as biostimulants more often because they have the potential to improve plant growth, health, and yield sustainability. These rhizosphere-dwelling soil bacteria work in harmony with the plant host to promote plant development. The physiological advantages of this chemical interaction are carried out by several processes, such as the solubility of mineral phosphates, the synthesis of growth-stimulating phytohormones, and the fixation of nitrogen. Biological stimulants, like PGPR formulation, are becoming more and more popular as cutting-edge tactics to increase crop output, quality, and resistance to unfavorable environmental factors. Bio-stimulants are a variety of compounds or microorganisms that are designed to activate a plant's internal processes in order to increase plant production via various mechanisms of action. Plants treated with PGPR show increased ability to resist the hormone ethylene, a substance generated in response to a variety of stressors such as pathogen invasions, heavy metal exposure, floods, drought, and salt (Zahir *et al.* 2008, Khan *et al.* 2013).The application of bacterial inoculating agents to reduce salt stress in agricultural plants has been investigated in recent research (Sharma *et al.* 2021). Biological fixation of nitrogen, phytohormone production, nutrient solubilization, improved nutrient absorption, and strengthening plant tolerance to biotic and abiotic stressors are some of these processes (Maxton *et al.* 2018, Kang *et al.* 2014). Additionally, it has been discovered that PGPR inoculation enhances plant development and yield in a variety of plants at both favorable and unfavorable circumstances (Arruda *et al.* 2013, Barnawal *et al.* 2014).

MATERIALS AND METHODS

The present investigation entitled was conducted at Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh during *kharif* 2023. The experimental material comprised of 15 mung bean genotypes which were collected from different sources grown in individual pots with two replications by adapting Completely Randomized design. Our own soil isolated and characterized plant growth promoting rhizobacteria i.e., *Bacillus cereus* (LC 820408) was used during the study. The NaCl was collected from the lab of the same department. In order to select the best yield giving genotype in the agro climatic conditions of prayagraj region observations were recorded for various quantitative traits like days to 50% flowering, days to 100% flowering, days to maturity, number of primary and secondary branches per plant, number of clusters and pods per plant, plant height, seed yield per plant, biological yield and harvest index.

List of mung bean genotypes under study are; IC-282079, IC- 38995, IC- 9887, IC- 43600, IC- 119604, IC- 22456, IC- 333090, IC- 103979, IC- 76464, IC- 76599, IC- 249656, IC- 211220, IC- 76569, IC-119005, IC- 76414.

Statistical analysis

Genetic variability

The degree of genetic variability within the population under study is measured by the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV). Coefficients of variation related to genotype and phenotype were calculated according to Burton and Devane (1953) based on the estimate of genotypic and phenotypic variances. Heritability in broad sense refers to the proportion of genetic variance to the total observed variance in the population. It has been estimated from the formula given by Lush (1940). The expected genetic advance

and genetic gain per cent of mean for each character was estimated by the formula given by Johnson *et al.* (1955).

Correlation coefficient analysis

Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariances were then calculated as per the formulae given by Johnson *et al.* (1955). Appropriate variances and covariances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.* 1955). The phenotypic and genotypic correlation coefficient's significance was examined by referring to Fisher and Yates (1963).

Path coefficient analysis

First, the genotypic and phenotypic correlation co-efficient was divided into direct and indirect effects using path analysis, as proposed by Dewey and Lu (1959) and developed by Wright (1921), in order to demonstrate the cause and effect link.

RESULTS AND DISCUSSION

Variability studies

The results of the analysis of variance (Table 1) showed that, all eleven of the characters: Days to 50% flowering, days to 100% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per cluster, harvest index, and seed yield; the genotypes differ significantly at the one percent significance level. This implies that there is a considerable amount of variation among the genotypes being studied. Similar outcomes were discovered by Sharma *et al.* (2022a), Nalajala *et al.* (2022), Saikumar *et al.* (2022) and Navya *et al.* (2023).

The genetic yield parameters and their constituent parts are provided in Table 2. High estimates of PCV and GCV was recorded in the traits like biological yield followed by number of pods per cluster, number of clusters per plant, number of primary branches and number of secondary branches. Moderate estimates of PCV and GCV was recorded in the traits like harvest index, plant height and seed yield. Whereas the low estimates of PCV and GCV was observed in days to 50% flowering, days to 100% flowering and days to maturity.

All the traits recorded high estimates of heritability at broad sense, are noted in decreasing order viz., plant height, number of pods per cluster, seed yield, harvest index, number of clusters per plant, number of secondary branches, days to 100% flowering, biological yield, number of primary branches, days to maturity and days to 50% flowering. It proves that if selection for these qualities is carried out in the hybridization procedure, these traits might be successfully passed on to progeny. This was in line with

Table 1. Analysis of variance for 11 characters of mung bean genotypes (At 1% level of significance).

		ANOVA summary			
		Mean sum of squares (MSS)			
Sl. No.	Sources	Genotype	Treatment	Genotype × Treatment	Error
	Degrees of freedom	14	7	98	120
1	Days to 50% flowering	0.098	242.254 **	5.652	4.977
2	Days to 100% flowering	0.004	252.969 **	6.124 **	3.62
3	Days to maturity	0.127	241.660 **	5.769	7.747
4	Number of primary branches	34.774 **	35.468 **	1.062 **	0.037
5	Number of secondary branches	68.123 **	85.388 **	3.066 **	0.149
6	Plant height (cm)	664.607 **	87.571 **	6.813 **	2.268
7	Number of clusters per plant	33.918 **	106.178 **	2.608 **	0.041
8	Number of pods per cluster	714.179 **	11135.240 **	297.343 **	2.787
9	Biological yield (g)	0.097 **	0.444 **	0.018 **	0
10	Seed yield (g)	148.824 **	1843.612 **	36.621 **	6.837
11	Harvest index (%)	159.557 **	1850.959 **	40.440 **	3.844

Table 2. Estimation of various genetic parameters in mung bean genotypes.

Sl. No.	Genetic parameters	GCV	PCV	h^2 (Broad sense)	GA	GAM
1	Days to 50% flowering	5.765	5.862	96.7	6.178	11.68
2	Days to 100% flowering	5.239	5.286	98.2	6.416	10.697
3	Days to maturity	4.561	4.637	96.8	6.191	9.242
4	Number of primary branches	38.425	38.939	97.4	3.792	78.109
5	Number of secondary branches	31.207	31.459	98.4	5.678	63.773
6	Plant height (cm)	15.951	15.966	99.8	13.72	32.83
7	Number of clusters plant	48.181	48.476	98.8	5.079	98.65
8	Number of pods per cluster	79.8	80.003	99.5	45.517	163.971
9	Biological yield (g)	88.727	89.563	98.1	0.326	181.071
10	Harvest index (%)	19.939	20.007	99.3	18.386	40.936
11	Seed yield (g)	13.501	13.544	99.4	18.115	27.726

the studies by Nalajala *et al*. (2022), Sharma *et al*. (2022a), Navya *et al*. (2023) Supreetha *et al*. (2023) Jain *et al*. (2024) for plant height, number of pods per cluster, days to flowering, days to 50% flowering and days to maturity.

High estimates of genetic advancement was recorded in number of pods per cluster, followed by

Table 3. Estimation of phenotypic correlation in mung bean genotypes for yield and yield contributing traits.

	Days to 50% flowering	Days to 100% flowering	Days to maturity	Number of primary branches	Number of secondary branches	Plant height (cm)
			Phenotypic correlation matrix			
Days to 50% flowering	1	0.780**	0.596**	-0.601**	-0.558**	-0.440**
Days to 100 flowering		1	0.572**	-0.610**	-0.555**	-0.354*
Days to maturity			1	-0.463**	-0.463**	-0.354*
Number of primary branches				1	0.930**	0.831**
Number of secondary branches					1	0.801**
Plant height (cm)						1
Number of clusters per plant						
Number of pods per cluster						
Biological yield (g)						
Harvest index (%)						
Seed yield (g)						

Table 3. Continued.

	Number of clusters per plant	Number of pods per cluster	Biological yield (g)	Harvest index (%)	Yield per plant (g)
			Phenotypic correlation matrix		
Days to 50% flowering	0.2	-0.362*	0.076	-0.329*	-0.303*
Days to 100% flowering	0.087	-0.438**	-0.124	-0.355*	-0.338*
Days to maturity	0.257*	-0.118	0.028	-0.095	-0.091
Number of primary branches	-0.012	0.322*	-0.009	0.349*	0.448**
Number of secondary branches	-0.039	0.18	-0.08	0.185	0.310*
Plant height (cm)	-0.045	0.149	-0.085	0.214	0.263*
Number of clusters per plant	1	0.629**	0.717**	0.546**	0.617**
Number of pods per cluster		1	0.772**	0.730**	0.750**
Biological yield (g)			1	0.492**	0.498**
Harvest index (%)				1	0.795**
Seed yield (g)					1

Table 4. Estimation of genotypic correlation in mung bean genotypes for yield and yield contributing traits.

| | Genotypic correlation matrix | | | | | |
	Days to 50% flowering	Days to 100% flowering	Days to maturity	Number of primary branches	Number of secondary branches	Plant height (cm)
Days to 50% flowering	1	0.783**	0.779**	-0.718**	-0.674**	-0.574**
Days to 100% flowering		1	0.765**	-0.750**	-0.700**	-0.532**
Days to maturity			1	-0.536**	-0.558**	-0.430**
Number of primary branches				1	0.947**	0.892**
Number of secondary branches					1	0.887**
Plant height (cm)						1
Number of clusters per plant						
Number of pods per cluster						
Biological yield (g)						
Harvest index (%)						
Seed yield (g)						

Table 4. Continued.

| | Genotypic correlation matrix | | | | |
	Number of clusters per plant	Number of pods per cluster	Biological yield (g)	Harvest index (%)	Yield per plant (g)
Days to 50% flowering	0.238	-0.425**	0.088	-0.390*	-0.342*
Days to 100% flowering	0.111	-0.533**	-0.151	-0.434**	-0.492**
Days to maturity	0.292*	-0.139	0.03	-0.106	-0.097
Number of primary branches	-0.011	0.324*	-0.01	0.354*	0.475**
Number of secondary branches	-0.039	0.183	-0.082	0.197	0.319*
Plant height (cm)	-0.054	0.164	-0.095	0.231	0.317*
Number of clusters per plant	1	0.630**	0.721**	0.555**	0.659**
Number of pods per cluster		1	0.775**	0.744**	0.793**
Biological yield (g)			1	0.501**	0.530**
Harvest index (%)				1	0.853**
Seed yield (g)					1

harvest index and seed yield while the moderate estimates of genetic advancement was recorded in plant height. The low estimates of genetic advancement was recorded in biological yield, number of primary branches, number of clusters per plant, number of secondary branches, days to 50% flowering, days to maturity and days to 100% flowering.

High estimates of genetic advance as percent mean was recorded in biological yield followed by number of pods per cluster, number of clusters per plant, number of primary branches, number of secondary branches, harvest index, plant height and seed yield. While the low estimates of genetic advance as percent mean was recorded in days to 100% flowering, days to 50% flowering and days to maturity. High genetic advance and high heritability

(h^2) were observed in traits such as plant height, number of primary branches, number of secondary branches, harvest index, number of pods per cluster, and number of clusters per plant. These traits suggest that additive gene action predominates and that phenotypic selection may lead to improvements in these traits. Similar outcome was reported by Nalajala *et al.* (2022), Sharma *et al.* (2022a), Navya *et al.* (2023) Supreetha *et al.* (2023) and Jain *et al.* (2024).

Correlation coefficient analysis

Correlation studies help us understand the associations between yield-related variables and how they affect overall yield collectively. They facilitate our understanding of the ways in which different traits interact and impact one other's manifestation. From

Table 5. Estimation of phenotypic path coefficients in mung bean genotypes for yield and yield contributing traits.

	Phenotypic path matrix					
	Days to 50% flowering	Days to 100% flowering	Days to maturity	Number of primary branches	Number of secondary branches	Plant height (cm)
Days to 50% flowering	0.002	0.002	0.001	-0.001	-0.001	-0.001
Days to 100% flowering	0.064	0.082	0.047	-0.05	-0.046	-0.029
Days to maturity	-0.016	-0.016	-0.027	0.013	0.013	0.01
Number of primary branches	-0.304	-0.308	-0.234	0.505	0.47	0.42
Number of secondary branches	0.068	0.067	0.056	-0.112	-0.121	-0.097
Plant height (cm)	0.075	0.061	0.061	-0.142	-0.137	-0.171
Number of clusters per plant	0.067	0.03	0.087	-0.004	-0.013	-0.015
Number of pods per cluster	-0.121	-0.147	-0.04	0.108	0.06	0.05
Biological yield (g)	-0.015	0.024	-0.006	0.002	0.016	0.017
Harvest index (%)	-0.123	-0.133	-0.036	0.13	0.069	0.08
Seed yield (g)	-0.303*	-0.338*	-0.091	0.448**	0.310*	0.263*

Table 5. Continued.

	Phenotypic path matrix				
	Number of clusters per plant	Number of pods per cluster	Biological yield (g)	Harvest index (%)	Yield per plant (g)
Days to 50% flowering	0.001	-0.001	0.001	-0.001	-0.303*
Days to 100% flowering	0.008	-0.036	-0.011	-0.029	-0.338*
Days to maturity	-0.007	0.004	-0.001	0.003	-0.091
Number of primary branches	-0.006	0.163	-0.005	0.177	0.448**
Number of secondary branches	0.005	-0.022	0.01	-0.023	0.310*
Plant height (cm)	0.008	-0.026	0.015	-0.037	0.263*
Number of clusters per plant	0.336	0.211	0.241	0.184	0.617**
Number of pods per cluster	0.21	0.334	0.258	0.244	0.750**
Biological yield (g)	-0.139	-0.149	-0.193	-0.095	0.498**
Harvest index (%)	0.204	0.272	0.184	0.373	0.795**
Seed yield (g)	0.617**	0.750**	0.498**	0.795**	

Table 6. Estimation of genotypic path coefficient in mung bean genotypes for yield and yield contributing traits.

	Genotypic path matrix					
	Days to 50% flowering	Days to 100% flowering	Days to maturity	Number of primary branches	Number of secondary branches	Plant height (cm)
Days to 50% flowering	-0.573	-0.598	-0.446	0.411	0.386	0.329
Days to 100% flowering	0.117	0.112	0.086	-0.084	-0.079	-0.06
Days to maturity	0.125	0.123	0.161	-0.086	-0.09	-0.069
Number of primary branches	-0.808	-0.844	-0.603	1.125	1.066	1.003
Number of secondary branches	0.544	0.565	0.45	-0.764	-0.806	-0.715
Plant height (cm)	0.082	0.076	0.061	-0.127	-0.126	-0.142
Number of clusters per plant	0.148	0.069	0.182	-0.007	-0.024	-0.034
Number of pods per cluster	0.116	0.145	0.038	-0.088	-0.05	-0.045
Biological yield (g)	0.014	-0.023	0.005	-0.002	-0.013	-0.015
Harvest index (%)	-0.106	-0.117	-0.029	0.096	0.053	0.063
Seed yield (g)	-0.342*	-0.492**	-0.097	0.475**	0.319*	0.317*

Table 6. Continued.

	Genotypic path matrix				
	Number of clusters per plant	Number of pods per cluster	Biological yield (g)	Harvest index (%)	Yield per plant (g)
Days to 50% flowering	-0.137	0.244	-0.051	0.224	-0.342*
Days to 100% flowering	0.013	-0.06	-0.017	-0.049	-0.492**

Table 6. Continued.

| | Genotypic path matrix | | | | |
	Number of clusters per plant	Number of pods per cluster	Biological yield (g)	Harvest index (%)	Yield per plant (g)
Days to maturity	0.047	-0.023	0.005	-0.017	-0.097
Number of primary branches	-0.013	0.364	-0.012	0.398	0.475**
Number of secondary branches	0.032	-0.147	0.066	-0.159	0.319*
Plant height (cm)	0.008	-0.024	0.014	-0.033	0.317*
Number of clusters per plant	0.622	0.392	0.448	0.346	0.659**
Number of pods per cluster	-0.172	-0.272	-0.211	-0.203	0.793**
Biological yield (g)	0.11	0.118	0.152	0.076	0.530**
Harvest index (%)	0.15	0.201	0.135	0.27	0.853**
Seed yield (g)	0.659**	0.793**	0.530**	0.853**	

the Tables 3-4 seed yield recorded highest positive significant correlation with harvest index followed by number of pods per cluster, number of clusters per plant, biological yield, number of primary branches, number of secondary branches and plant height. Whereas, the negative significant correlation was observed with days to 100% flowering, days to 50% flowering and days to maturity at phenotypic level. Seed yield recorded highest positive significant correlation with harvest index followed by number of pods per cluster, number of clusters per plant, biological yield, number of primary branches, number of secondary branches and plant height. Whereas, the negative significant correlation was observed with days to 100% flowering, days to 50% flowering and days to maturity at genotypic level.

Path- coefficient analysis

Through a variety of intermediate qualities, this method enables a through investigation of the direct and indirect impacts of a set of independent variables on the dependent variable. Path coefficient analysis offers a more in-depth and through representation of the relationships between various characters or variables by analyzing the correlation coefficient. The direct and indirect possessions of various characters along with their phenotypic and genotypic path coefficients with seed yield are presented in Tables 5-6. In the present investigation, path coefficients were analyzed by taking seed yield as dependent character and remaining eleven characters viz., days to 50% flowering, days to flowering, days to maturity, number of primary branches, number of secondary branches, plant height, number of clusters per plant, number of

pods per cluster, biological yield, harvest index and seed yield as independent variables.

The number of primary branches had the most direct and positive effect on seed yield, followed by the harvest index, number of clusters per plant, number of pods per cluster, days to 100% flowering and days to 50% flowering according to the critical estimation of path coefficient analysis, in which diagonal values signified direct effects. In contrast, at the phenotypic level, biological yield had the highest negative direct effect on seed yield, followed by plant height, number of secondary branches and days to maturity. The highest direct and positive influence on seed yield at the genotypic level was seen in number of primary branches, which was followed by number of clusters per plant, harvest index, days to maturity, biological yield and days to 100% flowering. Conversely, the greatest direct negative impact on seed yield was observed in relation to number of secondary branches, which was followed by days to 50% flowering, number of pods per cluster and plant height. These findings have also been reported by Sharma *et al.* (2022b), Jadhav *et al.* (2022), Saikumar *et al.* (2022) and Navya *et al.* (2023).

CONCLUSION

The current study concludes that the results of the analysis of variance, which are further corroborated by the findings of the genetic variability parameters, provide evidence for the existence of vast variability in the genetic material. It is advised for plant breeding to use direct selection for traits such as plant height, number of primary branches, number of clusters per

plant, number of pods per clusters, harvest index and seed yield that show high heritability combined with high genetic gain. Because of the quantitative interaction, the remaining qualities are not advised; it would not be possible to select characters directly for seed yield. Seed yield is positively correlated with factors like harvest index, pod and cluster numbers, biological yield, and branch numbers at both phenotypic and genotypic levels. Plant height also shows a positive correlation. Conversely, the number of days to flowering and maturity are negatively correlated with seed yield, with these relationships being more pronounced at the genotypic level.

At the phenotypic level, primary branches boost yield through harvest index but are hindered by plant height, while secondary branches and plant height influence yield in both directions. Genotypically, primary branches are influenced by flowering times, and secondary branches affect yield through complex interactions. Understanding these dynamics is essential for trait selection to improve seed production and achieve successful crop development. Understanding these relationships can guide the selection of traits to improve crop yield. Thus seed bio priming with our *Bacillus cereus* even under salinity stress for the genotypes IC- 119604, IC- 22456 and IC- 282079 will be best for salinity tolerance. As a result, these data provide plant breeders with a through overview of how to increase green gram seed output.

REFERENCES

Anon MC, Quiroga A, Scilingo A, Tironi V (2023) Plant Bioactive Peptides: From Oilseed, Legume, Cereal, Fruit, and Vegetable. In Handbook of Food Bioactive Ingredients: Properties and Applications. Cham: Springer International Publishing, pp 907-940.
doi.org/10.1007/978-3-030-81404-5_18-1

Arruda L, Beneduzi A, Martins A, Lisboa B, Lopes C, Bertolo F (2013) Screening of rhizobacteria isolated from maize (*Zea mays* L.) in Rio Grande do Sul State (South Brazil) and analysis of their potential to improve plant growth. *Applied Soil Ecology* 63: 15-22. doi.org/10.1016/j.apsoil.2012.09.001

Barnawal D, Bharti N, Maji D, Chanotiya CS, Kalra A (2014) ACC deaminase-containing arthrobacterprotophormiae induces NaCl stress tolerance through reduced ACC oxidase activity and ethylene production resulting in improved nodulation and mycorrhization in *Pisum sativum*. *Journal of Plant Physiology* 171: 884-894.

doi.org/10.1016/j.jplph.2014.03.007

Burton GW, Devane EM (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 45: 478-481.
doi.org/10.2134/agronj1953.00021962004500100005x

Dewey D, Lu KH (1959) A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*. 51: 515-518.
doi.org/10.2134/agronj1959.00021962005100090002x

Fisher RA, Yates F (1963) Statistical Tables for Biological Agricultural and Medical Research. Oliver and Boyd, London pp 46-63.

Jadhav RA, Mehtre SP, Patil DK, Gite VK (2022) Characters association and path analysis studies in mung bean (*Vigna radiata* (L.) Wilczek). *The Pharma Innovation Journal* 11(12): 105-118.

Jain N, Sikarwar RS, Tripathi MK, Sushma T (2024) Evaluation of genetic parameters for yield and its attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. *International Journal of Environment and Climate Change* 14(20): 482-487. Doi:10.9734/ijecc/2024/v14i23963

Johnson HW, Robinson HF, Compstock RE (1955) Estimates of genetic and environmental variability in soyabean. *Agronomy Journal* 47: 314-318.
doi.org/10.2134/agronj1955.00021962004700070009x

Kang SM, Khan AL, Waqas M, You YH, Kim JH, Kim JG (2014) Plant growth-promoting rhizobacteria reduce adverse effects of salinity and osmotic stress by regulating phytohormones and antioxidants in *Cucumis sativus*. *Journal of Plant Interaction* 9: 673-682.
doi.org/10.1080/17429145.2014.894587

Khan MY, Asghar HN, Jamshaid MU, Akhtar MJ, Zahir ZA (2013) Effect of microbial inoculation on wheat growth and phytostabilization of chromium contaminated soil. *Pakistan Journal of Botany* 45: 27-34. doi.org/10.1016/j.stress.2023.100206

Lush JL (1940) Heritability of quantitative characters in farm animals. *Proceedings of 85th Congress on Genetics and Heriditas* (*Supplement*) 35: 356-375.

Maxton A, Singh P, Masih SA (2018) ACC deaminase producing bacteria mediated drought and salt tolerance in *Capsicum annum*. *Journal of Plant Nutrition*. doi.org/10.1080/01904 167.2017.1392574

Mayak S, Tirosh T, Glick BR (2004) Plant growth-promoting bacteria confer resistance in tomato plants to salt stress. *Plant Physiology Biochemistry* 42: 565-572.
doi.org/10.1016/j.plaphy.2004.05.009

Nalajala S, Brajendra NS, Samuel MJ, Sastry VD, Sonika Y, Bireshwar S, Okendro S (2022) Genetic variability, correlation and path analysis in mung bean genotypes (*Vigna radiata* L. Wilczek): An experimental investigation. *International Journal of Environment and Climate Change* 12(11): 1846-1854. DOI: 10.9734/ijecc/2022/v12i1131170

Navya C, Gabriyal ML, Neha T (2023) Direct and indirect effects of yield contributing characters on seed yield in green gram (*Vigna radiata* L.). *International Journal of Plant Soil Science* 35(19): 612-622.
Doi: 10.9734/ijpss/2023/v35i193591

Saikumar SS, Gaibriyal ML, Roopa GL, Bimal S, Prameela S, Shakeer S (2022) Direct and indirect effects of yield contributing characters on seed yield in green gram (*Vigna*

radiata (L.) Wilczek). *International Journal of Environment and Climate Change*12(11): 3300-3310. Doi: 10.9734/ijecc/2022/v12i111380

Sharma A, Dev K, Sourirajan A, Choudhary M (2021) Isolation and characterization of salt-tolerant bacteria with plant growth-promoting activities from saline agricultural fields of Haryana, India. *Journal of Genetic Engineering and Biotechnology* 19: 99. doi.org/10.1186/s43141-021-00186-3. doi.org/10.1186/s43141-021-00186-3

Sharma A, Sharma NK, Ravindra K, Sanjay KS, Smrutishree S (2022b) Correlation and path analysis for seed yield and components traits in mung bean under arid environment. *The Pharma Innovation Journal* 11(2): 2418-2420.

Sharma A, Sharma NK, Ravindra K, Sanjay KS, Smrutishree S, Mukesh KY (2022a) Study of genetic variability parameters for seed yield and its component traits in mung bean germplasm under arid environment. *The Pharma Innovation Journal* 11(2): 2411-2414.

Supreetha K, Suma, Mogali C, Sumangala B, Patil RH (2023) Genetic variability and correlation studies on seed yield and yield components in advanced breeding lines of mung bean [*Vigna radiata* (L.) Wilczek.]. *Journal of Farm Sciences* 36(4): 329-332.

Wright S (1921) Correlation and causation. *Journal of Agricultural Research* 20: 557-585.

Zahir ZA, Munir A, Asghar HN, Shaharoona B, Arshad M (2008) Effectiveness of rhizobacteria containing ACC deaminase for growth promotion of peas (*Pisum sativum*) under drought conditions. *Journal of. Microbiology and Biotechnology* 18: 958-963. doi.org/10.1016/S1002-0160(08)60055-7