



RESEARCH ARTICLE

Genotype × environment interactions for resistance to northern corn leaf blight and sorghum downy mildew in maize

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Abstract

Stability of disease resistance is critical in maize breeding because genotype × environment interaction (GEI) can substantially influence trait expression. In the present study, 31 multi-parent advanced generation intercross (MAGIC) recombinant inbred lines (RILs), along with 2 checks, were evaluated for northern corn leaf blight (NCLB) across 3 locations, while 32 RILs were assessed for their reaction to sorghum downy mildew (SDM) across 3 rainy seasons. Pooled analysis of variance (ANOVA) revealed a non-significant GEI for SDM, indicating stable genotype performance across seasons, whereas NCLB showed significant GEI. Correlation analysis further supported these results: SDM exhibited very high inter-season correlations, suggesting minimal genotype re-ranking, while NCLB showed moderate to low correlations among environments, reflecting environmental divergence and crossover interactions. Unweighted pair group method with arithmetic mean (UPGMA) clustering grouped the genotypes into three major clusters for both diseases but did not distinctly separate resistant and susceptible classes, suggesting quantitative inheritance and continuous phenotypic variation. Further stability analysis using additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) biplot models identified G13, G15 and G2 as stable and resistant for NCLB, while G15, G10, G16 and G32 exhibited broad adaptation across environments. These stable MAGIC RILs for NCLB disease represent valuable genetic resources for breeding durable resistance in NCLB prone maize production regions.

Keywords: AMMI; genotype by environment interactions; GGE; MAGIC; maize; stability

Introduction

Maize (*Zeamays* L.) is one of the most important cereal crops worldwide due to its wide adaptability, high productivity and diverse end uses in food, feed, fodder, fibre and biofuel industries. Globally, it ranks among the leading cereals in terms of production and economic value. Asia is the second largest maize-producing region, contributing approximately 31 % of global production from about 34 % of the harvested area (1), highlighting its critical role in ensuring food and nutritional security. However, the widespread cultivation of genetically uniform hybrids with a relatively narrow genetic base, combined with shifting climatic patterns, has increased the vulnerability of maize to several biotic and abiotic stresses. Such genetic uniformity often accelerates the spread of disease epidemics, thereby threatening yield stability and productivity. Maize is reported to be affected by more than 60 diseases worldwide (2), many of which can cause severe yield losses under favourable environmental conditions.

Among the major foliar diseases, Northern corn leaf blight (NCLB) and Sorghum downy mildew (SDM) are of particular concern in India because of their widespread occurrence and economic impact. Northern corn leaf blight, caused by *Exserohilum turcicum*

(Pass.) (3), is a destructive foliar disease capable of causing yield losses ranging from 25–90 % depending on disease severity, crop growth stage and prevailing environmental conditions (4, 5). The disease is favoured by high humidity, moderate temperatures and prolonged leaf wetness, which promote lesion development and rapid disease spread (6). Severe infection results in extensive leaf blighting, premature senescence and significant reduction in photosynthetically active leaf area, ultimately affecting grain filling and yield. Sorghum downy mildew, caused by *Peronosclerospora sorghi* [(W. Weston & Uppal) C.G. Shaw] (7), is another economically important disease that primarily infects seedlings younger than one month. Environmental conditions such as temperatures between 21–33 °C, relative humidity above 90 % and intermittent drizzling favour disease establishment and systemic infection (7). Infected plants exhibit pale yellow discolouration, chlorosis, downy fungal growth on the abaxial leaf surface, stunted growth and in severe cases complete plant mortality (8). The frequent outbreaks of NCLB and SDM across maize-growing regions highlight the urgent need to identify stable and durable sources of resistance. Screening of diverse germplasm panels has revealed substantial genetic variability for resistance to these diseases, providing opportunities for genetic improvement (9).

Among the available disease management strategies, host plant resistance is considered the most economical, environmentally safe and sustainable approach. Unlike chemical control, genetic resistance provides season-long protection and reduces production costs. The success of resistance breeding largely depends on the availability of genetically diverse parental lines carrying favourable and complementary alleles. In this context, multi-parent advanced generation intercross (MAGIC) populations (10) have emerged as valuable genetic resources for the improvement of complex traits. The MAGIC populations are developed by intercrossing multiple founder parents (commonly 4, 8, or 16) through structured funnel crossing schemes (11), followed by repeated selfing to generate recombinant inbred lines (RILs). These lines represent random mosaics of founder haplotypes, resulting in high levels of recombination and allelic diversity (12). Compared with biparental populations, MAGIC provide greater genetic resolution and broader variation, making them highly suitable for dissecting complex quantitative traits such as resistance to disease (13). Consequently, evaluating MAGIC RILs for disease resistance can facilitate the identification of novel and diverse resistance sources for maize breeding programs.

The expression of disease resistance is influenced not only by genetic factors but also by environmental conditions such as temperature, humidity, rainfall and other edaphic factors that affect pathogen development and host–pathogen interactions. As a result, genotype $\times$ environment (G $\times$ E) interactions play a crucial role in determining disease severity and resistance expression (14). A genotype exhibiting strong resistance in one environment may show moderate or even susceptible reactions under different environmental conditions, complicating selection decisions in breeding programs. Therefore, understanding G $\times$ E interactions is essential for identifying stable genotypes and delineating mega-environments for targeted breeding strategies (15, 16). Genotypes that consistently express resistance across diverse environments are particularly valuable for hybrid development and resistance introgression programs.

To quantify and interpret G $\times$ E interactions in multi-environment trials, several statistical models have been developed. Among them, the additive main effects and multiplicative interaction (AMMI) model (17) is widely used because it integrates analysis of variance (ANOVA) to estimate additive main effects with principal component analysis (PCA) to partition multiplicative interaction effects (18). The AMMI model effectively explains changes in genotype ranking across environments and improves the precision of stability assessment (19–22). In addition, genotype plus genotype-by-environment (GGE) biplot analysis provides a graphical representation of genotype performance, stability and mega-environment delineation, facilitating the identification of ideal genotypes and representative test environments (15). The combined use of AMMI and GGE biplot approaches has therefore become a standard and reliable method for evaluating genotype stability and adaptability in maize and other crops.

Therefore, the present study was undertaken to (i) quantify genotype $\times$ environment interactions (GEI) for resistance to NCLB and sorghum downy mildew in maize MAGIC recombinant inbred lines and (ii) identify stable and resistant genotypes suitable for hybrid development and introgression breeding programs. Identification of such stable resistance sources will strengthen

breeding strategies aimed at developing resilient maize cultivars adapted to diverse agro-ecological conditions.

Materials and Methods

Development of the multi-parent generation intercross population

An eight-parent MAGIC population was developed using a simple funnel crossing design (13). The founders were initially crossed in a half-diallel scheme to generate 28 single crosses, which were subsequently intercrossed to obtain 14 double crosses. These double crosses were further crossed to produce seven 8-way crosses following the funnel scheme (11). The resulting F₃s were advanced through selfing using the single seed descent (SSD) method up to the F₆ generation, resulting in approximately 1400 recombinant inbred lines.

Planting material and experimental design for northern corn leaf blight and sorghum downy mildew disease screening

From a total population of approximately 1400 F₆ MAGIC RILs, a subset representing the phenotypic variability of the population, based on preliminary disease response and agronomic performance, was selected for detailed multi-environment evaluation. In the present study, the stability of 31 MAGIC RILs for resistance to NCLB and 32 MAGIC RILs for sorghum downy mildew was assessed. The maize inbred lines SKV50 and CM202 were included as resistant and susceptible checks respectively, for both diseases. The experiments were conducted using a randomized complete block design (RCBD) with 2 replications. Each genotype was planted in a 2 m row with a spacing of 60 cm between rows and 20 cm between plants.

Evaluation for NCLB was carried out at 3 locations during the rainy season of 2024: Zonal Agricultural Research Station (ZARS), V.C. Farm, Mandya (E1); M/s. Advanta seeds disease screening facility, Hassan (E2); and M/s. Corteva Agriscience disease screening facility, Hassan (E3). Screening for SDM was conducted at ZARS, V C Farm, Mandya, across 3 consecutive rainy seasons, namely 2022, 2023 and 2024. Standard agronomic practices recommended for maize cultivation were followed at all locations and seasons. The list of genotypes along with their disease responses to NCLB and SDM is presented in Tables 1 and 2 respectively. The geographic coordinates and rainfall details of the test environments are provided in Supplementary Table 1.

Disease screening for northern corn leaf blight

Artificial disease inoculation was performed to ensure uniform disease spread across all the test entries at all the locations. The artificial inoculation method called the leaf whorl technique was followed, wherein the sorghum grains infected with *Exserohilum turcicum* were ground to fine powder and a pinch of this powder was applied to the leaf whorl of each plant at 30 DAS, followed by a water spray to permit spore germination, to ensure uniform disease spread (2). The symptoms started to develop after a week of artificial inoculation. Observations were recorded based on symptoms on the 75th day using a 1–9 scale (23, 24). The genotypes with a score less than or equal to 3 were considered as resistant, scores from 3.1 to 5.0 were grouped as moderately resistant, scores from 5.1 to 7.0 were considered as moderately susceptible and scores more than 7.1 were categorised as

susceptible. The per cent disease severity was computed using the formula given below:

$$\text{Percent disease severity} = \frac{\text{Sum of the individual disease ratings}}{\text{Total number of plants observed} \times \text{Maximum grade}} \times 100 \quad (\text{Eqn. 1})$$

Table 1. List of selected MAGIC RILs and their response to northern corn leaf blight disease (PDI %) across locations

Genotype	ZARS, Mandya		Advanta, Hassan		Corteve, Hassan	
	R1	R2	R1	R2	R1	R2
G1	68.52	51.39	53.33	61.11	20.99	38.89
G2	34.44	19.44	33.33	41.67	37.04	25.00
G3	34.13	38.89	37.78	36.11	64.81	33.33
G4	30.56	33.33	24.44	47.22	32.32	24.44
G5	23.61	22.22	33.33	47.22	39.63	27.78
G6	74.44	85.56	77.78	86.11	65.56	75.00
G7	25.56	55.56	44.44	44.44	81.48	44.44
G8	23.06	38.89	35.56	33.33	33.33	50.00
G9	43.83	28.89	24.44	41.67	58.33	38.89
G10	35.56	28.15	33.33	27.78	38.89	36.11
G11	67.78	64.44	88.89	69.44	29.63	36.11
G12	23.33	27.78	31.11	69.44	36.11	33.33
G13	24.07	33.33	33.33	33.33	25.55	33.33
G14	100.00	85.78	66.67	86.11	68.89	80.56
G15	33.33	33.33	33.33	38.89	37.04	33.33
G16	56.11	33.33	44.44	59.26	62.22	22.22
G17	55.56	59.26	44.44	77.78	71.11	55.56
G18	89.26	88.15	80.00	75.55	80.00	85.00
G19	58.33	44.44	46.67	66.67	57.78	30.56
G20	45.06	27.78	31.11	33.33	33.33	33.33
G21	65.56	44.44	80.00	100.00	33.33	25.00
G22	68.06	61.11	60.11	61.11	53.33	77.77
G23	66.67	61.11	35.56	41.67	60.00	33.33
G24	48.15	27.78	31.11	41.67	73.33	33.33
G25	55.55	61.11	31.11	44.44	53.33	44.44
G26	36.11	22.22	33.33	33.33	33.33	44.44
G27	46.30	27.78	33.33	41.67	44.44	33.33
G28	44.44	55.56	55.56	40.74	73.33	50.00
G29	25.00	38.89	33.33	38.89	60.00	52.78
G30	91.58	61.11	97.78	69.44	88.88	85.00
G31	56.94	44.44	40.00	40.74	53.33	22.22
G32 (RC)	22.22	21.22	33.33	15.55	11.11	23.57
G33 (SC)	77.78	66.59	88.89	95.56	77.89	90.00

RC: Resistant check; SC: Susceptible check.

Table 2. List of selected MAGIC RILs and their response to sorghum downy mildew disease (disease incidence %) across seasons

Genotype	2022	2023	2024	Genotype	2022	2023	2024
G1	31.25	33.33	16.67	G18	0.00	12.50	0.00
G2	83.33	100.00	33.33	G19	83.33	100.00	80.00
G3	0.00	14.29	10.00	G20	10.00	33.33	6.67
G4	100.00	100.00	81.82	G21	70.00	100.00	100.00
G5	75.00	50.00	42.85	G22	57.14	31.25	25.00
G6	86.67	60.00	87.50	G23	100.00	100.00	83.33
G7	100.00	100.00	50.00	G24	100.00	100.00	100.00
G8	0.00	0.00	22.22	G25	100.00	100.00	75.00
G9	75.00	100.00	83.33	G26	15.00	15.00	25.00
G10	100.00	100.00	100.00	G27	83.33	83.33	75.00
G11	20.00	0.00	14.29	G28	25.00	33.33	50.00
G12	62.50	100.00	60.00	G29	100.00	100.00	100.00
G13	100.00	100.00	76.92	G30	60.00	92.31	0.00
G14	100.00	50.00	12.50	G31	66.67	100.00	100.00
G15	70.00	60.00	0.00	G32	100.00	100.00	80.00
G16	100.00	100.00	100.00	G33(RC)	0.00	10.00	0.00
G17	100.00	100.00	100.00	G34(SC)	100.00	85.00	90.00

Disease screening for sorghum downy mildew

Artificial inoculation was employed to screen the MAGIC RILs for their response to SDM (25). The spreader rows (highly susceptible entry: African tall) were sown 15–20 days before the sowing of the test entries and artificial inoculation was done for these spreader

rows. Inoculum from the spreader rows is known to cause infection in the test entries. Artificial inoculation was also carried out when the seedlings were one week old. By 2.30 am, the diseased leaves with good sporulation were searched and washed in water at a rate of 15 leaves per litre of water collected in the buckets. This operation was completed by 3.00 am. Then the collected spore suspension in different buckets was thoroughly mixed and made up to 25 L. This spore suspension was used for inoculation and the entire process was completed by 4.00 am. Between 6.00 am and 6.00 pm, water spray was given to the inoculated plot to create the required humidity artificially. This method ensures 100 % disease incidence. Further, the observations were recorded at 30 days after sowing. The disease incidence was computed using the following formula,

$$\text{Percent disease incidence} = \frac{\text{Number of diseased plants}}{\text{Total number of plants}} \times 100 \quad (\text{Eqn. 2})$$

The progenies with per cent disease incidence ≤ 10 were grouped as resistant, 10.1 to 25 as moderately resistant, 25.1 to 50 as moderately susceptible and > 50 as susceptible.

Statistical analysis

The obtained per cent disease incidence data on NCLB and SDM diseases were transformed using arcsine transformation to make the means and variances independent and normally distributed using the 'asin' function available in R software version 4.4.3. The transformed data were used in further statistical analyses.

Detection and characterisation of genotype $\times$ environment interaction

The pooled ANOVA was performed to detect the presence of genotype $\times$ environment interaction using the 'agricolae' package available in R 4.4.3. The general linear model for detecting the presence of genotype by environment interactions is given as:

$$Y_{ijk} = \mu + G_i + E_j + B_{k(j)} + (GE)_{ij} + \varepsilon_{ijk} \quad (\text{Eqn. 3})$$

Where,

Y_{ijk} is the observed value of the i^{th} genotype in the j^{th} environment and k^{th} replication; μ is the overall mean; G_i is the effect of the i^{th} genotype; E_j is the effect of the j^{th} environment and $(GE)_{ij}$ is the interaction effect between the i^{th} genotype and the j^{th} environment; $B_{k(j)}$ is the effect of k^{th} block nested in environment j and ε_{ijk} is the residual error.

Additive main effects and multiplicative interaction and genotype plus genotype-by-environment biplot analysis

Characterisation of genotype by environment interaction was done employing a multiplicative model called AMMI (20). The AMMI uses ANOVA to fit genotypic and environmental main effects and PCA to dissect the interaction and residual components (26). Most of the interaction components are captured in initial IPCs and noise is captured in later IPCs (27). The AMMI stability model is a graphics-based tool to model genotype-by-environment interactions, but it fails to accommodate the linear mixed effect model in the structure (28); however, it is known to enhance the selection accuracy by separating interaction patterns from the residual noise in an additive model. AMMI1 and AMMI2 biplots are the most widely used for assessing genotypes' stability.

The first two IPC axes, viz., IPCA1 and IPCA2, were used to

compute AMMI stability values (ASV) (29). It provides a single stability index that weighs IPCA1 by the relative contribution of IPCA1 and IPCA2 to the genotype $\times$ environment sum of squares.

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}} \cdot (IPCA1)^2 + (IPCA2)^2 \quad (\text{Eqn. 4})$$

Where, SS_{IPCA1} and SS_{IPCA2} are the sum of squares for IPCA1 and IPCA2 from AMMI ANOVA and IPCA1 and IPCA2 are the genotype scores on the respective axes. Lower AMMI stability value (ASV) values indicate greater stability across environments. Further, the ranking of genotypes was done based on ASV and trait mean value. Genotypes having a low trait mean and a lower ASV value are highly desirable.

AMMI stability value and mean disease score scatter plot

The scatter plot was constructed by plotting the average disease score on the x-axis and AMMI stability value (ASV) values on the y-axis. Further, the genotypes are grouped into 4 quadrants based on the following considerations;

Quadrant	X-axis (mean disease score)	Y-axis (ASV)	Interpretation
Q1	$\leq$ mean	$>$ mean	Low disease score but unstable (high ASV)
Q2	$>$ mean	$>$ mean	High disease score and unstable
Q3	$\leq$ mean	$\leq$ mean	Low disease score and stable
Q4	$>$ mean	$\leq$ mean	High disease score but stable

The genotypes falling in the Q3 quadrant display low disease score and high stability for disease response as indicated by a lower ASV value.

Genotype + Genotype $\times$ Environment biplot is another approach to detect and characterise GEI. It comprises of a) which won where biplot, which recommends the genotypes to specific environments, b) the mean vs. stability biplot, which identifies the stable genotype that can be recommended across all locations and c) the discriminativeness vs. representativeness biplot for location evaluation and it explains the discriminative power of the location to effectively discriminate the genotypes under study (15).

Correlation analysis

Pearson's correlation analysis was performed to determine the association among genotypes for disease response across seasons and environments. The average disease incidence values were used for the analysis. The correlation coefficients were computed using the `cor()` function in the R software (version 4.4.3).

Cluster analysis using unweighted pair group with arithmetic mean

To assess the genetic divergence among MAGIC RILs based on disease response, hierarchical cluster analysis was performed using the unweighted pair group method with arithmetic mean (UPGMA) (30). The analysis was carried out using standardised data of average disease incidence. Euclidean distance was used as the measure of dissimilarity among genotypes. The distance matrix was computed using the `dist()` function in R (version 4.4.3) and hierarchical clustering was performed using the `hclust()` function with the method set to "average" (UPGMA method). A dendrogram was generated to visualise the grouping pattern of genotypes and the clustering pattern was interpreted to identify groups of genotypes exhibiting similar disease responses.

Results and Discussion

Pooled analysis of variance

The ANOVA partitioned total variation into genotype, environment and GEI components. Significance of mean sum of squares due to environment and genotype by environment interactions in pooled ANOVA indicated the significant role of environment in northern corn leaf blight disease response (Table 3). However, the non-significance of the mean sum of squares due to the environment and its interaction suggested a limited effect of the environment on sorghum downy mildew disease response (Table 4). Hence, no stability analyses were performed for sorghum downy mildew

Table 3. Pooled ANOVA for northern corn leaf blight disease response of multi-parent advanced generation intercross recombinant inbred lines

Sources of variation	Degrees of freedom	Mean sum of squares
Genotypes	32	7.29***
Environments	2	4.18*
Genotype $\times$ Environment	64	1.90**
Environment (Replication)	3	0.10***
Residuals	96	0.014

*, ** and *** indicate the significance at 0.05, 0.01 and 0.001 % respectively.

Table 4. Pooled ANOVA for Sorghum downy mildew disease response

Sources of variation	Degrees of freedom	Mean sum of squares
Genotypes	33	32.35***
Environments	2	2.67
Genotype $\times$ Environment	66	0.63
Environment (Replication)	3	5.27**
Residuals	99	0.02

*, ** and *** indicate the significance at 0.05, 0.01 and 0.001 % respectively.

disease response.

Correlation analysis

Pearson's correlation analysis among environments for NCLB revealed a moderate and significant positive correlation between E1 (ZARS, V.C. Farm, Mandya) and E2 (M/s. Advanta seeds disease screening facility, Hassan) ($r = 0.63$), followed by E2 (M/s. Advanta seeds disease screening facility, Hassan) and E3 (M/s. Corteva Agriscience disease screening facility, Hassan) ($r = 0.46$), indicating partial consistency in genotype performance across these environments. However, the correlation between E1 (ZARS, V.C. Farm, Mandya) and E3 (M/s. Corteva Agriscience disease screening facility, Hassan) was low and non-significant ($r = 0.31$) (Fig. 1a), suggesting substantial genotype re-ranking under contrasting environmental conditions. The declining magnitude of correlation from E1–E2 to E1–E3 indicated increasing environmental divergence and supports the presence of crossover genotype $\times$ environment interaction. These results justify the use of multi-environment trials and stability analyses for reliable identification of resistant genotypes.

In contrast to NCLB, the correlation analysis for SDM revealed very high and significant positive associations among years, with correlation coefficients of 0.96 between kharif 2022 and kharif 2023, 0.85 between kharif 2023 and kharif 2024 and 0.86 between kharif 2022 and kharif 2024 (Fig. 1b). The consistently strong correlations indicated minimal genotype re-ranking across environments and suggested the absence or very limited magnitude of genotype $\times$ environment interaction. The stability of genotype

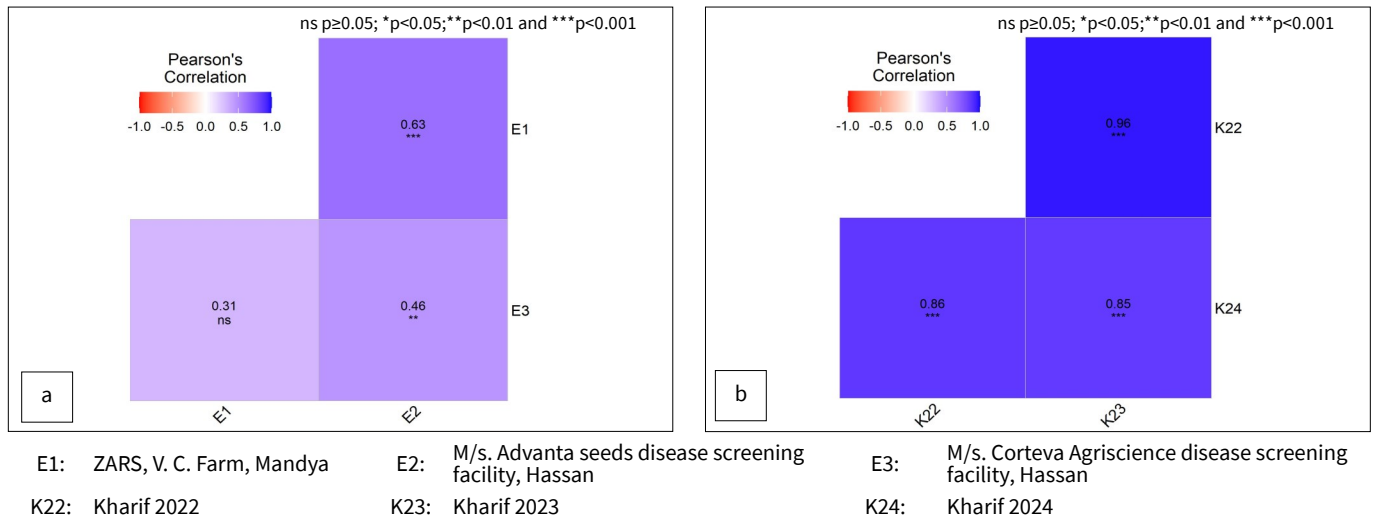


Fig. 1. Correlation heatmap of genotype performance across environments for (a) northern corn leaf blight (NCLB) and (b) sorghum downy mildew (SDM).

performance across years highlights the robustness of resistance expression against SDM. This consistency can be considered as a strength of the evaluated MAGIC RILs, as it reflects stable and reliable resistance under varying environmental conditions.

Clustering of multi-parent advanced generation intercross recombinant inbred lines based on unweighted pair group method with arithmetic mean

Hierarchical clustering using the UPGMA method based on mean disease response to NCLB, grouped the MAGIC RILs into 3 major clusters (Fig. 2), indicating substantial phenotypic variability for disease resistance. Cluster I was the largest with 25 genotypes and was further subdivided into 3 distinct sub-clusters, reflecting differences in the magnitude of disease response among genotypes within this group. However, cluster II was the smallest with only 2 genotypes (G11 and G21).

Further, UPGMA clustering based on SDM disease response classified MAGIC RILs into 3 clusters, with cluster I being the largest, with the highest number of MAGIC RILs (20), followed by cluster III and cluster II with 8 and 6 MAGIC RILs, respectively (Fig. 3). Hierarchical clustering based on disease response did not distinctly separate resistant and susceptible genotypes for either NCLB or SDM. This pattern suggests that the resistance in the experimental material is governed by quantitative genetic effects, resulting in

continuous phenotypic variation (31–34) rather than sharply defined classes. Such overlapping distributions are common in polygenic resistance, where minor additive effects cumulatively contribute to disease resistance. The absence of discrete clustering further supports the need for stability and multi-environment analyses to reliably identify superior genotypes.

Additive main effects and multiplicative interaction analysis of variance for northern corn leaf blight

The genotype-by-environment interaction consists of a predictable component called the signal and an unpredictable component called noise. The AMMI model dissects the total GEI into signal and noise using several interaction principal components (IPCs). The initial IPCs are expected to capture most of the signal, while later IPCs capture the noise. For NCLB disease response, the GEI was partitioned into the sum of squares attributable to GEI_{signal} and GEI_{noise} . The sum of squares attributable to GEI_{signal} was 86.14 %, whereas it was 13.86 per cent for GEI_{noise} (Table 5). Total GEI was split into two IPCs, each of which explained a proportion of GEI. The proportion of variation explained by each of the components is given in Table 5.

The contribution of the environment to the total sum of squares was the highest (20.30 %), followed by GEI (5.06 %) and genotypes (3.07 %), indicating the strong influence of environmental

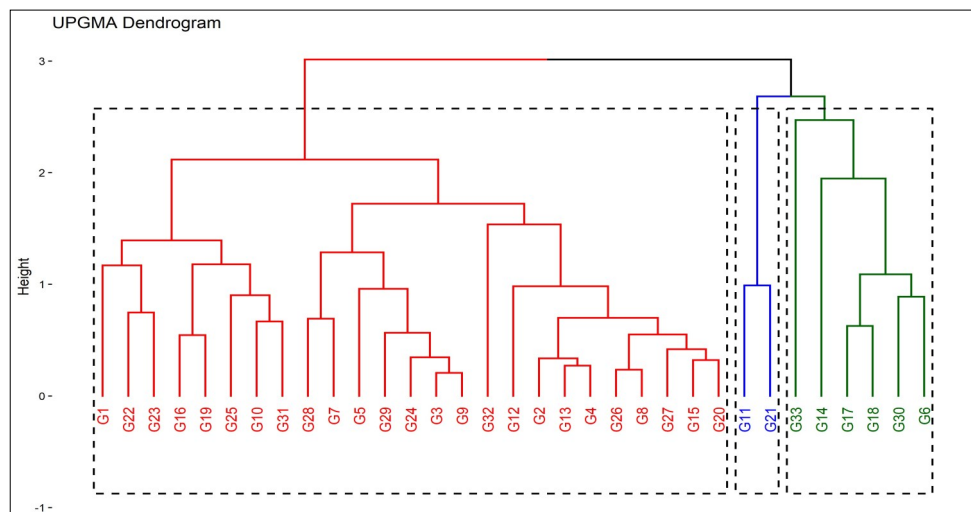


Fig. 2. Unweighted pair group method with arithmetic mean -based clustering of multi-parent advanced generation intercross recombinant inbred lines based on northern corn leaf blight disease response.

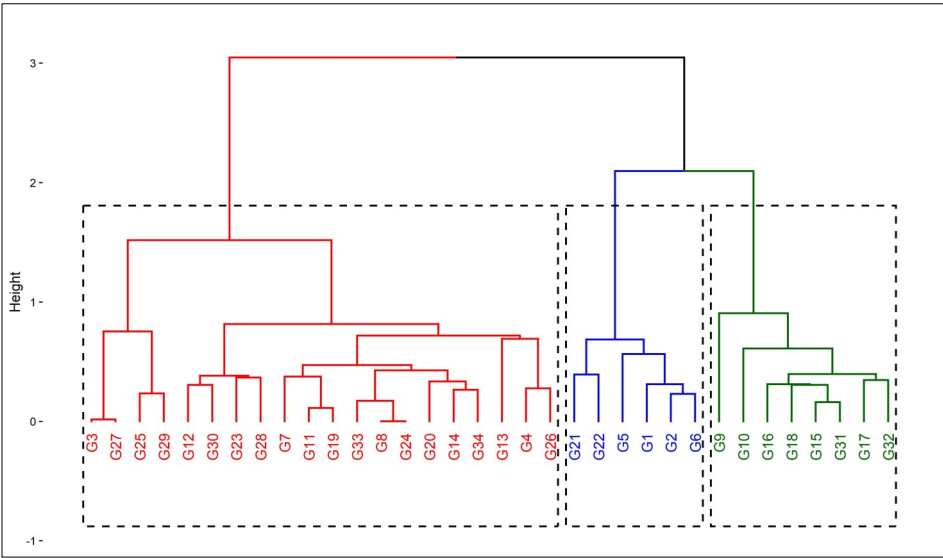


Fig. 3. Unweighted pair group method with arithmetic mean (UPGMA) -based clustering of MAGIC RILs based on sorghum downy mildew (SDM) disease response.

Table 5. additive main effects and multiplicative interaction (AMMI) analysis of variance for northern corn leaf blight disease response of MAGIC RILs evaluated across 3 locations

Source of variation	df	Northern corn leaf blight disease response	
		MSS	VE (%)
Environment	2	0.067*	20.30
Genotype	32	0.109**	3.27
Genotype × Environment	64	0.101*	5.06
IPCA1	33	0.033*	60.20
IPCA2	31	0.023*	39.80
Error	96	0.014	0.46
GLI _{noise} =EMSS × df of GLI		0.95	13.86 % of GLI
GLI _{signal} = GLI SS-GLI _{noise}		2.30	86.14 % of GLI

*, ** and *** indicate the significance at 0.05, 0.01 and 0.001 % respectively; MSS: mean sum of squares; VE: variance due to environment; SS: sum of squares; GLI: genotype × location interaction; EMSS: error mean sum of squares.

conditions on disease expression. The AMMI analysis revealed two IPCs axes (IPC1 and IPC2), as only 3 environments were evaluated. IPC1 and IPC2 explained 60.20 % and 39.80 % of the GEI sum of squares respectively, together accounting for 100 % of the interaction variation. The significant GEI and IPC effects highlight the importance of identifying stable genotypes and discriminating environments to enhance selection efficiency for disease resistance.

Thus, selection of stable genotypes based on AMMI1 and AMMI2 biplots is found to be very effective (1, 27, 35–36).

The genotype G13 exhibited the lowest ASV (0.009), indicating high stability across environments for disease response, followed by G15 with an ASV value of 0.031. Further, the genotypes G3, G31, G12, G8, G26, G20, G4, G2, G27, G15, G13, G16 and G32 located in the third quadrant of the scatter plot have relatively lower average disease scores accompanied by lower ASV values (stable performance), suggesting their practical utility in introgression or hybrid breeding programs. Conversely, the genotypes G28, G6, G18, G17, G33 and G19 recorded a lower ASV value with a higher average disease score, suggesting stable and susceptible response to NCLB disease. However, the genotypes G9, G24, G5, G29 and G10 located in the first quadrant possess lower average disease score with higher ASV values suggesting a prominent genotype × environment interaction (Fig. 4). The genotypes located in the second quadrant viz., G25, G22, G23, G7, G1, G30, G14, G11 and G21 possess higher ASV value coupled with higher average disease scores indicating unstable and susceptible response. Further, ranking of the genotypes was carried out by adding ASV with the mean disease score and the genotypes G13, G15 and G2 were found to be promising lines for NCLB disease resistance breeding (Table 6).

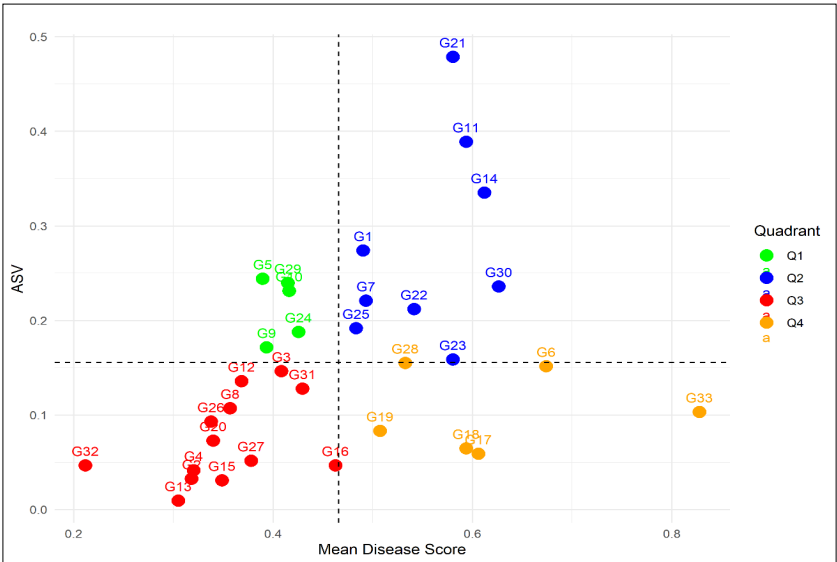


Fig. 4. Scatter plot depicting the distribution of genotypes based on AMMI stability value (ASV) and average disease score.

Table 6. Table depicting PC1, PC2, additive main effects and multiplicative interaction (AMMI) stability values along with ranks

Genotype	PC1	PC2	ASV	Av. disease score	Rank
G13	0.001022	0.009324	0.009409	0.30	1
G15	0.019638	0.019413	0.03098	0.35	2
G2	-0.00306	-0.03251	0.03273	0.32	3
G4	-0.02974	0.019864	0.04161	0.32	4
G32	-0.03024	0.028336	0.046745	0.21	5
G16	-0.03808	-0.00193	0.04686	0.46	6
G27	0.031704	0.033943	0.051685	0.38	7
G17	0.047588	0.007977	0.059046	0.61	8
G18	-0.03034	-0.05307	0.064864	0.59	9
G20	0.016271	0.070016	0.072817	0.34	10
G19	-0.06644	0.016191	0.083271	0.51	11
G26	0.075726	-0.00016	0.093098	0.34	12
G33	0.009336	-0.10267	0.103308	0.83	13
G8	0.087172	0.002867	0.107209	0.36	14
G31	-0.03089	0.122033	0.127804	0.43	15
G12	-0.03597	-0.12851	0.135907	0.37	16
G3	0.11807	0.019359	0.146441	0.41	17
G6	-0.03862	-0.144	0.151622	0.67	18
G28	0.122769	0.034971	0.154931	0.53	19
G23	-0.11794	0.064855	0.158841	0.58	20
G9	0.135055	0.043276	0.171585	0.39	21
G24	0.151128	0.028128	0.187914	0.43	22
G25	0.050448	0.181515	0.191818	0.48	23
G22	-0.09136	0.179871	0.212062	0.54	24
G7	0.179267	-0.01587	0.220962	0.49	25
G10	0.000647	0.231232	0.231233	0.42	26
G30	-0.13812	-0.16373	0.23589	0.63	27
G29	0.194211	-0.02042	0.239636	0.41	28
G5	0.17644	-0.11203	0.244136	0.39	29
G1	-0.2081	0.09788	0.273927	0.49	30
G14	0.130086	-0.29441	0.335047	0.61	31
G11	-0.31641	0.003154	0.389009	0.59	32
G21	-0.37126	-0.14489	0.478877	0.58	33

Similar approaches of combining AMMI based stability and mean performance have been successfully used in disease resistance and yield stability studies in maize and other crops (37–39).

The heatmap constructed using average disease scores across environments, along with ASV values (Fig. 5) revealed distinct patterns of genotype response. Genotypes G33 and G30 exhibited both higher mean NCLB severity and high ASV values, indicating greater environmental sensitivity and poor stability. The high ASV suggests that their disease response was strongly

influenced by environmental fluctuations, reflecting possible susceptibility due to weaker quantitative resistance mechanisms. Environments E2 (M/s Advanta disease screening facility, Hassan) and E3 (M/s Corteva Agriscience disease screening facility, Hassan) consistently recorded higher disease severity across genotypes, identifying them as highly disease-conducive locations. This may be attributed to favourable environmental conditions for pathogen development, such as optimal humidity, prolonged leaf wetness duration and moderate temperature, which are known to enhance NCLB progression. The consistent high disease pressure in these environments strengthens their utility as reliable screening sites for resistance evaluation. In contrast, the genotypes G13, G32, G15 and G20 maintained lower disease severity even under these high-pressure environments, coupled with a lower ASV values. Such genotypes are particularly valuable for breeding programs, as they offer durable resistance and broad adaptation, making them suitable candidates for deployment in NCLB-prone regions.

Additive main effects and multiplicative interaction biplots

AMMI1 biplot

AMMI1 biplot was plotted by considering average NCLB disease response on the abscissa, representing main effects, while the ordinates were depicted by IPCA I scores, indicating the multiplicative or GEI effects (14, 40). The AMMI1 biplot reveals the relationship between environments and genotypes. In the present study, the environment E3 (M/s. Corteva Agriscience disease screening facility Hassan) was placed farthest from the origin, with the longest vector indicating the presence of strong genotype by environment interaction. Whereas the environment E1 (ZARS, V. C. Farm, Mandya) had the shortest vector and was close to the origin, implying its low GEI influence. The environment E2 (M/s. Advanta seeds disease screening facility Hassan) was placed on the right-hand side of the biplot, indicating that it is favourable for the evaluation of genotypes for NCLB disease response (Fig. 6).

The MAGIC RILs, viz., G32, G4, G13 and G2, that were located on the right side of the quadrant recorded a resistant phenotype against the NCLB disease. Further, the genotypes G16, G19 and G10 that were located close to the origin displayed a wider adaptability to all the test

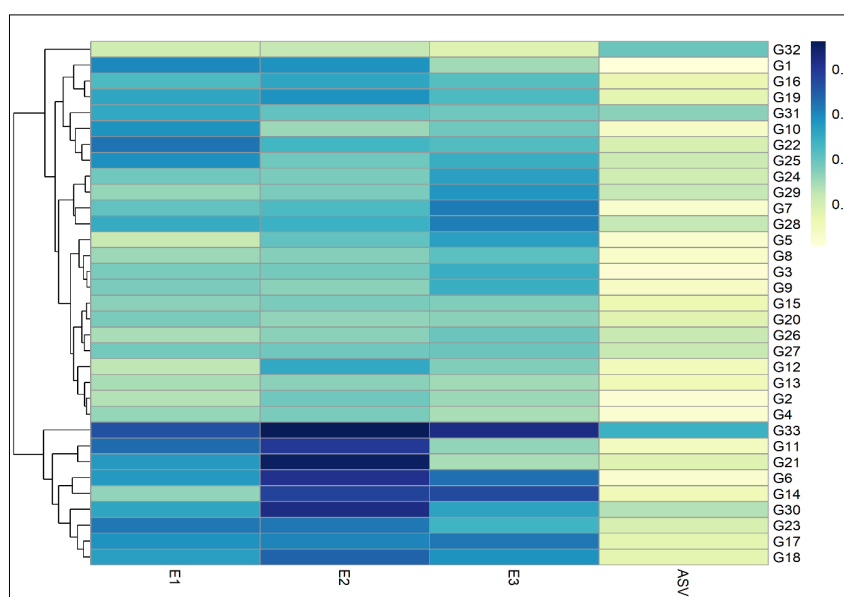


Fig. 5. Heatmap of northern corn leaf blight (NCLB) disease severity across genotypes and environments in comparison to AMMI stability value (ASV).

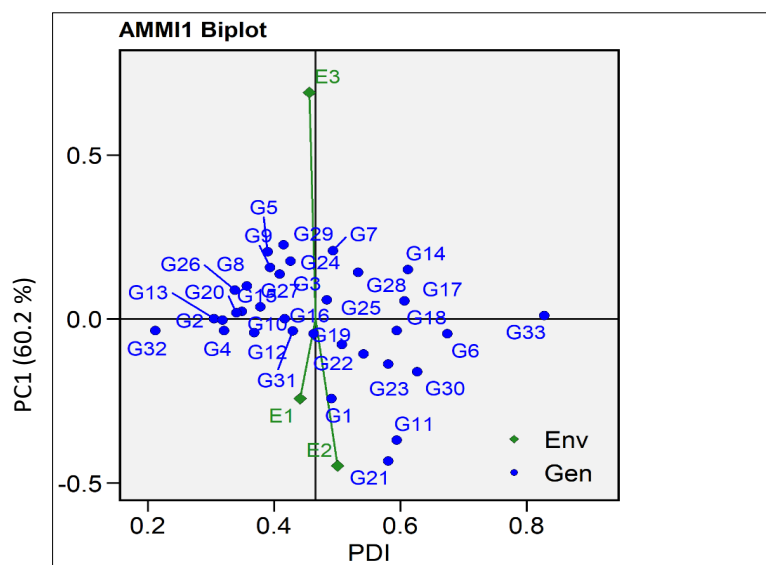


Fig. 6. Additive main effects and multiplicative interaction (AMMI 1) biplot for northern corn leaf blight (NCLB) disease response of MAGIC RILs.

environments. Several researchers employed AMMI1 in identifying better-performing and stable genotypes for various economically important traits like yield potential and other traits in maize (1, 14, 41).

AMMI2 biplot

The AMMI2 biplot was constructed using IPCA1 and IPCA2. It denotes the genotype-by-environment interaction to understand the genotype's response in each of the test environments. The first two principal components together explained 100 % of the total variation. The AMMI2 biplot uses the distances from the biplot origin to give an insight into the degree of interaction recorded by the genotypes across locations. The genotypes G3, G28, G2, G16, G12 and G32, which were located closer to the biplot's origin, were considered to possess wider adaptability. Meanwhile, the genotypes G14, G21, G11 and G10, which were located farther from the origin, are specifically adapted to a particular location (Fig. 7). Many researchers employed AMMI2 biplot for identifying the widely and specifically adaptable genotypes in various crops for different traits, such as grain yield in maize (41), sucrose content in sugarcane (42) and green cob yield in sweetcorn (1).

Genotype plus genotype-by-environment interaction (GGE) biplots

The GGE biplots are considered as the most powerful tool for successful analysis and better interpretation of multi-environment trial data (1, 43). In GGE biplot, several graphical representations facilitate the interpretation of genotype by environment interactions (44, 45).

Which won where biplot

The which-won-where view of the GGE biplot facilitates the identification of genotypes exhibiting the highest trait expression in specific mega-environments (46). Since disease severity was recorded such that higher values indicate greater susceptibility, the vertex genotypes in sectors containing environments represent the most susceptible genotypes in those respective mega-environments. The polygon view revealed that genotypes G33, G21 and G14 formed vertices on the negative side of PC1, whereas G5 and G32 were positioned on the positive side of the biplot (Fig. 8). The three environments were grouped into 2 mega-environments, wherein E2 (M/s. Advanta disease screening facility, Hassan) and E3 (M/s. Corteva Agriscience disease screening facility, Hassan)

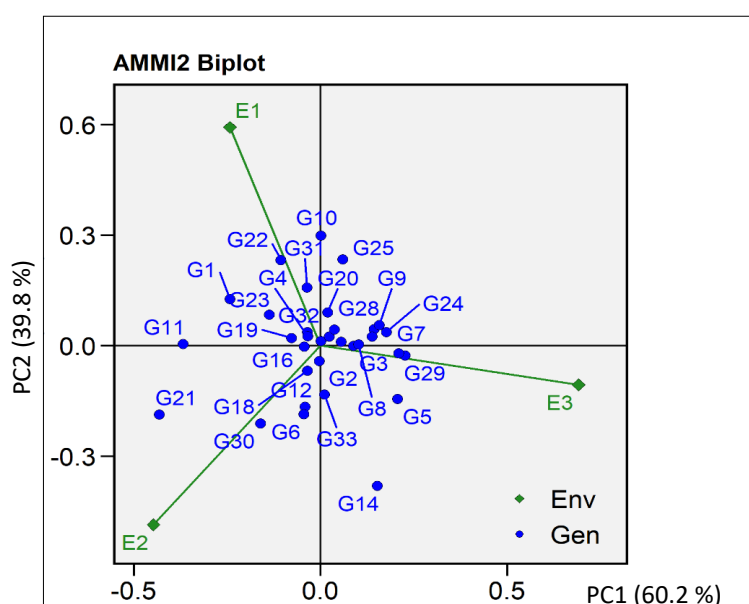


Fig. 7. Additive main effects and multiplicative interaction (AMMI 2) biplot for northern corn leaf blight (NCLB) disease response of MAGIC RILs.

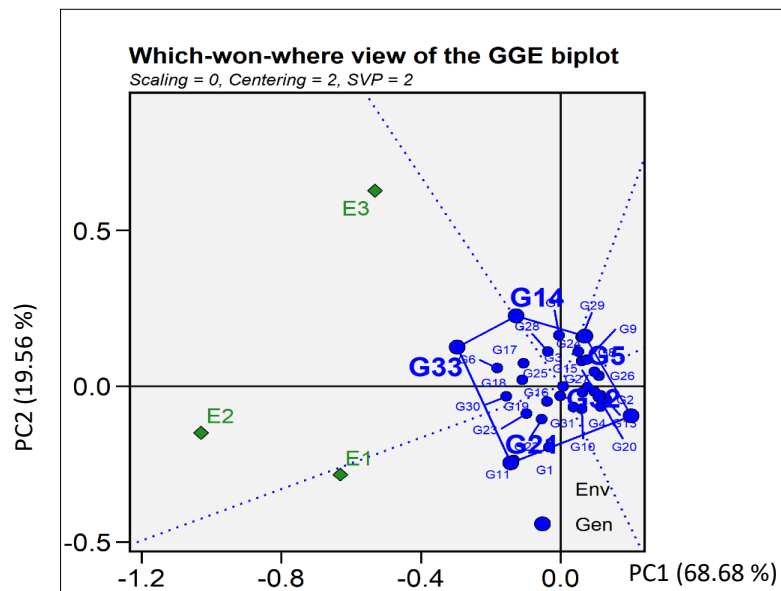


Fig. 8. Which won where biplot for northern corn leaf blight disease (NCLB) response of MAGIC RILs.

together formed one mega-environment, while E1 (ZARS, V.C. Farm, Mandya) constituted a separate mega-environment.

The genotypes G33 and G21, located at the vertices of the sectors containing mega-environments 1 and 2 respectively, were identified as the most susceptible genotypes in those environments. In contrast, genotypes positioned on the opposite side of the environment vectors, particularly G5 and G32, exhibited lower disease scores and were therefore considered resistant. Genotypes such as G2, G16 and G3, located closer to the origin, showed relatively stable and moderate disease response across environments. The identification of sector-specific genotypes through the which-won-where biplot enables delineation of mega-environments and assists in selecting genotypes adapted to specific environmental conditions (1, 47).

Mean vs. stability biplot

The mean vs. stability view of GGE biplot is a 2D visualisation of average disease resistance vs. stability based on IPC1 and IPC2 (35). An average environment coordinate was plotted to visualise the genotype's stability. The length of the perpendicular line drawn from the environmental abscissa indicates stability. The shorter the projection, the wider the adaptability. Genotypes aligned in the

direction of the average environment coordination (AEC) arrow display higher mean performance, while the genotypes located in the opposite direction show poor performance. In the mean vs. stability biplot from the current study, the genotype G33 with a shorter projection from the AEC abscissa displayed a higher stability with a higher disease score (indicating the highly susceptible response). The genotypes which were located on the opposite side of the AEC abscissa with shorter projections from the environment abscissa, viz., G15, G27, G13 and G10, were considered resistant with a lower disease score (Fig. 9).

Discriminativeness vs. representativeness biplot

Discrimination and a representative view of GGE biplot was employed to display the discriminative and representative ability of the test environments in different crops (1, 48, 49). The discriminativeness vs. representativeness biplot tests the environment's potential to identify the environments that effectively identify the stable genotypes within a given mega environment. The length of the environment vector and its angle with the AEC indicate their discriminating and representative abilities respectively. A discriminative environment distinguishes between genotypes, while a representative one averages all test environments. Longer environment vectors signify higher discriminative ability. Small

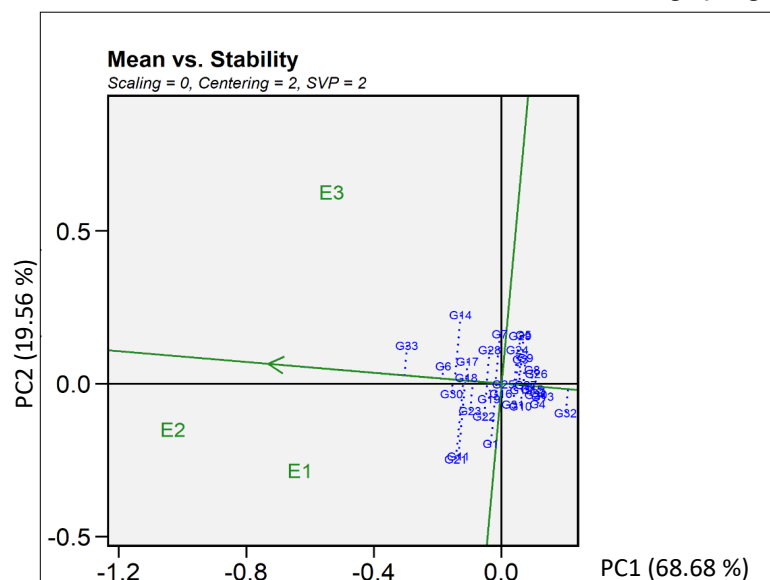


Fig. 9. Mean vs. stability biplot for northern corn leaf blight (NCLB) disease response of MAGIC RILs.

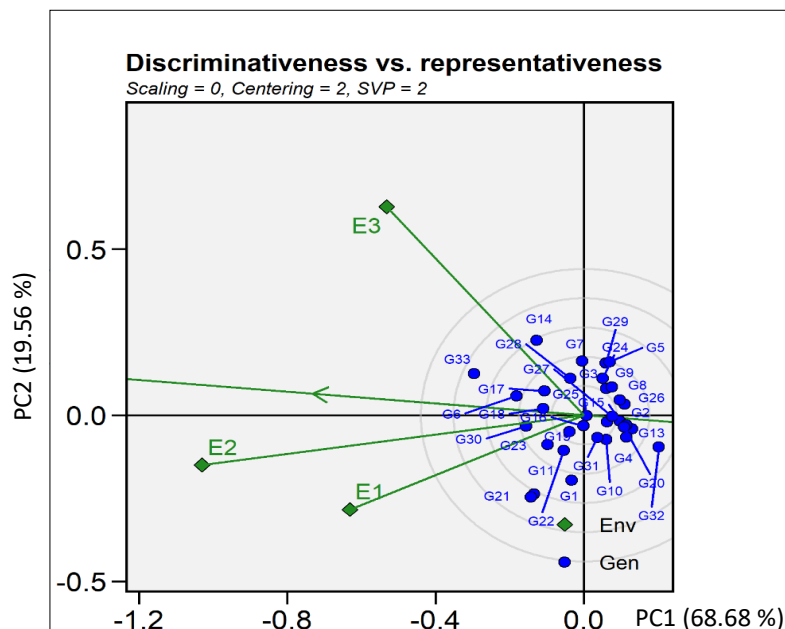


Fig. 10. Discriminativenss and representativeness biplot. angles indicate higher representativeness, while large angles indicate poor representativeness. Acute angles show similarity between test environments, while obtuse angles reflect dissimilarity.

In the given study, the environment E2 (M/s. Advanta seeds disease screening facility at Hassan) was highly discriminative, indicating that it effectively distinguishes between genotypes and the same environment with the lowest angle with the environment abscissa was highly representative, also implying it represents all test environments (Fig. 10).

Conclusion

The present study revealed contrasting patterns of genotype × environment interaction for northern leaf corn blight (NCLB) and sorghum downy mildew (SDM) reaction in the evaluated MAGIC RILs. While SDM exhibited stable genotype performance across seasons, supported by very high inter-season correlations and minimal genotype re-ranking, NCLB showed significant environmental influence and moderate correlations among locations, indicating crossover interaction and the need for multi-location testing. Unweighted pair group method with arithmetic mean (UPGMA) clustering for both diseases grouped genotypes into major clusters but did not distinctly separate resistant and susceptible classes, suggesting quantitative inheritance and continuous phenotypic variation. Stability analyses using additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment (GGE) biplots consistently identified G15, G10, G13, G16 and G32 as stable and broadly adapted genotypes. These lines constitute valuable genetic resources for breeding durable and environment-resilient disease resistance. Future research should validate these stable genotypes across diverse agro-climatic regions and integrate phenotypic stability analysis with genomic approaches to identify loci associated with consistent resistance, thereby accelerating marker-assisted introgression and hybrid development.

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disease screening facility.

Authors' contributions

SMS participated in the design of the study and performed the statistical analysis. LHC conceived the study and participated in its design and coordination. MP, MN and JG provided resources and coordination. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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References

1. Patel R, Parmar DJ, Patel DA, Memon J, Patel MB, Patel JK. Dissection of genotype × environment interaction for green cob yield using AMMI and GGE biplot with MTSI for selection of elite genotype of sweet corn (*Zea mays* conva. *saccharata* var. *rugosa*). Indian J Genet. 2023;83(1):59–68.
2. Hooda KS, Bagaria PK, Khokhar M, Kaur H, Rakshit S. Mass screening techniques for resistance to maize diseases. ICAR-Indian Inst Maize Res, PAU Campus, Ludhiana. 2018;93 pp.
3. Leonard KJ, Suggs EG. *Setosphaeria turcica* n. comb., the ascigerous state of *Helminthosporium turcicum* Pass. Phytopathol. 1974;64 (9):1130–1.
4. Pant SK, Kumar P, Chauhan VS. Effect of turcicum leaf blight on photosynthesis in maize. Indian Phytopathol. 2000;54:251–2.
5. Nwanosike MR, Mabagala R, Kusolwa PM. Effect of northern corn leaf blight (*Exserohilum turcicum*) severity on yield of maize (*Zea mays* L.) in Morogoro, Tanzania. Int J Sci Res. 2015;4(9):466–75.
6. Singh R, Mani VP, Koranga KS, Khendelwal RS, Bhandari P, Pant SK. Identification of additional sources of resistance to *Exserohilum turcicum* in maize (*Zea mays* L.). SABRAO J Breed Genet. 2004;36:45–7.

7. Schuh W, Frederiksen R, Jeger M. Analysis of spatial patterns in sorghum downy mildew with Morisita's index of dispersion. *Phytopathology*. 1986;76:446–50. <https://doi.org/10.1094/phyto-76-446>
8. Renfro BL. Introduction and decision taken on downy mildew issue. *Indian Phytopathol*. 1973;23:177–9.
9. Zhao L, Wu Y, Yu X, Shi J. Genetic approaches and breeding strategies for enhancing northern corn leaf blight resistance in maize (*Zea mays* L.). *Maize Genom Genet*. 2024;15(6):282–92. <https://doi.org/10.5376/mgg.2024.15.0027>
10. Mackay I, Powell W. Methods for linkage disequilibrium mapping in crops. *Trends Plant Sci*. 2007;12:57–63.
11. Huang BE, Verbyla KL, Verbyla AP, Raghavan C, Singh VK, Gaur P. Magic populations in crops: current status and future prospects. *Theor Appl Genet*. 2015;128:999–1017. <https://doi.org/10.1007/s00122-015-2506-0>
12. Scott MF, Ladejobi O, Amer S, Bentley AR, Biernaskie J, Boden SA, et al. Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. *Heredity*. 2020;125(6):396–416. <https://doi.org/10.1038/s41437-020-0336-6>
13. Desai SP, Lohithaswa HC, Mallikarjuna N. Genetic characterization and comparative assessment of response of biparental and multi-parental populations to northern corn leaf blight in maize (*Zea mays* L.). *Indian J Genet*. 2022;82(3):304–10.
14. Mwendo MM, Mbega ER, Ndunguru J, Philipo M. AMMI and GGE biplot analysis of maize genotypes for seed yield across different maize growing location in Tanzania. *Cogent Food Agric*. 2025;11(1):2438909. <https://doi.org/10.1080/23311932.2024.2438909>
15. Yan W, Hunt LA, Sheng Q, Szlavnic Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci*. 2000;40:597–605.
16. Supriadi D, Bimantara YM, Zendrato YM. Assessment of genotype × environment and yield performance of tropical maize hybrids using stability statistics and graphical biplots. *PeerJ*. 2024;12:e18624. <https://doi.org/10.7717/peerj.18624>
17. Gollob HF. A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*. 1968;33:73–115.
18. Ajay BC, Ramya KT, Fiyaz AR, Govindaraj G, Bera SK, Kumar N, et al. R-AMMI-LM: Linear-fit Robust-AMMI model to analyze genotype-by environment interactions. *Indian J Genet Plant Breed*. 2021;81(1):87–92. <https://doi.org/10.31742/IJGPB.81.1.9>
19. Crossa J, Gauch HG, Zobel RW. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci*. 1990;30(3):493–500. <https://doi.org/10.2135/cropsci1990.0011183X003000030003x>
20. Gauch HG Jr. Model selection and validation for yield trials with interaction. *Biometrics*. 1988;44:705–15. <https://doi.org/10.2307/2531585>
21. Ma C, Liu C, Ye Z. Influence of genotype × environment interaction on yield stability of maize hybrids with AMMI model and GGE biplot. *Agron*. 2024;14(5):1000. <https://doi.org/10.3390/agronomy14051000>
22. Bocianowski J, Nowosad K, Rejek D. Genotype-environment interaction for grain yield in maize (*Zea mays* L.) using the additive main effects and multiplicative interaction (AMMI) model. *J Appl Genet*. 2024;65(4):653–64. <https://doi.org/10.1007/s13353-024-00899-4>
23. Chung C, Longfellow JM, Walsh EK, Kerdieh Z, Esbroeck GV, Balint-Kurti P, et al. Resistance loci affecting distinct stages of fungal pathogenesis: use of introgression lines for QTL mapping and characterization in the maize-*Setosphaeria turcica* pathosystem. *BMC Plant Biol*. 2010;10:103.
24. Mitiku M, Eshte Y, Shiferaw W. Evaluation of maize variety for northern leaf blight (*Trichometasphaeria turcica*) in South Omo zone. *World J Agric Res*. 2014;2(5):237–9.
25. Lal S, Singh IS. Breeding for resistance to downy mildews and stalk rots in maize. *Theor Appl Genet*. 1984;69:111–9.
26. Zobel RW. A powerful statistical model for understanding genotype-by-environment interaction. In: Kang MS, editor. *Genotype-by-environment interaction and plant breeding*. Louisiana State University; 1990. p.126–40.
27. Farshadfar E, Sutka J. Biplot analysis of genotype-environment interaction in durum wheat using the AMMI model. *Acta Agron Hung*. 2006;54:459–67.
28. Olivoto T, Lúcio ADC. Metan: an R package for multi-environment trial analysis. *Methods Ecol Evol*. 2020;11(6):783–9.
29. Purchase JL, Hatting H, van Deventer CS. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability of cultivars and recommendations for stable cultivars. *Euphytica*. 2000;112:1–12.
30. Sokal RR, Michener CD. A statistical method for evaluating systematic relationships. *Univ Kans Sci Bull*. 1958;38:1409–38.
31. Sowmya MS, Lohithaswa HC, Jadesha G, Mahadevu P, Mallikarjuna N, Mohan Rao A. Genetic variability studies on resistance to sorghum downy mildew disease in MAGIC population of maize (*Zea mays* L.). *Mysore J Agric Sci*. 2024;58(4):110–4.
32. Lohithaswa HC, Balasundara DC, Mallikarjuna MG, Sowmya MS, Mallikarjuna N, Kulkarni RS, et al. Experimental evaluation of effectiveness of genomic selection for resistance to northern corn leaf blight in maize. *J Appl Genet*. 2024;66(3):493–521.
33. Ranganatha HM, Lohithaswa HC, Pandravada A. Mapping and validation of major quantitative trait loci for resistance to northern corn leaf blight along with the determination of the relationship between resistances to multiple foliar pathogens of maize (*Zea mays* L.). *Front Genet*. 2021;11:548407.
34. Rashid Z, Sofi M, Harlapur SI, Kachapur RM, Dar ZA, Singh PK, et al. Genome-wide association studies in tropical maize germplasm reveal novel and known genomic regions for resistance to northern corn leaf blight. *Sci Rep*. 2020;10:21949.
35. Yan W, Cornelius PL, Crossa J, Hunt LA. Two types of GGE biplots for analyzing multi-environment trial data. *Crop Sci*. 2001;41(3):656–63. <https://doi.org/10.2135/cropsci2001.413656x>
36. Gauch HG Jr. A simple protocol for AMMI analysis of yield trials. *Crop Sci*. 2013;53(5):1860–9. <https://doi.org/10.2135/cropsci2013.04.0241>
37. Kang MS. Simultaneous selection for yield and stability in crop performance trials: consequences for growers. *Agron J*. 1993;85:1860–9.
38. Gauch HG, Piepho HP, Annicchiarico P. Statistical analysis of yield trials by AMMI and GGE. *Crop Sci*. 2008;48:866–89.
39. Bose LK, Jambhulkar NN, Pande K, Singh ON. Stability analysis of rice genotypes for grain yield and its components under irrigated ecosystem. *African J Agric Res*. 2014;9(26):2044–50.
40. Ebdon JS, Gauch HG Jr. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype × environment interaction. *Crop Sci*. 2002;42(2):489–96. <https://doi.org/10.2135/cropsci2002.4890>
41. Bozovic D, Zivanovic T, Popovic V, Tatic M, Gospavic Z, Miloradovic Z, et al. Assessment stability of maize lines yield by GGE-biplot analysis. *Genetika*. 2018;50(3):755–70.
42. Elayaraja K, Govindaraj P, Mahadevswamy HK, Appunu C, Hemaprabha G, Rajesh V, et al. Stability analysis for identification of stable genotypes of sugarcane (*Saccharum* spp.) through AMMI model. *Indian J Genet Plant Breed*. 2022;82(4):480–9. <https://doi.org/10.31742/ISGPB.82.4.12>
43. Samonte SOP, Wilson LT, McClung AM, Medley JC. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analyses. *Crop Sci*. 2005;45(6):2414–24. <https://doi.org/10.2135/cropsci2005.062414a>

doi.org/10.2135/cropsci2004.0627

44. Kumar A, Sharma A, Kumar R, Rana M, Sharma S, Kumar P, et al. Precision agriculture innovation focuses on sustainability using GGE biplot and AMMI analysis to evaluate GE interaction for quality essential oil yield in *Eucalyptus citriodora* Hook. *Biochem Syst Ecol.* 2023;107:104603. <https://doi.org/10.1016/j.bse.2023.104603>
45. Zhang H, Liu Z, Li X, Wang Q, Yang Y, Zhang W, et al. Genotype by environment interaction for grain yield in foxtail millet (*Setaria italica*) using AMMI model and GGE biplot. *Plant Growth Regul.* 2023;99(1):101–12. <https://doi.org/10.1007/s10725-022-00885-y>
46. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: principles and applications. *Can J Plant Sci.* 2006;86:623–45. <https://doi.org/10.4141/P05-169>
47. Ohunakin AO, Odiyi AC, Akinyele BO. Genetic variance components and GGE interaction of tropical maize genotypes under northern leaf blight disease infection. *Cereal Res Commun.* 2020;49(2):277–83. <https://doi.org/10.1007/s42976-020-00100-6>
48. Reddy PS, Satyavathi CT, Khandelwal Patil HT, Narasimhulu R, Bhadarge HH, Iyanar K, et al. GGE biplot analysis for identification of ideal cultivars and testing locations of pearl millet (*Pennisetum glaucum* L.R. Br.) for peninsular India. *Indian J Genet Plant Breed.* 2022;82(2):167–76. <https://doi.org/10.31742/IJGPB.82.2.5>
49. Kottawa-Arachchi JD, Ranatunga MAB, Abeysiriw Ardena DS. Utilization of within location non-replicated multi-locational yield trials and GGE biplot methods for testing adaptability of tea (*Camellia sinensis* (L.) O. Kuntze) over diverse environments. *Indian J Genet Plant Breed.* 2022;82(3):342–9. <https://doi.org/10.31742/IJGPB.82.3.9>

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