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Research Paper

Simple and Efficient Method to Identify Genotypes with Stable Resistance to Diseases over Diverse Environments by Assessing GE Interaction

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Abstract

Stable, disease-resistant genotypes in crop plants are commonly identified using methods such as regression analysis, AMMI, and GGE biplot. However, these approaches are complex and mainly based on the dynamic concept of stability, making them less suitable for identifying stable resistance across diverse environments. Therefore, the objective of the present study was to develop a simple, efficient, and effective method based on the static concept of stability to evaluate genotype × environment (GE) interaction, using Mungbean Yellow Mosaic Virus (MYMV) disease as a model. A total of 60 mungbean genotypes were screened across six diverse environments. Disease severity index (DSI) was calculated, and genotypes were classified into six categories: highly resistant, resistant, moderately resistant, moderately susceptible, susceptible, and highly susceptible. Based on this classification, ranks from 1 to 6 were assigned respectively, and GE interaction was analyzed using a newly introduced ranking method aligned with the static stability concept. The genotype VC 6371-94 was identified as the most stable and highly resistant across environments. In addition, VC 6369 (53-97), VC 6370 (30-65), VC 6372 (45-8-1), VC 6370-92, and VC 6486 (10-51) exhibited stable resistance to MYMV. Among the six environments tested, only three were found to be most suitable for effective screening of genotypes.

Keywords: Diseases of crop plants, Diverse environments, GE interaction, Ranking method, Stable resistance

Introduction

Diseases is one of the major causes for yield losses in crop plants approaching even 100% in susceptible varieties under severe infestation. It is a well-known fact that plant resistance is the most efficient, cost effective and environmentally friendly method to control any disease in crop plants. However, the disease resistance has to be stable over diverse environments where the crop is grown. Thus, the methods to identify resistant genotypes that are stable over diverse environments are essential.

The stability of crop performance across diverse environments is defined in different ways, depending on whether the focus is on yield consistency, adaptability, or the ability to maintain performance under varying conditions. Depending on the characteristic under consideration, there are two different concepts viz. Static or biological and dynamic or agronomic concepts of stability (Becker, 1981). In agronomic measurements of stability, stable genotype should improve its performance as the environment improves. This type of stability is ideal for traits like crop yield which is expected to improve as the environment improves. The static concept of stability is ideal and useful for traits, almost the same level of which has to be maintained in all environments. Examples for such traits are resistance against pests and diseases and quality traits. However, understanding the genotype × environment (GE) interaction is crucial for identifying genotypes with stable resistance to crop diseases (Yan & Kang, 2002) and for this, evaluating crop genotypes for disease resistance across diverse environments is essential.

In most of the studies, stable resistance to diseases of crop plants have been assessed by analysing GE interaction using dynamic or agronomic concept of stability. Regression model has been applied to identify stable resistance to bacterial blight (Nayak and Chakrabarti, 1986; Nayak *et al*., 2008) and blast (Mukherjee *et al*., 1998) diseases in rice and anthracnose disease in sorghum (Koima *et al*., 2023). The additive main effect and multiplicative interaction effect (AMMI) model has been used to identify stable blast resistance in rice (Abamu *et al*., 1998), stable broomrape resistance in Faba beans (Flores *et al*., 1996), stable late blight resistance in potato (Forbes *et al*., 2005) and stable *rhizomania* resistance in sugar beet (Rajabi *et al*., 2023). GGE biplot method which is comparatively more complex has been used to identify stable resistant varieties to diseases of different crop plants (Egesi *et al*., 2009; Sharma *et al*., 2015; Sharma *et al*., 2016; Parihar *et al*., 2017a; Parihar *et al*., 2017b; Tamang *et al*., 2022; Rizal and Sana, 2024). Robinson and Talli (1999) used regression and AMMI models on comparative basis to identify stable net blotch resistance in barley. All these statistical methods of regression analysis, AMMI and GGE biplot are strongly related to dynamic or agronomic concept of stability. However, no study is available where the static concept of stability which is ideal for traits like diseases, has been used to assess stable resistance to diseases of crop plants over diverse environments. Thus, the objective of the present study was

to introduce a simple, efficient and effective method which is easy to understand and use and related to static concept of stability to identify genotypes with stable resistance to diseases by assessing GE interaction. Mungbean Yellow Mosaic Virus (MYMV) disease which is one of the major diseases in mungbean in Sri Lanka was taken as an example. The most conducive environments to screen genotypes for reaction to disease can also be identified by this method. This method can also serve as a model in crop improvement programs aiming to address similar challenges.

Materials and Methods

The proposed ranking method will be explained using experimental results published earlier by the same authors (Kumararathna *et al*., 2024) so that some parts of the materials and methods and results and discussion published in the earlier study are repeated in the present study.

Plant materials and experimental locations

Sixty mungbean genotypes including known resistant and susceptible checks were included in the study (Table 1). The resistant check was MIMB 7 which has been identified as a moderately resistant genotype in the previous tests 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 to represent location diversity, over four growing seasons to represent seasonal diversity. Four growing seasons were two *Yala* or dry seasons (2021 *Yala* and 2022 *Yala*) and two *Maha* or wet seasons (2021/2022 *Maha* and 2022/23 *Maha*). If the season × year interaction is not significant, data from two *Yala* seasons and two *Maha* seasons could be averaged separately, to represent *Yala* and *Maha* seasons. Three locations combined with the two seasons (location × season combinations) constituted six distinct environments in the study to represent environmental diversity (Table 2). Thus, genotypic reaction to MYMV disease could be studied over diverse environments to identify stable resistant genotypes using GE interaction.

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

Genotype $	Source of Origin *	No.	Genotype	Source of Origin
MIMB59/V3476	Dept.	31	VO27094B-G	Exotic
ksp1/NM54	Dept.	32	VO2817B-G	Exotic
MIMB101/V2802	Dept.	33	VO3131A-G	Exotic
AC8419	PGRC	34	Eoul	Exotic
AC8429	PGRC	35	J71	Exotic
AC8449	PGRC	36	Dahyeon	Exotic
AC8452	PGRD	37	Sohyeon	Exotic
VC 6370-92	Exotic	38	Jangahn (SC)	Exotic

Genotype $	Source of Origin *	No.	Genotype	Source of Origin
VC6371-94	Exotic	39	AC0099	PGRC
VC1973A(ksp1)(SC)	Exotic	40	AC0259	PGRC
VC6351B-20G	Exotic	41	AC2943	PGRC
VC 6368 (46-40-4)	Exotic	42	AC3022	PGRC
VC 6369(53-97)	Exotic	43	AC1570	PGRC
VC 6370 (30-65)	Exotic	44	AV8421	PGRC
VC 6370a	PGRC	45	AC8421	PGRC
VC 6372 (45-8-1)	Exotic	46	AC8431	PGRC
VC 6469-12-3-4A	Exotic	47	AC8417	PGRC
VC 6486-10-51	Exotic	48	AC8416	PGRC
VC6489-9-1	Exotic	49	AC8446	PGRC
VC6492-59A	Exotic	50	AC8455	PGRC
VC6493-44-1	Exotic	51	AC8433	PGRC
VC6510-151-1	Exotic	52	AC8436	PGRC
MIMBAUS923	Local	53	AC84287	PGRC
TVO1251A-G	Exotic	54	AC8425	PGRC
TVO1270A-G	Exotic	55	AC8434	PGRC
TVO1596A-G	Exotic	56	AC8447	PGRC
TVO3981A-G	Exotic	57	AC8430	PGRC
TVO3982A-G	Exotic	58	AC8445	PGRC
VO11282A-G	Exotic	59	AC8435	PGRC
VO11254A-G	Exotic	60	MIMB 7(MRC)	Dept.

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

**PGRC- Germplasms received from Plant Genetic Resource Center, Department of agriculture, Exotic- Germplasm received from other countries, Dept. - Mungbean lines developed by the Department of agriculture.*

Experimental design

The field experiment in each environment was established in a randomized complete block design (RCBD) with two replications. 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*" (*Macroptilium lathyroides*) was planted after each genotype to be evaluated for reaction to MYMV disease. Insecticides were intentionally omitted to maintain an optimal vector (whitefly) population to create a high inoculum pressure of the MYMV disease. Regular surveillance of the crops was carried out to detect any symptoms of MYMV disease.

Table 2. 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	6.3297° N	80.8567° E	117m above sea level
Field Crops Research and Development Institute (FCRDI)	*Maha*	E4			
Agunakolapalassa (South)	*Yala*	E5	8.1114° N	80.4703° E	51m above sea level
Grain Legumes and Oil Crops Research and Development Centre (GLOCRDC)	*Maha*	E6			

Data recorded

Degree of infection with MYMV disease for each of 120 individual plants within a genotype was recorded separately using the disease score scale of 0 to 9 (Table 3) 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 (Bashir *et al*., 2006). The DSI for MYMV disease for each genotype was calculated as follows;

After calculating DSI, different DSI ranges were used to categorize mungbean genotypes for reaction to MYMV disease into six groups (Ttable 4). If the DSI of populations were 0 or <1, 1 - 10, 11 - 20, 21 – 30, 31 – 50 and > 50%, they were recorded as highly resistant, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible, respectively (Malathi *et al*., 2008; Kumara *et al*., 2014).

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

Table 3. Degree of infection as measured by disease score scale based on visual symptoms of MYMV disease for each individual plant.

Disease score scale	Visual symptoms
0	Complete absence of symptoms
1	Small yellowing spots scattered on some 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 shrivelled seeds

Table 4. Disease severity index ranges used for categorization of mungbean genotypes for reaction to MYMV disease and ranks allocated for each disease reaction category.

Disease Severity Index range	Disease Reaction category	Rank
0	Highly resistant (HR)	1
1 to 10	Resistant (R)	2
11 to 20	Moderately resistant (MR)	3
21 to 30	Moderately susceptible (MS)	4
31 to 50	Susceptible (S)	5
>51	Highly susceptible (HS)	6

Statistical analysis

The DSI data were analysed using pooled ANOVA over environments by SAS (V 9.3). In the analysis, the total variance was partitioned into components due to genotypes (G), environments (E), and their interaction (GE). As original data were percentages of which the range was more than 40% they were subjected to arcsine transformation before analysis.

If the GE interaction is found to be significant, the disease performance and stability of genotypes over diverse environments will be further studied by analysing GE interaction using the ranking method introduced by the present study where analysis is performed on ranks that are allocated to disease reaction categories.

Ranking method

In the ranking method, disease reaction categories are assigned ranks (Table 4). The highly resistant category is assigned rank 1 and this is continued assigning ranks up to 6 for the highly susceptible variety. Thus, the genotypes in each environment are assigned ranks based on the disease reaction category and for each genotype average rank and variance in ranks across environments are calculated. The most resistant genotype is the one with the lowest average in rank. In static mean of stability,

a stable genotype is the one possessing a constant performance irrespective of any changes in environmental conditions (Becker and Leon, 1988). Thus, the most stable resistant genotype would be the one with the lowest average rank and the lowest variance in rank across environments and vice versa. Ranks can be converted back to disease reaction categories when presenting results.

Ranking method can also be used to identify the best environments for screening genotypes for reaction to MYMV disease. In each environment, average rank and the variance of ranks among genotypes tested in that environment should be calculated. The environments with the average rank equals to median (3.5) and the highest variance in ranks would be the best environments for screening genotypes for reaction to MYMV disease. Thus, the environments should be selected simultaneously for average rank close to 3.5 and the higher variance in rank while giving equal weights to both parameters. The environments with average rank equals to 3.5 will contain genotypes with disease reaction towards susceptibility as well as towards resistance and environments with comparatively higher variances will cover most of the disease reaction groups.

Results and Discussion

When data were analysed for each season separately over years in each location, season × year interaction was found to be not significant in each location so that data from two *Yala* seasons and two *Maha* seasons were averaged separately, to represent *Yala* and *Maha* seasons in each location. Disease severity index for MYMV disease of 60 mungbean genotypes in six environments are presented in Table 5. The mean disease severity index (DSI) ranged from 0.00 (highly resistant) to 55.56% (highly susceptible). The severity of MYMV disease 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 combined analysis of variance over environments (Table 6).

Table 5. Disease severity index for 60 mungbean genotypes for yellow mosaic virus disease in six environments.

Genotype*	Disease severity index						
	Environments (E)						Average
	E1	E2	E3	E4	E5	E6	
MIMB59/V3476	8.66	25.05	48.31	25.41	9.12	4.70	20.21
ksp1/NM54	5.86	16.90	36.45	44.03	11.68	5.77	20.12
MIMB101/V2802	6.74	16.39	48.61	37.78	6.71	6.95	20.53
AC8419	4.25	17.96	27.52	33.33	7.83	6.01	16.15
AC8429	9.74	16.13	34.58	49.09	10.29	5.89	20.95
AC8449	9.59	7.13	35.64	23.35	12.21	11.38	16.55
AC8452	4.10	18.05	18.45	28.92	4.05	3.15	12.79
VC 6370-92	0.30	2.22	1.28	0.70	0.00	0.00	0.75
VC6371-94	0.00	0.34	0.04	0.87	0.00	0.00	0.21
VC1973A(ksp1)(SC)	14.66	34.99	48.03	47.39	24.29	30.21	33.26
VC6351B-20G	5.95	13.89	12.41	18.97	6.03	5.76	10.50
VC 6368 (46-40-4)	7.64	3.46	10.63	20.12	7.64	8.12	9.60
VC 6369(53-97)	4.03	3.61	2.16	4.63	5.67	4.31	4.07
VC 6370 (30-65)	6.33	4.63	7.44	9.04	7.21	2.56	6.20
VC 6370a	12.95	22.68	9.48	26.06	5.62	8.82	14.27
VC 6372 (45-8-1)	0.00	0.00	0.06	1.05	0.00	0.00	0.19
VC 6469-12-3-4A	7.92	8.87	7.12	15.63	7.30	5.88	8.79
VC 6486-10-51	3.61	2.04	9.14	2.48	6.20	4.47	4.66
VC6489-9-1	8.39	37.06	11.78	28.10	7.95	8.18	16.91
VC6492-59A	10.08	26.16	16.38	32.06	8.45	8.10	16.87
VC6493-44-1	12.31	28.89	17.95	42.86	9.17	7.89	19.85
VC6510-151-1	6.55	18.48	10.54	16.33	11.63	6.06	11.60
MIMBAUS923	0.94	2.77	18.96	10.38	12.46	7.68	8.87
TVO1251A-G	2.97	4.71	11.12	25.04	10.83	5.86	10.09
TVO1270A-G	0.87	3.25	14.57	19.52	10.74	5.77	9.12
TVO1596A-G	2.41	8.67	15.50	18.75	8.34	5.98	9.94
TVO3981A-G	1.97	11.79	20.06	18.06	10.79	6.66	11.56
TVO3982A-G	5.11	13.10	11.95	39.18	11.12	6.90	14.56
VO11282A-G	5.17	8.41	27.97	36.32	10.10	10.77	16.46
VO11254A-G	3.37	12.18	14.19	39.47	11.52	12.83	15.59
VO27094B-G	5.84	8.32	12.88	32.32	12.92	8.26	13.42
VO2817B-G	3.19	12.93	19.80	34.88	11.45	7.64	14.98
VO3131A-G	3.95	5.97	19.50	30.77	13.18	8.57	13.66
Eoul	5.86	10.19	15.83	35.28	18.32	9.69	15.86
J71	5.89	12.00	21.01	9.21	12.29	7.01	11.24

Genotype*	Disease severity index						
	Environments (E)						Average
	E1	E2	E3	E4	E5	E6	
Dhyeon	11.62	21.20	38.02	12.14	15.13	18.51	19.44
Sohyeon	7.26	15.37	32.69	37.99	14.69	8.23	19.37
Jangahn (SC)	15.19	42.84	36.36	55.56	15.67	28.94	32.43
AC0099	11.34	25.50	13.45	16.94	16.45	23.78	17.91
AC0259	7.69	27.37	28.96	15.11	19.30	14.38	18.80
AC2943	13.13	28.65	31.05	8.76	18.81	23.10	20.58
AC3022	12.44	28.01	29.13	16.70	15.79	16.77	19.81
AC1570	7.12	23.49	21.85	18.16	17.30	9.41	16.22
AV8421	11.78	30.06	20.13	29.04	17.65	12.04	20.12
AC8421	9.74	12.72	36.54	22.08	27.61	17.90	21.10
AC8431	11.75	21.47	20.85	32.08	28.16	22.18	22.75
AC8417	14.97	20.68	35.77	31.81	20.67	22.30	24.37
AC8416	12.88	17.00	15.93	47.64	20.20	13.37	21.17
AC8446	12.00	12.37	18.10	54.19	25.60	22.09	24.06
AC8455	6.95	34.18	32.80	38.03	12.88	12.82	22.94
AC8433	7.95	17.06	33.85	48.20	25.50	11.76	24.05
AC8436	3.53	10.65	31.81	8.56	24.47	10.08	14.85
AC84287	14.15	28.76	39.00	11.35	23.30	12.58	21.52
AC8425	5.45	14.09	32.88	32.36	25.45	11.86	20.35
AC8434	5.61	17.28	36.20	19.63	30.30	12.77	20.30
AC8447	4.06	37.93	45.87	35.42	30.45	12.89	27.77
AC8430	6.97	28.08	44.60	16.94	17.07	16.60	21.71
AC8445	6.04	10.12	16.84	18.33	20.75	8.98	13.51
AC8435	11.48	22.07	30.70	13.37	19.72	9.65	17.83
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,*

Table 6. Analysis of variance of MYMV disease severity index in 60 mungbean genotypes tested in six environments.

Source of variance	DF	SS	MS	F value	P value
Environments (E)	5	52140.3	10428.8	995.4	<0.0001
Genotypes (G)	59	3892.7	659.7	62.98	<0.0001
Reps/E	6	11.76	11.76	1.2	0.29
G × E	295	23947.6	111.65	10.66	<0.001
Error	354	3760.8	10.47		

As the GE interaction effect was found to be significant, the different genotypes reacted to MYMV disease differently in different environments. Thus, the GE effects was further studied to identify resistant genotypes that are stable across different environments using ranking method introduced by the present study.

Disease reaction categories and ranks in tested environments and average and variance in ranks across environments for each genotype and the average and variance in rank among genotypes for each environment are presented in Table 7.

Table 7. Disease reaction categories and ranks in tested environments and average and variance in ranks across environments for each genotype and the range and variance of ranks among genotypes for each environment

Genotypes *	Disease reaction category and rank						Rank	
	Environments (E)							
	E1	E2	E3	E4	E5	E6	Mean	Variance
MIMB59/V3476	R(2)	MS(4)	S(5)	MS(4)	R(2)	R(2)	3.3(MR)	1.77
ksp1/NM54	R(2)	MR(3)	S(5)	S(5)	MR(3)	R(2)	3.3(MR)	1.87
MIMB101/V2802	R(2)	MR(3)	S(5)	S(5)	R(2)	R(2)	3.2(MR)	2.17
AC8419	R(2)	MR(3)	MS(4)	S(5)	R(2)	R(2)	3.0(MR)	1.60
AC8429	R(2)	MR(3)	S(5)	S(5)	MR(3)	R(2)	3.3(MR)	1.87
AC8449	R(2)	R(2)	S(5)	MS(4)	MR(3)	MR(3)	3.2(MR)	1.37
AC8452	R(2)	MR(3)	MR(3)	MS(4)	R(2)	R(2)	2.7(MR)	0.67
VC 6370-92	HR(1)	R(2)	R(2)	HR(1)	HR(1)	HR(1)	1.3(R)	0.27
VC6371-94	HR(1)	HR(1)	HR(1)	HR(1)	HR(1)	HR(1)	1.0(HR)	0.00
VC1973A(ksp1)(SC)	MR(3)	S(5)	S(5)	S(5)	MS(4)	S(5)	4.5(MS)	0.70
VC6351B-20G	R(2)	MR(3)	MR(3)	MR(3)	R(2)	R(2)	2.5(R)	0.30
VC 6368 (46-40-4)	R(2)	R(2)	MR(3)	MS(4)	R(2)	R(2)	2.5(R)	0.70
VC 6369(53-97)	R(2)	R(2)	R(2)	R(2)	R(2)	R(2)	2.0(R)	0.00
VC 6370 (30-65)	R(2)	R(2)	R(2)	R(2)	R(2)	R(2)	2.0(R)	0.00
VC 6370a	MR(3)	MS(4)	R(2)	MS(4)	R(2)	R(2)	2.8(MR)	0.97
VC 6372 (45-8-1)	HR(1)	HR(1)	HR(1)	R(2)	HR(1)	HR(1)	1.2(R)	0.17
VC 6469-12-3-4A	R(2)	R(2)	R(2)	MR(3)	R(2)	R(2)	2.2(R)	0.17
VC 6486-10-51	R(2)	R(2)	R(2)	R(2)	R(2)	R(2)	2.0(R)	0.00
VC6489-9-1	R(2)	R(2)	MR(3)	MS(4)	R(2)	R(2)	3.0(MR)	1.60
VC6492-59A	MR(3)	MS(4)	MR(3)	S(5)	R(2)	R(2)	3.2(MR)	1.37
VC6493-44-1	MR(3)	MS(4)	MR(3)	S(5)	R(2)	R(2)	3.2(MR)	1.37
VC6510-151-1	R(2)	MR(3)	MR(3)	MR(3)	MR(3)	R(2)	2.7(MR)	0.27
MIMBAUS923	HR(1)	R(2)	MR(3)	MR(3)	MR(3)	R(2)	2.3(R)	0.67
TVO1251A-G	R(2)	R(2)	MR(3)	MS(4)	MR(3)	R(2)	2.7(MR)	0.67
TVO1270A-G	HR(1)	R(2)	MR(3)	MR(3)	MR(3)	R(2)	2.3(R)	0.67
TVO1596A-G	R(2)	R(2)	MR(3)	MR(3)	R(2)	R(2)	2.3(R)	0.27

Genotypes *	Disease reaction category and rank						Rank	
	Environments (E)							
	E1	**E2**	**E3**	**E4**	**E5**	**E6**	**Mean**	**Variance**
TVO3981A-G	R(2)	MR(3)	MS(4)	MR(3)	MR(3)	R(2)	2.8(MR)	0.57
TVO3982A-G	R(2)	MR(3)	MR(3)	S(5)	MR(3)	R(2)	3.0(MR)	1.20
VO11282A-G	R(2)	R(2)	MS(4)	S(5)	MR(3)	MR(3)	3.2(MR)	1.37
VO11254A-G	R(2)	MR(3)	MR(3)	S(5)	MR(3)	MR(3)	3.2(MR)	0.97
VO27094B-G	R(2)	R(2)	MR(3)	S(5)	MR(3)	R(2)	2.8(MR)	1.37
VO2817B-G	R(2)	MR(3)	MR(3)	S(5)	MR(3)	R(2)	3.0(MR)	1.20
VO3131A-G	R(2)	R(2)	MR(3)	S(5)	MR(3)	R(2)	2.8(MR)	1.37
Eoul	R(2)	MR(3)	MR(3)	S(5)	MR(3)	R(2)	3.0(MR)	1.20
J71	R(2)	MR(3)	MS(4)	R(2)	MR(3)	R(2)	2.7(MR)	0.67
Dhyeon	R(2)	MS(4)	S(5)	MR(3)	MR(3)	MR(3)	3.5(MR)	0.70
Sohyeon	R(2)	MR(3)	S(5)	S(5)	MR(3)	R(2)	3.3(MR)	1.87
Jangahn (SC)	MR(3)	S(5)	S(5)	HS(6)	MR(3)	MS(4)	4.3(S)	1.47
AC0099	MR(3)	MS(4)	MR(3)	MR(3)	MR(3)	MS(4)	3.3(MR)	0.27
AC0259	R(2)	MS(4)	MS(4)	MR(3)	MR(3)	MR(3)	3.2(MR)	0.57
AC2943	MR(3)	MS(4)	S(5)	R(2)	MR(3)	MS(4)	3.5(MR)	1.10
AC3022	MR(3)	MS(4)	MS(4)	MR(3)	MR(3)	MR(3)	3.3(MR)	0.27
AC1570	R(2)	MS(4)	MS(4)	MR(3)	MR(3)	R(2)	3.0(MR)	0.80
AV8421	MR(3)	S(5)	MS(4)	MS(4)	MR(3)	MR(3)	3.7(MS)	0.67
AC8421	R(2)	MR(3)	S(5)	MS(4)	MS(4)	MR(3)	3.5(MR)	1.10
AC8431	MR(3)	MS(4)	MS(4)	S(5)	MS(4)	MS(4)	4.0(MS)	0.40
AC8417	MR(3)	MS(4)	S(5)	S(5)	MS(4)	MS(4)	4.7(S)	0.57
AC8416	MR(3)	MR(3)	MR(3)	S(5)	MS(4)	MR(3)	3.5(MR)	0.70
AC8446	MR(3)	MR(3)	MR(3)	HS(6)	MS(4)	MS(4)	3.8(MS)	1.37
AC8455	R(2)	S(5)	S(5)	S(5)	MR(3)	MR(3)	3.8(MS)	1.77
AC8433	R(2)	MR(3)	S(5)	S(5)	MS(4)	MR(3)	3.7(MS)	1.47
AC8436	R(2)	MR(3)	S(5)	R(2)	MS(4)	MR(3)	3.7(MS)	1.37
AC84287	MR(3)	MS(4)	S(5)	MR(3)	MS(4)	MR(3)	3.7(MS)	0.67
AC8425	R(2)	MR(3)	S(5)	S(5)	MS(4)	MR(3)	3.7(MS)	1.47
AC8434	R(2)	MR(3)	S(5)	MR(3)	S(5)	MR(3)	3.0(MR)	1.50
AC8447	R(2)	S(5)	S(5)	S(5)	S(5)	MR(3)	4.7(S)	1.77
AC8430	R(2)	MS(4)	S(5)	MR(3)	MR(3)	MR(3)	3.3(MR)	1.07
AC8445	R(2)	MR(3)	MR(3)	MR(3)	MS(4)	R(2)	2.8(MS)	0.57
AC8435	MR(3)	MS(4)	S(5)	MR(3)	MR(3)	R(2)	3.3(MR)	1.07
MIMB 7 (MRC)	HR(1)	R(2)	R(2)	R(2)	R(2)	R(2)	1.8(R)	0.17
Average rank	2.17	3.13	3.67	3.78	2.87	2.48		
Variance in rank	0.345	1.033	1.379	1.596	0.795	0.661		

** SC – Susceptible check, MRC – Moderately resistant check,*

On the average, genotypes exhibited considerable differences in their reaction to MYMV disease as measured by ranks. Based on the average performance across environments, ranks of susceptible checks, VC1973A-ksp1 and Jangahn were 4.5 and 4.3, respectively showing susceptible reaction as expected. However, the rank of MIMB 7 which is expected to be moderately resistant was 1.8 so that it could be categorized as resistant. Further, it was revealed that genotype VC 6371 -94 recorded average rank 1 with 0 variance indicating that it is the only highly stable resistant genotype in the test. This is really important as this is the only highly stable resistant mungbean genotype found in the country to date. The genotypes VC 6369 (53-97), VC 6370 (30-65), VC 6372 (45-8-1), VC 6370-92 and VC 6486 (10-51) showed stable resistance similar to MIMB 7. Genotypes AC8417 and AC8447 expressed susceptibility to the disease consistently over environments.

Results of the mungbean genotypic screening against the MYMV disease in the present study are only in partial agreement with the results reported by Kumararathna *et al*., (2024) (same authors of the present study) on the same data set of the same experiment by analysing GE interaction using GGE biplot technique. Using GGE biplot technique, only the genotypes namely VC 6370-92, VC 6372 (45-8-1) and VC6371-94 were identified but not the genotypes VC 6369 (53-57), VC 6370 (30-65) and VC 6486 (10-51) as the most resistant and stable genotypes for MYMV disease over diverse environments. In addition, GGE biplot technique identified VC 8431 as a genotype which is consistently susceptible over diverse environments but not the ranking method in the present study. Furthermore, the VC 6371-94 was identified as the only highly stable resistant genotype by the ranking method but GGE biplot technique did not identify any highly stable resistant genotypes over diverse environments. Although GGE biplot technique identified MIMB 7 as moderately resistant, the ranking method in the present study identified MIMB 7 as a stable resistant genotype. However, the findings made by the Kumararathna *et al*. (2024) are in agreement with the earlier reports by Yan *et al*. (2000) who also used the GGE biplot method. The observed differences in identifying stable resistant and susceptible genotypes between ranking and GGE biplot methods may be purely due to the conceptual differences between two methods.

The environments with the average rank closer to 3.5 (median) or more and comparatively higher variances in ranks should be the best environments out of tested environments for screening of mungbean germplasm for reaction to MYMV disease. Such environments record the highest number of disease reaction categories (representativeness) particularly including highly susceptible category showing the presence of favourable environmental conditions and adequate genotypic differences (discriminating power) for the disease. Thus, out of the six environments used, E4 which is the *Maha* season at FCRDI, MI, recorded the average

rank closer to 3.5 including both highly susceptible and highly resistant categories and highest variance in rank confirming the presence of all the disease reaction categories indicating that it is the best out of six environments to screen mungbean germplasm for reaction to MYMV disease. The next favourable environment to screen mungbean germplasm for reaction to MYMV disease appeared to be the E3, the *Yala* season at FCRDI, MI which recorded the average rank closer to 3.5 and higher variance in ranks. Thus, as a location FCRDI, MI is the best to screen mungbean germplasm for reaction to MYMV disease. E2 also appeared to be appropriate to screen mungbean germplasm for reaction to MYMV disease as it recorded an average rank closer to 3.5 and high variance in ranks. This environment is the *Maha* season at RARDC, Kilinochchi. Based on the spearman's correlations, E2 was dissimilar to E3 (r = - 0.820*) but was similar to a certain degree to E4 (r = 0.461*). E3 was also similar to a certain degree to E4 (r = 0.428*). This again confirms that selection of environments is appropriate.

Selection of environments for mungbean genotypic screening against the MYMV disease in the present study is not in agreement with the results reported by Kumararathna *et al*. (2024) by analysing GE interaction using GGE biplot technique. The GGE biplot technique selected E4, E5 and E6 as environments suitable for mungbean genotypic screening against the MYMV disease. Most of the disease reaction categories recorded in E5 and E6 are towards moderately resistant to resistant so that their ability to produce full range of disease reaction categories is remote. Therefore, as these environments are not conducive for high disease infestation, they are not suitable for screening genotypes against MYMV disease. However, E4 has been selected by both ranking and GGE biplot methods as an ideal environment for screening mungbean genotypes for reaction to MYMV disease.

Ranking method with static concept of stability appears ideal for identifying genotypes with stable resistance to diseases. GGE biplot method is comparatively less efficient in identifying genotypes possessing constant performance irrespective of any changes in environmental conditions as it is strongly related to dynamic concept of stability. In addition, ranking method is simple and less complex as it is easy to understand and use and more efficient as it identifies comparatively more number of stable resistant as well as susceptible genotypes which have been missed by the GGE biplot method. Identification of comparatively less number of stable resistant as well as susceptible genotypes by the GGE biplot method cannot be judged as conservative.

Conclusion

Importance of the use of GE interaction for identification of stable resistant genotypes in crop improvement programs for disease resistance is highlighted. Ranking method that analyses GE interaction using static concept of stability introduced by the present study was found to be ideal for identifying genotypes with stable

resistance over diverse environments to MYMV disease in mungbean. This method appears to be simple, less complex, efficient and easy to understand and use.

VC 6371 -94 was found to be the only highly stable resistant genotype while VC 6369 (53-97), VC 6370 (30-65), VC 6372 (45-8-1), VC 6370-92 and VC 6486 (10-51) were identified as stable resistant genotypes to MYMV disease over diverse environments. Genotypes AC8417 and AC8447 expressed susceptibility to the disease consistently over diverse environments.

The three environments of *Yala* and *Maha* seasons at FCRDI and *Maha* season at RARDC, kilinochchi, were identified as the most suitable environments for screening genotypes for reaction to MYMV disease in mungbean.

Author Contribution

MJMPK conducted the experiment, collected data, and prepared the manuscript. DSZA provided guidance for carrying out the research, data collection, data analysis, and manuscript preparation. DMJBS and DMC provided instructions for conducting the trials and guidance in writing the manuscript.

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