Journal of Food Legumes
38(2): 209-216, 2025
DOI: 10.53550/jfl.v38.i2.261

Research Paper

^{60}CO induced mutations for yellow mosaic disease resistance and productivity traits in mungbean

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Received: *August 31, 2024*
Accepted: *September 24, 2024*

ABSTRACT

In the present study, 21 advanced mungbean mutant lines developed from gamma-ray irradiation of seeds of YMD susceptible mungbean varieties SML 668, SML 832 and TMB 37 were evaluated for key agronomic traits and Yellow Mosaic Disease (YMD) resistance across different seasons. All the mutants were highly resistant to YMD with a coefficient of infection < 3. A wide range of variability was observed for the number of pods per plant, 100-seed weight, biological yield, grain yield,and harvest index. Mutants of TMB 37 exhibited a lesser extent of variability than those of SML 668 and SML 832. MML 2637 and MML 2593 were identified as the best mutant lines for summer and *kharif* season, respectively. MML 2664 and MML 2629 showed potential as dual season lines owing to stable yields across the environments.

Key words: Gamma rays, Mungbean, Mutants, Variability, YMD resistance

INTRODUCTION

Food legumes are an indispensable component of vegetarian diets, especially in the Indian subcontinent. Amongst the pulses, mungbean is an important short-duration crop of India that grows in four seasons *i.e., Kharif*, spring, summer and *Rabi*. It is a low-input crop with the ability to tolerate varying levels of heat and drought. The legume fits perfectly in the fallow period between wheat and rice (Nair *et al.* 2020). Thus, mungbean is a promising option for intensification as well as diversification of cropping systems. This is of utmost significance in developing tropical countries, particularly India where the majority of farmers are marginal or small (Nair *et al.* 2020). It adapts well to various cropping systems and improves soil health by fixing atmospheric nitrogen in symbiosis with the biological nitrogen-fixing bacteria *Rhizobium*. In a single cropping season, the quantity of fixed nitrogen ranges from 30 to 50 kg/ha (Chadha 2010).

Mungbean is cultivated as a summer (sown in March-April) and *kharif* (sown in July) crop in Punjab state of India. Traditionally, the *kharif* season is the main season and mungbean was cultivated on 3.8 thousand hectares during 2022-23 (Anonymous 2024). Being a poor competitor economically, as compared to paddy, the area under *kharif* crop is less. However, as an additional crop between wheat and rice, significant acreage is under mungbean. During 2022 summer mungbean was sown on 38900 ha, substantially higher than the main season crop (Anonymous 2022). The phenomenon of global climate change has impacted cropping systems considerably. The popular varieties of the summer season *i.e.,* SML 668, SML 832, and TMB 37 are susceptible to the Yellow Mosaic Disease (YMD), which is the major disease attacking the crop. The begomovirus complex causing YMD is transmitted by whitefly. Owing to the erratic rainfalls and anomalies in temperature regimes, the summer crop of mungbean, which earlier escaped whitefly infestations, is now being attacked by the same leading to the outbreak of YMD in the summer cropping season. Vector control and the development of resistant genotypes are the only two techniques for the management of YMD. Out of these, insecticide-mediated control of whiteflies is unfavorable environmentally and economically, along with chances of insect resurgence (Kumar *et al.* 2024).

Genetic variation is one of the prerequisites for any breeding program. To enable effective selection, every breeding program that aims to be successful needs to have a high level of genetic variation. In recent years, induced mutations have proven to be a useful supplement to other time-consuming conventional plant breeding methods, improving harvests and developing new plant varieties. Mutation breeding is a mimicry of the spontaneous mutation process. Induced mutations have been successfully used for generating genetic variability, inducing stress tolerance, and developing higher-yielding crop genotypes since the 1900's (Javed *et al*. 2016). The available sources of disease resistance in mungbean do not provide complete resistance against YMD and are not stable (Parihar *et al.* 2017, Nair *et al.* 2017). Mutation breeding targeted at the induction of resistance can also lead to the creation of novel genes, which might provide complete and durable resistance. Further more, mutations have also been used to create genetic variation for productivity traits. Induction of mutations and screening for the desired traits presents itself as an efficient and cost-effective solution in the mungbean scenario. Out of 3365 total mutants released across the globe, 1703 have been developed using gamma rays. Even in India, 70 % of the mutant varieties are physical mutagen-based (Kumar *et al.* 2021). Keeping in view the importance of crop and the dire need for genetic variability, gamma rays have been used to create mutations in three elite genotypes of mungbean *viz.*, SML 668, SML 832, and TMB 37. The present investigation was thus focusedon the characterization of advanced mutants of mungbean for YMD resistance and key agronomical characters.

MATERIALS AND METHODS

Plant materials and growing conditions

The present study was conducted at the Pulses Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana (Punjab) over two seasons during 2020. Seeds of summer mungbean cultivars, 150 g of each variety; SML 668, SML 832, and TMB 37 were irradiated with 500 Gy and 600 Gy doses of gamma rays. After germination of the M_2 generation plant stand was counted and 1600 plants of SML 832, 1525 plants of TMB 37 and 1350 plants of SML 668 were recorded. Further generation advancement and selections were made from M_2 onwards till M_7, culminating in a set of 21 mutant lines (7 lines from each of the parental genotypes). From M_2 onwards visual selection for YMD resistance, podding potential, and other agronomic traits was performed. The susceptible check, SML 1082 was used as infector rows, repeated after 4 rows to ensure uniform disease incidence. The set of mutants was the experimental material for both the cropping seasons *viz.*, summer and *kharif*. The parental genotypes were included as checks for the summer season while ML 818, ML 2056, and SML 1082 were included as *kharif* checks. ML 818 and ML 2056 were the varieties released for cultivation in the state, while SML 1082 was the susceptible check for YMD evaluation.

Experimental design and data recording

The mutant lines were evaluated for key agronomic traits and YMD resistance in both summer and *kharif* seasons. Both the experiments were sown in Randomized Complete Block Design (RCBD). The summer season trial was sown on 27th March 2020. Each entry was sown in 4 rows of 4 m each in 3 replications; with rows spaced at 22.5 cm and plants spaced at 10-15 cm. The *kharif* season trial was sown on 31st July 2020, which was similar to the summer trial except row-to-row distance of 30 cm. The recommended package of practices was followed. Observations were recorded ondays to 50% flowering, days to maturity, pods per plant, 100-seed weight, biological yield, grain yield, and harvest index. YMD data was recorded as per the Singh and Singh (2000) scale in the *kharif* season. Percent disease incidence (PDI) and Disease severity (DS) were calculated and used to assign Severity Grades (SG) and Response values (RV). The Coefficient of Infection (CI) was calculated as PDI × RV. CI and disease reaction (DR) categories were used as per the scale.

Statistical analysis

Data wereanalyzed using the R package 'variability' (Popat *et al.* 2020) in RStudio. ANOVA, descriptive stats, and estimates of genetic variability were obtained. Correlation analysis and heatmaps were produced using the package 'Performance Analytics' (Peterson *et al.* 2018). Box plots and bar graphs were produced using 'ggplot2' (Wickham 2016). GGE biplots were produced using the package 'metan' (Olivoto and Lucio 2020).

RESULTS AND DISCUSSION

Yellow mosaic disease resistance

The summer crop didn't have any disease incidence hinting at disease escape in place of non-favourable vector conditions. Disease incidence data recorded on a per-plot basis in the *kharif* season were analyzed according to Singh and Singh (2000) (Table 1). The susceptible check, SML 1082 had a disease severity (DS) of 100 with 99.4% disease incidence (PDI). The coefficient of infection (CI) was

Table 1. Disease reaction of genotypes and checks

Sr. No.	Entry Name	PDI	DS	SG	RV	CI	DR
1	MML 2593	1.99	16.16	1.00	0.25	0.50	HR
2	MML 2594	0.54	8.73	1.00	0.25	0.14	HR
3	MML 2595	2.43	48.07	2.00	0.50	1.22	HR
4	MML 2596	1.52	37.78	2.00	0.50	0.76	HR
5	MML 2597	2.00	11.89	1.00	0.25	0.50	HR
6	MML 2600	2.74	45.33	2.00	0.50	1.37	HR
7	MML 2601	5.16	24.24	1.00	0.25	1.29	HR
8	MML 2629	2.74	23.13	1.00	0.25	0.68	HR
9	MML 2630	2.68	15.36	1.00	0.25	0.67	HR
10	MML 2637	6.50	23.19	1.00	0.25	1.62	HR
11	MML 2643	1.61	6.67	1.00	0.25	0.40	HR
12	MML 2644	4.57	11.11	1.00	0.25	1.14	HR
13	MML 2645	4.60	26.38	2.00	0.50	2.30	HR
14	MML 2647	1.24	0.00	0.00	0.00	0.00	HR
15	MML 2657	2.39	9.44	1.00	0.25	0.60	HR
16	MML 2658	2.70	21.34	1.00	0.25	0.68	HR
17	MML 2661	2.68	45.00	2.00	0.50	1.34	HR
18	MML 2662	4.13	13.93	1.00	0.25	1.03	HR
19	MML 2664	6.43	19.87	1.00	0.25	1.61	HR
20	MML 2667	3.24	16.19	1.00	0.25	0.81	HR
21	MML 2668	1.08	0.00	0.00	0.00	0.00	HR
22	ML 2056	0.74	0.00	0.00	0.00	0.00	HR
23	ML 818	0.78	0.00	0.00	0.00	0.00	HR
24	SML 1082	99.40	100.00	4.00	1.00	99.40	HS
25	SML 668	72.50	60.50	3.00	0.75	54.38	S
26	SML 832	94.00	100.00	4.00	1.00	94.00	HS
27	TMB 37	98.00	100.00	4.00	1.00	98.00	HS

Abbreviations used: - DS: Disease Severity, SG: Severity Grade, RV: Response value, PDI: Percent Disease Incidence, CI: Coefficient of Infection, DR: Disease Reaction

also calculated to be 99.4, thus highly susceptible (HS) reaction was observed for the susceptible check. Similarly, parental genotypes SML 668, SML 832, and TMB 37 had DS of 60.5, 100, and 100%, respectively. The CI for SML 668 was 54.4 and hence it was classified as susceptible (S), while SML 832 (CI of 94) and TMB 37 (CI of 98) were HS against the disease. Contrastingly, the *kharif* checks ML 2056 and ML 818 had DS and CI values of 0, and were classified as highly resistant (HR). Figure 1 contains the photographs of the field disease reaction of checks, mutants, and parents.

The DS values of mutants ranged from 0 to 48.1, while PDI values ranged from 0.5 to 6.5. The CI for the mutants was calculated to lie between 0 to 2.30; hence, all the mutants were observed to be highly resistant against the YMD. Out of 21 mutants MML 2647 (mutant of SML 832) and MML 2668 (Mutant of SML 668) had DS and CI values of 0 same as the resistant check. Several other workers have documented the successful use of mutations to generate YMD resistance (Khattak *et al.* 2008, Reddy 2009, Vairam *et al.* 2016, Emam *et al.* 2017, Raihan *et al.* 2018, Sardar 2019, Khalil *et al.* 2020).

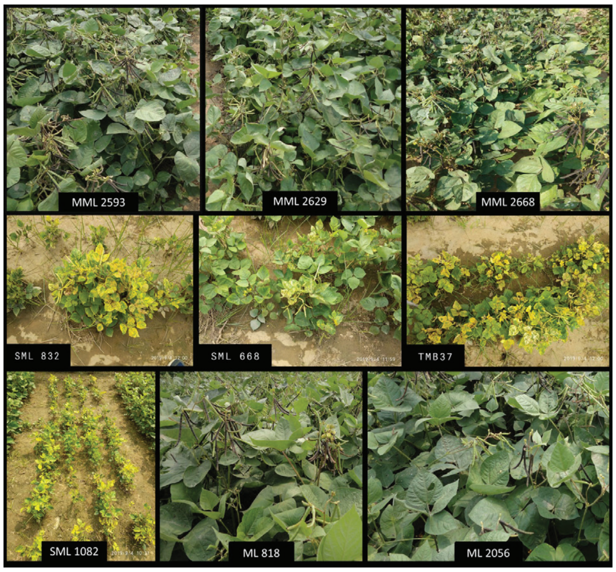

Fig. 1. Field photographs of checks (including parents) and mutants depicting disease reaction

Performance of mutants with respect to checks

In the present study, ANOVA revealed that a substantial degree of variation was exhibited by the mutants in both seasons. For the summer season trial, 24 genotypes' data (21 mutants + 3 checks) was used for ANOVA and subsequent analyses. In the *kharif* season, susceptible check *i.e.,* SML 1082 was decimated by the disease hence no data could be recorded for the same. Phenotypic data of the rest of the entries was used for ANOVA and other analyses. The mean sum of squares revealed significant differences among the genotypes for all the characters under study during both the summer and *kharif* seasons at alpha 0.01 (data not shown).

A comparison was made between mutants and the checks for both the seasons separately and best genotypes for different traits were identified (Table 2a and 2b). The minimum and maximum values for the traits depicted the expanse of variation induced in mutants during both seasons. During the summer season checks were early to exhibit 50% flowering and maturity than the mutants, while

Table 2a. Mean and descriptive statistics for summer season

Sr. No.	Yield parameters	Genotypes	Mean	Range	Promising genotypes
1	Days to 50% flowering	Mutants	39	38-45	MML 2593, MML 2594, MML 2595, MML 2596, MML 2597, MML 2601
		Checks	38	38 - 38	SML 668, TMB 37, SML 832
2	Days to maturity	Mutants	62	60 - 63	MML 2593, MML 2601
		Checks	60	59 - 61	SML 668
3	No. of pods / plant	Mutants	21.8	17.3-33.2	MML 2637
		Checks	23.9	22.2-25.1	TMB 37
4	100 Seed weight (g)	Mutants	5.4	4.4-6.1	MML 2661
		Checks	5.0	4.3 - 6.1	SML 668
5	Biological yield (g)	Mutants	27.5	18.6-45.1	MML 2637
		Checks	29.7	27.0-31.6	TMB 37
6	Grain yield (g)	Mutants	8.6	6.3-12.2	MML 2637
		Checks	9.3	9.0 -9.9	SML 832
7	Harvest index (%)	Mutants	31.7	25.2 - 38.0	MML 2600
		Checks	31.5	28.4 - 33.6	SML 668

Table 2b. Mean and descriptive statistics for *kharif* season

Sr. No.	Yield parameters	Genotypes	Mean	Range	Promising genotypes
1	Days to 50% flowering	Mutants	39	38-40	MML 2600
		Checks	43	42 - 44	ML 818
2	Days to maturity	Mutants	68	67-71	MML 2593
		Checks	72	72 - 73	ML 818
3	No. of pods / plant	Mutants	21.6	13.2 - 31.0	MML 2601
		Checks	16.7	12.8 - 20.7	ML 818
4	100 Seed weight (g)	Mutants	3.9	3.0 - 4.7	MML 2668
		Checks	3.3	3.2 - 3.3	ML 2056
5	Biological yield (g)	Mutants	28.3	20.2 - 40.2	MML 2593
		Checks	24.7	19.3-30.1	ML 818
6	Grain yield (g)	Mutants	7.8	4.9-10.9	MML 2593
		Checks	5.9	4.8 -6.9	ML 818
7	Harvest index (%)	Mutants	27.5	24.4-32.5	MML 2601
		Checks	23.9	23.0 -24.8	ML 2056

the scenario was reversed for the *kharif* season. The mean biological yield of mutants (27.5 g) fell a little short of checks' mean biological yield (29.7 g) during the summer season. However, the best mutant genotype, MML 2637 had a significantly higher biological yield (45.1 g) than the best check TMB 37 (31.6 g). The *kharif* checks had a lower mean biological yield (24.7 g) than mutants (28.3 g). The best mutant, MML 2593, and best check, ML 818 had respective biological yields of 40.2 g and 30.1 g. The mean grain yield of mutants for summer and *kharif* was 8.6 g and 7.6 g, respectively, while checks were recorded to yield 9.3 g and 5.9 g in summer and *kharif*. The best check for the summer season was SML 832 which had a grain yield of 9.9 g, which was significantly out performed by the best mutant MML 2637 with 12.2 g grain yield. Similarly, the best *kharif* check, ML 818 was also out-yielded by the best mutant MML 2593 with respective mean yields of 6.9 g and 10.9 g. Hence, MML 2637 and MML 2593 were the best mutants for both biological and grain yield during summer and *kharif* season, respectively. The mean harvest index (%) of mutants was greater than that of checks during both seasons. MML 2600 (38.0%) and MML 2601 (32.5%) had the highest harvest index during summer and *kharif* season significantly greater than the respective best checks; SML 668 (33.6%) and ML 2056 (24.8%).These results are in accordance with numerous other studies that have studied variability generated in mutant populations and reported mutants better than parents/check for many traits such as yield, yield stability, harvest index, number of pods per plant, etc (Khan and Goyal 2009, Sarkar *et al.* 2009, Yuliasti and Reflinur 2015, Dewanjee and Sarkar 2017, Sarkar and Kundagrami 2018).

Mutants vis-à-vis respective parent varieties

Lack of suitability of the parental genotypes and sub-optimal trait expression during the *kharif* season restricted the comparison of mutants with their respective parents to the summer season only. Hence, summer season data was used for the comparison. The mean and range of mutants have been compared with the respective parental genotypes in Table 3. The mean and range of all the mutants showed extensive contrast to the parental genotypes for pods per plant, biological yield, grain yield, and harvest index. The values for biological yield of mutants derived from SML 832 exhibited the highest variation amongst all the traits and mutant groups, while the lowest variability was observed for days to 50% flowering of mutants of SML 668. The biological yield of SML 832 ranged from 29.4 - 31.7 g, while its mutants ranged from 18.6 - 45.1 g. A similar trend was observed for grain yield in mutants of SML 832 with a range of 6.3 - 12.2 g as opposed to 9.2 - 10.7 of the parent. The harvest index of SML 832 was calculated to lie in the range of 31.4 - 33.6%, whereas its mutants exhibited a much wider range (25.2 - 36.9%). Overall highest degree of variation as assessed by the range of traits was recorded in mutants of SML 832 followed by SML 668, then TMB 37.

Genetic advance, genetic variability and heritability

Estimates of PCV were somewhat higher than GCV in both seasons (Table 4a and 4b). In

Table 3. Comparison of mutants with their respective parent varieties

Trait	Mean		Range		Mean		Range		Mean		Range	
	Mutants of TMB 37	TMB 37	Mutants of TMB 37	TMB 37	Mutants of SML 832	SML 832	Mutants of SML 832	SML 832	Mutants of SML 668	SML 668	Mutants of SML 668	SML 668
Days to 50% flowering	38	38	38 - 39	38 - 38	40	38	39 - 41	38 - 38	39	38	39 - 39	38 - 38
Days to maturity	61	60	60 - 61	60 - 60	63	60	62 - 63	60 - 60	62	59	61 - 63	59 - 59
No of pods / plant	19.3	25.1	17.6 - 22.4	24.7 - 25.7	23.3	24.3	17.3 - 33.2	23.7 - 25.0	22.8	22.2	19.5 - 28.2	21.7 - 22.7
100 seed weight (g)	5.8	4.3	5.6 - 6.0	4.0 - 4.5	4.6	4.6	4.4 - 4.9	4.5 - 4.7	5.8	6.1	5.5 - 6.1	5.9 - 6.1
Biological yield (g)	25.7	31.6	20.5 - 29.5	30.7 - 32.5	29.6	30.4	18.6 - 45.1	29.4 - 31.7	27.2	27.0	24.5 - 31.6	26.2 - 27.5
Grain yield (g)	8.1	9.0	7.3 - 8.8	8.6 - 9.4	8.7	9.9	6.3 - 12.2	9.2 - 10.7	9.1	9.1	8.3 - 10.4	8.6 - 9.4
Harvest index (%)	31.8	28.4	29.2 - 38.0	27.9 - 28.9	29.9	32.6	25.2 - 36.9	31.4 - 33.6	33.4	33.6	29.9 - 35.4	33.0 - 34.2

the summer season, all the traits had low PCV and GCV (<20%). In *kharif* season pods per plant (25.34 and 24.96%) and grain yield (23.23 and 22.37%) had moderate PCV and GCV. Biological yield in the *kharif* season had moderate PCV (20.06%), but low GCV (19.59%), and the rest of the traits had low PCV and GCV. Hemavathy *et al.* (2015) and Raturi *et al.* (2015) also concluded similar results in mungbean. Moderate PCV and GCV for pods per plant and grain yield in the *kharif* season were also reported by Paul *et al.* (2017). Heritability estimates were high for days to maturity (98.09%), pods per plant (97.43%), biological yield (97.47%), 100-seed weight (84.15%), grain yield (89.39%) and harvest index (88.58%) during the summer season. Like wise, high heritability for pods per plant (97.04%), 100-seed weight (84.11%), biological yield (95.36%), and grain yield (92.74%) were observed in the *kharif* season. Similar heritability estimates were calculated by other researchers (Dhole and Reddy 2018, Khan and Goyal 2009, Makeen *et al.*2007, Wani and Khan 2007).

Table 4a. Variability, heritability and genetic advance in summer season

Character	h^2	GA%	GA	PCV	GCV	CV
Days to 50% flowering	54.90	1.19	3.06	2.71	2.00	1.82
Days to maturity	98.09	2.41	3.91	1.94	1.92	0.27
No. of pods/plant	97.43	7.47	33.85	16.87	16.65	2.70
100 Seed weight (g)	84.15	1.16	21.64	12.48	11.45	4.97
Biological yield (g)	97.47	10.30	37.07	18.46	18.22	2.93
Economical yield (g)	89.39	2.34	26.86	14.59	13.79	4.75
Harvest index (%)	88.58	5.88	18.58	10.18	9.58	3.44

Table 4b. Variability, heritability and genetic advance in *Kharif* season

Character	h^2	GA %	GA	PCV	GCV	CV
Days to 50% flowering	67.01	1.99	5.05	3.66	3.00	2.10
Days to maturity	52.78	1.99	2.89	2.66	1.93	1.83
No. of pods/plant	97.04	10.73	50.65	25.34	24.96	4.36
100 Seed weight (g)	84.11	0.94	24.09	13.90	12.75	5.54
Biological yield (g)	95.36	11.04	39.41	20.06	19.59	4.32
Economical yield (g)	92.74	3.39	44.38	23.23	22.37	6.26
Harvest index %	74.72	3.84	14.11	9.17	7.92	4.61

Correlation with grain yield

In the summer season, significant and positive correlations were observed for pods per plant-grain yield (r=0.85) and biological yield-grain yield (r=0.84) (Table 5). For the *kharif* season, pods per plant also had a significantly positive correlation grain yield (r=0.84). Biological yield and harvest index were also positively correlated with grain yield, having r values of 0.92 and 0.55, respectively. Pods per plant were reported to show a high correlation with yields by Saxena *et al.* (2007) and Sarma *et al.* (2022). A contrasting correlation of 100-seed weight-grain yield was observed. During the summer a negative correlation (r= -0.23) was documented as opposed to a positive correlation of a similar magnitude (r=0.25) during the *kharif* season. Thus, to obtain higher yield in the summer season medium seed-size genotypes are required but during *kharif* season large seeded varieties would be desirable. A negative and statistically significant correlation of days to 50 % flowering and days to maturity with grain yield was observed during the *kharif* season. It

Table 5. Correlation of different traits with grain yield (g)

Trait **Season**	Days to 50% flowering	Days to maturity	No. of pods / plant	100 Seed weight (g)	Biological yield (g)	Harvest index (%)
Summer	0.12	0.11	0.85**	-0.23*	0.84*	-0.02
Kharif	-0.35**	-0.47**	0.84**	0.25*	0.92**	0.55**

appears that to obtain higher grain yields optimum level of biomass is required. When biomass exceeds the said optimum due to longer flowering and maturity, it leads to suboptimal conversion of the biomass into yield, thus, an adverse effect on grain yield was observed.

Environmental suitability and stability of genotypes

GGE analysis of data of both seasons was carried out in RStudio using the metan package and results were interpreted as per Yan and Tinker (2006). The Analysis indicated that no relationship existed between the summer and *kharif* environment (Figure 2a). Also, *kharif* was closer than summer to the ideal environment therefore was more representative as well as informative amongst the two. Which-won-where biplot (Figure 2b) depicts clearly that in terms of economic yield, MML 2593 was the best genotype for *kharif*, MML 2637 for summer while MML 2664 performed well in both environments. The same results were reinforced by the mean v. stability biplot; MML 2664 had the best combination of average yield and stability amongst the mutant lines. The mutant genotype MML 2664 was also the closest to the ideal genotype, while MML 2629 and MML 2661 were next in order of proximity to the ideal genotype.

Mungbean occupies an area of more than 7 million hectares on the world agriculture map. Global productivity averages around 0.5 t/ha which is quite low when compared to the yield potential of 2.5 to 3.0 t/ha (Nair *et al*. 2020). The lacuna in yield has been attributed to poor management, abiotic stresses such as drought, and untimely rains; and biotic stresses which include diseases such as YMD and pests such as bruchids. The variability in mungbean cultivars is towards the lower side, owing to breeding efforts focused on the use of few parents (Nair *et al*. 2020). Therefore, the need arises to widen the genetic base. Mutation breeding programs have been used successfully and churned out 39 cultivars of mungbean worldwide. ANOVA tables revealed considerable variation in the genotypes for all the traits across both seasons which can be efficiently exploited in breeding programmes. The generated variation also contributes towardsthe widening of a narrow genetic base. The utility of induced mutations is thus reinforced by these results. The summer season trial revealed that mutants and checks were at par for days to 50 % maturity, days to

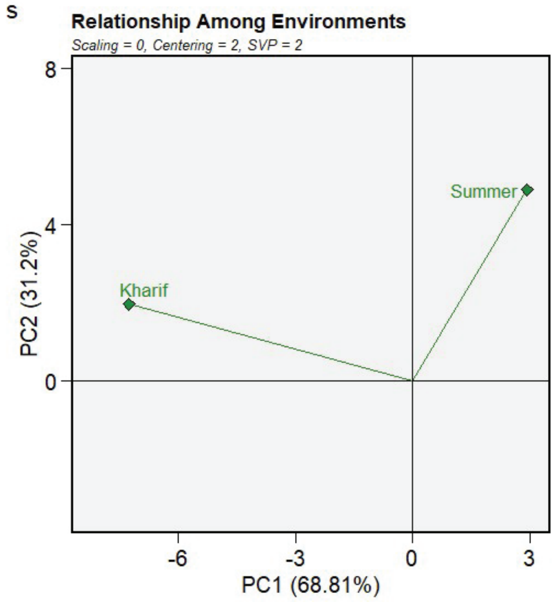

Fig. 2a. Relationship among environments' biplot

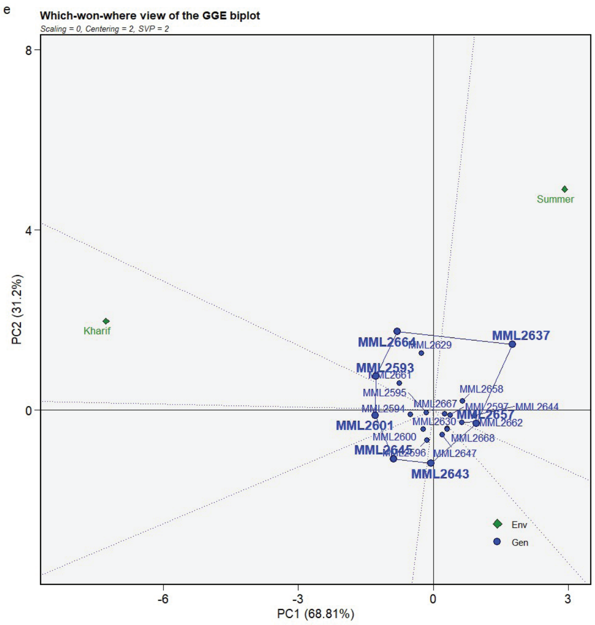

Fig. 2b. Which-won-where biplot

maturity, and 100-seed weight. MML 2637 emerged to be the best mutant line for pods per plant, biological yield, and grain yield. MML 2600 had the best harvest index for the summer trial. In the *kharif* season too, mutants out performed the checks; MML 2668 was the best mutant line for 100-seed weight. Mutant line MML 2593 significantly outperformed the best check both in terms of biological yield and grain yield. Moreover, MML 2629 and MML 2664 out-yielded the best checks in both seasons and, therefore could be used as dual-season varieties.

YMD is a severe nuisance for the mungbean growing pockets across the globe, particularly in India, where yield losses of up to 85% have been reported (Karthikeyan *et al.* 2014). Based on the CI, all of the mutant entries were completely resistant to YMD. Generation of a mutant panel of 21 lines all having HR reaction against YMD is a promising outcome and the lines, at the least, can be used as donors. Since the mutants have been sourced from three different parents *viz.,* SML 832, SML 668, and TMB 37, the probability of these mutations being distinct from each other prevails. Further studies are needed to confirm this fact.

CONCLUSION

The present study documents a genetic stock of 21 mutant lines which could prove to be an important resource against YMD, the main bottle neck for mungbean cultivation and yield. The set of mutants exhibited a wide range of variability for all traits under study except days to flowering, which can be effectually exploited to widen the crop's genetic base. Global climate scenarios are predominated by climatic vagaries which take their toll on farming communities as well. Highly stable and resistant mutant MML 2664 could help stabilize yield levels across seasonal and climatic variation and contribute effectively towards global nutritional security. Moreover, a dual-season cultivar shall alleviate the problem which many farmers are facing *viz.,* quality seed. Thus, the findings of the study will help in the efficient utilization of the mutant lines in the mungbean breeding program along with reinforcing the significance of mutation breeding programs in crops with limited genetic resources such as mungbean.

Authors' contributions

Conceptualization and designing of the work (T.S. Bains, R.K. Gill, K.S. Mandahal); Execution of field/lab experiments and data collection (K.S. Mandahal, S. Nagpal, J. Singh); Analysis of data and interpretation (A. Sirari, T.S. Bains, K.S. Mandahal); Preparation of manuscript (K.S. Mandahal, P. Sharma, A. Sirari, B. S. Gill).

Declaration

The authors declare no conflict of interest.

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