



Evaluation of mungbean genotypes for yellow mosaic disease resistance using principal component analysis

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Summary

The study was conducted to evaluate the response of various mungbean genotypes against yellow mosaic disease (YMD) in different locations of India. Key findings indicate that some genotypes, such as MH 1142, MH 1908, MI 2023-01, ML 2748 and OBBG 107, consistently exhibited resistance across multiple locations, making them potential candidates for breeding YMD-resistant genotypes. However, genotypes like Kopargaon, BM 2021-4, JLPM 818-8 and RVSM 2213 displayed high susceptibility, highlighting the need for effective disease management strategies. Principal Component Analysis (PCA) was performed to analyse variations in disease response among genotypes based on location. PC1 explained the highest variance (43.61%), primarily influenced by locations like Hisar, Ludhiana, Shilongani, Dholi and Jhansi, which contributed significantly to overall disease susceptibility and resistance patterns. PC2 (13.92%) captured additional variability, mainly driven by Ayodhya and Raipur, while PC3 (11.43%) and PC4 (9.21%) were influenced by Sagar and Vamban, respectively, indicating regional disease response variations. Correlation analysis between locations and principal components revealed strong associations of PC1 with disease responses in Hisar, Ludhiana, Shilongani, Dholi and Jhansi. PC2 was strongly linked to Ayodhya and Raipur, suggesting location-specific differences in disease susceptibility. The study underscores the importance of selecting resistant genotypes for breeding programs and tailoring disease management strategies based on regional variations in YMD incidence.

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Introduction

Mungbean [*Vigna radiata* (L.) R. Wilczek] is a short-duration legume crop and known as a rich source of protein. The crop is highly vulnerable to several viral diseases, with yellow mosaic disease (YMD) being the most severe (Pratap et al. 2018). YMD caused by mungbean yellow mosaic virus (MYMV) belongs to begomoviruses of the family Geminiviridae, with bipartite genome (Bos 1999; Karthikeyan et al. 2004). In India, YMD was first reported in 1955 at IARI, New Delhi (Nairani 1960). This disease is transmitted by whitefly (*Bemisia tabaci* Genn) in a persistent (calculative)

manner (Nene 1972). It has been confirmed that at least two viruses, i.e. MYMV and MYMIV species causing yellow mosaic disease, are prevalent in the Indian subcontinent. Viral particles associated with YMD are found to be isometric and geminate, having 18-30 nm in size with two single-stranded DNA molecules (DNA A & DNA B) of 2726 and 2775 nucleotides, respectively (Morinaga et al. 1990; Morinaga et al. 1993; Bos 1999; Hull 2004). One of these species, mungbean yellow mosaic India virus is considered to be more predominant in northern, central and eastern India and other MYMV in the peninsular region of India (Karthikeyan et al. 2004; Malathi et al. 2008; Gupta et al. 2013; Nair et al. 2017; Sachin et al. 2019). It caused infection on other legume crops like urdbean, soybean, and cowpea in Sri Lanka, Pakistan, Bangladesh, and India (Qazi et al. 2007; Biswas et al. 2008; John et al. 2008). The disease reduces the yield of 5–100 per cent depending upon disease severity, host resistance level and prevailing environmental conditions (Rathi 2002). The yield loss from the YMD depends on the stage of infection; late infection causes a 32–78 per cent reduction in mungbean grain yield and infection at early growth stages may even lead up to 100 per cent yield loss (Khattak et al. 2000).

The management of YMD is focused mainly on the vector (whitefly) population, which depends on the weather conditions of a particular region (Alam et al. 2014). However, pesticides can provide temporary

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management of whitefly, but do not give effective control of the disease. A more efficient and environmentally safe long-term solution is the development of mungbean cultivars resistant to both the virus and its vector, *B. tabaci*. A good deal of research efforts has been directed towards the screening of mungbean germplasm against YMD, thus identifying promising cultivars possessing resistance to mungbean yellow mosaic virus is a top priority for most pulse crops (Akhtar et al. 2011; Mishra et al. 2020; Singh et al. 2020; Pratap et al. 2021; Mariyappan and Nandini 2022; Pathan et al. 2023). Aski et al. (2015) studied mode of inheritance for resistance against MYMIV in mungbean. Nair et al., 2017 identified the mungbean lines with tolerance or resistance to yellow mosaic in fields in India where different begomovirus species and different *Bemisia tabaci* cryptic species predominate. Host resistance is the most efficient and environmentally friendly approach to reducing yellow mosaic disease damage in mungbean. Understanding the inheritance of disease resistance is essential for breeding resistant cultivars. Inheritance of resistance to disease in mungbean has been studied extensively using different resistant sources but results were contradictory. Although needed to study using various resistant sources at different geographical conditions. Understanding the nature and organization of variation is essential for the genetic improvement of crop species. Numerous traits are often assessed for germplasm evaluation, screening and characterization against major stresses. However, screening large germplasm collections across different geographical conditions presents challenges in consolidating information and drawing valid conclusions. In such cases, Principal

Component Analysis (PCA) is a valuable technique for reducing large datasets with multiple variables into key principal components, enhancing data interpretation (Haldhar et al. 2019). This statistical method is commonly used for data compression, reduction and transformation. By simultaneously analysing multiple measurements per individual, PCA is widely applied in selecting elite genotypes. With these considerations, this study was conducted for screening genotypes against disease to evaluate the relationship among locations and establish selection criteria for identifying genetic variations associated with disease resistance within a population.

Materials and Methods

A total of sixty-one mungbean genotypes were evaluated against yellow mosaic disease (YMD) under natural field conditions in different zone of India during *kharif* season of year 2023. All genotypes were grown in randomized block design with two replications in paired row of four-meter length and kept the spacing of 30×10 cm. Local infector line was also raised after five test genotypes for providing the better spread of the infection of YMD. Conventional agronomic practices were employed to keep the crop in good conditions at all locations. No pesticides were applied against the whitefly to ensure high inoculum pressure throughout the season. The data for YMD were recorded following the rating system (Table 1) at 30 (Ist time) and 45 days after sowing (IInd time) of crop. The second time data was used for determined the response of genotypes against disease and farther statistical analysis by GRAPES 1.0.0 (Gopinath et al. 2020).

Table 1. Disease scoring scale (0-9) for yellow mosaic disease based on the percentage of disease intensity of symptoms

Disease Scale	Percent infection	Visual symptoms	Reaction
0	All plants free of the disease symptoms	Complete absence of symptoms	Immune (HR)
1	0.1-10 % infection	Small yellowish spots scattered on some leaves	Resistant (R)
3	10.1-20 % infection	Yellowish bright spots common on leaves, easy to observe	Moderately Resistant (MR)
5	20.1-30% infection	Yellowish bright specks common on leaves, easy to observe with larger patches of symptoms	Moderately Susceptible (MS)
7	30.1-50% infection	Bright yellow specks or spots on all leaves, minor stunting of plants and less number of pods	Susceptible (S)
9	>50% and more infection	Yellowing of all leaves, shortening of internode, deformed pods produced with small, immature and shriveled seeds	Highly Susceptible (HS)

Results and Discussion

Location-specific disease response of YMD

Fig. 1 depicted the disease reaction of YMD on mungbean genotypes varied notably across the locations. The summarize results from all the locations revealed to table 2, some genotypes exhibited high resistance (R, score 1) to moderate resistance (MR,

score 3) across multiple locations, including MH 1142, MH 1908, MI 2023-01, ML 2748 and OBGG 107. While, DGG 214, IGKM 2021-1, IPM 02-3, MH 1890, MH 2-15, MI 13-47, ML 2738, ML 2878, MI 2844, ML 818, OBGG 110 and PM 2015 at selected locations. The susceptibility levels of these genotypes varied by location, indicating that disease severity may be influenced by

environmental conditions. Several genotypes were classified as susceptible (S, score 7) or highly susceptible (HS, score 9) across locations, indicating severe disease vulnerability includes BM 2021-4, JLPM 818-8, Kopargaon, RVSM 2213, LGG 628, LGG 657, LGG 685, MGG 514, MGG 519, RMG 1183, RMG 1188 and VBN 5. The similar studies conducted by Karthikeyan et al. (2014); Vijaya Bhaskar (2017); Saable et al. (2024), they reported that YMD incidence in mungbean germplasm lines ranged from 0-100%. The large variability in the incidence and severity of YMD depends on variety, location and year reported by Bashir et al.

(2006); Singh et al. (2000); Mohan et al. (2014). A good deal of research efforts have also been directed towards the screening of mungbean germplasm against YMD, identifying promising cultivars possessing resistance to YMD is a top priority for most pulse crops (Mishra et al. 2020; Pratap et al. 2021; Singh et al. 2020). It was previously reported (Bashir et al. 2006; Singh et al. 2000; Mohan et al. 2014) that large variability in the incidence and severity of YMD depends on variety, location and year. Parihar et al. (2017) also reported the seasonal effects on outbreak of yellow mosaic disease in mungbean cultivars.

Table 2. Reaction of mungbean genotypes to YMD across multiple locations of India

S. No	Genotype	Hisar	Ludhiana	Pantnagar	Vamban	Jhansi	Sagar	Raipur	Ayodhya	Dholi	Shilongani
1	AKM 1606	5	7	7	3	5	5	1	3	7	5
2	BCM 20-5	5	5	3	3	3	5	3	3	7	1
3	BCM 20-73	5	5	1	5	3	3	3	1	7	3
4	BM 2021-4	9	9	5	7	9	1	3	3	9	9
5	BM 4	9	9	7	5	8	1	6	5	7	7
6	DGG 214	3	5	3	5	5	3	3	3	5	1
7	IGKM 2021-1	3	5	5	5	3	5	1	3	5	3
8	IPM 02-3	5	5	3	3	3	1	1	3	7	1
9	IPM 1718-3	5	5	3	1	3	3	3	5	7	1
10	IPM 2-14	3	3	3	5	3	1	1	3	7	1
11	IPM 410-3	5	5	1	5	5	7	1	5	7	1
12	JLPM 707-27	9	9	5	7	7	3	5	5	7	7
13	JLPM 818-8	9	9	7	9	9	1	3	7	7	9
14	KM 2241	5	5	3	3	5	1	3	3	7	1
15	KM 2401	5	5	5	7	3	5	5	5	7	1
16	KM 2417	5	5	3	5	3	5	5	3	7	1
17	LGG 628	5	5	3	9	3	7	1	7	7	1
18	LGG 657	6	5	1	9	3	1	3	7	7	1
19	LGG 685	5	5	5	9	5	5	3	7	7	3
20	MGG 514	3	3	3	9	3	5	7	7	7	1
21	MGG 519	5	5	3	9	3	1	5	7	7	1
22	MH 1142	1	3	3	1	3	1	3	3	3	1
23	MH 1890	3	5	1	5	5	5	1	1	5	5
24	MH 1908	1	3	1	1	3	3	3	3	3	1
25	MH 2-15	3	7	3	5	3	3	1	3	5	1
26	MI 13-47	3	5	3	1	3	5	1	3	5	5
27	MI-2023-01	3	3	1	1	3	3	1	3	3	1
28	ML 2738	1	3	3	7	3	3	1	1	3	1
29	ML 2748	1	1	1	1	3	3	3	1	3	1
30	ML 2878	1	1	1	3	3	5	3	1	3	1
31	ML 2844	1	1	5	1	3	5	1	1	3	1
32	ML 818	1	1	3	5	3	1	1	3	1	1
33	OBGG 107	1	3	1	3	3	3	3	3	3	3
34	OBGG 110	1	5	3	3	3	5	2	3	5	1
35	PM 2015	3	5	3	3	3	3	1	1	5	5
36	PM 1918	5	5	3	1	3	1	7	5	7	1
37	PM 2031	3	7	3	3	3	1	3	5	7	3
38	PM 4	3	5	5	3	3	1	7	7	7	1

39	PM- 6	5	7	5	7	7	1	1	5	7	5
40	PMD 15	5	7	5	1	3	3	3	3	7	1
41	PMS 8	5	7	1	1	7	5	3	1	7	3
42	PUSA 0672	3	5	1	3	3	5	3	5	7	3
43	PUSA 1371	5	5	1	1	5	5	1	5	7	3
44	PUSA 2371	5	5	3	3	3	3	3	3	5	5
45	RM 03-79	5	5	5	3	5	3	3	3	7	5
46	RMB 15-14	5	7	5	1	7	5	5	5	7	3
47	RMG 1164	7	7	5	3	7	3	3	3	7	7
48	RMG 1181	7	9	5	3	3	5	1	3	7	7
49	RMG 1183	7	9	5	1	5	3	1	7	9	7
50	RMG 1188	7	9	5	1	7	5	5	7	7	9
51	RVSM 2213	7	9	5	3	5	5	3	5	9	7
52	RVSM 22-3	5	9	5	3	7	1	5	5	7	5
53	SKNM 2105	7	9	1	3	5	5	1	3	7	7
54	SVM 106	5	3	5	5	5	3	1	3	3	5
55	T-44	7	9	7	3	5	1	3	3	7	9
56	TAKM 141	5	5	5	1	3	3	5	7	7	5
57	VBN 5	5	5	3	9	3	5	1	7	7	3
58	VGG 20-157	3	5	3	1	3	5	1	7	7	1
59	VGG 20-234	5	5	3	5	3	3	1	3	7	1
60	IPM 512-1	5	5	3	5	9	3	3	5	7	3
61	Kopargaon	9	9	7	9	9	7	5	5	7	9

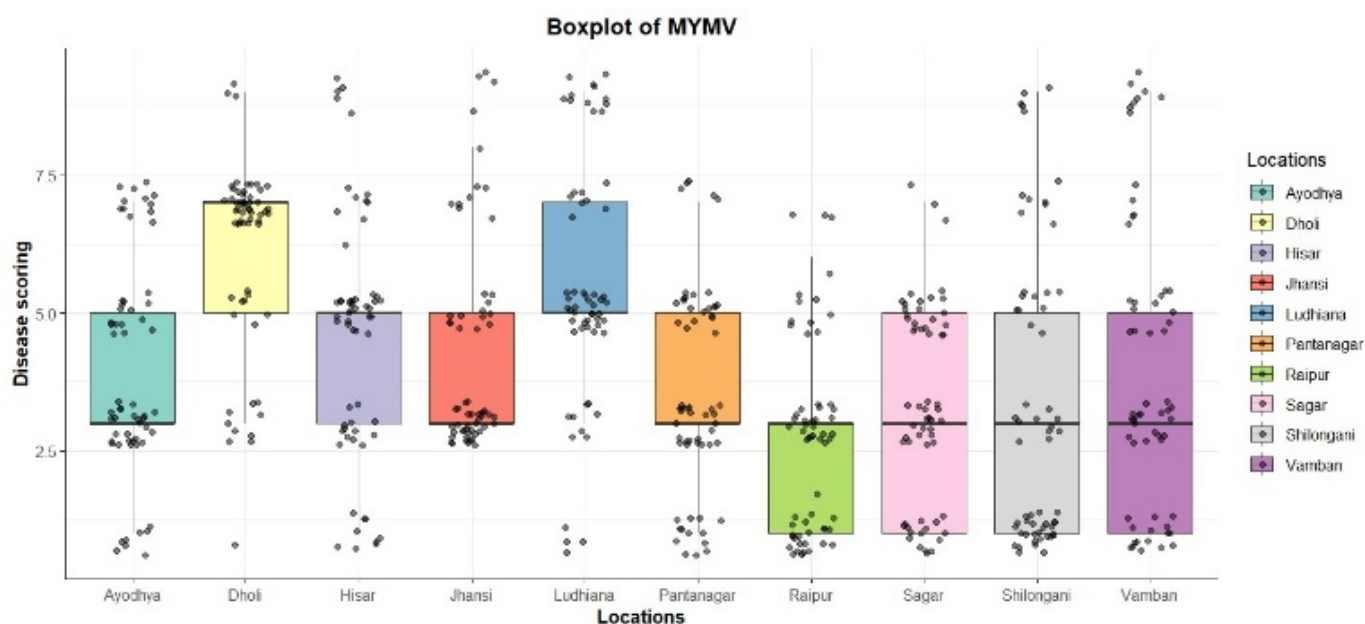


Figure 1. Boxplot for location wise response of yellow mosaic disease on mungbean genotypes

Principal component analysis (PCA)

In this present study PCA was performed for variable (location) and response of YMD with mungbean genotypes. The loadings indicate how strongly each location is associated with a particular principal component, helping to identify patterns of variation among mungbean genotypes in response to YMD (Table 3). The loadings represent the contribution of each location to the respective principal components (PC1 to PC10). PC1 has high negative loadings for most locations, highest negative loadings are observed in

Hisar (−0.442), Ludhiana (−0.427), Shilongani (−0.373), Dholi (−0.362) and Jhansi (−0.361). These locations contribute significantly to PC1, indicating they share a common pattern of variability in YMD response across mungbean genotypes, likely representing overall disease susceptibility or resistance trends. PC2 is second most important pattern of variation which shows strong negative loadings for Ayodhya (−0.575), Raipur (−0.477) and Vamban (−0.368), while other variables show positive contributions. This suggests that PC2 differentiates locations where genotypes exhibit

contrasting responses to YMD. Sagar (-0.794) shows the highest negative loading, making it the dominant driver of PC3 (third major pattern of variation), indicating a contrast reflection between Sagar and other locations, suggesting a possible regional variation in disease expression. Vamban (0.792) has the highest positive loading, suggesting PC4, which indicates that this location contributes uniquely to a distinct disease response pattern compared to other sites. PC5–PC10 is explaining less variation across locations.

PCA biplot is illustrating the distribution of genotypes and the contribution of different traits to the first two principal components, where PC1 accounts for 43.6% and PC2 13.9% of the total variation. The black dots represent genotypes, with their positions indicating similarity or dissimilarity based on the YMD. The arrows represent different traits with their directions which indicated the positive correlations with similar directions, whereas those pointing in opposite directions are negatively correlated. Genotypes positioned closer

together exhibit similar characteristics (Fig 2). PCA variable plot illustrates the contribution of different variables. The colour intensity represents the quality of representation, where red and orange arrows contribute more strongly to the principal components, while blue and green arrows have a weaker influence. Variables pointing in the same direction are positively correlated, while those pointing in opposite directions are negatively correlated. Locations such as Hisar, Ludhiana and Shilongani have strong positive contributions to Dim1, suggesting that they share common disease resistance patterns captured by this axis. In contrast, Sagar is positioned separately with a distinct contribution, primarily along Dim2, indicating a unique disease response pattern. Locations like Ayodhya, Vamban and Raipur also contribute significantly but in a different direction, implying variability in disease response across these sites (Fig. 3). This biplot helps in visualizing how different locations cluster based on their influence responses to disease.

Table 3. Loadings of each variable (location) evaluation of mungbean genotypes against yellow mosaic disease under natural condition

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Hisar	-0.442	0.048	-0.078	0.003	-0.154	0.152	-0.156	0.1	0.657	0.532
Ludhiana	-0.427	0.175	-0.038	-0.178	-0.199	0.017	-0.108	0.161	-0.723	0.393
Pantnagar	-0.333	0.065	0.219	0.158	0.31	-0.738	-0.273	-0.31	0.027	-0.006
Vamban	-0.142	-0.368	-0.297	0.792	0.001	0.147	-0.246	0.125	-0.157	-0.075
Jhansi	-0.361	0.229	0.082	0.204	0.246	0.427	0.444	-0.568	-0.062	-0.047
Sagar	0.029	0.127	-0.794	-0.242	0.535	-0.032	-0.069	-0.019	-0.002	0.047
Raipur	-0.173	-0.477	0.383	-0.283	0.562	0.329	-0.228	0.19	-0.046	-0.021
Ayodhya	-0.243	-0.575	-0.16	-0.109	-0.074	-0.33	0.667	0.095	0.009	0.066
Dholi	-0.362	-0.198	-0.212	-0.342	-0.400	0.093	-0.31	-0.309	0.052	-0.552
Shilongani	-0.373	0.402	0.043	0.077	0.113	-0.041	0.184	0.623	0.108	-0.494

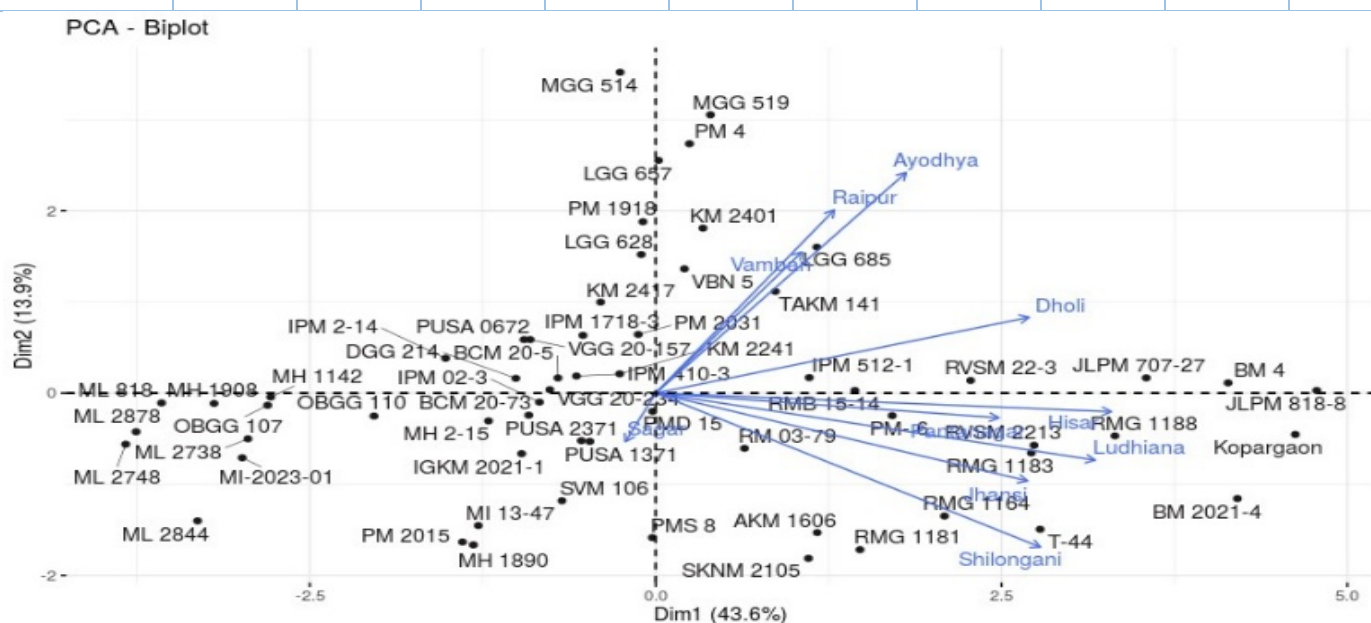


Figure 2. Biplot showing the distribution of genotypes and contribution of all the characters in first two principal components (PC-1 and PC-2)

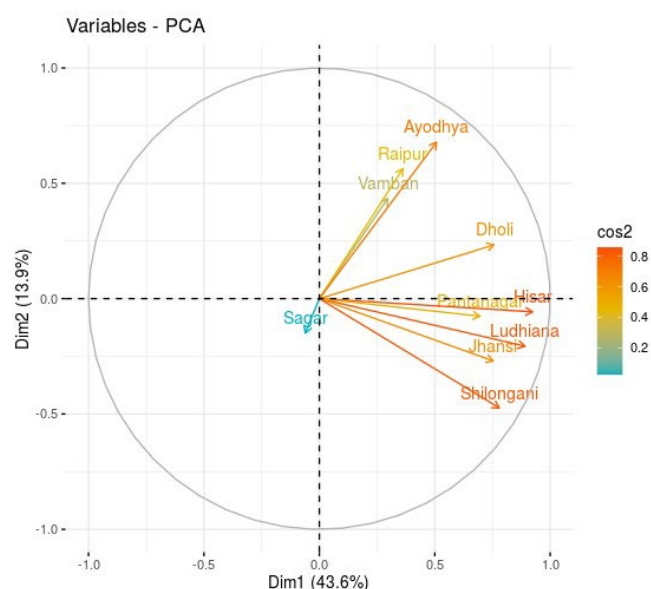


Figure 3. PCA variable plot illustrates the contribution of different variables to two principal components (PC-1 and PC-2)

Table 4 presents the eigenvalues, percentage of variation and cumulative percentage of variance for the principal components in the evaluation of mungbean genotypes against YMD. PC1 has the highest eigenvalue (4.361) and accounts for 43.61% of variation (Fig. 4), indicating that it is the most influential component in explaining the differences in YMD response among genotypes. PC2 contributes an additional 13.92%, bringing the cumulative variance explained to 57.53%, suggesting that the first two components together capture more than half of the total variability. PC3 and PC4 explain 11.43% and 9.21%, respectively, increasing the cumulative variance to 78.17%. PC5 to PC7 contribute smaller percentages (6.89%, 5.70% and 3.88%) and PC8 to PC10 contribute minimally (less than 3% each), leading to a total of 100% variance explained. PC1 to PC4 are the most significant components, capturing more than 78% of the total variation. This suggests that these components effectively summarize the major patterns in disease response across mungbean genotypes, while the remaining PCs contribute marginally to the overall variation.

Table 4. Eigen values, percentage of total variation and cumulative percentage for corresponding mungbean genotypes against YMD

Prin_comp	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	4.361	43.609	43.609
PC2	1.392	13.921	57.529
PC3	1.143	11.43	68.959
PC4	0.921	9.21	78.169
PC5	0.689	6.889	85.058
PC6	0.569	5.695	90.753
PC7	0.388	3.884	94.637
PC8	0.278	2.785	97.422
PC9	0.146	1.457	98.879
PC10	0.112	1.121	100

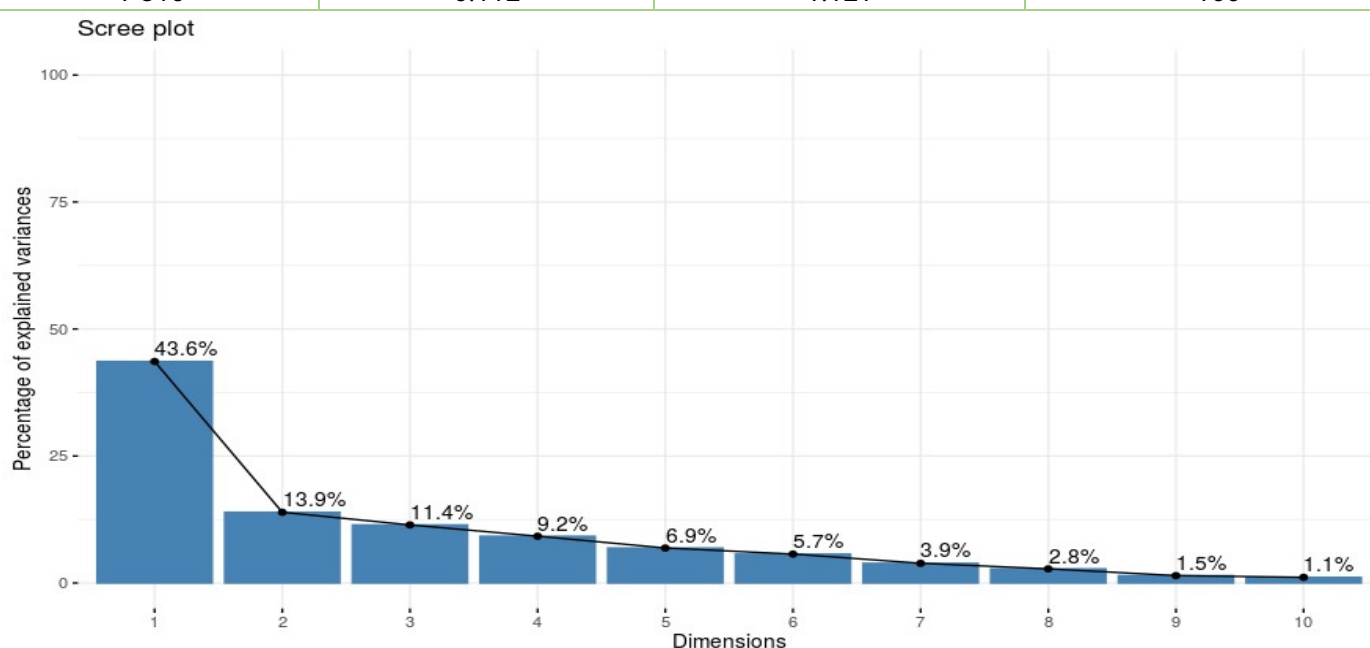


Figure 4: Scree plot constructed using 10 PCA

Table 5 presents the percentage contribution of different locations (variables) to the principal components (PCs) in the evaluation of mungbean genotypes against YMD. The percentage values indicate the extent to which each location influences a particular principal component. PC1 is primarily influenced by Hisar (19.57%), Ludhiana (18.21%), Shilongani (13.94%), Dholi (13.13%) and Jhansi (13.03%). This indicates that these locations are the primary drivers of the variation captured by PC1. PC2 is heavily dominated by Ayodhya (33.06%) and Raipur (22.79%), indicating these locations play a crucial role in explaining additional variability in YMD resistance among mungbean genotypes. PC3 is mainly driven by Sagar (62.99%) and PC4 is overwhelmingly influenced by Vamban (62.78%). In view, different locations contribute variably across the principal components, with some (e.g., Sagar, Vamban, Raipur and Ayodhya) showing dominance in specific components, indicating regional variations in the disease response of mungbean genotypes.

Table 5. Percentage contribution of variables on PCs of mungbean genotypes against YMD

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Hisar	19.571	0.235	0.606	0.001	2.367	2.31	2.429	1.007
Ludhiana	18.205	3.056	0.144	3.17	3.971	0.029	1.173	2.602
Pantnagar	11.104	0.416	4.808	2.502	9.622	54.423	7.444	9.603
Vamban	2.016	13.551	8.813	62.782	0	2.171	6.062	1.568
Jhansi	13.031	5.246	0.673	4.149	6.038	18.243	19.71	32.303
Sagar	0.086	1.601	62.993	5.872	28.607	0.103	0.474	0.038
Raipur	3.003	22.793	14.697	8.018	31.588	10.823	5.203	3.622
Ayodhya	5.913	33.063	2.573	1.19	0.552	10.868	44.494	0.907
Dholi	13.13	3.908	4.502	11.726	15.983	0.864	9.639	9.535
Shilongani	13.941	16.13	0.189	0.59	1.272	0.167	3.373	38.814

Figure 5 presents the correlation coefficients between different locations (variables) and the principal components (PC1 to PC8) derived from the principal component analysis (PCA) of mungbean genotypes in response to YMD. These correlation values indicate how strongly each location contributes to the respective principal components. PC1 exhibits strong positive correlations with Hisar (0.924), Ludhiana (0.891), Shilongani (0.78), Dholi (0.757) and Jhansi (0.754), indicating that these locations contribute significantly to the variation explained by the first principal component. Since PC1 captures the highest variance in the dataset, it suggests that disease response at these locations plays a major role in differentiating mungbean genotypes. PC2 is highly correlated with Ayodhya (0.678), Raipur (0.563), and Vamban (0.434), implying that these locations contribute distinct variability not captured by PC1. Conversely, Shilongani (-0.474), Jhansi (-0.27), and Ludhiana (-0.206) show negative correlations with PC2, suggesting that their variation is negatively associated with this component. PC3 is strongly associated with Sagar (0.849) and PC4 is dominated by Vamban (0.760), meaning that disease response in this location is a unique factor influencing this principal component. Later components (PC5 to PC8) generally explain minor variations in the dataset (Table 6).

Table 6. Correlation between variables (location) and PCs of mungbean genotypes in response to YMD

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Hisar	0.924	-0.057	0.083	0.002	-0.128	0.115	0.097	0.053
Ludhiana	0.891	-0.206	0.041	-0.171	-0.165	0.013	0.067	0.085

Correlation Plot of variables VS PCs

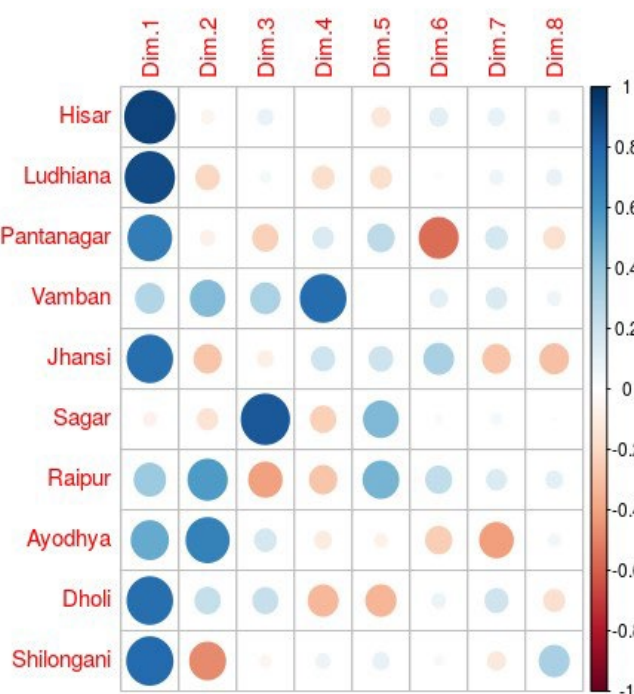


Figure 5. Correlation between different locations (variables) and PCs in the response to YMD

Pantnagar	0.696	-0.076	-0.234	0.152	0.257	-0.557	0.17	-0.164
Vamban	0.296	0.434	0.317	0.760	0.001	0.111	0.153	0.066
Jhansi	0.754	-0.27	-0.088	0.195	0.204	0.322	-0.277	-0.300
Sagar	-0.061	-0.149	0.849	-0.233	0.444	-0.024	0.043	-0.010
Raipur	0.362	0.563	-0.41	-0.272	0.466	0.248	0.142	0.100
Ayodhya	0.508	0.678	0.171	-0.105	-0.062	-0.249	-0.416	0.050
Dholi	0.757	0.233	0.227	-0.329	-0.332	0.07	0.193	-0.163
Shilongani	0.78	-0.474	-0.047	0.074	0.094	-0.031	-0.114	0.329

Conclusion

The study evaluates the response of various mungbean genotypes to yellow mosaic disease (YMD) in different locations of India. Key findings indicate that some genotypes, such as MH 1142, MH 1908, MI 2023-01, ML 2748 and OBG 107 consistently exhibited high resistance across multiple locations, making them potential candidates for breeding YMD-resistant mungbean. However, genotypes like Kopargaon, BM 2021-4, JLP 818-8 and RVSM 2213 displayed high susceptibility, highlighting the need for effective disease management strategies. Principal component analysis (PCA) revealed that PC1 explained 43.6% of the variance, primarily influenced by Hisar, Ludhiana and Shilongani. Other PCs highlighted region-specific disease pressures. The study underscores the importance of selecting resistant genotypes for breeding programs and tailoring disease management strategies based on regional variations in YMD incidence.

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Declarations of interests

All authors of this manuscript declare that they have no conflict of interest.

Data sharing

All relevant data are within the manuscript.

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