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UNVEILING THE EMS-INDUCED MUTATIONAL VARIABILITY AND IDENTIFICATION OF STABLE DISEASE TOLERANT MUTANT LINES OF MUNGBEAN (*Vigna radiata* L. WILCZEK)

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ABSTRACT

A total of 176 M_3 lines of DGGV 2 induced with EMS were grown in an augmented design during the *kharif* season of 2023. Fiftyfive M_4 lines were selected from the M_3 generation based on the yield performance and resistance to foliar diseases. The selected lines were grown in an alpha lattice design with two replications in protected and unprotected environment during the summer season of 2024. The data were analysed for genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percent of the mean. A pooled analysis of variance of the data generated for M_3 and M_4 generations from the protected and unprotected environments revealed significant Genotype × Environment interaction for plant height, number of branches, number of clusters, number of pods, and yield per plant. The mean values for number of clusters and pods were found to be higher in the M_4 generations than the control DGGV 2 and the M_3 generation. The estimates of PCV and GCV were found to be similar for the protected and unprotected environments, indicating that the incidence of foliar diseases did not contribute to the variation in the M_3 generation. All the traits except days to fifty percent flowering and pod length had a high heritability and genetic advance as a percent of the mean. The identification of genotypes with high yield and stable performance in both the protected and unprotected environments was considered as an ideal selection criterion for selecting mutants. Among the ten stress tolerance indices, the Stress tolerance index (STI), Mean Productivity (MP), and Geometric Mean Productivity (GMP) were highly correlated with the yield. The combined index was obtained by using the rank mean procedure for combining the correlated indices. The superior mutants identified using the combined index were DGGM 131, DGGM 63, DGGM 13 and DGGM 55.

Key words : Mean productivity, EMS, Genetic advance, Heritability, Mungbean.

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is an important grain legume, next only to chickpea and pigeon pea, which is cultivated throughout India for its high content of protein, carbohydrates, vitamins and minerals and its ability to fix atmospheric nitrogen (Singh and Ahlawat, 2005; Dhoot *et al*., 2017). Despite its nutritional and economic importance, productivity is limited due to its narrow genetic base, susceptibility to biotic and abiotic stresses and adverse effects of climate change.

Since mungbean is a self-pollinated crop with cleistogamous flowers and no reliable male-sterile system,

hybridization to create genetic variability is difficult, and the availability of genetic variability is a major constraint in mungbean breeding.Foliar diseases like anthracnose, cercospora leaf spot, powdery mildew, and mungbean yellow mosaic virus (MYMV) are major constraints, reducing the yield potential of the crop, and causing plants to fail to realize their genetic potential (Nair *et al*., 2019).

The popular variety DGGV 2 grown in northern Karnataka is highly susceptible to foliar diseases, while *Vigna trilobata* is resistant but has poor crossing ability, hybrid viability and seed yield (Pandiyan *et al*., 2012).

Induced mutagenesis is an effective method for broadening the genetic base of mungbean (Singh and Singh, 2001). Ethyl methane sulfonate (EMS) is a potent chemical mutagen that causes point mutations and is effective in creating genetic variability (Kaur, 2006). Therefore, the present study was undertaken to induce mutations in the popular variety DGGV 2 to develop and identify high-yielding mutants with resistance to foliar diseases.

Genetic variability is the basis of any successful plant breeding program because selection is possible only when there is variability among the genotypes under evaluation. However, the identification of superior genotypes for complex traits such as yield under stress is a challenging task because yield is a polygenic quality with low heritability and is highly influenced by the environment.

Therefore, direct selection based solely on yield under stress or non-stress (protected) conditions may not be effective in identifying genotypes that perform well under both conditions.Selection under protected conditions alone may lead to the identification of stress-sensitive high-yielding mutants, while selection under unprotected conditions may identify disease-tolerant mutants with low yield potential.Consequently, breeders are increasingly interested in developing mutants that perform well under both conditions, with high yield potential and yield stability under stress (Rosielle and Hamblin, 1981; Fernandez, 1992; Das *et al*., 2016).

Several stress tolerance indices have been developed that combine yield information from stressed and non-stressed environments into a single index for selecting stress-tolerant and high-yielding mutants. This paper discusses (a) the variability generated in the M_3 generation under protected and unprotected conditions and (b) the identification of high-yielding disease-tolerant mutants based on the stress tolerance indices.

Materials and Methods

The present experiment was conducted at the Main

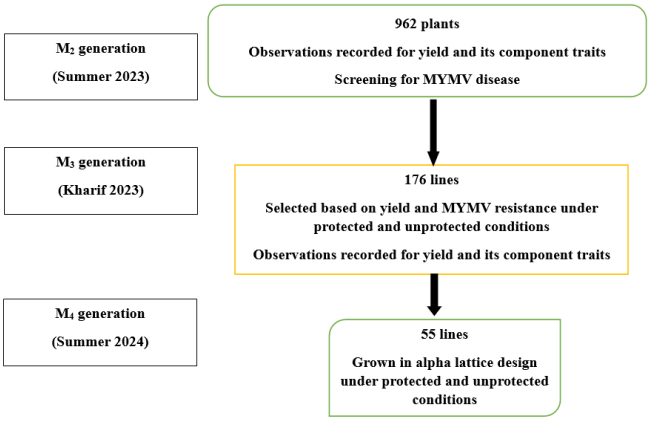


Fig. 1 : The experimental plan from M_2 to M_4 generations.

Agricultural Research Station, Dharwad, Karnataka, during the *kharif* season of 2023. The experiment involved evaluating 176 M_3 lines of DGGV 2 for foliar disease resistance and genetic variability for yield and yield components in an augmented design. The experimental material was evaluated under protected and unprotected conditions for foliar disease resistance.

Out of the 176 M_3 lines evaluated, 55 lines were selected based on high yield and resistance to foliar diseases and advanced to the M_4 generation. The M_4 generation of the selected lines was evaluated in an alpha lattice design with two replications during the summer season of 2024 to evaluate resistance to MYMV and estimate genetic variability for yield and yield components under protected and unprotected conditions (Fig. 1).

Under protected conditions, appropriate plant protection measures were taken to manage foliar diseases, while under unprotected conditions, plants were exposed to natural disease incidence. In both environments, each entry was sown in a single row 3.0 m long with 0.6 m between rows. The mutant lines were grown as progeny rows, and five plants were selected at random for recording observations.

The following observations were recorded for each plant: plant height, number of branches, number of clusters, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, yield per plant and hundred-seed weight.

The mutant lines were evaluated for foliar disease resistance during the kharif season of 2023 and for MYMV resistance during the summer season of 2024. The disease reaction of the mutant lines to foliar diseases was recorded on a 0-9 scale as per the procedure outlined by Singh and Singh (2001). Resistance to MYMV was recorded according to the scale proposed by Mayee and Datar (1986).

The average data from five randomly selected plants

Table 1 : Disease stress tolerance indices.

Stress tolerance index	Formula	Reference
Stress Tolerance Index (STI)	$STI = \frac{Y_p \times Y_s}{(\bar{Y}_p)^2}$	Fernandez (1992)
Mean Productivity (MP)	$MP = \frac{Y_p + Y_s}{2}$	Rosielle and Hamblin (1981)
Geometric Mean Productivity (GMP)	$GMP = \sqrt{Y_p \times Y_s}$	Fernandez (1992)
Harmonic Mean (HM)	$HM = \frac{2Y_pY_s}{Y_p + Y_s}$	Kristin *et al*. (1997)
Tolerance Index (TOL)	$TOL = Y_s - Y_s$	Rosielle and Hamblin (1981)
Stress Susceptibility Index (SSI)	$SSI = \frac{1-(Y_p/Y_s)}{1-(\bar{Y}_p/\bar{Y}_s)}$	Fischer and Maurer (1978)
Yield Stability Index (YSI	$YSI = \frac{Y_s}{Y_p}$	Bouslama and Schapaugh (1984)
Yield Index (YI)	$YI = \frac{Y_s}{\bar{Y}_s}$	Gavuzzi*et al*. (1997)
Stress Resistance Index (SRI)	$SRI = STI \times \frac{Y_s}{Y_p}$	Fernandez (1992)
Stress Susceptibility Percentage Index (SSPI)	$SSPI = \frac{(Y_p - Y_s)}{2\bar{Y}_p} \times 100$	Moosavi *et al*. (2008)

and the calculated PDI scores were used for statistical analysis with R software version 4.6.1. Genetic variability, heritability, and genetic gains were calculated. The Bartlett's test was conducted to assess the homogeneity of variances across the conditions (Ashram and Lovric, 2011). The stress tolerance indices that were used to identify disease-resistant mutants are given in Table 1. Among these indices, those with correlation values greater than 0.7 were considered significant for the selection of disease-tolerant mutants. As more than one index showed significant correlation, the rank mean method (Farshadfar and Javadinia, 2011; Farshadfar and Elyasi, 2012) was applied to identify the disease-tolerant mutants.

Results and Discussion

Analysis of Variance

The analysis of variance showed highly significant differences in all studied traits among the EMS-induced mungbean mutants under both protected and unprotected conditions (Tables 2 and 3). This indicates that a substantial amount of genetic variability has been successfully induced. Such variability is fundamental for effective selection and genetic improvement, especially for traits that are inherited quantitatively, such as seed yield and disease resistance. Similar findings of significant genetic variability in mungbean have been reported by Roychowdhury *et al*. (2012), Arulbalachandran and Mullainathan (2009), Deepthi (2023), Sofia *et al*. (2023) and Basnet *et al*. (2024).

The variance across the environment indicated to be homogenous, as indicated by Bartlett's test. The significant genotype × environment interaction observed for plant height, branches per plant, clusters per plant, pods per plant and seed yield further demonstrated that mutants responded differently under protected and disease-prone conditions (Table 4). This emphasizes the importance of evaluating genotypes in diverse environments (Ceccarelli, 1996; Cooper *et al.*, 1996). Under unprotected conditions, disease incidence reduced yield potential by negatively

Table 2 : Analysis of variance for yield and its component traits in M_3 lines of mungbean during *kharif* 2023 under protected and unprotected condition.

Protected Condition											
Source of variation	**d.f.**	**DFF**	**PH**	**BPP**	**CPP**	**PPC**	**PPP**	**PL**	**SPP**	**YPP**	**HSW**
Block (eliminating Check+Mutants)	3	1.42	21.11	0.02	0.20	0.02	2.60	0.52	0.93	0.18	0.12
Entries (ignoring Blocks)	179	15.93 **	64.91 **	0.39 **	7.50 **	0.34 **	66.27 **	1.08 **	3.32 *	4.48 **	1.44 **
Checks	3	24.42 **	141.73 **	0.17 *	10.32 **	0.23 **	126.87 **	1.61 *	4.47 *	8.68 **	1.07 **
Mutants	175	13.44 **	60.81 **	0.40 **	7.45 **	0.35 **	64.81 **	1.05 *	3.24 *	4.35 **	1.33 **
Checks vs. Mutants	1	425.52 **	552.38 **	0.06 *	7.69 **	0.12 *	139.81 **	5.40 **	13.57 **	14.54 **	21.89 **
Error	9	0.47	10.73	0.04	0.11	0.02	3.54	0.24	0.78	0.26	0.08

Unprotected Condition														
Source of variation	**d.f.**	**DFF**	**PH**	**BPP**	**CPP**	**PPC**	**PPP**	**PL**	**SPP**	**YPP**	**HSW**	**PDI (CLS)**	**PDI (PM)**	**PDI (ANT)**
Block (eliminating Check+Mutants)	3	1.56	2.60	0.04	2.60	0.05	5.07	0.02	0.04	0.42	0.13	8.54	1.36	3.21
Entries (ignoring Blocks)	179	8.65**	65.91**	0.40**	6.45**	0.29**	51.74**	0.91**	3.90**	2.77**	1.83**	102.57**	106.44**	158.38**
Checks	3	14.06**	34.27**	1.00**	6.48*	0.75**	71.22 **	2.85**	6.28**	4.12**	2.33**	1072.64**	1164.69**	1000.35**
Mutants	175	7.25**	62.87**	0.39**	6.47**	0.29**	51.71**	0.82**	3.73**	2.76**	1.63**	85.63**	80.61**	115.74**
Checks vs. Mutants	1	237.34**	693.57**	0.13*	3.25*	0.15*	8.90*	10.91**	25.95**	0.89*	35.93**	156.92**	1452.15**	5094.37**
Error	9	0.62	4.84	0.06	1.16	0.04	3.19	0.15	0.17	0.43	0.09	5.88	2.85	0.99

* Significant at 5 % level of probability
** Significant at 1 % level of probability
d.f. -degrees of freedom
DFF - Days to fifty per cent flowering
PH - Plant height (cm)
BPP - Number of branches per plant
TY – Total seed yield (quintals/ hectare)
CPP - Number of clusters per plant
PDI (PM)-PDI score of Powdery mildew
PPP - Number of pods per plant
PL - Pod length (cm)
SPP- Number of seeds per pod
YPP -Yield per plant (g)
HSW – Hundred seed weight (g)
PDI(CLS)- PDI score of Cercospora leaf spot
PDI (ANT)- PDI score of Anthracnose

Table 3 : Analysis of variance in M_4 lines of mungbean during summer 2024 under protected and unprotected conditions.

Protected Conditions											
Source of variation	**df**	**DFF**	**PH**	**NBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**YPP**	**HSW**
Replication	1	0.3	7.4	0.92	2.24	1.68	55.68	0.06	0.67	0.08	0.1
Blocks (within replication)	8	20.98	20.65	0.96	1.57	1.39	64.42	0.58	3.86	0.27	0.13
Mutants (adjusted for blocks)	59	26.07**	35.27**	1.26**	20.72**	1.67*	98.82*	1.16*	4.77**	5.8**	2.45**
Error	51	5.5	17.25	0.54	2.24	1.01	58.53	0.39	1.26	1.55	0.29
Unprotected Conditions											
Source of variation	**df**	**DFF**	**PH**	**NBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**YPP**	**HSW**	**PDI**
Replication	1	0.01	10.02	0.96	6.46	1.65	54.99	0.13	0.35	5.39	0.13	0.25
Blocks (within replication)	8	2.35	23.0	0.94	2.13	1.4	64.20	0.57	3.48	1.79	0.13	22.97
Mutants (adjusted for blocks)	59	24.47**	36.79*	1.09*	12.99**	1.66*	98.71*	0.93**	3.6 **	6.09**	2.49**	812.70**
Error	51	5.11	19.45	0.54	2.26	1.01	58.79	0.27	1.28	1.5	0.29	156.09

* Significant at 5 % level of probability
** Significant at 1 % level of probability
d.f. -degrees of freedom
DFF - Days to fifty per cent flowering
PH - Plant height (cm)
BPP - Number of branches per plant
CPP - Number of clusters per plant
PDI - Per cent Disease Incidence (Mungbean Yellow Mosaic Virus)
PPP - Number of pods per plant
PL - Pod length (cm)
SPP- Number of seeds per pod
YPP -Yield per plant (g)
HSW – Hundred seed weight (g)
TY – Total seed yield (quintals/ hectare)

Table 4 : Pooled analysis of variance of quantitative characters in M_3 and M_4 generations under different environments (protected and unprotected).

M_3 generation											
Source of variation	**df**	**DFF**	**PH**	**NBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**YPP**	**HSW**
Genotype	54	120.8**	135**	1.862**	17.21**	24.84	180**	3.2*	60.52*	10.1*	5.32*
Environment	1	932	5264**	9.182**	250.31**	3.03	2062**	35.95	111.36	357.1*	91.76
Genotype × Environment	54	20.1	115**	0.525**	11.35**	0.59	69**	1.05	3.86	3.9**	0.61
Environment × Replication	2	2.3	0.23	1.35	0.45	2.14	2.87	4.57	5.4	4.7	1.65
Error	108	0.152	1.45	0.54	0.14	1.25	4.7	5.2	4.6	7.9	4.8
M_4 generation											
Source of variation	**df**	**DFF**	**PH**	**NBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**YPP**	**HSW**
Genotype	54	43.11**	35.1**	1.847**	18.501*	1.32*	120.9**	1.1195**	1.1949*	8**	5.171**
Environment	1	0.04	321**	6.334**	26.629**	1.968	2478.5**	0.1039	2.2261	383	0.867

Table 4 continued...

Table 4 continued...

Genotype × Environment	54	4.07	32.3**	1.343**	15.913**	1.105	96.9*	0.5152	1.7256	3.3**	0.001
Environment × Replication	2	1.59	17.6	0.403	2.165	2.702	59.5	0.4181	0.6363	2.6	0.08
Error	108	5	17.8	0.547	2.591	1.156	67.2	0.3668	1.3521	1.7	0.288

* Significant at 5 % level of probability ** Significant at 1 % level of probability
d.f. -degrees of freedom
DFF - Days to fifty per cent flowering
PH - Plant height (cm)
BPP - Number of branches per plant
CPP - Number of clusters per plant
PDI - Per cent Disease Incidence (Mungbean Yellow Mosaic Virus)
PPP - Number of pods per plant
PL - Pod length (cm)
SPP- Number of seeds per pod
YPP -Yield per plant (g)
HSW – Hundred seed weight (g)
TY – Total seed yield (quintals/ hectare)

Table 5 : Mean values of quantitative characters in M_3 and M_4 generations compared to the control (DGGV2).

Trait	Condition	Mean [DGGV 2]	Mean±SE [M_3]	Shift in mean values in M_3 compared to DGGV 2	Mean±SE [M_4]	Shift in mean values in M_4 compared to DGGV 2
DFF	Protected	49	52.40 ± 0.28	3.4	47.58 ± 1.95	-1.42
	Unprotected	47	50.11 ± 0.2	3.11	47.42 ± 1.54	0.42
PH	Protected	58.125	57.86 ± 0.53	-0.265	37.86 ± 2.97	-20.265
	Unprotected	48.275	52.39 ± 0.59	4.115	36.87 ± 3.46	-11.405
NBP	Protected	3.6	3.81 ± 0.05	0.21	3.20 ± 0.71	-0.4
	Unprotected	3.15	3.58 ± 0.05	0.43	3.74 ± 3.79	0.59
NCP	Protected	9.2	9.33 ± 0.2	0.13	10.99 ± 1.03	1.79
	Unprotected	6.475	8.11 ± 0.2	1.635	10.59 ± 1.06	4.115
NPC	Protected	3.25	3.67 ± 0.04	0.42	5.49 ± 0.72	2.24
	Unprotected	4.35	3.80 ± 0.04	-0.55	5.66 ± 0.72	1.31
NPP	Protected	28.025	30.73 ± 0.61	2.705	42.77 ± 4.71	14.745
	Unprotected	23.45	27.22 ± 0.51	3.77	39.98 ± 5.45	16.53
NSP	Protected	15.35	7.53 ± 0.08	-7.82	12.89 ± 0.90	-2.46
	Unprotected	9.425	7.09 ± 0.07	-2.335	11.70 ± 0.89	2.275
PL	Protected	8.275	12.87 ± 0.14	4.595	7.39 ± 0.45	-0.885
	Unprotected	7.525	12.02 ± 0.14	4.495	7.86 ± 0.39	0.335
YPP	Protected	5.13	6.14 ± 0.15	1.01	9.34 ± 0.83	4.21
	Unprotected	4.31	4.70 ± 0.13	0.39	7.31 ± 0.90	3
HSW	Protected	4.5475	3.74 ± 0.09	-0.8075	3.20 ± 0.36	-1.3475
	Unprotected	4.1275	3.02 ± 0.1	-1.1075	3.68 ±0.36	-0.4475
PDI(CLS)	Unprotected	53.52	20.01 ± 0.71	-	-	-
PDI(PM)	Unprotected	78.67	27.20 ± 0.69	-	-	-
PDI(ANT)	Unprotected	52.96	41.58 ± 0.84	-	-	-
PDI (MYMV)	Unprotected	65.55	-	-	39.09 ± 8.52	-

BPP - Number of branches per plant
DFF - Days to fifty per cent flowering
PH - Plant height (cm)
CPP - Number of clusters per plant
PPP - Number of pods per plant
PL - Pod length (cm)
SPP- Number of seeds per pod
YPP -Yield per plant (g)
PDI(CLS)- PDI score of Cercospora leaf spot
PDI (ANT)- PDI score of Anthracnose
PDI (PM)-PDI score of Powdery mildew
HSW – Hundred seed weight (g)

Table 6 : Estimates of genetic variability parameters for yield and its component traits and PDI scores of diseases during *kharif* 2023 in M_3 lines of mungbean under protected and unprotected conditions.

Trait	Condition	Range		Coefficient of variation		Heritability (h^2_{bs})	GAM
		Minimum	Maximum	PCV (%)	GCV (%)		
DFF	Protected	41	53	7.00	6.87	93.49	13.93
	Unprotected	44	57	5.37	5.14	91.48	10.14
PH	Protected	40.52	73.39	13.48	12.23	82.36	22.90
	Unprotected	32.95	70.27	15.13	14.54	92.30	28.82
NBP	Protected	2.12	5.47	26.63	25.72	89.30	30.64
	Unprotected	2.07	5.90	27.50	26.05	84.03	30.34
NCP	Protected	3.71	16.61	29.25	29.02	93.47	59.42
	Unprotected	2.15	16.15	31.38	28.43	82.08	53.14
PPC	Protected	2.43	6.56	26.01	25.43	92.94	30.69
	Unprotected	2.83	6.28	24.10	23.11	86.45	25.15
PPP	Protected	11.79	58.77	26.20	25.47	94.54	51.10
	Unprotected	13.93	62.92	26.42	25.59	93.84	51.14
NSP	Protected	5.66	11.36	13.58	11.89	76.72	21.49
	Unprotected	4.64	9.38	12.78	11.56	81.72	21.55
PL	Protected	5.41	17.21	13.99	12.19	76.01	21.93
	Unprotected	5.08	15.48	16.07	15.71	95.56	31.69
YPP	Protected	1.73	11.83	33.96	29.92	83.99	55.85
	Unprotected	1.08	9.72	35.36	32.50	84.48	61.63
HSW	Protected	0.41	6.20	19.86	18.94	94.14	59.3
	Unprotected	0.29	6.09	12.23	11.00	94.26	82.12
SY	Protected	3.07	17.81	33.83	32.45	91.98	64.20
	Unprotected	1.79	14.29	34.89	32.30	85.71	61.69
PDI(CLS)	Unprotected	0.74	46.67	46.24	44.62	93.14	88.85
PDI(PM)	Unprotected	10.67	82.67	33.01	32.02	92.47	65.70
PDI(ANT)	Unprotected	0.74	59.26	25.87	24.76	91.14	52.92

BPP - Number of branches per plant
DFF - Days to fifty per cent flowering
PH - Plant height (cm)
CPP - Number of clusters per plant
PPP - Number of pods per plant
PL - Pod length (cm)
SPP- Number of seeds per pod
YPP -Yield per plant (g)
PDI(CLS)- PDI score of Cercospora leaf spot
PDI (ANT)- PDI score of Anthracnose
PDI (PM)-PDI score of Powdery mildew
HSW – Hundred seed weight (g)

affecting plant growth and the partitioning of assimilates, leading to significant yield losses, as also reported by Yadav and Brar (2010) and Venkariya *et al*. (2020).

Comparing mutant generations with the parent cultivar DGGV 2 and between the M_3 and M_4 generations showed an improvement in the mean values of important yield-related traits, especially clusters per plant, pods per plant and seed yield per plant (Table 5). This directional improvement suggests that selection has been effective in increasing favourable alleles and enhancing the performance of the population across generations (Kumar *et al*., 2011; Raina *et al.*, 2017).

The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all traits, indicating that environmental effects had a minor role in the observed variability. High PCV and GCV estimates for branches per plant, clusters per plant, pods per plant, and seed yield suggest that there is ample exploitable genetic variability for these economically important traits (Tables 6 and 7). Such

Table 7 : Estimates of genetic variability parameters for yield and its component traits and DI of MYMV in M_4 lines of mungbean during summer 2024 under protected and unprotected conditions.

Trait	Condition	Range		Coefficient of variation		Heritability (h^2_{bs})	GAM
		Minimum	Maximum	PCV (%)	GCV (%)		
DFF	Protected	33.5	55	8.62	6.38	74.01	9.74
	Unprotected	40.5	56.5	8.05	6.62	82.23	11.21
PH	Protected	25	45.54	13.59	11.82	86.97	21.27
	Unprotected	25.5	46.29	15.35	11.13	72.50	26.61
NBP	Protected	2.26	5.5	30.20	27.87	92.28	52.99
	Unprotected	2.06	5.3	22.67	21.49	94.79	30.17
NCP	Protected	4.9	16.95	31.05	30.26	97.45	60.78
	Unprotected	5.35	20.8	26.16	24.47	93.53	47.15
PPC	Protected	3.21	7.8	21.38	18.99	88.82	34.77
	Unprotected	3.71	8.3	21.76	20.70	95.12	28.12
PPP	Protected	24.48	55.35	17.69	16.16	91.35	35.15
	Unprotected	26.78	58.35	19.07	18.98	95.06	25.95
NSP	Protected	6.68	14.75	15.56	14.66	94.21	28.45
	Unprotected	9.18	17.15	12.24	11.34	92.64	21.65
PL	Protected	5.75	9.43	11.76	9.30	79.08	15.14
	Unprotected	6.65	11.41	10.06	8.57	85.18	20.31
YPP	Protected	2.68	9.72	25.06	20.00	79.80	40.12
	Unprotected	5.24	13.97	26.12	24.44	93.56	47.10
HSW	Protected	0.43	5.24	42.44	38.46	90.62	71.78
	Unprotected	0.57	5.35	31.77	31.3	98.52	63.55
SY	Protected	3.39	14.99	27.11	25.85	95.35	50.87
	Unprotected	3.31	16.23	26.87	26.22	97.58	52.72
PDI (MYMV)	Unprotected	5.2	81.4	55.32	52.92	95.66	78.53

results were also obtained in studies in mungbean by Roychowdhury *et al*. (2012), Divya *et al*. (2018), Deepthi (2023) and Sofia *et al*. (2023), and in other legumes such as chickpea (Babbar *et al*., 2012) and lentil (Tyagi and Khan, 2011). The relatively small differences between PCV and GCV under both protected and unprotected environments suggest that the variability generated through EMS mutagenesis was primarily genetic and only slightly affected by disease incidence. A decrease in variability was observed from the M_3 to the M_4 generation for several traits, including pods per plant, pods per cluster, and seed yieldis expected as selection promotes the stabilization of favourable alleles, thereby reducing the amount of segregating variation in later generations. Likewise, declines in genetic variability after selection have been reported in mutation breeding programs for mungbean and other crops (Ajay *et al*., 2014; Ahmed *et al*., 2017).

High broad-sense heritability and a high genetic advance as a percentage of the mean were observed for most yield-related traits, indicating that additive gene action predominates and that these traits can be effectively improved through direct phenotypic selection (Tables 6 and 7). This combination is widely recognized as the most reliable indicator of selection efficiency because it reflects both the inheritance of a trait and the expected improvement from selection (Johnson *et al*., 1955; Hanson *et al*., 1956). These findings align with studies in mungbean by Khan *et al*. (2004), Reddy (2011), Das and Barua (2015), Usharani and Anandakumar (2016) and Sofia *et al*. (2023). Earlier studies by Frey (1969) also demonstrated that mutagen-induced quantitative variation is highly heritable and responds effectively to selection.

Table 8 : Superior mutants identified during present investigation based on yield and disease resistance.

Mutant	STI	Rank	MP	Rank	GMP	Rank	Rank mean
DGGM 131	1.49937	1	12.1275	1	11.9875	1	1
DGGM 63	1.24667	2	11.02	2	10.9307	2	2
DGGM 13	1.13398	3	10.4505	4	10.425	3	3.44
DGGM 55	1.12099	4	10.645	3	10.3651	4	3.56
DGGM 8	1.05158	5	10.045	6	10.0391	5	5.44
DGGM 78	1.04718	6	10.135	5	10.0181	6	5.56
DGGM 16	1.03449	7	10.02	7	9.95721	7	7
DGGM 72	1.01899	8	9.89	10	9.88231	8	8.89
DGGM 7	1.00572	9	9.925	8	9.81777	9	8.56
DGGM 140	0.98753	10	9.871	12	9.72854	10	10.89

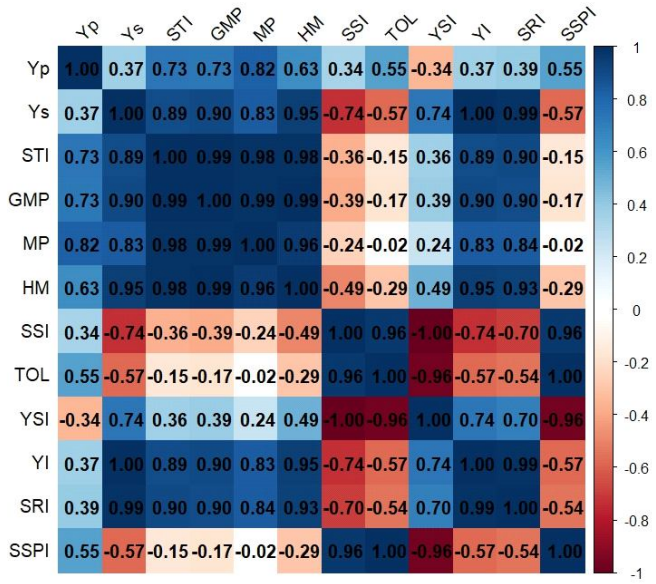


Fig. 2 : Correlation between the stress tolerance indices and yield.

Identification of correlated Stress Tolerant indices and Stress Tolerant genotypes

Out of the 10 indices (Table 1), STI, GMP and MP showed highly significant correlation with yield (Figure 2). These indices have been found to be effective in classifying genotypes by several researchers (Das *et al*., 2016 in barley; Nagamallika *et al*., 2022 in chickpea; Bennani *et al*., 2017 and Singh *et al*., 2021 in wheat). Pour-Aboughadareh *et al*. (2019) supported the use of these indices for any stress conditions provided that the plants are grown under protected and unprotected conditions. The rank mean method was applied to combine these indices into a single desirable index for identifying disease-tolerant mutants in the study. DGGM 131, DGGM 63, DGGM 13 and DGGM 55 were identified as stable, disease-tolerant mutants in this study (Table 8). These mutants can be further used in breeding programs to develop high-yielding disease-tolerant mutants.

References

Ahmad, M., Iqbal M., Khan B.A., Khan Z.U., Akbar K., Ullah I., Muhammad S. and Rehman A. (2017). Response to selection and decline in variability, heritability and genetic advance from F_2 to F_3 generation of tomato (*Solanum lycopersicum*). *Int. J. Plant Res.*, **7(1)**, 1–4. https://doi.org/10.5923/j.plant.20170701.01

Ajay, B.C., Byregowda M., Prashanth Babu H., Veera Kumar G.N. and Reena M. (2014). Variability and transgressive segregation for yield and yield contributing traits in pigeonpea crosses. *Elect. J. Plant Breed.*, **5(4)**, 786–791. https://ejplantbreeding.org

Arulbalachandran, D. and Mullainathan L. (2009). Changes in quantitative traits of black gram (*Vigna mungo* (L.) Hepper) induced by EMS in the M_2 generation. *J. Phytol.*, **1(4)**, 230–235. https://updatepublishing.com/journal/index.php/jp

Ashram, H. and Lovric M. (2011). Bartlett's test. In : Lovric, M. (Ed.). *International encyclopedia of statistical science* (pp. 87–88). Springer. https://doi.org/10.1007/978-3-642-04898-2_84

Babbar, A., Prakash V., Tiwari P. and Iquebal M.A. (2012). Genetic variability for chickpea (*Cicer arietinum* L.) under late-sown season. *Legume Res.*, **35(1)**, 1–7. https://arccjournals.com/journal/legume-research

Basnet, B., Upreti U. and Thapaliya K.P. (2024). Genotypic variations in post-fertility traits and yield components of mungbean (*Vigna radiata* (L.) Wilczek) germplasms in Chitwan, Nepal. *Heliyon*, **10(20)**, e39226. https://doi.org/10.1016/j.heliyon.2024.e39226

Ceccarelli, S. (1996). Adaptation to low/high input cultivation. *Euphytica*, **92**, 203–214. https://doi.org/10.1007/BF00022846

Cooper, M. and Hammer G.L. (Eds.). (1996). *Plant adaptation and crop improvement*. CAB International. https://www.cabi.org

Das, R.T. and Barua P.K. (2015). Association studies for yield and its components in green gram. *Int. J. Agricult., Environ. Biotechnol.*, **8(3)**, 561–565. https://doi.org/10.5958/2230-732X.2015.00068.3

Das, S., Mudi N. and Mahapatra S. (2016). Assessment of *Helminthosporium* blight resistance in barley using disease stress tolerance index. *Indian Phytopathology*, **69(1)**, 24–31. https://link.springer.com/journal/42360

Deepthi (2023). *Studies on induced mutagenesis in mungbean* (*Master's thesis*). University of Agricultural Sciences, Dharwad,

Karnataka, India. https://krishikosh.egranth.ac.in

Dhoot, R., Modha K.G, Kumar D. and Dhoot M. (2017). Correlation and path analysis studies on yield and its components in mungbean (*Vigna radiata* L. Wilczek). *Int. J. Curr. Microbiol. Appl. Sci.*, **6(5)**, 370–378. https://doi.org/10.20546/ijcmas.2017.605.043

Divya, R.C.K., 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. Appl. Sci.*, **7(3)**, 2753–2761. https://doi.org/10.20546/ijcmas.2018.703.318

Farshadfar, E. and Elyasi P. (2012). Screening quantitative indicators of drought tolerance in bread wheat (*Triticum aestivum* L.) landraces. *Europ. J. Exp. Biol.*, **2(3)**, 577–584. https://www.imedpub.com/european-journal-of-experimental-biology

Farshadfar, E. and Javadinia J. (2011). Evaluation of chickpea (*Cicer arietinum* L.) genotypes for drought tolerance. *Seed Plant Improv. J.*, **27(4)**, 517–537. https://sj.areeo.ac.ir

Fernandez, G.C.J. (1992). Effective selection criteria for assessing plant stress tolerance. In : *Proceedings of the International Symposium on Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress* (pp. 257–270). Asian Vegetable Research and Development Center (AVRDC). https://avrdc.org

Frey, K.J. (1969). Release of mutagen-induced genetic variability in oats by outcrossing. *Japanese J. Gen.*, **44**, 396–403. https://doi.org/10.1266/jjg.44.396

Hanson, C.H., Robinson H.F. and Comstock R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.*, **48(6)**, 268–272. https://doi.org/10.2134/agronj1956.00021962004800060008x

Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agron. J.*, **47(7)**, 314–318. https://doi.org/10.2134/agronj1955.00021962004700070009x

Kaur, L. (2006). Multiple disease resistant sources of mungbean. In : *Proceedings of the First International Conference on Indigenous Vegetables and Legumes: Prospectus for Fighting Poverty, Hunger and Malnutrition* (pp. 423–426). https://www.actahort.org

Khan, S., Wani M.R. and Kouser P. (2004). Induced genetic variability for quantitative traits in mungbean (*Vigna radiata* (L.) Wilczek). *Pak. J. Bot.*, **36(4)**, 845–850. https://www.pakbs.org/pjbot

Kumar, R., Sharma N.K., Meena S. and Balakrishnan A.P. (2021). Mutation breeding: A way forward for genetic improvement in mungbean. *Int. J. Plant Environ.*, **7(4)**, 255–262. https://doi.org/10.18811/ijpen.v7i04.2

Nair, R.M., Pandey A.K., War A.R., Hanumantharao B., Shwe T., Alam A.K.M.M., Pratap A., Malik S.R., Karimi R., Mbeyagala E.K. and Douglas C.A. (2019). Biotic and abiotic constraints in mungbean production—Progress in genetic improvement. *Front. Plant Sci.*, **10**, 1340. https://doi.org/10.3389/fpls.2019.01340

Nair, R.M., Schafleitner R., Kenyon L., Srinivasan R., Easdown W.J., Ebert A.W. and Hanson P. (2019). Mungbean (*Vigna radiata* L.) production constraints and improvement strategies. *Front. Plant Sci.*, **10**, 1340. https://doi.org/10.3389/fpls.2019.01340

Pandiyan, M., Ramamoorthi N., Ganesh S.K., Jebaraj S., Pagarajan P. and Balasubramanian P. (2008). Broadening the genetic base and introgression of mungbean yellow mosaic virus resistance and yield improvement through unexplored genes from wild relatives in mungbean. *Plant Mutation Reports*, **1(2)**, 33–38. https://www.iaea.org/resources/databases/mutation-breeding-newsletter

Pour-Aboughadareh, A., Yousefian M., Moradkhani H., Moghaddam Vahed M., Poczai P. and Siddique K.H.M. (2019). iPASTIC: An online toolkit to estimate plant abiotic stress indices. *Applic. Plant Sci.*, **7(7)**, e11278. https://doi.org/10.1002/aps3.11278

Raina, A., Laskar R.A., Khursheed S., Khan S., Parveen K. and Amin R. (2017). Induced physical and chemical mutagenesis for improvement of yield-attributing traits and their correlation analysis in chickpea. *Int. Lett. Nat. Sci.*, **64**, 61–65. https://doi.org/10.18052/www.scipress.com/ILNS.64.61

Reddy, K.R.D., Venkateswarlu O., Obaiah M.C. and Jyothi G.L.S. (2011). Studies on genetic variability, character association and path coefficient analysis in green gram (*Vigna radiata* (L.) Wilczek). *Leg. Res.*, **34(3)**, 202–206. https://arccjournals.com/journal/legume-research

Rosielle, A.A. and Hamblin J. (1981). Theoretical aspects of selection for yield in stress and non-stress environments. *Crop Sci.*, **21(6)**, 943–946. https://doi.org/10.2135/cropsci1981.0011183X002100060033x

Roychowdhury, R., Datta S., Gupta P. and Tah J. (2012). Analysis of genetic parameters on mutant populations of mungbean (*Vigna radiata* L.) after ethyl methane sulphonate treatment. *Notulae Scientia Biologicae*, **4(1)**, 137–143. https://doi.org/10.15835/nsb417327

Singh, D.P. and Ahlawat I.P.S. (2005). Green gram (*Vigna radiata*) and black gram (*Vigna mungo*) improvement in India: Past, present and future prospects. *Indian J. Agricult. Sci.*, **75**, 243–250. https://epubs.icar.org.in/index.php/IJAgS

Sofia, S., Reddy D.M., Reddy K.H.P., Latha P., Reddy B.R. and Devi M.S. (2023). Evaluation of induced genetic variability for yield and yield contributing traits in M„ generation of mungbean (*Vigna radiata* (L.) Wilczek). *Int. J. Plant Soil Sci.*, **35(22)**, 940–947. https://journalijpss.com

Tyagi, S.D. and Khan M.H. (2011). Correlation, path coefficient and genetic diversity in lentil (*Lens culinaris* Medik.) under rainfed conditions. *Int. Res. J. Plant Sci.*, **2(7)**, 191–200. https://interesjournals.org/IRJPS

Usharani, K.S. and Anandakumar C.R. (2016). Estimation of variability, heritability and genetic advance in mutant populations of black gram (*Vigna mungo* (L.) Hepper). *SABRAO J. Breed. Gen.*, **48(3)**, 258–265. https://sabraojournal.org

Vekariya, P.V., Andani V.P. and Chudasama M.K. (2020). Assessment of yield loss caused by powdery mildew disease in mungbean. *Int. J. Chem. Stud.*, **8(2)**, 229–231. https://www.chemijournal.com

Yadav, M.S. and Brar K.S. (2010). Assessment of yield losses due to mungbean yellow mosaic India virus and evaluation of mungbean genotypes for resistance in south-west Punjab. *Indian Phytopathology*, **63(3)**, 318–320. https://www.indianphytopath.org