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AMMI Model and YREM - Based Grain Yield Stability of Horse Gram [*Macrotyloma uniflorum* (Lam.) Verdc.] YMV Disease Resistant Genotypes

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Abstract

Horse gram yellow mosaic virus (HgYMV) disease is one of the major biotic constraints in horse gram production. Development and deployment of cultivars resistant to HgYMV disease are considered as the most eco-friendly and sustainable approach to mitigate the production losses caused by the disease. However, for easy acceptance of such HgYMV disease-resistant cultivars by farmers, they should be in high yielding background. Under these premises, nine HgYMV disease-resistant genotypes including two checks were field-evaluated in triplicated randomized complete block design (RCBD) to identify those that exhibit stable grain yield plant^{-1} across four (two location-two years combination) environmrnts during 2020 and 2021 late rainy seasons. Additive Main effects and Multiplicative Interaction (AMMI) model was used to detect and characterize genotype × environment interaction (GEI). Genotype + Genotype × environment (GGE) bi-plot was used to visually (subjective criterion) interpret GEI patterns of genotypes and identify those that are stable across four environments. AMMI Stability Value (ASV) and Stability Index (SI) were used as objective criteria to assess relative stability of genotypes. A simple statistic, namely, yield relative to environment maximum (YREM) was also used to detect cross-over GEI and to quantify genotypes' attainable grain yield loss attributable to crossover GEI. The genotypes differed significantly and displayed significant GEI for grain yield. GEI_{signal} explained over 50 per cent of total SS due to GEI. AMMI 2 model family was adequate to explain detected variation attributable to GEI. One genotype namely, 'Palem 2' was found highly stable across four test environments based on three criteria, namely GGE bi-plot, ASV and SI with high mean grain yield plant^{-1}. 'Palem 2' with unit YREM is likely to maintain its high grain yield potential across temporal environments without reduction in grain yield even in the presence of cross over GEI.

Keywords: GEI, HgYMV disease, GGE bi-plot, AMMI stability value, Stability index, Resistance, YREM

Horse gram is one of the important climate-resilient indigenous grain legume crops in India. It is the fifth most widely grown legume crop in India (Fuller and Murphy, 2018). It is self-pollinated crop with 2n=20 chromosomes (Halder, 2012). It is one of the good sources of protein to a large number of people, especially those depending on vegetarian diet for source of energy (Morris, 2008). The productivity of horse gram is rather low (Fuller and Murphy, 2018) as it is grown in marginal soils in rainfed ecosystems by resource-poor farmers. Besides this, its production is constrained by several biotic stresses. Among these, horse gram yellow mosaic virus (HgYMV) disease transmitted by whiteflies (*Bemacia tabaci*) is most devastating (Durga *et al.,* 2014).

Genetic management through the development and deployment of cultivars resistant to HgYMV disease

is considered as the most eco-friendly and sustainable approach to mitigate the production losses caused by the HgYMV disease. Host plant resistance is not only effective, safe, reliable and long-lasting method of control, but also forms an important component of integrated disease management (IDM). However, for easy acceptance of HgYMV disease resistant cultivars by the farmers, they should be in high yielding background. The use of high- yielding HgYMV disease resistant cultivars is expected to contribute to sustainable horse gram production. Identification and deployment of YMV disease resistant genotypes within the working germplasm is a short-term strategy to cater to the immediate YMV disease resistant cultivar requirement of the farmers. Towards this effort, a few genotypes with high levels of resistance to HgYMV disease from among 196 germplasm accessions were selected based on their evaluation in two hotspot locations, namely Main Research Station (MRS), Hebbal, Bengaluru and Krishi Vignana Kendra (KVK), Chamarajnagar during 2021 and 2022 summer seasons. We hypothesize that at least one of these HgYMV disease resistant genotypes would serve as potential candidate cultivar if it displays grain productivity better than or at least as good as the check cultivars with high stability. To test this hypothesis, the HgYMV disease resistant geno types were field evaluated to (i) detect genotype × environment interaction (GEI) (if any), (ii) characterize GEI and (iii) identify the genotypes with high grain yield potential and stability across temporal environments.

Material and Methods

Experimental Material

The material for the study consisted of seven HgYMV disease resistant genotypes namely, Palem 1, Palem 2, Paiyur 1, Paiyur 2, IC-121640, IC-43516 and IC-392329 and two check varieties *viz.,* PHG 9 and BGM 1 (Table 1). PHG 9 and BGM 1 are high-yielding varieties released by the University of Agricultural Sciences (UAS), Bangalore, India for commercial horse gram production.

Table 1

Details of the HgYMV disease-resistant genotypes used for the study

Genotypes	Source of collection	YMV disease response score
Palem 1	Agriculture Research Station (ARS), Palem, Andhra Pradesh (AP)	2
Palem 2	ARS, Palem, AP	2
Paiyur 1	Regional Research Station (RRS), Paiyur, Tamil Nadu (TN)	2
Paiyur 2	RRS, Paiyur, TN	2
IC-121640	Kerala	2
IC-43516	Karnataka	1
IC-392329	Jharkhand	2
Yield checks		
PHG 9	UAS, GKVK, Bengaluru, Karnataka	2
BGM 1	Karnataka	2

The genotypes were scored for their response to HgYMV disease on 1-6 scale, where. 1=highly resistant and 6=highly susceptible

Methods

The seeds of 9 HgYMV disease resistant genotypes were sown in randomized complete block design (RCBD) with three replications at two locations, namely Gandhi Krishi Vignana Kendra (GKVK), Bengaluru and Zonal Agricultural Research station (ZARS), VC Farm, Mandya during 2020 and 2021 late rainy seasons. Each accession was sown in a single row of 3m length with a row-to-row spacing of 0.45m. Fifteen-days after sowing, the seedlings were thinned to maintain plant-to-plant spacing of 0.15m. A total of 15 to 16 plants survived to maturity in each genotype. Recommended crop management practices were followed during the crop growth period to raise a healthy crop. Data were recorded on ten randomly chosen plants (avoiding border ones) in each genotype on grain yield plant^{-1} (g).

Statistical Analysis

The replication-wise mean grain yield of HgYMV disease resistant genotypes was used for all statistical analysis as described in following sections.

ANOVA

Analysis of variance (ANOVA) (Panse and Sukhatme, 1984) was performed to detect significant differences, if any, among the HgYMV disease resistant genotypes.

Detection and Characterization of Genotype × Environment Interaction (GEI)

For purpose of detection of genotype × environment interaction (GEI), two location-two years combination was considered as four different temporal environments. Replication-wise mean grain yield data recorded from four environments was subjected to Additive main effects and multiplicative interaction (AMMI) model (Gauch and Zobel,1988). The additive main effects of genotypes and environments were fitted by univariate ANOVA, followed by fitting multiplicative GEI by interaction principal component (IPC) analysis (Gauch and Zobel,1988). The sum of squares attributable to signal-rich component of GEI (GEI_{Signal}) was computed as GEI SS - GEI_{Noise}, where, GEI_{Noise} = GEI degrees of freedom × error mean squares from the AMMI ANOVA (Gauch, 2013). The following model was used to estimate main effects of genotypes and environments, and GEI effects.

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where, 'Y_{ij}' is the mean grain yield of i^{th} genotype in the j^{th} environment, 'μ' is the experimental mean grain yield, 'g_i' and 'e_j' are the i^{th} genotype and j^{th} environment mean deviation from 'μ' respectively. 'λ_k' is the square root of eigen value of the k^{th} IPC axis, 'α_{ik}' and 'γ_{jk}' are the IPC scores for i^{th} genotype and j^{th} environment, respectively and 'ε_{ij}' is the residual. All the analyses were implemented using RStudio software v.4.2.1.

GGE Bi-Plot for Interpretation of GEI

Genotype + Genotype × environment (GGE) bi-plot is a subjective / qualitative means of characterizing GEI patterns and assessment of relative stability of test genotypes. GGE bi-plot utilises a combination of GGE concepts and AMMI bi-plot (Yan *et al.,* 2000). GGE bi-plot has been suggested for visual interpretation of patterns of GEI, representativeness and discriminating ability of the environments and relative stability of test genotypes. The GGE bi-plot is based on the following model.

$$Y_{ij} - Y_i = \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where, 'Y_{ij}' is the mean grain yield of i^{th} genotype in the j^{th} environment, 'Y_i' is mean grain yield of all the test genotypes in the j^{th} environment, 'λ_1' and 'λ_2' are square roots of eigen values of first and second IPC axes, 1 and 2, 'α_{i1}' and 'α_{i2}' are scores of the first and second IPC, respectively, for the i^{th} genotype and γ_{j1} and γ_{j2} are first and second IPC's respectively for j^{th} environment.

AMMI model-based parameters to identify stable genotypes

The relative stability of genotypes can be assessed objectively based on the estimates of AMMI stability value (ASV) (Purchase *et al*., 2000) and Stability Index (SI) (Farshadfar, 2011). The procedure and formulae for estimating ASV and SI are described in the following sections.

AMMI Stability Value (ASV)

ASV was estimated as,

$$\text{ASV} = \sqrt{\left[\frac{SSIPC1}{SSIPC2}(\text{IPC1 score})\right]^2 + (\text{IPC2 score})^2}$$

Where, SSIPC 1 and SSIPC 2 are sum of squares (SS) attributable to first two IPC's. Conceptually, ASV is the distance from zero in a two-dimensional scatter diagram of IPC 1 *vs.* IPC 2 scores (Purchase *et al*., 2000). Since the IPC 1 score generally contributes proportionately more to GEI, it is weighted by the proportional difference between IPC 1 and IPC 2 scores in order to compensate for the relative contribution of IPC 1 and IPC 2 scores to the total

GEI sum of squares. Lower the magnitude of estimates of ASV, greater in the stability of the test genotypes. Higher the magnitude of estimates of ASV, lower is the stability of test genotypes (Purchase *et al*., 2000).

Stability Index (SI)

As ASV considers only stability, regardless of grain yield potential of genotypes, SI was estimated to facilitate simultaneous selection of test genotypes with high stability and high mean grain yield. SI was estimated as SI = RASV + RY where, RASV is rank of the test genotypes based on ASV and RY is the rank of test genotype based on mean grain yield (Farshadfar, 2011) across four environments. The test genotypes with low SI were regarded as those with high mean grain yield and high stability.

Estimation of Yield Relative to Environment Maximum (YREM)

A simple statistic, namely YREM was used to detect crossover GEI and to quantify reduction in grain yield potential of test genotypes due to crossover GEI. Higher the value of YREM of a genotype, lower is the magnitude of crossover GEI and the lower is the extent of reduction in grain yield potential of that genotype even in the presence of crossover GEI. The grain YREM (Yan, 1999) was estimated as $Y_{ij} = X_{ij} / MAX_{ij}$, where, '$Y_{ij}$' and '$X_{ij}$' are the YREM and mean grain yield, respectively, of i^{th} genotype in j^{th} environment. MAX_{ij} is the grain yield of highest performer in j^{th} environment. The analysis was implemented using statistical analysis option available in Microsoft Excel software.

YREM is a special type of standardized estimate of genotypes' performance, with nullified environment main effect. It is also an intuitive and genotypes' attendance-independent measure of test genotype's performance (Yan, 1999). It is a dynamic measure of genotypes' performance, as it varies with the performance of best genotypes in a given environment and the best genotype also varies with the environment. The performance of best genotype is its potential attainable in a given environment. Hence, YREM is an indicative of magnitude of cross-over GEI. Therefore, in the absence of crossover GEI, the average YREM of a genotype tested across environment must be 1.0. Any departure of a genotype's YREM from 1.0 is interpreted as loss in its attainable grain yield attributable to crossover GEI (Yan, 1999). For example, if a genotype has an across-environments' average YREM = 0.90, then 10 per cent of its attainable grain yield is lost due to crossover GEI.

Results and Discussion

ANOVA

ANOVA is the diagnostic step to detect different sources of variation relevant to the results of field experiments such as those being reported in the present study. Location-wise ANOVA revealed significant mean squares attributable to test genotypes in all four environments for grain yield plant^{-1} (Table 2). These results indicated substantial differences among the test genotypes for grain yield plant^{-1} and thus provide justification for their use in

Table 2

ANOVA of HgYMV disease-resistant genotypes for grain yield plant^{-1} (g) at GKVK, Bengaluru and Zonal Agricultural Research Station, Mandya

Source of variation	Degrees of freedom	GKVK, Bengaluru						ZARS, Mandya					
		2020			2021			2020			2021		
		MSS	'F' Statistic	P≥F	MSS	'F' Statistic	P≥F	MSS	'F' Statistic	P≥F	MSS	'F' Statistic	P≥F
Genotypes	08	2.22	59.92	0.00	2.39	61.18	0.00	2.11	140.07	0.00	2.05	51.16	0.00
Replication	02	0.07	2.02	0.16	0.22	5.72	0.01	0.28	18.79	0.00	0.05	1.28	0.30
Error	16	0.04			0.04			0.01			0.04		

MSS: Mean sum of squares

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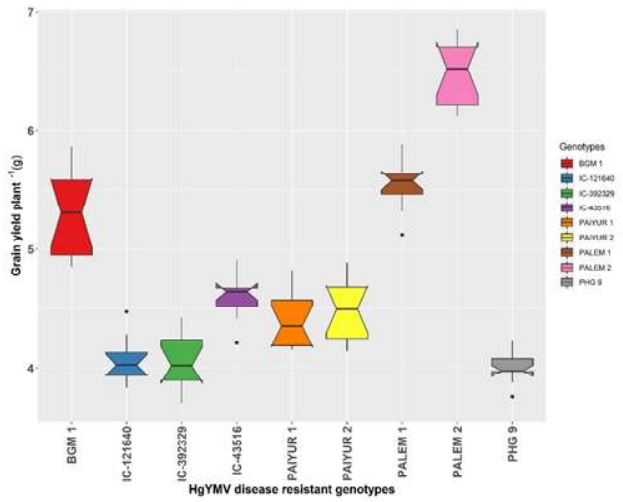

Fig. 1 : Box-Whisker plots showing significant differences among HgYMV disease-resistant genotypes for grain yield plant^{-1}

the present study. Box-Whisker plots depicts the range of grain yield plant^{-1} of seven test genotypes and two checks across the four environments. The genotype Palem 2 was the highest grain yielder followed by Palem 1 and BGM 1 (Fig. 1).

AMMI model - based detection and characterization of GEI effects

Additive ANOVA detects GEI only when the average of all (g-1) (e-1) degrees of freedom (df) contrasts is significant. Classical additive ANOVA indicate a lack of GEI, even when there exists significant GEI for some of the contrasts. Hence, classical additive ANOVA is not a desirable method for detecting GEI. Researchers can declare absence of GEI only if GEI sum of squares of one df is not significant (Gauch, 1988). As an intermediate approach between 1 and (g-1) (e-1) df, AMMI model is widely used to unambiguously detect GEI (Gauch, 1988). AMMI model uses additive ANOVA for detection of main effects of genotypes and environments and multiplicative IPC analysis of GEI effects. The rationale behind the AMMI model is that the observed performance of test genotypes in a particular environment is not the best estimate of true performance of that genotypes in that environment. This is because, most often than not test genotypes interact significantly with test environment (s) and hence GEI is a rule rather than an exception (Bernardo, 2020). The GEI effects consists of (1) signal / pattern attributable to repeatable and predictable component and (2) noise attributable to non-repeatable and un-predictable component. AMMI model effectively dissects GEI in to 'signal' and 'noise' components using several IPC's. While the first few IPC's tend to capture most of the repeatable and predictable components, later IPC's capture non-repeatable and un-predictable component (Gauch, 2013). AMMI model estimates GEI for ith genotype and jth environment not only from data pertaining to ith genotype and jth environment, but also from data of all the genotypes' performance in all the test environments (Bernardo, 2020).

In the present study, sum of squares (SS) attributable to GEI was partitioned into those attributable to GSI_{Signal} and GSI_{Noise}. Differences among test genotypes and environments are necessary for existence of GEI effects. In the present study, significant mean squares (Table 3) suggested presence of substantial variability among the test genotypes for grain yield plant^{-1}. Significant mean squares attributable to the GEI suggested differential performance of test genotypes across the four environments. However, over 50 per cent of SS due to GEI_{signal} contributes to SS due to GEI. Thus, a substantial portion of detected GEI effects are repeatable and hence predictable. However, mere detection of GEI does not provide information on the relative performance of genotypes across different test environments. Stability analysis help the researcher to examine the performance of genotypes relative to each other in different environments. Stability analysis requires AMMI model diagnosis, as AMMI constitutes a model family, not a single model. Consequently, model diagnosis is required to determine which member of this model family is best for a given data set and research purpose. The significance of mean squares attributable to IPC's is widely used as a criterion to diagnize the best AMMI model family member for given data set (Gauch, 2013). In the present study, sum of squares (SS) attributable to the first two IPC's explain >99.9 per

TABLE 3

AMMI ANOVA of HgYMV disease-resistant genotypes for grain yield plant^{-1} (g)

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	'F' Statistic	P≥F	Proportion
Genotypes	08	68.69	8.58	261.61	0.00	-
Environment	03	0.45	0.15	0.94	0.04	-
G×E interaction	24	1.51	0.06	1.91	0.02	-
PC1	10	1.13	0.11	3.43	0.00	74.70
PC2	08	0.37	0.05	1.41	0.02	24.60
PC3	06	0.01	0.01	0.06	0.99	0.70
Residual	64	2.10	0.03	-	-	-
GEI signal	-	0.79				52.31
GEI noise	-	0.72				47.68

GEI signal SS (0.79) = GEI SS (1.51) - GEI noise SS (0.72), where, GEI noise SS (0.72) = GEI degrees of freedom (24) × AMMI Error MSS (0.03)

cent of SS due to GEI. Further, the significance of mean squares attributable to first two IPC's indicate AMMI 2 is the best model family member that captures predictable component of GEI. Selection of the best AMMI model family member is the key for reliable estimates of genotypes' performance and selection of best genotype (s) with highly predictable performance in future years as well. This argument stems from the fact that it is rather difficult to exploit genotype × temporal environments (such as years) interaction, as breeders cannot establish independent breeding programs for different years. This is because, climate conditions that generate genotype × year interaction variation are not known *apriori.* From grower's point of view, location is a constant-not-variable factor and grain yield consistency over years is the only relevant component of genotypes' performance (Annicchiarico *et al.* 2006). This is because, success of identified best genotype as cultivar in growers production environments depends on the stability of its performance in future years after its release for commercial production (Spoorthi *et al.* 2021b). Several researchers such as Arunkumar and Konda (2014) and Bhardwaj *et al*. (2014) in mungbean, Vaijayanthi *et al.* (2017) in dolichos bean and Khan *et al.* (2021) in bambara groundnut have also detected significant GEI for grain yield and its component traits. Further, several previous researchers such as Piepho (1994) in fababean, Annicchiarico *et al*. (2006) in wheat, Ebdon and Gauch (2011) in turfgrass, Sadiyah and Hadi (2016) in rice and Spoorthi *et al.* (2021a) in dolichos bean have also reported adequacy of most parsimonious AMMI model family *i.e.* AMMI 2 model to explain the observed variation attributable to GEI.

The significant repeatable component of GEI effects detected in the present study warrants identification of HgYMV disease-resistant genotypes that are specifically suitable to each environment to maximize horse gram production in each environment with/ without the presence of YMV infection. The relative stability of test genotypes was assessed based on visual interpretation using GGE bi-plot and stability parameters. While assessment of stability based on GGE bi-plot visualization is a subjective method, that based on stability parameters is an objective method.

Assessment of Stability based on GGE Bi-Plot

A major purpose of yield - trial research is the selection of best genotypes for use as a cultivar in target environment. Stability of test genotypes across temporal environments as is the case in the present study is particularly important as it reduces susceptibility to unpredictable component of GEI

effects. The stability of test genotypes across four temporal environments can be qualitatively assessed using the graphical representation of test genotypes based on their first two IPC's in GGE bi-plot (Yan *et al.* 2000). GGE bi-plot is a multivariate analytical tool that graphically displays the interaction between each genotype and each environment. It is a two-dimensional graph and allows visualization of the inter-relationship among environments and test genotypes. There are numerous ways to use and interpret GGE bi-plot. However, four views of the GGE bi-plot are most relevant (Segherloo *et al.,* 2010). These are (i) average environment coordination (AEC) view based on test genotype-focused scaling for ranking of the test genotypes relative to ideal genotype; the ideal genotype is the one whose point is located in the centre of concentric circles in the GGE bi-plot (ii) discriminating and representativeness of test environments view (iii) polygon view based on symmetrical scaling for determining 'which-won-where' pattern of test genotypes in test environments, and (iv) AEC view based on environment-focused scaling for interpreting mean performance of the genotypes *vs.* their stability patterns (Yan and Kang, 2003). The results of the four views of GGE bi-plot are discussed in the following sections.

Genotype (s) Relative to Ideal Genotype

An ideal genotype is the one with high mean performance and high stability across the test environments. A single arrowed line passing through the origin in the biplot and center of the circle is referred to as an average environment coordinate (AEC). The average environment is represented by the small circle at the end of the arrow (Yan and Tinker, 2006). An ideal genotype is present at the center of concentric circles with AEC passing through it in positive direction and has a vector length equal to the longest vector of the genotype on the positive side of AEC. Using the ideal genotype as center, several concentric circles are drawn around to help in easy visualization of the distance between each test genotype and ideal genotype. Stable genotypes are the ones which are located closer to the ideal genotype. The test genotypes namely IC-43516 and Paiyur 2 were identified as near ideal ones on account of being closer to ideal genotype which is located at origin (Fig. 2a).

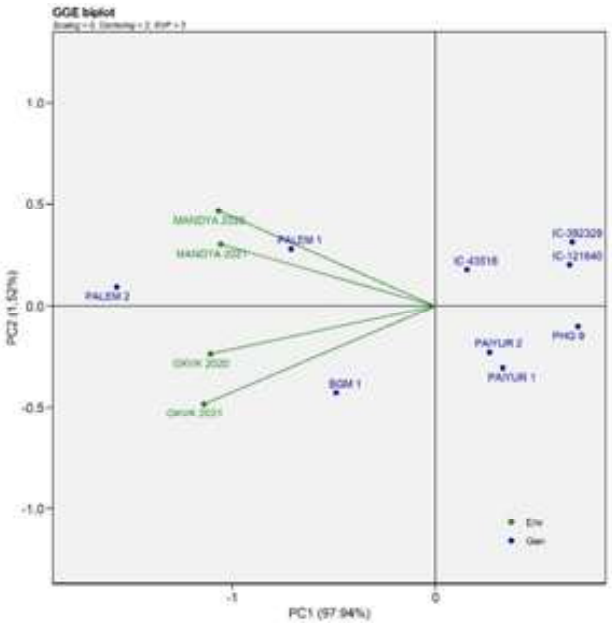

Fig. 2a : Average environment coordination (AEC) view of GGE-biplot for identification of test genotypes relative to ideal genotypes for grain yield plant^{-1}

Discriminative ability and representativeness of test environments

Dotted line connecting the test environment pointing to the origin is called environment vector. The length of environment vectors and angle between the respective environment vector with AEC helps in identifying the discriminating ability and representativeness of the test environments. A discriminative environment is the one which has the ability to discriminate between test genotypes while a representative environment should represent average of the four test environments. Shorter and longer environment vectors indicate lower and higher discriminative ability of the environments, respectively. Small and large angle between environment vectors and AEC indicate most and least representativeness of environments, respectively. The acute and obtuse angle between the test environment vectors indicate similarity and dissimilarity between the test environments, respectively. In the present

study, GKVK 2021 late rainy season is discriminative as its environment vector is longer than other environmental vectors. On the other hand GKVK 2020 late rainy season is a representative environment as the vectors of these environments are oriented in acute angle relative to AEC (Fig. 2b).

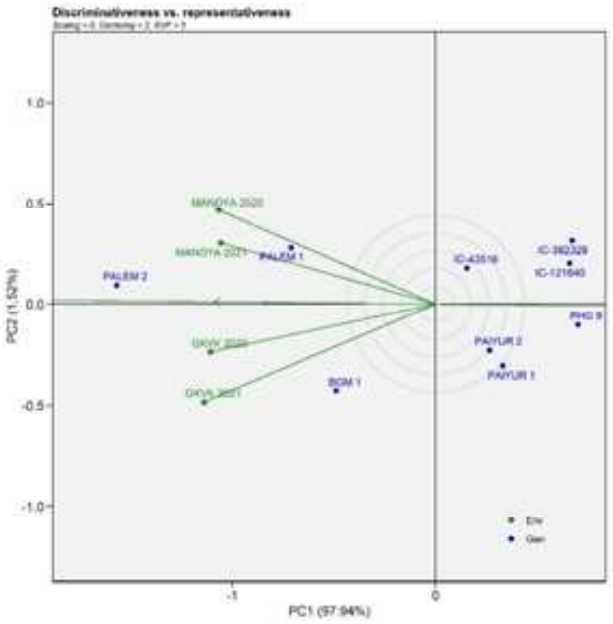

Fig. 2b : Descriminative *vs.* representativeness view of GGE-biplot for grain yield plant^{-1}

'Which-won-where' View

Polygon view of GGE biplot helps in identifying which won where pattern of genotypes. A polygon is formed by joining all the test genotypes farther from the biplot origin in such a way that all of them fell within the polygon. Perpendicular lines called equality lines, originating from biplot origin are drawn to each side of the polygon. The equality lines divide the bi-plot into sectors. The vertex genotype in each sector is the winning genotype at environments whose markers (point) fall into the respective sector (Yan *et al*., 2000). Thus, environments whose markers fall in the sector will have the same winning genotype, while environments of different sectors have different winning genotypes. Thus, polygon view of GGE biplot indicates the presence or absence of crossover GEI. In the present study, test genotypes such as Palem 1 and Palem 2 occupied vertices of the polygon. While Palem 1 was the winner in ZARS, Mandya during both 2020 and 2021 late rainy seasons, Palem 2 was the winner in GKVK, Bengaluru during both 2020 and 2021 late rainy seasons for grain yield plant^{-1} (Fig. 2c).

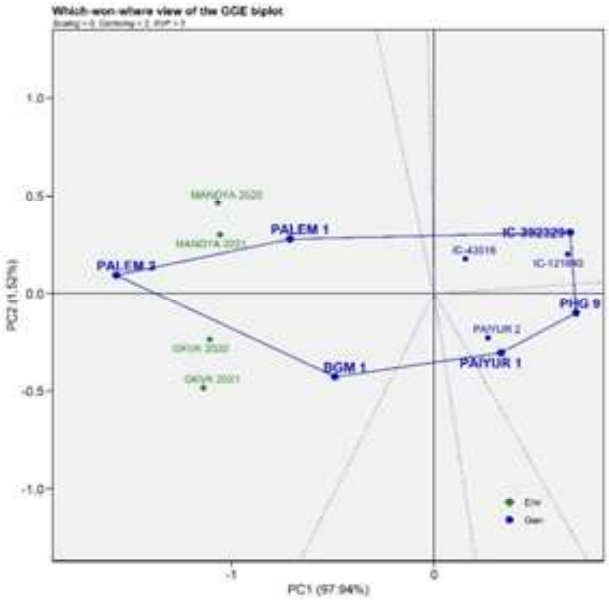

Fig. 2c : Polygon view of GGE-biplot based on the symmetrical scaling for "which won-where" pattern of test genotypes and environments for grain yield plant^{-1}

Mean Performance *vs.* Stability Patterns

The mean performance and stability could be visualized based on the location of genotypes in relation to AEC using AEC view of GGE bi-plot. The single-arrowed AEC points to higher mean performance of the genotypes across test environments (Yan, 1999). The genotypes with their points located towards AEC arrow are considered to exhibit high mean performance. On the contrary, the genotypes with their points located opposite to AEC arrow are considered to exhibit lower performance. Further, the relative lengths of projections of the genotypes from AEC are indicative of their relative stability. Shorter the length of the projections of genotypes from AEC, greater is the stability of the genotypes. Longer the projections of genotypes, poorer in their stability (Yan and Kang, 2003). In the present study, Palem 2 with shortest vector from the AEC line, was identified as a highly stable genotype across test environments with higher mean grain yield plant^{-1} (Fig. 2d).

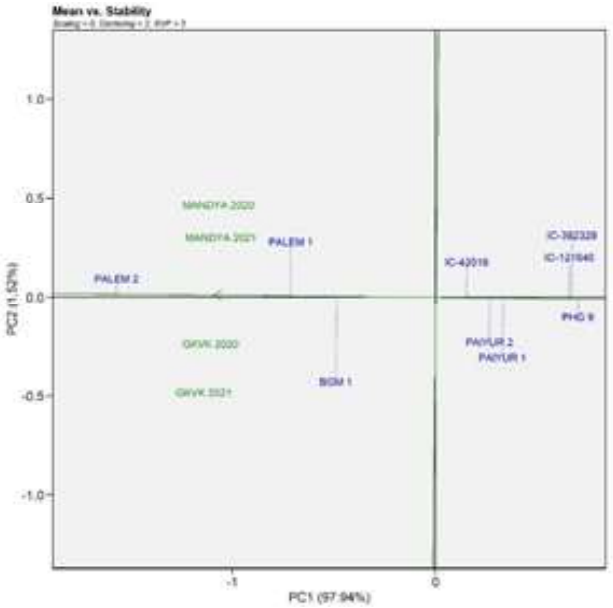

Fig. 2d : Average environment coordination (AEC) view of GGE-biplot based on environment-focused scaling for the mean performance *vs.* stability of test genotypes for grain yield plant^{-1}

AMMI Model-based Stability Parameters

AMMI Stability Value (ASV)

ASV provides an objective criterion of assessment of stability and hence help to identify test genotypes stable across the four environments. ASV is the distance from zero in a two-dimensional scatter-plot of IPC 1 scores against IPC 2 scores. In the present study, ASVs were estimated using both IPC 1 and IPC 2, as they significantly contributed towards total GEI variance of grain yield plant^{-1} (Table 3). In the present study, Palem 2 and PHG 9 with lower magnitude of the estimates of ASV (Table 4), were adjudged as stable genotypes across the four test environments for grain yield plant^{-1}.

Stability Index (SI)

SI which takes into account of both mean grain yield and stability in a single criterion helps in simultaneous selection of genotypes with desired performance for mean grain yield coupled with stability. The genotypes with low SI are regarded as those with high grain yield and stability. In the present study, Palem 2 and Palem 1 with lower magnitude of SI (Table 4), were regarded as the best genotypes with high grain yield and stability. Several researchers such as Patel *et al.* (2009), Arunkumar and Konda (2014), Bharadwaj *et al.* (2014), Vaijayanthi *et al.* (2016), Vaijayanthi *et al*. (2017), Kavya and Rangaiah (2019) have also identified genotypes stable across

TABLE 4

Estimates of AMMI model-based parameters to assess stability of nine HgYMV disease-resistant genotypes for grain yield plant^{-1} (g)

Genotypes	Mean	RY	ASV	RASV	SI	Average YREM
Palem 1	5.56	2	0.66	4.5	06.5	0.85
Palem 2	6.49	1	0.15	2.0	03.0	1.00
Paiyur 1	4.41	6	0.84	7.0	13.0	0.68
Paiyur 2	4.48	5	0.66	4.5	09.5	0.69
IC-121640	4.06	7	0.78	6.0	13.0	0.62
IC-43516	4.61	4	0.59	3.0	07.0	0.71
IC-392329	4.04	8	1.20	8.0	16.0	0.62
Yield checks						
PHG 9	4.01	9	0.13	1.0	10.0	0.62
BGM 1	5.30	3	1.42	9.0	12.0	0.82
SEm±	0.28					
CD @P=0.05	0.60					

RY: Rank of the test genotype based on mean grain yield, ASV: AMMI Stability Value, RASV: Rank of the test genotype based on ASV, SI: Stability Index, YREM: Yield relative to environment maximum.

temporal environments based on SI. Of these two genotypes, Palem 2 was found highly stable across four test environments based on three criteria, namely GGE bi-plot, ASV and SI with high mean grain yield plant^{-1}.

YREM

Considering that YREM is a simple statistic which is independent of genotypes' attendance, it could be used as a predictor of genotypes' performance in future years (Yan, 1999). In the present study, unit YREM of Palem 2 (Table 4) indicates that its interaction with the four test environments is of non-crossover type. Unit YREM of Palem 2 also indicates that it remained highest yielder in all the four environments and its grain yield potential as assessed in the present study is attainable in all the test temporal environments without any loss, even if there exists cross-over GEI. Ashwini *et al.* (2021) and Spoorthi *et al.* (2021b) have also used YREM to detect crossover GEI, and to identify stable horse gram and dolichos bean genotypes respectively. Thus, Palem 2 with significantly higher grain yield potential and stability than both the checks, and unit YREM could be used as a cultivar for commercial production in GKVK, Bengaluru and ZARS, Mandya.

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