Research Paper

Multi-environmental Screening of Mungbean for Reaction to Yellow Mosaic Virus Disease to Identify Stable Resistant Genotypes by Assessing GE Interaction

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Abstract

Mungbean is an important legume crop cultivated in Sri Lanka. Yellow mosaic virus disease (YMVD) is the major distructive disease affecting mungbean cultivation. Screening of 60 genotypes of mungbean was performed following infector row method over six environments representing Norhern, Suthern and Central regions of th Dry Zone in *Yala* and *Maha* seasons. The experiment in each environment was conducted in a randomized complete block design with two replicaions. Disease severity index was calculated and data were analysed by assessing Genotype × Environment (GE) interaction. GGE biplot analysis was performed to identify the most stable resistant genotypes to YMVD over diverse environments and the suitable environments for disease screening. Three mungbean genotypes namely VC 6370-92 (8), VC6371-94 (9) and VC 6372 (45-8-1) (16) were identified as the most stable resistant genotypes to YMVD over diverse environments and genotypes, VC1973A (ksp1) and Jangahn could be confirmed as susceptible checks. Out of the six tested environments, *Maha* seasons at the Field Crops Research and Development Institute (FCRDI), Mahailluppallama and *Yala* and *Maha* seasons at the Grain Legumes and Oil Crops Research and Development Center (GLOCRDC), Agunakolapalassa, were identified as the most suitable environments for screening mungbean genotypes for stable resistance to YMVD. Multi-environment testing and assessing GE interaction to identify genotypes with stable resistance to disease appeared highly valuable and beneficial in crop improvement programs for disease resistance. It may serve as a model for any crop improvement program.

Keywords: Disease resistance, GE interaction, Mungbean, Yellow mosaic virus disease

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is an essential leguminous crop cultivated across South and South-East Asia, Africa, South America and Australia (Kumara *et al*., 2014). As the global climate changes, breeding Mungbean for stability and resilience becomes increasingly important. In Sri Lanka, mungbean is primarily grown in the Dry and Intermediate zones. The rising price of mungbean is due to insufficient production to meet the country's needs, with an average productivity of 0.9 t ha^{-1} (Socio Economics and Planning Centre, 2022). Globally, mungbean productivity averages between 0.7 to 1.2 t ha^{-1}, varying by region due to factors such as climate, soil fertility, farming practices and technology access (FAO, 2023). Low productivity is mainly caused by pest and diseases, suboptimal fertilizer uses and inadequate irrigation (FAO, 2023; IFPRI, 2022). Among these, Yellow Mosaic Virus disease (YMVD) significantly impacts yields, causing yellow mosaic patterns on leaves, stunted growth, malformed pods and reduced seed quality (Kumar *et al*., 2021). Transmitted by the whitefly (*Bemisia tabaci*), YMVD is challenging to manage with traditional pest control methods (Nair *et al*., 2020). Therefore, developing mungbean varieties resistant to YMVD is vital for sustainable production and food security.

Crop improvement programs focusing on disease-resistance require an understanding of Genotype × Environment (GE) interaction. By integrating GE interaction analysis into the selection process, breeders can develop crop varieties that meet current agricultural demands and be prepared for future challenges. GE interaction occurs when genotype performance across environments varies differently among genotypes, complicating breeder selection as a genotype performing well in one setting may not do so in another (Gauch, 2013). Thus, evaluating mungbean genotypes for YMVD resistance over diverse environments is essential to identify stable resistant lines. Stability refers to consistent genotype performance across different conditions and it is crucial for developing resilient mungbean varieties that maintain high yields despite environmental variability.

Identification of new mungbean varieties with enhanced stable resistance to YMVD, will contribute to sustainable production by reducing yield losses due to YMVD ensuring a stable supply of this nutritious crop (Kumar *et al*., 2019). Additionally, by accounting for GE interaction, breeders can select genotypes that are not only resistant to YMVD but also stable in yielding ability across diverse environments. This approach increases the likelihood of developing resilient crop varieties that thrive under variable conditions (Cooper *et al*., 2021).

The stability and performance of genotypes across diverse environments using GE interaction can be evaluated by the GGE Bi-plot method (Yan *et al*., 2002). In

addition to identifying stable resistant lines, this method also provides valuable information on relative performance of different environments indicating which environments are exerting the highest stress on genotypes and which are more conducive to resistance. This information is crucial for selecting appropriate testing sites for future breeding trials and developing location-specific management strategies for YMVD (Yan *et al*., 2007). The GGE Bi-plot method has been developed to visualize the average tester coordinate (ATC) and a polygon view, which is useful for identifying the best genotypes and environments. In addition, the GGE Bi-plot method utilizes principal component analysis (PCA) and Bi-plot visualization techniques (Jolliffe and Cadima, 2016). Bi-plots, graphical representations of PCA results, allow simultaneous visualization of genotypes and environments, providing insights into GE interaction and genotype stability (Gabriel, 1971).

The present study aimed at screening a wide range of mungbean genotypes for resistance to YMVD over diverse environments, assessing GE interaction to identify the most stable resistant lines. The study also aimed at highlighting the value of multi-environmental testing and benefits of assessing GE interaction in identifying stable resistant genotypes to diseases in crop improvement programs.

Materials and Methods

Plant Materials and Experimental locations & seasons

Sixty mungbean genotypes including known resistant and susceptible checks to YMVD were used in the study (Table 1). The genotype included as the resistant check, MIMB 7 is only moderately resistant and the susceptible checks were VC 1973A (ksp 1) and Jangahn.

The genotypes were evaluated across three locations representing northern, central and southern parts of the Dry Zone of Sri Lanka, over four growing seasons: two *Yala* or *dry* seasons (2021 *Yala* and 2022 *Yala*) and two *Maha* or *Wet seasons* (2021/2022 *Maha* and 2022/23 *Maha*).

Experimental Design

The field experiments were established in a Randomized Complete Block Design (RCBD) with two replications in each location in each season in each year. The experimental plot size was 3 × 1.2 m^2 with 120 plants/plot. To increase disease pressure and ensure uniform disease spread, single row of infector plant called "*Lathoroid or Phasey beans*" (*Macroptilium lathyroides*) was planted after each genotype to be evaluated for reaction to YMVD. Insecticides were intentionally omitted to maintain an optimal vector (whitefly) population to create a high inoculum pressure of the YMVD. Regular surveillance of the crops was carried out to detect any symptoms of YMVD.

Table 1. Mungbean genotypes used in the study and their sources of origin

No.	Genotype [$]	Source of origin *	No.	Genotype [$]	Source of origin *
1	MIMB59/V3476	DOASL	31	VO27094B-G	Exotic
2	ksp1/NM54	DOASL	32	VO2817B-G	Exotic
3	MIMB101/V2802	DOASL	33	VO3131A-G	Exotic
4	AC8419	PGRC	34	Eoul	Exotic
5	AC8429	PGRC	35	J71	Exotic
6	AC8449	PGRC	36	Dahyeon	Exotic
7	AC8452	PGRD	37	Sohyeon	Exotic
8	VC 6370-92	Exotic	38	Jangahn (SC)	Exotic
9	VC6371-94	Exotic	39	AC0099	PGRC
10	VC1973A(ksp1)(SC)	Exotic	40	AC0259	PGRC
11	VC6351B-20G	Exotic	41	AC2943	PGRC
12	VC 6368 (46-40-4)	Exotic	42	AC3022	PGRC
13	VC 6369(53-97)	Exotic	43	AC1570	PGRC
14	VC 6370 (30-65)	Exotic	44	AV8421	PGRC
15	VC 6370a	PGRC	45	AC8421	PGRC
16	VC 6372 (45-8-1)	Exotic	46	AC8431	PGRC
17	VC 6469-12-3-4A	Exotic	47	AC8417	PGRC
18	VC 6486-10-51	Exotic	48	AC8416	PGRC
19	VC6489-9-1	Exotic	49	AC8446	PGRC
20	VC6492-59A	Exotic	50	AC8455	PGRC
21	VC6493-44-1	Exotic	51	AC8433	PGRC
22	VC6510-151-1	Exotic	52	AC8436	PGRC
23	MIMBAUS923	Local	53	AC84287	PGRC
24	TVO1251A-G	Exotic	54	AC8425	PGRC
25	TVO1270A-G	Exotic	55	AC8434	PGRC
26	TVO1596A-G	Exotic	56	AC8447	PGRC
27	TVO3981A-G	Exotic	57	AC8430	PGRC
28	TVO3982A-G	Exotic	58	AC8445	PGRC
29	VO11282A-G	Exotic	59	AC8435	PGRC
30	VO11254A-G	Exotic	60	MIMB (MRC)	DOASL

[$] *SC- Susceptible check, MRC – Moderately Resistant check.*

**PGRC- Genetic Resource Center, Department of agriculture, Exotic- Germplasm received from other countries, DOASL - Department of agriculture, Sri Lanka*

Data Recorded

Weather parameters of rainfall, temperature and relative humidity were obtained from the Natural Resource Management Center over eight weeks period within which the peak disease incidence was observed in each environment. Degree of infection to YMVD for each of 120 individual plants within a genotype was recorded separately using the disease score scale of 0 to 9 (Table 2) introduced by Bashir *et al*. (2006). The number of infected plants was counted in each plot at weekly intervals after the onset of symptoms and continued for a duration of eight weeks. To quantify disease severity of a genotype as a whole, disease severity index (DSI) was calculated. The DSI for YMVD for each genotype was calculated as follows;

$$DSI = \frac{\textit{Sum of (disease score} \times \textit{No.of individuals with the relevant score}}{\textit{Total no.of individuals observed} \times \textit{maximum disease score}} \times 100$$

After calculating DSI, different DSI ranges were used to categorize mungbean genotypes for reaction to YMVD as presented in Table 3. Thus, if the DSI of a genotype was 0, it was recorded as highly resistant and if the DSI of a genotype was >50, it was recorded as highly susceptible.

Table 2. Degree of infection as measured by disease score scale based on visual symptoms of yellow mosaic virus disease for each individual plant

Disease score scale	Visual symptoms
0	Complete absence of symptoms
1	Small yellowing spots scattered on same leaves
3	Yellowish bright spots common on leaves, easy to observe
5	Yellowish bright spots common on leaves, easily observed with large patches of symptoms
7	Bright yellow specks or spots on all leaves, Minor stunting of plants & a smaller number of pods
9	Yellowing or chlorosis of all leaves on whole plants, shortening of internodes, severe stunting of plants with no yield or few flowers and deformed pods with small immature and shriveled seeds

Table 3. Disease Severity Index range used for categorization of mungbean genotypes for reaction to yellow mosaic virus disease

Disease Severity Index range	Disease Reaction category
0	Highly resistant (HR)
1 to 10	Resistant (R)
11 to 20	Moderately resistant (MR)
21 to 30	Moderately susceptible (MS)
31 to 50	Susceptible (S)
>51	Highly susceptible (HS)

Statistical Analysis

Analysis of data in different locations separately indicated that Season × Year interaction was not significant within each location. The reason may be that the weather parameters between different years for the same season are almost the same so that the differences observed in DSI between years for the same season is totally random. This, allowed to remove the year factor and data from two *Yala* seasons and two *Maha* seasons were averaged separately over years, to represent *Yala* and *Maha* seasons. Averaging of DSI for the same season over two years instead of taking only one season results, represented a season more accurately. After removing the year factor, the experiment was initially analysed as a three factor factorial experiment where factors being Genotype, Location and Season and the three way interaction effect of Genotype × Location × Season was found to be highly significant. Thus, the three way interaction effect was further studied considering Location × Season combination as an environment as the genotypic stability of resistant to YMVD over diverse environments was the main objective of the study. This provided six different environments (Table 4) that were significantly different from each other for DSI of mungbean YMVD to perform an efficient and effective stability analysis. Navrood *et al*. (2023) also considered Location × Season combination as an environment in yield stability analysis of groundnut genotypes.

Table 4. Locations, seasons and environments used in the study and their respective geographical coordinates

Location	Season	Environment	Latitude	Longitude	Altitude
Kilinochchi (North)	*Yala*	E1	9.3803° N	80.39066° E	30m above sea level
Regional Agriculture Research and Development Centre (RARDC)	*Maha*	E2			
Mahailluppallama (North Central)	*Yala*	E3	8.1167° N	80.41067° E	117m above sea level
Field Crops Research and Development Institute (FCRDI)	*Maha*	E4			
Agunakolapalassa (South)	*Yala*	E5	6.2586° N	80.9993° E	51m above sea level
Grain Legumes and Oil Crops Research and Development Centre (GLOCRDC)	*Maha*	E6			

Finally, the data were analysed as a two factor factorial, factors being Genotypes and Environments, using pooled ANOVA over environments by SAS (V 9.3). As original data were percentages of which the range was more than 40% they were subjected to arcsine transformation before analysis. In the analysis, the total variance was partitioned into components due to Genotypes (G), Environments (E), and Genotype × Environment interaction (GE).

As the GE interaction effect was found to be highly significant, the stability and performance of genotypes over diverse environments were evaluated by the GGE biplot method (A site regression model) using R studio computer programme. The GGE biplot analysis was performed using the first two principal components (PC1 and PC2), which were symmetrically scaled to visualize the interaction patterns effectively. The model used for the GGE biplot analysis was:

$$y_{ij} - \mu - \beta_j = \lambda_1 \ \Sigma_{i1} \ \eta_{j1} + \ \lambda_2 \Sigma_{i2} \ \eta_{j2} + \in_{ij}$$

Where;

y_{ij} is the performance of genotype i in environment j

μ is the grand mean

β_j is the average effect of environment j

λ_1& λ_2 are the singular values for PC1 and PC2

Σ_{i1} & Σ_{i2} are genotype scores for PC1 and PC2

η_{j1}& η_{j2} are the environment scores for PC1 and PC2

$\in_{ij}$ is the residual error

The GGE Bi-plot was developed to visualize the average tester coordinate (ATC) which is useful for identifying the best genotypes and environments. The Average Tester Coordinate (ATC) in the GGE Biplot simplifies genotype evaluation by combining performance and stability. It identifies the best genotypes based on their alignment with the ATC direction and revealed stability through their perpendicular distance from the line. The cosine of the angles between the vectors of environments was considered to adjust the associations among various environments (Yan and Tinker 2006).

Results & Discussion

The whitefly population which transmits the virus, is dependent on environmental factors such as temperature, humidity and rainfall (Rahman *et al*., 2006, Khan *et al*., 2006, Islam *et al*., 2008, Livinder *et al*., 2009, Srivasrava *et al*., 2012). Thus, the influence of weather factors on disease severity was studied. Comparatively higher DSI values were observed in environments where higher rainfall and relative humidity were recorded (Table 5). The significant positive leaner relationship (P< 0.0075) with significant coefficient of correlation (r = 0.86) between weekly rainfall and DSI indicated a strong positive relationship, suggesting that as rainfall increases, disease incidence also tended to rise significantly. High humidity prolongs leaf wetness and creates an environment to increase vector activity. Thus, rainfall and relative humidity were the main factors that have influenced synergistically to amplify disease severity in the studied environments.

DSI for mungbean yellow mosaic virus disease of 60 mungbean genotypes in six environments are presented in Table 6. The mean DSI ranged from 0.00 (highly resistant) to 55.56% (highly susceptible). The severity of YMVD was comparatively higher on the susceptible checks and much lower on the moderately resistant check across all environments indicating that the results of the study are valid and acceptable. Genotypic (G), environment (E) and GE interaction effects were found to be highly significant in the analysis (Table 7).

Table 5. Weather parameters and average disease severity index of the two most susceptible mungbean genotypes in the six environments over a period of eight weeks within which the peak disease incidence was observed

Environment*	weekly average rainfall (mm)	Temperature (°C)	RH[$] (%)	DSI (%)
RARDC Kilinochchi –*Yala* (E1)	1.08	30.25	79.14	14.92
RARDC Kilinochchi –*Maha* (E2)	5.01	30.46	78.37	38.91
FCRDI, MI-*Yala* (E3)	4.81	32.62	80.34	42.19
FCRDI, MI – *Maha* (E4)	5.06	32.60	87.11	51.47
GLORDC, ANK-*Yala* (E5)	0.42	33.22	75.00	19.98
GLORDC, ANK-*Maha* (E6)	1.16	32.33	74.86	9.95

Table 6. Disease severity index for 60 mungbean genotypes for yellow mosaic virus disease in six environments.

No.	Genotype*	Environments (E)						
		DSI[$]						
		E1	E2	E3	E4	E5	E6	Average
1	MIMB59/ V3476	8.66	25.05	48.31	25.41	9.12	4.70	20.21
2	ksp1/NM54	5.86	16.90	36.45	44.03	11.68	5.77	20.12
3	MIMB101/ V2802	6.74	16.39	48.61	37.78	6.71	6.95	20.53
4	AC8419	4.25	17.96	27.52	33.33	7.83	6.01	16.15
5	AC8429	9.74	16.13	34.58	49.09	10.29	5.89	20.95
6	AC8449	9.59	7.13	35.64	23.35	12.21	11.38	16.55
7	AC8452	4.10	18.05	18.45	28.92	4.05	3.15	12.79
8	VC 6370-92	0.30	2.22	1.28	0.70	0.00	0.00	0.75
9	VC6371-94	0.00	0.34	0.04	0.87	0.00	0.00	0.21
10	VC1973A (ksp1)(SC)	14.66	34.99	48.03	47.39	24.29	30.21	33.26
11	VC6351B-20G	5.95	13.89	12.41	18.97	6.03	5.76	10.50
12	VC 6368 (46-40-4)	7.64	3.46	10.63	20.12	7.64	8.12	9.60

No.	Genotype*	Environments (E)						
		DSI[$]						
		E1	E2	E3	E4	E5	E6	Average
13	VC 6369 (53-97)	4.03	3.61	2.16	4.63	5.67	4.31	4.07
14	VC 6370 (30-65)	6.33	4.63	7.44	9.04	7.21	2.56	6.20
15	VC 6370a	12.95	22.68	9.48	26.06	5.62	8.82	14.27
16	VC 6372 (45-8-1)	0.00	0.00	0.06	1.05	0.00	0.00	0.19
17	VC 6469-12-3-4A	7.92	8.87	7.12	15.63	7.30	5.88	8.79
18	VC 6486-10-51	3.61	2.04	9.14	2.48	6.20	4.47	4.66
19	VC6489-9-1	8.39	37.06	11.78	28.10	7.95	8.18	16.91
20	VC6492-59A	10.08	26.16	16.38	32.06	8.45	8.10	16.87
21	VC6493-44-1	12.31	28.89	17.95	42.86	9.17	7.89	19.85
22	VC6510-151-1	6.55	18.48	10.54	16.33	11.63	6.06	11.60
23	MIMBAUS923	0.94	2.77	18.96	10.38	12.46	7.68	8.87
24	TVO1251A-G	2.97	4.71	11.12	25.04	10.83	5.86	10.09
25	TVO1270A-G	0.87	3.25	14.57	19.52	10.74	5.77	9.12
26	TVO1596A-G	2.41	8.67	15.50	18.75	8.34	5.98	9.94
27	TVO3981A-G	1.97	11.79	20.06	18.06	10.79	6.66	11.56
28	TVO3982A-G	5.11	13.10	11.95	39.18	11.12	6.90	14.56
29	VO11282A-G	5.17	8.41	27.97	36.32	10.10	10.77	16.46
30	VO11254A-G	3.37	12.18	14.19	39.47	11.52	12.83	15.59
31	VO27094B-G	5.84	8.32	12.88	32.32	12.92	8.26	13.42
32	VO2817B-G	3.19	12.93	19.80	34.88	11.45	7.64	14.98
33	VO3131A-G	3.95	5.97	19.50	30.77	13.18	8.57	13.66
34	Eoul	5.86	10.19	15.83	35.28	18.32	9.69	15.86
35	J71	5.89	12.00	21.01	9.21	12.29	7.01	11.24
36	Dhyeon	11.62	21.20	38.02	12.14	15.13	18.51	19.44
37	Sohyeon	7.26	15.37	32.69	37.99	14.69	8.23	19.37
38	Jangahn (SC)	15.19	42.84	36.36	55.56	15.67	28.94	32.43
39	AC0099	11.34	25.50	13.45	16.94	16.45	23.78	17.91
40	AC0259	7.69	27.37	28.96	15.11	19.30	14.38	18.80
41	AC2943	13.13	28.65	31.05	8.76	18.81	23.10	20.58
42	AC3022	12.44	28.01	29.13	16.70	15.79	16.77	19.81
43	AC1570	7.12	23.49	21.85	18.16	17.30	9.41	16.22
44	AV8421	11.78	30.06	20.13	29.04	17.65	12.04	20.12
45	AC8421	9.74	12.72	36.54	22.08	27.61	17.90	21.10

No.	Genotype*	Environments (E)						
		DSI[$]						
		E1	E2	E3	E4	E5	E6	Average
46	AC8431	11.75	21.47	20.85	32.08	28.16	22.18	22.75
47	AC8417	14.97	20.68	35.77	31.81	20.67	22.30	24.37
48	AC8416	12.88	17.00	15.93	47.64	20.20	13.37	21.17
49	AC8446	12.00	12.37	18.10	54.19	25.60	22.09	24.06
50	AC8455	6.95	34.18	32.80	38.03	12.88	12.82	22.94
51	AC8433	7.95	17.06	33.85	48.20	25.50	11.76	24.05
52	AC8436	3.53	10.65	31.81	8.56	24.47	10.08	14.85
53	AC84287	14.15	28.76	39.00	11.35	23.30	12.58	21.52
54	AC8425	5.45	14.09	32.88	32.36	25.45	11.86	20.35
55	AC8434	5.61	17.28	36.20	19.63	30.30	12.77	20.30
56	AC8447	4.06	37.93	45.87	35.42	30.45	12.89	27.77
57	AC8430	6.97	28.08	44.60	16.94	17.07	16.60	21.71
58	AC8445	6.04	10.12	16.84	18.33	20.75	8.98	13.51
59	AC8435	11.48	22.07	30.70	13.37	19.72	9.65	17.83
60	MIMB 7 (MRC)	0.15	2.50	1.66	1.98	1.57	1.59	1.58
	Average DSI	7.14	16.48	22.70	25.00	13.79	9.43	15.76

** SC – Susceptible check, MRC – Moderately resistant check, $ DSI – Disease severity index*

Table 7. Analysis of variance of yellow mosaic virus disease severity index in 60 mungbean genotypes tested in six environments.

Source of variation	Df	SS	MS	F value	P value
Environments (E)	5	18268.08	3653.61	1273.03	<0.0001
Genotypes (G)	59	30987.44	525.21	182.95	<0.0001
R/E	6	66.04	11.00	3.83	0.001
G × E	295	18318.33	62.09	21.63	<0.001
Error	354	1016.23	2.87		

As the environment effect was highly significant, different environments needed for the study have been achieved as expected so that the results of the study could be successfully utilized to screen mungbean genotypes against YMVD. This is further evidenced by the frequency distribution of six levels of genotypic reaction to YMVD in each environment (Figure 1). Different environments had different frequency distributions of six levels of genotypic reaction to YMVD and environment 3 had all six levels and environment 4 had five levels while both having highly susceptible level indicating the highest suitability of these two environments for relevant screening test. However, none of the other environments had highly susceptible level due to low disease incidence caused by unfavourable weather for disease infestation. In addition, Spearman's correlation analysis (<0.001) was conducted to assess the association

of YMVD incidence spectrum between each pair of environments. The results, as shown in Table 8, revealed the correlation coefficient for each pair illustrating the degree of similarity and dissimilarity in disease incidence across different environments. E1 had no relation with E2 and E6 but was similar in different degrees to E3, E4 and E5. E2 was dissimilar to E3 but closely similar to E4, E5 and E6. E3 was dissimilar to E5 but similar to E4 and E6. E4 was dissimilar to E5 but similar to E6. E5 and E6 showed no relation. This again indicated that environmental differences achieved for YMVD was adequate for the study.

On average, genotypes exhibited considerable differences in their reaction to YMVD (Table 6). Based on the average performance across environments, DSIs of susceptible checks (VC1973A-ksp 1 and Jangahn) were 30.21 and 28.94, respectively and the DSI of the moderately resistant check (MIMB 10) was 1.59 as expected. As the GE interaction effect was found to be significant, the different genotypes have reacted to YMVD differently in different environments. When genotypes are tested in multi-environment trials, shifts in the relative ranking due to genotype-by-environment interaction often occur (Alam *et al*., 2014, Basandri *et al*., 2016). Thus, both G and GE effects were further studied to identify resistant genotypes that are stable across different environments using GGE biplot analysis.

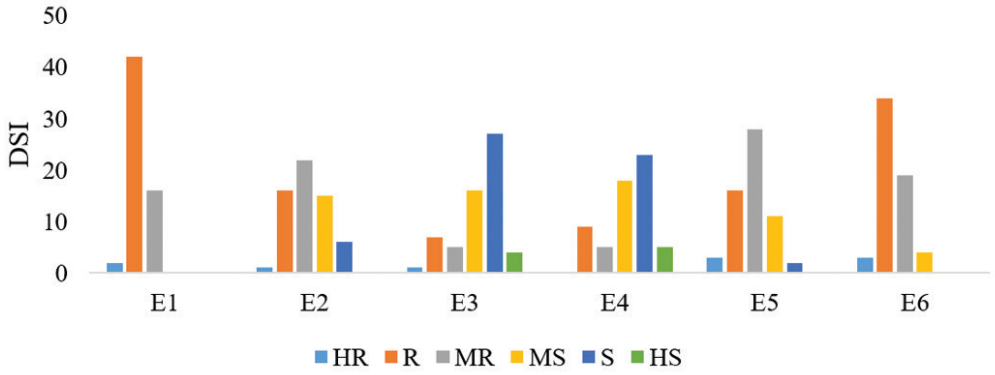

Figure 1. Frequency distribution of 60 mungbean genotypes for reaction to YMVD severity index at six environments (E). HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS- Moderately susceptible, S-Susceptible, HS-Highly susceptible.

Table 8. Spearman's correlations between each pair of tested environments (E) for YMV disease incidence spectrum.

Environment	E1	E2	E3	E4	E5	E6
E1	1	0.21341	0.172*	0.708**	0.560**	0.01174
E2		1	-0.082**	0.461**	0.622**	0.405**
E3			1	0.428**	-0.219**	0.113**
E4				1	-0.715**	0.328*
E5					1	0.204
E6						1

The GGE biplot (Figure 2) illustrates the relationship among 60 genotypes at six different environments (E1, E2, E3, E4, E5 and E6) regarding YMVD. As revealed by the analysis of GGE biplot, Principal Component 1 (PC1) and Principal Component 2 (PC2) collectively explained 71.4 percent (PC1 53.2% and PC2 18.2%) of the total variation.

PC1 represented the genotypic main effect of DSI, as there was a significant high correlation (r = 0.94) between PC1 and the genotypic main effect of DSI. In a GGE biplot, PC2 often captures variation that is not directly related to the primary trait but instead reflects the fluctuations of the trait across different environments. Thus, PC2 represents the stability of disease reaction among the genotypes across diverse environments. The environment vectors represented the direction and magnitude of the environmental effects while the genotypic vector summarized the collective interaction of all genotypes with the environments.

The biplot shows that the vectors of the environments are all relatively long, suggesting that all the environments had almost similar discriminating power and each environment significantly contributed to the variation in disease incidence. The spread of the environment vectors also indicated differences in disease pressure across these environments.

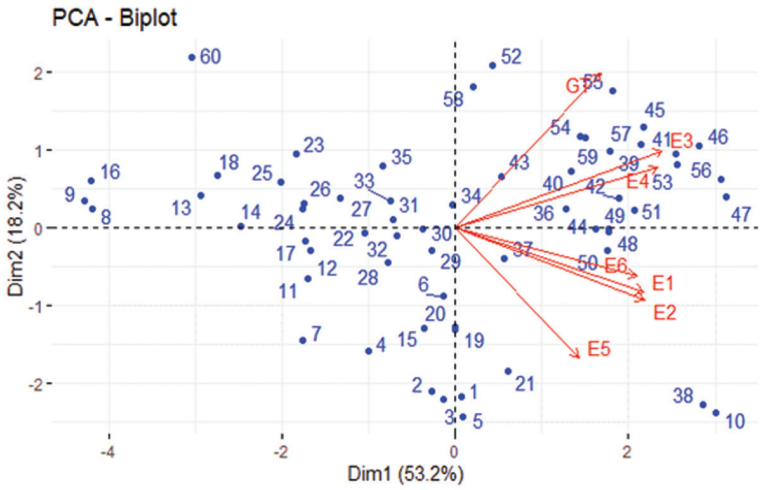

Figure 2. GGE biplot of PC1 (Dim1-Disease Severity Index) and PC 2 (Dim-2-Disease Reaction Stability) in relation to yellow mosaic virus disease severity index on 60 mungbean genotypes in six environments (E1 to E6). Environment (E) and Genotype (GT) vectors are indicated by red lines with arrowheads.

As PC1 showed a high correlation with the genotypic main effect of DSI, this axis effectively captured the variation in disease incidence across the environments, with environments or genotypes positioned in similar directions or further from the origin reflecting higher or lower disease incidence levels. Thus, PC1 can be used as an indicator of disease incidence levels helping to distinguish resistant genotypes from susceptible ones based on their proximity along the axis in the biplot. The genotypes positioned at the far left of the biplot (lower PC1 score) are comparatively more resistant and genotypes positioned towards the right side of the biplot are comparatively more susceptible to the disease.

In GGE biplot analysis, stability was identified by examining the proximity of genotypes to the Average Tester Coordinate (ATC) rather than by the sign of PC2 value. The ATC serves as a reference line indicating the average performance across all environments. Genotypes that are closer to the ATC are considered more stable because their disease response remains consistent across varying environments. Conversely, genotypes further from the ATC line exhibit greater variability in their response to YMVD across environments, indicating comparatively lower stability. Genotypes that combine both stability (proximity to the ATC perpendicular axis) and superior performance (positioned at the far left of the PC1 axis with lower PC1 score) are preferable for selection as they are the stable resistant ones for the disease.

The genotypes positioned on the far-left side of the PC1 axis or biplot, such as VC 6372 (45-8-1) (16), VC 6370-92 (8), VC 6371-94 (9), and MIMB 7 (60), exhibited low DSI values, indicating a high level of resistance to the disease. These genotypes are located closer to the highly resistant end of the spectrum, reflecting their ability to withstand the disease pressure effectively across environments. Conversely, genotypes positioned on the far-right side of the PC1 axis, including VC1973A (ksp1) (10), Jangahn (38), AC8417 (47), AC8447 (56), and AC8431 (46), displayed high DSI values, suggesting susceptibility to the disease. The clear separation of resistant and susceptible genotypes along the PC1 axis highlighted the significant role of genotypic main effects in influencing disease resistance, making PC1 a reliable indicator of overall disease performance.

Genotypes positioned on the left side and closer to the horizontal axis are the highly resistant and most stable. Therefore, the genotypes namely VC 6370-92 (8), VC 6372 (45-8-1) (16) and VC6371-94 (9) are identified as most resistant and stable genotypes for YMVD over diverse environments. These findings are in agreement with the earlier reports (Yan e*t al*., 2007). Level of resistance and stability of MIMB7 (60), the resistant check of the study, to YMVD were found to be less than that of the above three genotypes.

Biplot of the relationship among six environments and 60 mungbean genotypes for YMVD incidence and stability is presented in Figure 3.

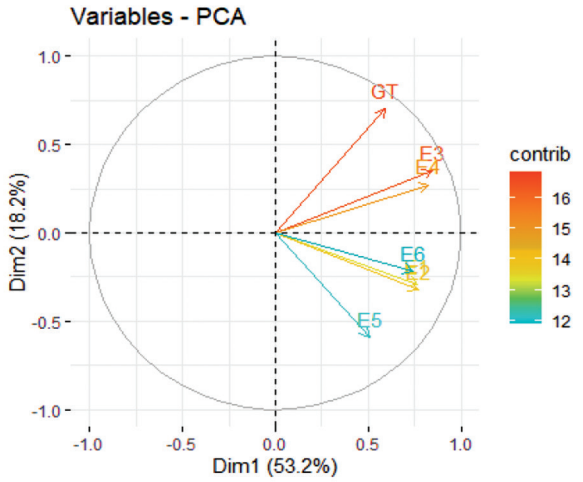

Figure 3. Biplot of the relationship among six environments (E) and 60 mungbean genotypes (GT) for YMVD severity index and stability.

The biplot visualizes the relationship among six environments (E1 to E6) and 60 mungbean genotypes (GT) based on their performance and stability for YMVD. The red arrow labeled GT, represents the genotypic vector summarizing the collective interaction of all genotypes with the environments. Each environment is indicated by its own vector (E), with the direction and length of these vectors reflecting their contribution to the variation in YMVD severity.

Four environments, E1 (Regional Agriculture Research and Development Center (RARDC), Kilinochchi *Yala* season), E2 (Regional Agriculture Research and Development Center (RARDC), Kilinochchi, *Maha* season), E5 (Grain Legumes and Oil Crops Research and Development Center (GLOCRDC), Agunakolapalassa, *Yala* season) and E6 (Grain Legumes and Oil Crops Research and Development Center (GLOCRDC), Agunakolapalassa, *Maha* season) are positioned in the lower division of the biplot. These environments demonstrated low disease incidence and low discriminating ability. Thus, they are not ideal test environments for YMVD. However, only E5 and E6 can be included in future tests conducted to evaluate genotypic stability of resistance to YMVD due to no correlation between these two environments for comparable performance of the genotypes leading to high representativeness, as evidenced by high cosign of the angle close to 90° between these two environments. The environments E1 and E2 and as a whole the location, Regional Agriculture Research and Development Center (RARDC), may be avoided from such tests due to their positive correlations with E6 leading to very low representativeness as evidenced by the small angle of much less than 90° between corresponding environments.

The environments E3 and E4 (Field Crops Research and Development Institute (FCRDI), mahailluppallama *Yala* and *Maha* seasons, respectively) demonstrated high disease incidence and high discriminating ability based on the positions of these environments which are located in the upper division of biplot (positive PC2). E4 can be identified as the ideal test environment for YMVD based on its very high discriminating ability and representativeness. However, E3 showed a positive correlation with E4 as evidenced by the small cosign of the angle which is much less than 90° showing low representativeness so that it should be avoided in future tests. Finally, the environments E4, E5 and E6 could be selected based on their representativeness and discrimination ability for screening of mungbean genotypes for reaction to YMVD to identify stable resistant genotypes over diverse environments.

The present study appeared highly efficient and effective in identifying stable resistant genotypes for YMVD over diverse environments and identifying the most suitable environments for YMVD screening in mungbean. The present study also highlighted the value of multi-environment testing and benefits of using GE interaction in identifying stable resistant genotypes in crop improvement programs for disease resistance. Thus, the approach used in the present study may be served as a model even for other crop improvement programs aiming to enhance disease resistance.

Conclusions

Three mungbean genotypes namely VC 6370-92 (8), VC6371-94 (9) and VC 6372 (45-8-1) (16) were identified as the most stable resistant genotypes to YMVD over diverse environments. Therefore, these genotypes should be used extensively for breeding resistant cultivars of mungbean. Genotypes VC1973A (ksp1) and Jangahn could be confirmed as susceptible checks consistently over diverse environments. Furthermore, among tested environments, *Maha* seasons at the Field Crops Research and Development Institute (FCRDI), Mahailluppallama and *Yala* and *Maha* seasons at the Grain Legumes and Oil Crops Research and Development Center (GLOCRDC), Agunakolapalassa, were identified as the most suitable environments for screening mungbean varieties for stable resistance to YMVD. Present study highlighted the value of multi-environment testing and benefits of assessing GE interaction in identifying stable resistant genotypes in crop improvement programs for disease resistance.

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