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Genotype × environment interaction and selection of maize (*Zea mays* L.) hybrids across moisture regimes

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ABSTRACT

Genotype × environment (GE) interaction effect is one of the major challenges in identifying cultivars with stable performance across environments and years. Objective of the present study was to identify maize hybrids with high and stable yields under different soil moisture regimes such as drought, waterlogged and well-watered conditions. The trials were carried out in subsequent winter (*Rabi)* and summer-rainy (*Kharif*) seasons of 2017 and 2018 totaling seven test environments at the two different locations of India *viz*, Banaras Hindu University, Varanasi and CIMMYT, Hyderabad. After observing substantial and statistically significant GE interaction for studied traits, the phenotypic stability of maize hybrids was analyzed by AMMI, GGE biplot and multi-trait stability index (MTSI) methods. The study emphasized on the significance of AMMI and GGE biplots in deciphering the GE interactions based on grain yield data. Estimation of stability indices, WAASB (Weighted Average of Absolute Scores from the singular value decomposition of the matrix of BLUPs) for the GE interaction effects and WAASBY (a combination of WAASB and yield) scores for identification of the best suitable genotypes with high stability and maximum yield potential was highlighted. The investigation delineated the applicability of MTSI that computed based on the genotype-ideotype distance considering the multiple variables. The methods studied were concordant in the identification of the promising maize hybrids with high mean performance and greater phenotypic stability across the different soil moisture conditions.

1. Introduction

Maize has emerged as the cereal with largest global production, which surpassed rice in 1996 and wheat in 1997, and its production is increasing at twice the annual rate of rice and three times that of wheat (Fischer et al., 2014). Asia, with its 31 % share in global maize production from about 34.0 % of the total global area harvested, is the second largest maize producer in the world. The current decade continued impressive growth in maize production, as in all the sub-regions showed significant increase in maize production, including Southeast Asia- 10.8 %, Southern Asia- 27.3 %, East Asia- 30.6 %, which resulted overall 27.7 % maize production increase in Asia within a short period of 2010–2016 (FAOSTAT, 2018). Even though, being a soil moisture sensitive crop, maize is affected by low as well as excess moisture availability at any stage of growth and development. The prevalence of drought or waterlogging stress at the vegetative or reproductive stage causes poor crop stand and under severe conditions leads to complete failure of the crop (Zeid and Nermin, 2001; Aslam et al., 2015). In India, out of total geographical area of 328.7 million hectare (mha), about 120.4 mha (37 %) is affected by various kinds of

Abbreviations: GEI, genotype × environment interaction; MET, multi-environment trials; AMMI, additive main effects and multiplicative interaction; GGE, genotype main effect plus genotype-environment interaction effect; AEC, average-environment coordinate; SVP, singular value partitioning; SVD, singular value decomposition; SREG, site regression; BLUP, best linear unbiased prediction; LMM, linear mixed model; WAASB, weighted average of absolute scores from the singular value decomposition of the matrix of BLUPs; MTSI, multi-trait stability index; ASV, AMMI stability value; YSI, yield stability index; IPCA, interaction principal component axis; DFF, days to 50 % anthesis; DFS, days to 50 % silking; ASI, anthesis-silking interval; PH, plant height; EH, ear height; EL, ear length; NKPR, number of kernels per row; NKRE, number of kernel rows per ear; TW, test weight; GYPH, grain yield per hectare.

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abiotic stresses in which drought and waterlogging occupied a greater amount. The coming decades are expected to see further increases in temperature, rising sea levels, more intense pest and disease pressures and water shortages. By 2050, when the global population is expected to reach 9.6 billion, demand for the cereals including rice, wheat and maize could become a total of 3.3 billion tonnes a year, or 30 percent more than that produced today. In India, maize is grown in 9.3 mha area with a national production of 28.72 million tonnes (MT) (FAOSTAT, 2020). It contributes up to 9.5 percent in the Indian food basket.

The global importance of maize and the worst effects of moisture stresses on maize growth, physiology and yielding potential prompted the plant breeders to develop maize germplasm that tolerant to multiple stresses including drought and waterlogging. In addition to this, the hybrids developed should be stable across the environments in order to be widely accepted by the farmers throughout a region (Kenga, 2001; Etoundi and Dia, 2008; Khalil et al., 2011). Hence, it is important to develop improved and climate-resilient maize hybrids that to be thoroughly evaluated at different sites and for a number of years/seasons before release (Badu-Apraku et al., 2011, 2012; Ndhlela, 2012). The AMMI model (Gauch, 2013) and GGE biplots has been widely used in the multi-environmental trial (MET) analysis because these provides more accurate estimates and easy interpretations of the GEI through nice graphical tools. Researchers have been using GT (genotype × trait) biplot technique in plant breeding for a long time. However, this method fails to give accurate results for breeders to know which cultivar to recommend, select, or eliminate (Kendal, 2019). Eventually, the GYT (genotype × yield × trait) biplot technique was developed to overcome the deficiencies encountered in the GT biplot model and enables a more efficient selection of genotypes based on their overall superiority across the yield-trait combinations and trait profiles which facilitates genotype evaluation and recommendation (Yan and Frégeau-Reid, 2018).

In this study, we applied the multi-trait stability index (MTSI) for simultaneous selection of high-performance and stable genotypes in METs based on multiple traits considering both a fixed-effect and a mixed-effect model (Olivoto et al., 2019a). It provides a unique selection process that facilitates the fine tuning of stability and mean performance by considering multiple traits based on positive or negative selection differential required for a particular trait (Olivoto et al., 2019b).

2. Materials and methods

2.1. Planting material and test environments

A total of 45 single cross hybrids along with five commercial checks (Supplemental Table S1) were evaluated under the different soil moisture regimes. The plant material were procured from CIMMYT, Hyderabad under 'Climate Resilient Maize for Asia' (CRMA) project. The experimental hybrids were developed through biparental crosses, obtained from a pool of CIMMYT maize germplasm (600 lines) crossed with two stress susceptible testers *viz*, CML451 and CL02450. These were globally released elite testers belonging to separate heterotic groups, A and B with high combining ability that resulted in stress-tolerant test crosses. The experimental material were evaluated in three soil moisture regimes such as optimal, low and excess soil moisture for two seasons, late *Rabi*/winter 2017−18 and subsequent *Kharif*/ summer-rainy 2018 at two locations *viz*, Banaras Hindu University (BHU), Varanasi and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad. Geographical information including coordinates and altitude of the two test locations was shown in the Fig. 1. In each environment, the experimental layout was alpha lattice (Patterson and Williams, 1976) design in two replications. Hand sowing was done in 2 rows of 4 m length. Trials were planted with 0.75 m inter-row spacing and 0.20 m in-row spacing. Plots were over-sown and followed by thinning to achieve a plant population of 66,666 plants ha^{-1}. The soil type of experiment site at Varanasi location was sandy loam whereas shallow black soils at Hyderabad location. The detailed information of seven environments studied including environment code (E1 to E7), seasons, soil moisture condition and planting

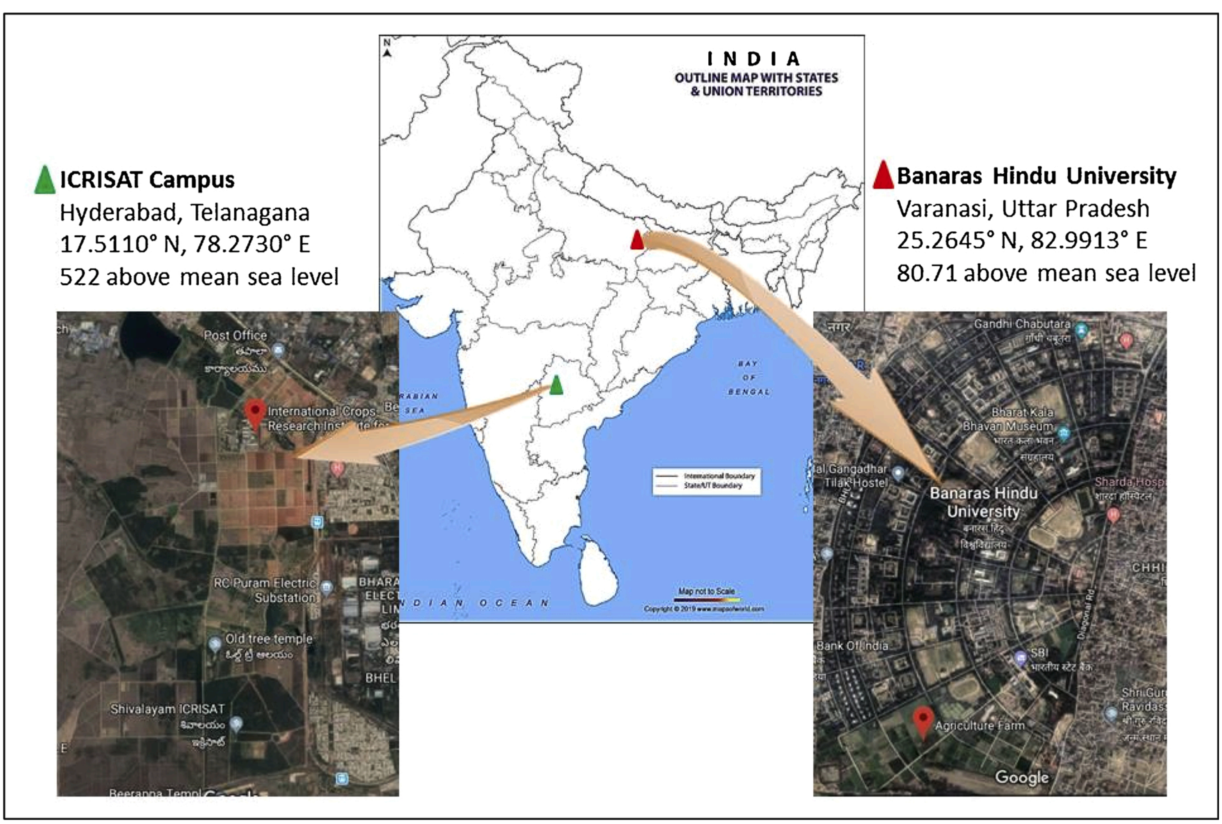


Fig. 1. Geographical information of the locations for the testing 50 maize hybrids under different soil moisture conditions during *Rabi* 2017–18 and *Kharif* 2018.

dates shown in the Table 1. Meteorological data including maximum, minimum temperatures and rainfall based on standard week during crop growing period during both the seasons at both the locations shown in Supplemental Fig. S1a and b.

A total of twelve stress related primary and secondary traits were recorded by following the standard CIMMYT abiotic stress phenotyping protocols (Zaidi et al., 2016; Zaman-Allah et al., 2016). The traits *viz*, days to 50 % anthesis (DFA), days to 50 % silking (DFS) and anthesis-silking interval (ASI) were recorded as number of days on plot basis. Whereas, average chlorophyll content (SPAD readings) recorded before and after imposing stress by SPAD-502 plant chlorophyll meter. Plant height (PH, in cm) and ear height (EH, in cm) were recorded as average of five randomly selected plants in each plot. At physiological maturity, ear length (EL, in cm), number of kernels per row (NKPR) and number of kernel rows per ear (NKRE) recorded based on average of five ears per plot. Test weight (TW, in g) was recorded by weighing 100 kernels. Moisture and shelling percent for each plot were measured for conversion of fresh weight of ears without husk in to grain yield per hectare (GYPH) at 12.5 % moisture.

2.1.1. Managed drought stress

Drought stress was imposed at flowering stage of the crop by modifying the irrigation schedule. To impose the drought stress at right stage in all the environments and seasons, cumulative growing degree days (GDD) were calculated from the day of life irrigation. The flowering stage of the crop was made exposed to severe moisture stress by withdrawing irrigation at 550 cumulative GDD (generally, very few days before anthesis) and withdrawal of drought period by 'rescue irrigataion' at 1000 cumulative GDD values (Zaman-Allah et al., 2016).

$$GDD = \Sigma\ ((T_{max}+T_{min})/2) - T_{base}$$

where, T_{max} = maximum temperature, T_{min} = minimum temperature, T_{base}=base temperature (10 °C)

Moisture depletion at different soil depths (10–100 cm) and progress in stress imposing was tracked by 'Delta-T PR2 soil moisture profile probe' readings. The data were recorded weekly, starting first week after withdrawal of irrigation in drought trials, until the stress is relieved. Rescuing the crop from the stress was confirmed by the soil moisture content at 30–40 cm soil depth reached the 'permanent wilting point' (PWP) value i.e. 16.8 % v/v.

2.1.2. Managed waterlogging stress

Well-leveled fields with zero inclination, good irrigation and drainage facilitates were selected for waterlogging phenotyping. Excess moisture stress was imposed at V_5-V_6 leaf ('Knee-high') stage of crop by stagnating water continuously for seven days. The same level of stagnation, a depth of 10 ± 0.5 cm was maintained by providing additional need based irrigation in consideration to the seepage and evaporation. After seven days the excess water in the experimental plots was drained out and normal irrigation schedule was resumed (Zaidi et al., 2016).

Table 1
Description of test environments including managed soil moisture condition, planting season and location for evaluation of 50 maize hybrids during *Rabi* 2017–18 and *Kharif* 2018.

Environment code	Soil moisture condition	Season*	Location
E1	Managed drought stress	*Rabi* 2017–18	BHU, Varanasi
E2	Optimal/Non-stress	*Rabi* 2017–18	BHU, Varanasi
E3	Managed drought stress	*Rabi* 2017–18	ICRISAT, Hyderabad
E4	Optimal/Non-stress	*Kharif* 2018	BHU, Varanasi
E5	Managed Waterlogging stress	*Kharif* 2018	BHU, Varanasi
E6	Optimal/Non-stress	*Kharif* 2018	ICRISAT, Hyderabad
E7	Managed waterlogging stress	*Kharif* 2018	ICRISAT, Hyderabad

* *Rabi* 2017–18 planting was done in second week of December, *Kharif* 2018 planting was done in first and second week of July.

2.2. Statistical analysis

2.2.1. Analysis of variance

The data from all the test environments were subjected to Shapiro-Wilk test for ANOVA residuals and confirmed data were normally distributed. Although Bartlett's test showed homogeneity of data from individual environments and also similar soil moisture conditions, but it was resulted in heterogeneity for the data all over the test environments. Hence, the data of studied traits including yield and its related traits under seven test environments (a combination of location, season and soil moisture condition) were analyzed by the general linear mixed model (GLMM) analysis of variance by assuming genotypes as fixed and environments, replications and blocks within replication as random factors as follows (Mhlaba et al., 2019; Rusinamhodzi et al., 2020):

$$Y_{ijkl} = \mu + G_i + E_j + R_{k(j)} + B_{l(jk)} + GE_{ij} + \alpha_{ijkl}$$

where, Y_{ijkl} is the observed value of i^{th} genotype (i = 1, 2, …, 50) in l^{th} block (l = 1, 2,. ., 10) and k^{th} (k = 1,2) replication of j^{th} environment (j = 1, 2,. ., 7), μ is the grand mean, G_i is the effect of i^{th} genotype, E_j is the j^{th} environment effect, $R_{k(j)}$ is the effect of k^{th} replication in j^{th} environment, $B_{l(jk)}$ is the effect of l^{th} block in j^{th} environment and k^{th} replication, GE_{ij} is the interaction effect of i^{th} genotype with j^{th} environment, and α_{ijkl} is the error (residual) effect of i^{th} genotype in l^{th} block and k^{th} replication of j^{th} environment

2.2.2. GEI analysis

2.2.2.1. AMMI analysis.
Grain yield per hectare (GYPH) data from all the test environments were subjected to AMMI method that integrates analysis of variance and principal component analysis (PCA) into a unified approach (Bradu and Gabriel, 1978; Gauch, 1988). The additive main effects of genotypes and test environments were fitted in the usual ANOVA and followed by PCA that revealed the non-additive portion, genotype by environment interaction (GEI). Stable genotypes for each environment were identified by AMMI analysis and statistically tested for significance by Gollob (1968) F-test procedure (Vargas and Crossa, 2000). AMMI biplots were constructed based on main effect of means versus the first Principal Component Axis (PCA1) and between first two principal component axes (PCA1 *vs* PCA2). The AMMI equation followed according to Gauch and Zobel (1988) for T genotypes and S environments is;

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

where, Y_{ij} is the mean yield of the genotype i (i = 1,2,..,T) in the environment j (j = 1,2,..,S); μ is the general mean, gi is the i^{th} genotypic effect; ej is the j^{th} location effect; λ_k is the eigenvalue of the PCA axis k; α_{ik} and γ_{jk} are the i^{th} genotype j^{th} environment PCA scores for the PCA axis k; θ_{ij} is the residual. Further, genotypes were ranked based on AMMI's stability values (ASV) and yield stability index (YSI). ASV were calculated by following the formula proposed by Purchase et al. (2000) as follows:

$$ASV = \sqrt{\left[\frac{PCA1_{ss}}{PCA2_{ss}} + (PCA1_{score})\right] + (PCA2_{score})^2}$$

where, $PCA1_{ss}$ and $PCA2_{ss}$ are the sum of squares of first and second principal component axes; $PCA1_{score}$ and $PCA2_{score}$ are the genotype scores of first and second axes in AMMI's model, respectively. The larger the absolute value of PCA indicates greater the adaptability of a specific genotype for a specific environment. Conversely, lower ASV values denote greater stability of a genotype in different environments.

The yield stability index (YSI) was calculated using the following formula:

$$YSI = r\overline{Y} + rASV$$

Where, r $\overline{Y}$ is genotype rank based on mean yield and rASV is genotype rank based on AMMI's stability values.

2.2.2.2. Construction of GGE biplot. Grain yield data from all the environments were subjected to construction of GGE biplot according to the model (Yan et al., 2000; Yan, 2002; Yan and Kang, 2003; Yan and Tinker, 2006) based on singular value decomposition (SVD) of the first two principal components by ignoring random error is

$$Y_{ij} = \mu + \beta_j + \alpha_i + \theta_{ij} + \varepsilon_{ij}$$

where, Y_{ij} is the value of mixed effect of the grand mean (μ) modified by the genotype main effect (α_i), the environment main effect (βj), and the genotype by environment interaction due to genotype i and environment j (θ_{ij}), plus any random error (ε_{ij})

GGE (Genotype Main Effect plus Genotype-Environment Interaction) biplots were constructed based on site regression analysis, SREG (Cornelius et al., 1996; Crossa and Cornelius, 1997; Crossa et al., 2002), GGE biplot tools were used to identify highly adaptable maize hybrids with maximum mean yield by 'Mean *vs* Stability' (Yan, 2001). The average-environment coordinate (AEC) view of GGE biplot revealed the high mean yielders and stable genotypes through AEC abscissa and AEC ordinate, respectively. The 'which-won-where' pattern, an intrinsic property of the GGE biplot exhibited by the inner-product property of the biplot of genotype by environment data set was also visually presented. Genotypes with PCA1 score more than 0 were considered as high yielders with maximum adaptability whereas less than 0 were identified as lower yielding hybrids and non-adaptable (Zerihun, 2011). Association within and among the genotypes and environments was visually shown in the 'Discriminativeness *vs* Representativeness' graph.

2.2.2.3. Multi-trait stability index (MTSI). This analysis was carried out by using singular value decomposition (SVD) of the matrix of BLUPs for the GE interaction effects generated by a linear mixed model (LMM) to quantify the stability of each genotype. The stability of each hybrid was quantified by estimating the weighted average of absolute scores from the singular value decomposition of the matrix of best linear unbiased predictions for the GEI effects generated by a linear mixed-effect model (WAASB); and simultaneous selection for mean performance and stability was performed by using the WAASBY index, weighting between mean performance (Y) and stability (WAASB). Further, the multi-trait stability index (MTSI), equation (Olivoto et al., 2019a):

$$MTSI_i = \sum_{j=1}^{f} \left[\left(F_{ij} - F_j \right)^2 \right]^{0.5}$$

where, MTSI is the multi-trait stability index for the i^{th} genotype, F_{ij} is the j^{th} score of the i^{th} genotype, and F_j is the j^{th} score of ideotype. The genotype with the lowest MTSI value is closer to the ideotype and therefore presents a high mean performance and stability across environments for all traits studied. The desirable genotypes with maximum productivity coupled with highest stability were selected with 15 % selection intensity *i.e.* eight best hybrids among all the hybrids studied. These selected and non-selected genotypes were shown graphically by plotting MTSI scores. The studied hybrids were grouped into four classifications by construction of GY × WAASB biplot which allowed the joint interpretation of stability and mean performance in different environments. This biplot with four quadrants was constructed with grain yield on the x-axis and WAASB values on y-axis.

2.3. Statistical software

Combined ANOVA and all the genetic variability parameters for each individual and across all the environments were calculated in ADEL-R (Pacheco et al., 2017) and META-R (Alvarado et al., 2015) software packages. GEI, GGE biplots and MTSI were carried out in RStudio, R version 4.0.3 (RStudio, 2020) by using 'GGEBiplotGUI' (Frutos et al., 2014) and 'metan' (Olivoto and Lúcio, 2020) R packages.

3. Results

3.1. ANOVA and mean performances of experimental hybrids

Combined ANOVA for all the test environments revealed the presence of highly significant variation for all the measured traits. Mean sum of squares for all the traits showed significant variation among environments, genotypes and GEI (Table 2). The analysis reported the per cent variation contributed towards total variability (G + E+GEI) by environment is maximum for DFA (98.7) followed by DFS (98.4), SPAD (75.2), EG (71.6) and EL (70.4) whereas genotype shared about 30.7 % for NKRE followed by EH (23.8 %), TW (22.1 %) and PH (18.8 %). Contribution of GEI is higher for NKRE (58.7 %) followed by TW (44.7 %), ASI (36.5 %) and NKPR (29.9 %) towards total variation. Grain yield (GYPH) showed 67.4 % variation contributed by environment whereas 18.6 % and 13.9 % was contributed by genotype and GEI towards total variability, respectively. GYPH recorded in the range of 4.15–8.16 t/ha with a mean of 6.99 t/ha. Mean values of the characters studied viz, DFA (73.02), DFS (76.33), ASI (3.26), PH (162.86), EH (91.36), TW (27.37), SPAD (44.53), EL (16.01), EG (4.02), NKRE (14.45) and NKPR (32.71) were recorded and shown in the Supplemental Table S2 and Supplemental Fig. S2.

3.2. GEI analysis

The AMMI analysis of variance for grain yield (t/ha) of 50 maize hybrids tested in seven environments is presented in Table 3. The analysis showed that maize grain yield was significantly ($p < 0.001$) affected by environments (E), genotypes (G) and GEI. Environment alone significantly explained about 67.2 % of the total sum of squares due to treatments (G + E+GEI). Only the small portion that is, 18.6 % of the total sum of squares was contributed by genotypic effects. 14.2 % of the treatments variation in grain yield is significantly explained by GEI. The analysis revealed the sizable differences among the genotypes across the test environments. Differential mean performances of all the characters including grain yields and ranks of genotypes across the environments represented the GEI was a crossover type (Supplemental Fig. S2). The application of AMMI model for partitioning of GEI reported that the first six interaction principal component axes (IPCA) of AMMI were significant using an approximate F-statistic (Gollob, 1968). In this study, the first and second IPCAs explained about 41.6 % and 18.2 % of GEI sum of squares, respectively. Further, the GEI was partitioned into 3rd, 4th, 5th and 6th multiplicative factors with per cent contribution towards total variation by GEI are 13.5, 12.8, 9.0 and 4.9, respectively (Table S3).

3.3. AMMI biplot

Yield potential of the genotypes, stability levels and association of test environments were represented visually by AMMI biplots. AMMI stability showing the relationship between stress tolerant maize genotypes and test environments with different soil moisture regimes is presented in 'grain yield *vs* IPC1 scores' *i.e.* AMMI1 (Fig. 2). The environments E4, E2 and E5 are far from the origin with longer vectors represents strong interaction forces whereas the environments E1, E3, E6 and E7 are with shorter vectors and very closure to the origin showed weak interaction forces. Hybrids *viz.,* 31 (ZH16929) followed by 16

Table 2
Analysis of variance for all the traits studied along with their contribution towards total variation among 50 maize hybrids in seven test environments during *Rabi* 2017–18 and *Kharif* 2018.

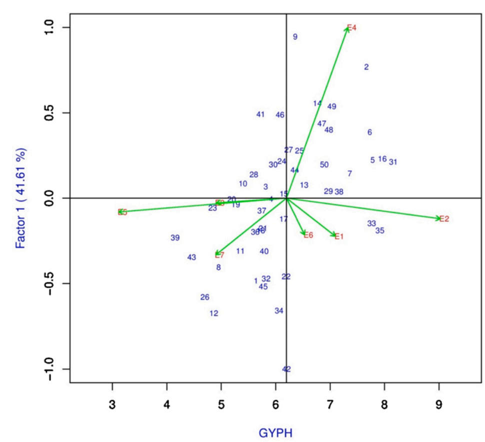
Source of variation	Environment		Genotype		GEI		Residual
Df	6		49		294		341
Traits	Mean Squares	% (G + E+GEI)	Mean Squares	% (G + E+GEI)	Mean Squares	% (G + E+GEI)	Mean Squares
DFA	51100.17***	98.68	56.84***	0.89	4.38***	0.41	2.58
DFS	52907.97***	98.41	65.73***	0.99	6.396***	0.58	3.45
ASI	214.34***	49.75	7.24***	13.72	3.21***	36.52	2.15
PH	35415.20 ***	63.94	1277.33***	18.83	194.61*	17.21	152.39
EH	13498.56***	50.90	773.61***	23.82	136.77*	25.27	107.91
SPAD	9991.46***	75.29	102.75***	6.28	49.88*	18.41	41.16
TW	457.15***	33.16	37.38***	22.14	12.57***	44.68	4.33
EL	522.47***	70.43	7.32***	8.05	3.25***	21.50	1.11
EG	21.21***	71.63	0.29***	8.14	0.12***	20.20	0.03
NKRE	18.85***	10.31	6.87***	30.71	2.19***	58.69	0.43
NKPR	1796.61***	58.37	44.33***	11.76	18.75***	29.85	6.10
GYPH	384.13***	67.37	13.01***	18.63	1.63***	13.98	0.59

df, degrees of freedom; G, genotype; E, environment; GEI, genotype × environment interaction; DFA, days to fifty per cent anthesis; DFS, days to fifty per cent silking; ASI, anthesis-silking interval; PH,Plant height; EH, ear height; SPAD, SPAD chlorophyll meter recordings; TW, test weight; EL, Ear length; EG, Ear girth; NKRE, number of kernel rows per ear; NKPR, number of kernels per row; GYPH, grain yield per hectare.
*** Significant at 0.1 %.
* Significant at 5 %.

Table 3
AMMI analysis of variance for grain yield among 50 maize hybrids across seven test environments during *Rabi* 2017–18 and *Kharif* 2018.

Source	df	SS	MSS	Total variation explained (%)	GEI contributed (%)
Environment	6	2304.8	384.1 ***	67.2	–
Genotype	49	637.6	13.0 ***	18.6	–
GEI	294	487.7	1.7***	14.2	–
IPC1	54	196.3	3.6***	–	41.6
IPC2	52	86.1	1.7***	–	18.2
IPC3	50	63.8	1.3***	–	13.5
IPC4	48	60.4	1.3***	–	12.8
IPC5	46	42.3	0.9***	–	9.0
IPC6	44	22.9	0.5*	–	4.9
Residuals	350	216.0	0.6	–	0.0

df-Degrees of freedom, SS-Sum of squares, MSS- Mean sum of squares, GEI-genotype × environment interaction.
*** Significant at 0.1 %.
* Significant at 5 %.



GYPH, grain yield per hectare; E1, managed drought, *Rabi* 2017-18 at Varanasi; E2, Optimal, *Rabi* 2017-18 at Varanasi; E3, managed drought-*Rabi* 2017-18 at Hyderabad; E4, Optimal, *Kharif* 2018 at Varanasi; E5, managed waterlogged, *Kharif* 2018 at Varanasi; E6, Optimal, *Kharif* 2018 at Hyderabad; E7, managed waterlogging, *Kharif* 2018 at Hyderabad

Fig. 2. AMMI1 Biplot (Mean grain yield *vs* IPC1) for grain yield (t/ha) of 50 maize hybrids and seven environments with different soil moisture regimes during *Rabi* 2017–18 and *Rabi* 2018.

(VH123021), 35 (ZH161034), 5 (ZH17191), 6 (VH131167) and 2 (ZH161032) showed higher grain yield than overall mean yield. Hybrids such as 15 (VH112733), 4 (VH11130), 17 (VH123045), 13 (ZH17192), 3 (VH113014) and 44 (ZH161529) are placed nearer to origin; those are broadly adoptable or insensitive to the environments with near to average overall mean yielding capacity. The AMMI2 biplot, constructed between first two principal components that explained 59.8 % of GEI, of which IPCA1 and IPCA2 contributed 41.6 % and 18.2 % of the total variation, respectively (Supplemental Fig. S3). Polygon view form dotted lines connected with the vertex genotypes that are showed maximum or minimum grain yields with specific adaptation to the environment. A perpendicular projection from the genotype to the environmental vector revealed the amount of interaction with the particular environment. The plot showed, entry number 16 (VH123021), 14 (VH12926), 9 (VH12186), 26 (VH12263), 42 (VH121043) and 45 (ZH161035) are with higher or lower grain yields and poor stable performance across the environments.

Yield stability index (YSI), a combination of AMMI's stability values and mean grain yield was estimated to quantify and classify the genotypes (Table 4). Lower YSI scores represent the hybrids with higher stability and greater productivity. According to YSI, genotypes *viz*, 16 (VH123021, YSI = 13), 33 (ZH16929-1, YSI = 14), 31 (ZH16929, YSI = 14), 38 (VH121082, YSI = 16), 13 (ZH17192 YSI = 18), 5 (ZH17191, YSI = 18), 35 (ZH161034, YSI = 22) and 7 (ZH161531, YSI = 26) were selected as top hybrids with high stability and higher grain yield (Table 4). It also revealed the genotypes viz, 12 (VH11129, YSI = 92), 26 (VH12263, YSI = 92), 8 (ZH114233, YSI = 82), 43 (VH12254, YSI = 79) and 45 (ZH161035-1, YSI = 78) were with poor productivity and lower stability.

3.4. GGE biplots

Genotype and genotype plus environment (GGE) biplots were constructed based on site regression (SREG) model (Yan et al., 2000, 2017) which explains only genotype main effects along with GEI effects by ignoring random error. It showed first six principal components were jointly explained significantly with 98.2 % of the total variation by genotype and GEI (Supplemental Table S3). The GGE analysis showed that

Table 4
Mean grain yield (t/ha), AMMI stability values (ASV), multi-trait stability index (MTSI) and ranking orders of the 50 maize hybrids tested across seven environments during *Rabi* 2017–18 and *Kharif* 2018.

Genotype code	Mean yield (t/ha)	rYield (A)	ASV	rASV (B)	YSI (A + B)	MTSI	rMTSI
1	5.64	38	1.232	39	77	6.278	18
2	7.67	**7**	2.028	48	55	6.887	30
3	5.82	31	0.236	5	36	6.302	20
4	5.92	29	0.218	3	32	6.072	14
5	7.78	**4**[a]	0.567	14	**18**	6.550	21
6	7.73	**6**	1.011	33	39	6.193	17
7	7.36	**8**	0.615	18	**26**	6.117	15
8	4.95	45	1.145	37	82	7.560	36
9	6.36	18	2.38	49	67	5.760	**10**
10	5.4	41	0.233	4	45	7.584	38
11	5.35	42	0.826	28	70	7.799	43
12	4.86	46	1.774	46	92	6.940	31
13	6.52	16	0.185	2	**18**	6.804	25
14	6.76	15	1.414	43	58	8.292	48
15	6.15	23	0.24	6	**29**	5.703	**9**
16	7.96	**2**	0.503	11	**13**	4.660	**2**
17	6.14	24	0.878	32	56	6.994	32
18	5.73	36	0.719	24	60	7.593	39
19	5.26	43	0.139	1	44	7.614	40
20	5.19	44	0.262	8	52	8.768	50
21	5.77	34	0.526	12	46	8.051	47
22	6.19	22	1.09	34	56	7.027	34
23	4.84	47	0.398	10	57	6.805	26
24	6.11	25	0.715	23	48	5.383	**6**
25	6.44	17	0.865	31	48	6.026	13
26	4.7	48	1.592	44	92	7.895	45
27	6.24	20	0.846	29	49	6.779	24
28	5.6	40	0.583	16	56	7.714	42
29	6.97	12	0.73	25	37	5.997	11
30	5.96	28	0.816	27	55	6.289	19
31	8.16	**1**	0.555	13	**14**	6.690	23
32	5.83	30	1.397	42	72	6.551	22
33	7.76	**5**	0.284	9	**14**	5.578	**7**
34	6.06	27	1.814	47	74	6.149	16
35	7.92	**3**	0.629	19	**22**	7.574	37
36	5.62	39	0.731	26	65	5.610	**8**
37	5.75	35	0.692	22	57	7.237	35
38	7.16	**9**	0.247	7	**16**	6.850	29
39	4.15	50	0.673	21	71	6.832	27
40	5.79	32	0.671	20	52	7.866	44
41	5.72	37	1.221	38	75	8.639	49
42	6.2	21	2.508	50	71	7.628	41
43	4.46	49	0.854	30	79	7.937	46
44	6.35	19	0.577	15	34	6.837	28
45	5.77	33	1.614	45	78	7.025	33
46	6.08	26	1.394	41	67	6.003	12
47	6.85	14	1.113	35	49	5.177	**4**
48	6.98	11	1.145	36	47	5.108	**3**
49	7.03	**10**	1.263	40	50	4.046	**1**
50	6.89	13	0.6	17	**30**	5.352	**5**

[a] bold values indicated top ten hybrids.

77.2 % variation explained by first two principal components in which PC1 with 62.9 % and PC2 with 14.3 % towards total variation by GEI. GGE biplot best fits for which-won-where pattern analysis, genotype, and test environment evaluation (Yan et al., 2017; Yan, 2002). All the GGE biplots in study were built with environment-centered data (centering = 2), not scaled (scale = 0), and with column singular value partitioning (SVP = 2) or genotypic-metric preserving (SVP = 1).

3.4.1. *Which-won-where and what*

This pattern allowed the visual grouping of environments based on crossed GEI between the high yielding genotypes shown in Fig. 3. Cumulative variation contributed by PC1 and PC2 was 77.2 %, which suggested sufficient for fitting GGE biplot model and construction of GGE biplots (Yang et al., 2009). The biplot showed three mega-environments whereas E1, E4, and E7 were fall under each mega-environment; and rest of four environments (E2, E3, E5, and E6) under same mega-environment. The plot showed that hybrid 35 (ZH161034) recorded with highest grain yield in E1 whereas genotypes 31 (ZH16929) in E2, E6, E2, E3, E5 and hybrid 2 (ZH161032) ranked highest in E4. No environment fell into the sector where hybrids 9 (VH12186), 39 (ZH116105), 12 (VH11129), and 42 (VH121043) were the vertex hybrids, indicating that these were the lowest yielding hybrids at some or across locations. Hybrids located close to the origin of the polygon *i.e.*, hybrids such as, 4 (VH11130), 30 (VH112563), 15 (VH112733), and 13 (ZH17192) were more adapted to low-yielding locations than the vertex hybrids.

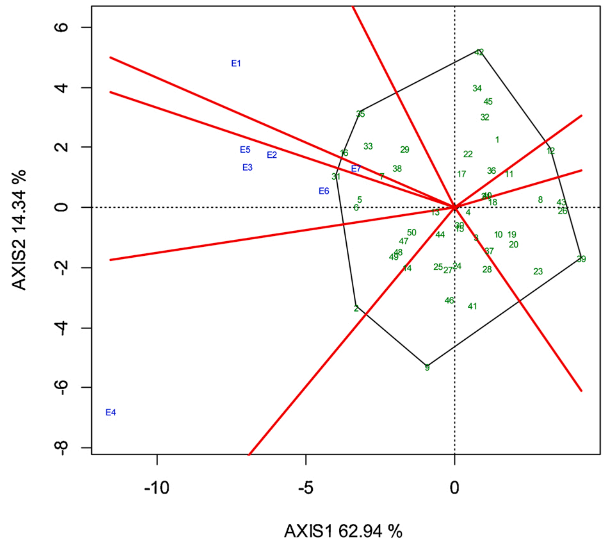
3.4.2. *Mean grain yield and stability of hybrids*

An AEC view of biplot was drawn to visualize mean grain yield and stability of the hybrids (Supplemental Fig. S4). The plot is more relevant for hybrid evaluation as it was constructed by genotype-metric preserving (SVP = 1). The AEC abscissa (represented by single-arrowed line) pointed to higher mean yield across the environments. Thus, hybrid 31 (VH16929) had maximum yield across environments followed by 16 (VH123021), 35 (VH161034), 5 (VH17191) and 33 (VH16929-1) while 39 (VH116105) followed by 43 (VH12254), 26 (VH12263), 23 (VH1230) and 12 (VH11129) were recorded lowest yields. A thick solid line perpendicular to the AEC, AEC ordinate pointed towards greater variability (poorer stability) in either direction. Thus, entry numbers 9 (VH12186), 42 (VH121043) and 34 (ZH137998) were showed more variability *i.e* highly unstable whereas entry 5 (ZH17191), 13 (ZH17192) and 4 (VH11130) were more stable. The 'discrimination and representativeness' view (Fig. 4) has the graphical ability to unravel the discriminating ability and representativeness present among the seven test environments.

3.5. *Multi-trait stability index (MTSI)*

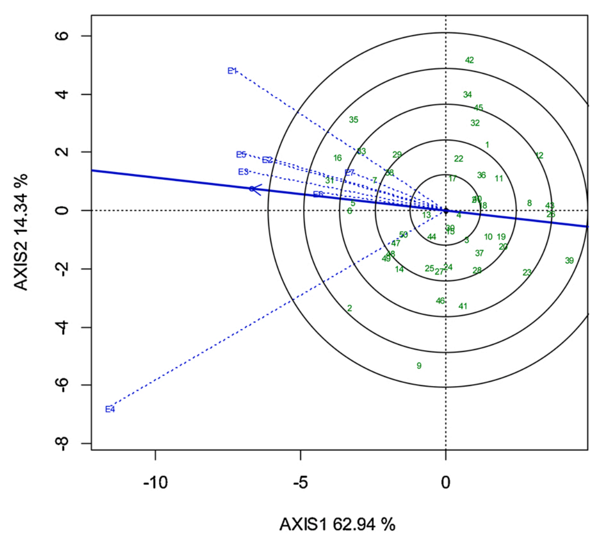
The p-values for likelihood ratio test of the analyzed traits reveled that all the variables studied in the experiment were showed significant ($p < 0.05$) genotype × environment interaction. A Pearson's correlation matrix for the WAASBY values was computed and extracted high magnitude associations are grouped as common factor. Five principal components were retained by an exploratory factor analysis (EPA), and the accumulated variance contributed by these components was 71.5 % (Supplemental Table S4). Maximum communality for DFS (0.82) and minimum for SPAD (0.56) with average communality (h) was 0.72 recorded after varimax rotation. The twelve traits were grouped in the five factors (FA) by extracting WAASBY values from each character given in the Table 5. The traits related to days to flowering, DFA and DFS along with TW and GYPH under FA1; plant height and ear height (PH and EH) in FA2; ear characters *viz*, EG and NKPE in FA3 whereas EL and NKPR in FA4 and lastly FA5 had ASI and SPAD (Table 5). The selection for mean performance and stability for multi-traits was based on the genotype–ideotype distance (Euclidian) using the scores obtained in an exploratory factor analysis and the scores for the 50 genotypes along with the ideotype estimated in the first five factors were given in Supplemental Table S5. Selection differential (SD) for both the mean performance and WAASBY index for measured traits were given in the Table 5. All the traits had positive SD for the WAASBY index and the mean SD% for the WAASBY was 17.4 % with a lowest one (3.8 %) for the NKPR and the highest (36.9 %) for the EG. A negative SD% for mean performance of the traits *viz*., DFA, DFS and ASI was observed.

The analysis resulted in a Y × WAASB biplot with mean grain yield on x-axis and WAASB values on y-axis which classified the genotypes in to four groups that allows the simultaneous selection of genotype that weight between stability along with mean performance (Fig. 5). The biplot showed 11 genotypes along with 3 environments (E5, E7 and E3) in quadrant I whereas 4 genotypes along with 4 environments (E1, E2, E4 and E6) in quadrant II. The third and fourth quadrants contained 19 and 16 genotypes, respectively. In this experiment, the simultaneous



Green and blue numbers stand for genotypes and environments, respectively.
E1, managed drought, *Rabi* 2017-18 at Varanasi; E2, optimal, *Rabi* 2017-18 at Varanasi; E3, managed drought, *Rabi* 2017-18 at Hyderabad; E4, optimal, *Kharif* 2018 at Varanasi; E5, managed waterlogged, *Kharif* 2018 at Varanasi; E6, optimal, *Kharif* 2018 at Hyderabad; E7, managed waterlogging, *Kharif* 2018 at Hyderabad

Fig. 3. Polygon view of the GGE-biplot for 50 maize hybrids evaluated across seven environments during *Rabi* 2017–18 and *Kharif* 2018.



Green and blue numbers stand for genotypes and environments, respectively.
E1, managed drought, *Rabi* 2017-18 at Varanasi; E2, optimal, *Rabi* 2017-18 at Varanasi; E3, managed drought, *Rabi* 2017-18 at Hyderabad; E4, optimal, *Kharif* 2018 at Varanasi; E5, managed waterlogged, *Kharif* 2018 at Varanasi; E6, optimal, *Kharif* 2018 at Hyderabad; E7, managed waterlogging, *Kharif* 2018 at Hyderabad

Fig. 4. The discrimination and representativeness view of GGE biplot for 50 maize hybrids tested across seven test environments during *Rabi* 2017–18 and *Kharif* 2018.

selection for mean performance and stability considering an LMM performed using the WAASBY index. According to lower MTSI values, the best hybrids with high stability with maximum mean performance in terms of all the measures traits were selected by assuming 15 % selection intensity. Genotypes viz, 49 (Check-1; 4.05) followed by 16 (VH123021; 4.66), 48 (Check-3; 5.11), 47 (Check-2; 5.18), 50 (Check-5; 5.35), 24 (ZH14435; 5.38), 33 (ZH16929-1; 5.58) and 36 (VH112986; 5.61) were selected as best hybrids. The genotype 36 (VH112986) with MTSI 5.61 was presented at cut point (Fig. 6, red circle) considered the selection intensity. The hybrids 20 (VH12316; 8.79) followed by 41 (VH112732; 8.64), 14 (VH112926; 8.29), 21 (ZH114250; 8.05), 43 (VH12254; 7.93) and 26 (VH12263; 7.89) recorded with high MTSI value representing poor performance and low stability (Fig. 6, genotypes nearer to the origin).

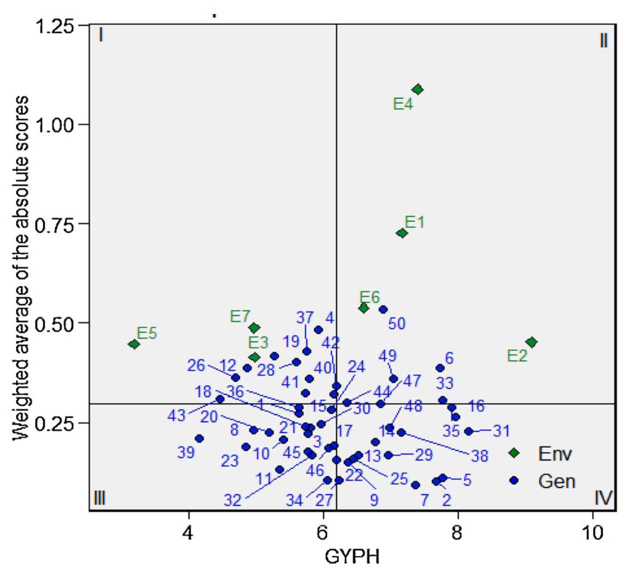
4. Discussion

In general, the cereal crops including maize in rainfed agro ecosystem are subjected to complete their life cycle by getting exposed to multiple and vagaries of abiotic stress *i.e.* low and high moisture conditions within same cropping season. The major part of maize mega environment in the Asian tropic falls in the rainfed environment is

Table 5
Selection differential for mean performance and WAASBY index for 12 traits of 50 maize hybrids across seven environments during *Rabi* 2017–18 and *Kharif* 2018.

Factor	Trait	Mean performance			WAASBY		
		Overall (Xo)	Selected genotypes (Xs)	SD (%)	Overall (Xo)	Selected genotypes (Xs)	SD (%)
FA 1	DFA	73.58	73.11	−0.64	60.30	66.40	10.10
FA 1	DFS	77.1	76.38	−0.93	67.70	70.90	4.75
FA 1	TW	27.03	27.45	1.55	52.20	60.40	15.70
FA 1	GYPH	6.198	6.901	11.35	54.10	63.50	17.50
FA 2	PH	157.5	166.2	5.52	54.60	65.61	19.90
FA 2	EH	84.18	90.58	7.60	58.50	75.71	29.30
FA 3	EG	3.893	4.014	3.09	48.80	66.51	36.10
FA 3	NKRE	14.39	14.35	0.26	56.10	58.30	3.86
FA 4	EL	15.73	16.31	3.73	53.30	62.70	17.70
FA 4	NKPR	30.27	31.96	5.57	61.70	76.11	23.30
FA 5	ASI	3.527	3.277	−7.10	61.10	68.40	11.90
FA 5	SPAD	44.15	45.68	3.46	52.70	62.30	18.20
Mean	–	–	–	–	56.77	66.40	17.38

FA1, factor 1; FA2, factor 2; FA3, factor 3; FA 4, factor 4; FA5, factor 5; SD, selection differential; DFA, days to fifty per cent anthesis; DFS, days to fifty per cent silking; ASI, anthesis-silking interval; PH, Plant height; EH, ear height; SPAD, SPAD recordings; TW, test weight; EL, ear length; EG, ear girth; NKRE, number of kernel rows per ear; NKPR, number of kernels per row; GYPH, grain yield per hectare.
X_O, mean of the original population; X_S, mean of the selected genotypes.



GYPH, grain yield per hectare; E1, managed drought, *Rabi* 2017-18 at Varanasi; E2, optimal, *Rabi* 2017-18 at Varanasi; E3, managed drought, *Rabi* 2017-18 at Hyderabad; E4, optimal, *Kharif* 2018 at Varanasi; E5, managed waterlogged, *Kharif* 2018 at Varanasi; E6, optimal, *Kharif* 2018 at Hyderabad; E7, managed waterlogging, *Kharif* 2018 at Hyderabad

Fig. 5. Yield × WAASB biplot based on joint interpretation of productivity (Y) and stability (WAASB) for 50 maize hybrids evaluated under seven environments during *Rabi* 2017–18 and *Kharif* 2018.

extremely vulnerable to climate change. Addressing the GEI complexity using appropriate statistical tool is the best way to identify adoptable and stable hybrids for the deployment of stress-resilient maize hybrids in the target environment. Statistically significant variation among evaluated hybrids across the moisture regimes would make possibility of selecting preferred hybrids suitable to both stress and non-stress environments. Earliness in flowering (DFA and DFS) and high ASI values whereas lower mean values for PH, EH, TW, EL, EG, NKPE and NKPR under stress conditions compared to optimal moisture environments were observed that resulted in poor grain yields, as expected. Different levels of grain yield reduction could be expected under drought and waterlogged conditions as a result of the intensity of stress to which the crop was exposed (Derera et al., 2008; Pswarayi and Vivek, 2008). Five commercial checks with three common across the seasons were included in the planting material, where most of the test hybrids showed better performance or at par with the performance of the checks. Several previous studies also reported the presence of significant variations among maize hybrids evaluated under different managed stress conditions for grain yield (Wegary et al., 2014; Abakemal et al., 2016; Njeri et al., 2017; Adeseye et al., 2018; Mebratu et al., 2019).

Combined analysis of variance across the locations reveled days to flowering (DFA and DFS) showed >98 % variation contributed solely by environment as delayed flowering was recorded in E1, E2 and E3. Maximum part of variability contributed by GEI for the traits NKRE, TW and ASI. It showed selection of these traits across the environments would be beneficial (Table 2). According to mean values and range of the traits under different environments (Supplemental Table S2) explained the impact of moisture level on the trait's expression. Some outliers in the box plots of measure traits were probably the result of inconsistent expressions as indicated severity of stress and interaction of genotype with soil moisture level (Supplemental Fig. S2). According to mean values, a large variation in days to 50 % flowering in two seasons

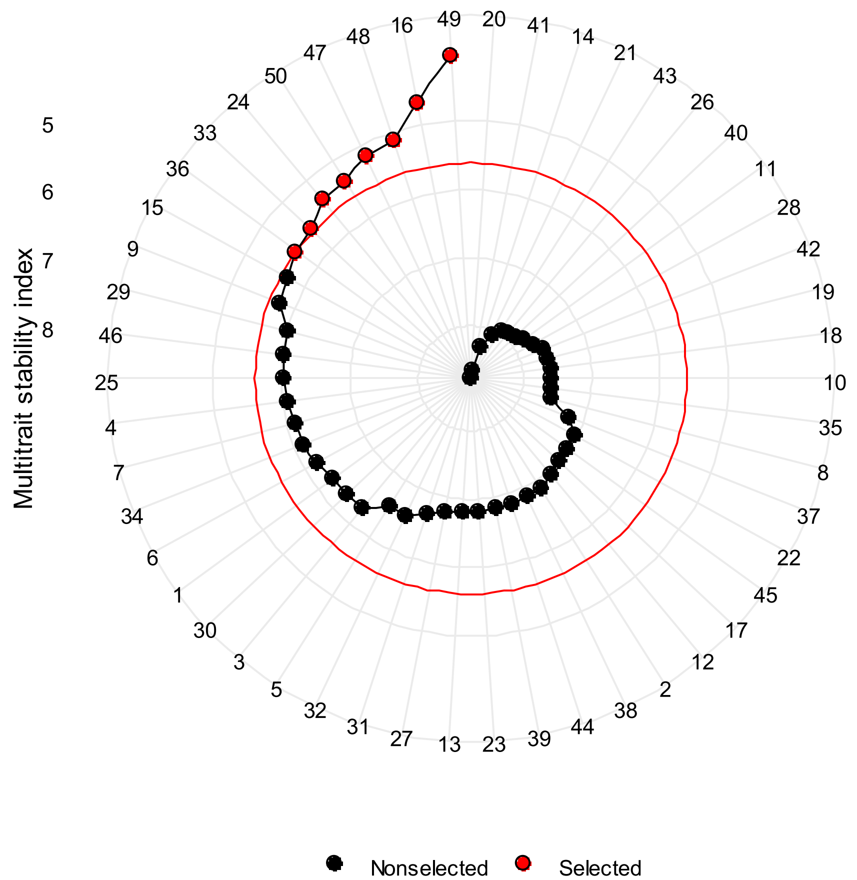


Fig. 6. Genotype ranking and selected genotypes among 50 maize hybrids for the multi- trait stability index considering a selection intensity of 15 %.

was observed, that exhibited delayed maturity in late *Rabi* maize crop. In general, dry-season maize crops records delayed in maturity due to a prolonged cold period at the early stages of crop growth from the seedling to knee-high stage. In winter or late *Rabi* plantings, adverse environmental conditions have a high probability of persisting for lengthy periods and consequenctly, survival depends on tolerance. This would resulted in reduction of grain yield up to 30–90 % depends on crop growth stage and period of soil moisture stress occurred in dry seasons connected with shortage of water availability (Sah et al., 2020). The variation in chlorophyll content was used to estimate the influence of abiotic stresses on plant growth and yield (Anjum et al., 2011a). Many studies reported that high SPAD values are associated with improved yield under water-limited conditions (Verma et al., 2004). In our study, the observed reduction of chlorophyll in moisture stressed plants might be due to early senescence that results a reduction in the lamellar content of the light harvesting chlorophyll proteins (Randall et al., 1977). Anjum et al. (2011b) reported the reduced chlorophyll contents under progressive drought stress in maize. Coefficient of variation (CV%) was very low (<10–15 %) for most of the traits evaluated, indicated the accuracy in implementing the experiment. The exception was ASI and GY where CV was nearly 30 % across the test environments. The larger CV for GY and ASI was due to the magnitude of the stress that undergone by the genotype which caused the larger variation in different soil moisture levels. The results were in agreement with previous reports of Al-Naggar et al. (2020), Asare et al. (2016) and Twumasi et al. (2017).

Despite of complexities of GEI, mostly all of the commercial hybrid maize breeding programmes focused on yield as a selection parameter. However, a better understanding of the yield components that assist to attain the higher yield potentiality under varied moisture regimes would improve the selection process. Thus, the knowledge of the effects of soil moisture stresses on the physiological processes of the maize plant would also enable the researchers to breed for promising cultivars for a drought or flood prone areas. Besides to drought, waterlogging stress also affects the crop growth. It has been reported that waterlogging causes a decline in the carotenoid content of maize leads to reducing leaf growth and worse effect on the cell turgour (El-Shihaby et al., 2002). Reduction in the PH, EH, EH, EG and NKRE and TW besides declining in the mean grain yield has been observed in waterlogging trials by Tripathi et al. (2003).

Significant variation among the effects of environment, genotype and GEI confirmed that each of the target environments were distinctly different from each other. Significant GEI in combination with combined ANOVA and IPCs from AMMI and GGE biplot results, indicated the existence of a crossover interaction which resulted in the response and ranking of the hybrids across the different soil moisture regimes. The study reported that, hybrids such as VH12186, ZH161032, VH112926, VH121043, VH11129 and ZH137998 placed farther from the biplot origin showed strong interaction with the specific environments, as evident from the higher positive as well negative IPCA1 scores (Fig. 2). These are very sensitive to an environment with specific adaptation and comparable grain yield, suggesting the existence of variation among the hybrids in response to the soil moisture condition. Hybrids such as VH112733, VH11130, VH12316, ZH17192, ZH161529 and VH121082 placed close to the biplot origin with IPCA1 score nearer to zero were considered as environment insensitive hybrids with mean yield across the moisture regimes (Ebdon and Gauch, 2002). AMMI1 biplot explained clearly that dominance of environment effect than genotype effect as it had long environment vectors and majority of genotypes scattered around the origin (Mebratu et al., 2019). The obtuse angle between vectors of environment with optimal water and waterlogging conditions (E2 with E5 and E7) represented negative association between them whereas right angle between E1 (drought) and E7 (waterlogging) represented absence of any specific association. The stability ranking of genotypes based on lower absolute IPC1 scores was identified and reported by Asfaw et al. (2009). YSI used for the screening of desired maize hybrids under different moisture conditions those with high productivity and stability. This stability measure was proved to have a significant correlation with other stability measures like Wricke (W_i), Shukla and Eberhart and Russel (S^2d_i); but Finlay and Wilkinson (b_i) and Linn and Binns (P_i) showed limited correspondence with any of the other methods (Purchase et al., 2000).

The GGE biplots for grain yield showed the potential usefulness for screening the genotypes in both the locations across different soil moisture regimes. Differences in moisture levels among the testing environments, as well as genetic variation in the hybrids studied eventually generated variable genotypic response over the locations and over the seasons. It can be useful tool for maize breeders to identify high yielding and stable genotypes by considering both genotype and its environment interaction factors, simultaneously. The potentially desirable maize hybrids those had high and low values of IPC1 and IPC2, respectively, could be easily selected through GGE biplot technique. The first two IPCs explained nearly 60 % of total variation from GEI in AMMI analysis whereas 77.2 % by IPC1 and IPC2 in GGE biplot analysis. 59.8 % contribution towards GEI by IPC1 and IPC2 was reported by Oyekunle et al. (2017) in maize hybrids at various agro-ecological zones belongs to Nigeria; 52.7 % recorded by Riaz et al. (2019) in cotton under normal and water deficit stress conditions at five locations of Pakistan; while, 87.5 percent contribution recorded by Kizilgeci et al. (2019) in wheat lines under thirteen environments using GGE biplot analysis.

High yielding hybrids under stress and stress-free environments with high stability across the locations were observed, which indicates that some hybrids can yield relatively high under optimal, drought as well as waterlogging environments. Thus, a specific breeding strategy could be formulated to develop hybrids with stable performance across different moisture regimes or hybrids with specific adaptation to the particular environment. The present investigation was in concordance with the few previous reports on maize hybrids under stress and non-stress environments (Sserumaga et al., 2016; Badu-Apraku et al., 2017; Ertiro et al., 2017; Mebratu et al., 2019). Asfaw et al. (2009) explained the relative adaptation of specific genotype and comparison of genotypes across different environments by GGE biplots. The polygon view of GGE biplot, 'Which-won-where' pattern of information is important in dividing all the environments into various mega-environments for recommending suitable cultivars for different mega-environments (Gauch and Zobel, 1997; Badu-Apraku et al., 2012; Abakemal et al., 2016 and Vaezi et al., 2019). We observed four mega-environments, among those three had different kind of moisture conditions (drought, waterlogged and optimal) whereas fourth mega-environment with four test environments with all the three soil moisture levels. The genotype, 31 (ZH16929) on the vertex of the polygon in a mega-environment, had the highest yield in two environments with optimal soil moisture condition at both the locations and it was one of the top-performing genotypes in the other environments. These results were in accordance with the reports of Yan and Rajcan (2002). A two-dimensional visualization of yield and stability based on PCA1 and PCA2 scores in this biplot pattern that constructed on SREG model was reported by Samonte et al. (2005), Yan et al. (2001) and Laurie and Booyse (2015).

The hybrids *viz*, 42 (VH121043), 12 (VH11129) and 39 (ZH16105) were found in on the vertices of the polygon where the environments were not fallen nearby indicating that these were the lowest yielding hybrids under both stress and non-stress environments used for the present study. An ideal genotype is with highest yielding and the most stable, but this rarely exists in reality (Yan and Kang, 2003). In present study, hybrids ZH16929, VH123021, ZH161034, VH131167, ZH17191 and ZH16929-1 were identified as most desirable genotypes across the test environments, indicating the inherent potential of these hybrids for higher yield and wider adaptation under optimal, drought and waterlogged conditions. The relative contributions of mean grain yield and stability by the GGE biplot methodology in our study was similar to previously reported studies on maize (Alwala et al., 2010; Oyekunle et al., 2017).

According to Yan (2002), the cosine of the angle between the two environmental vectors explains their association between them. Acute angles indicated similarity in hybrids performance between the environments, a right angle indicated the zero correlation, and obtuse angles indicated a negative relationship of hybrids performance between them. The vector view of the GGE biplot (Fig. 4) showed that all environments had positive correlations, in that, E1 (drought stress) and E4 (optimal moisture) had weak relationship as it evident from the angle between them is near to right angle while, rest of all showed strong association. Positive correlations indicated similarity in genotype performance among the test environments, whereas negative correlations revealed that the environments that are fairly different and highly influenced by GEI (Makumbi et al., 2015; Sserumaga et al., 2016). The drought stress environment at Varanasi (E2) and optimal moisture environment at Hyderabad (E4) are most decimating environments and these considered as 'ideal environments' to find out the desirable maize hybrids which give high yields with maximum stability. Ideal environments for selecting superior hybrids and for the provision of information that is important for the identification of desirable varieties was reported by Tukamuhabwa et al. (2012). Best hybrids with both stability and high grain yield under irrigated and rainfed conditions; suitable environment for optimal performance of the maize hybrids were reported by Boshev et al. (2014). Relative performances and GEI were studied for Nagina22 rice mutants under three soil conditions *viz*, normal irrigated, water limiting and low phosphorus content over twelve seasons using AMMI and GGE biplot analysis and reported stable lines across normal and input limited stresses by Yugandhar et al. (2018). Thungo et al. (2019) explained the GEI of elite heat tolerance and drought tolerant bread wheat lines under managed drought stress and non-stress conditions by both AMMI and GGE biplot methodology.

Successful selection of high-performance of the desirable traits and stable genotypes is the fundamental goal in stress breeding approach. Different stability measures including parametric, non-parametric, AMMI stability model and GGE biplots explains stability and performance of the genotypes by considering the yield or any other trait alone. Weighted average of absolute scores were computed for quantify the stability of all genotypes under different environments using linear mixed models (Olivoto et al., 2019a). Simultaneous selection based on all the traits studied by computing WAASB (stability alone) and WAASBY (stability and mean grain yield). Y $\times$ WAASB biplot classified all the genotypes in four groups showed in four quadrants (Fig. 5). The positive SD% of WAASBY scores for all the studied traits suggested that the method was efficient in selecting the best performing and stable genotypes while the desirable negative SD% for mean performance of the flowering traits *viz*., DFA, DFS and ASI was observed (Table 5). The genotypes or environments fall in quadrant I considered as unstable genotypes or environments with high discrimination ability, and with lower productivity than grand mean. Quadrant II included unstable genotypes, although with grain yield recorded above the grand mean. The environments fallen in this quadrant deserve special attention as they had good discrimination ability along with high magnitudes of the grain yield. Genotypes included in quadrant III have lower productivity than grand mean, but can be considered stable due to the lower WAASB values. The environments presented in this quadrant were considered as poorly productive with low discrimination ability. The genotypes included in the quadrant IV are highly productive in nature and broadly adapted due to the high magnitude of the productivity and high stability performance as projecting lower values of WAASB.

The main advantage of the simultaneous selection for mean performance and stability by MTSI is fine tuning of weights and rescaling across the traits based on the breeder's requirement. The exploratory factor analysis determined the number of latent variables or constructs that can be reduced into common factors based on associationship among them (Ullman, 2006). Followed by, the estimation of final factor scores allowed dealing with the multicollinearity (Olivoto et al., 2017). Compared with already used indexes, the WAASBY is not ambiguous and weights can be used when the selection of genotypes should prioritize the mean performance over the stability or vice versa. The MTSI analysis allowed easy and clear interpretation by taking the genotype-ideotype distance as criterion. Eight best entries were selected with 15 % selection intensity based on low MTSI values, in which four were commercial checks that indicated that rest of four selected hybrids *viz*, 16 (VH123021), 24 (ZH14435), 33 (ZH16929-1) and 36 (VH112986) were at par with checks in view of all the traits studied. The hybrid 15 (VH112733; MTSI = 5.70) was found just near to this circle of selected hybrids and could present desirable features. Thus, it would be interesting to investigate the performance of the genotypes that are very close to the cut-point in future studies.

Most of genotypes selected through MTSI were found to have placed nearer to the AEC in 'mean *vs* stability' biplot (Supplemental Fig. S4). The relative contribution (RC%) of each factor retained in the MTSI indicated the target traits that should be focused to improve to attain the stability. For example, ~55 % contribution of the distance from 9 (VH12186) to the ideotype was related to FA1 and FA4 (Supplemental Tables S5). In other words, hybrid VH12186 showed lower WAASBY values for the traits belongs to FA1 (DFA, DFS, TW and GYPH) and FA4 (EL and NKPR). In practice, this recommended that the breeding program should aim at improving the mentioned traits regarding the genotype to achieve the ideotypic performance. In contrast, for the hybrid 33 (ZH16929-1), the FA5 had the least contribution to the MTSI (~2 %). This revealed that hybrid ZH16929-1 is close to the ideotype regarding the traits ASI and SPAD, which are important traits for grain yields under moisture stress.

The theoretical basis and applicability of MTSI along with step-by-step guidelines for computing MTSI were explained by Olivoto et al. (2019b). Recently, Zuffo et al. (2020) screened promising soya bean genotypes under drought and saline stress condition through simultaneous selection by using MTSI tool. Koundinya et al. (2021) conducted an experiment for selection of cassava genotypes under rainy and water-stress environments using AMMI, WAAS, BLUP and MTSI techniques. The MTSI found to have a great advantage where the simultaneous selection for stability and mean performance based on several characters instead of yield alone. This procedure could have been useful for previous published works that evaluated the stability and mean performance of genotypes considering several traits including intra-trait interactions (GET biplots), yield × trait interactions (GYT biplots) (e.g., Yan and Frégeau-Reid, 2018; Kizilgeci et al., 2019; Kendal, 2019; Koundinya et al., 2019; Nduwumuremyi et al., 2017; Bocianowski et al., 2019).

5. Conclusion

The purpose of present investigation was to identify maize hybrids with wide adaptation for different moisture regimes with high agronomic performance along with high yield potential. The magnitude of GEI effect was different in AMMI and GGE biplots as the patterns obtained in the AMMI biplots allowed an investigation of the effects of the GEI, while in the GGE biplot included both GEI along with genotype effects in respective environments. The quantified stability along with yield performance estimated by YSI, reported best hybrids *viz*, VH123021, ZH16929-1, ZH16929, VH121082 and ZH17192 whereas genotypes *viz*, ZH16929, VH123021, ZH161034, ZH17191, VH131167, ZH16929-1 selected as best hybrids suitable all the environments. The simultaneous selection based on stability and performance of genotypes by subjecting all the traits evaluated was carried out by estimation of WAASBY. The fourth quadrant of Y × WAASB biplot represents stable genotypes with high mean performance. The MTSI allowed the selection of stable genotypes, with positive selection differentials for traits those wanted to improve like yield, chlorophyll content, test weight and ear components and negative selection differential for the traits those wanted to decrease such as flowering and ASI. The radar diagram of MTSI revealed that the hybrids *viz*, VH123021, ZH14435, ZH16929-1, VH112986, VH112733 and VH12186 were selected as best hybrids for with high stability and maximum mean performance of all the traits evaluated under environments with different moisture regimes.

CRediT authorship contribution statement

Ashok Singamsetti: Conceptualization, Methodology, Investigation, Formal analysis, Writing - original draft. **J.P. Shahi:** Supervision, Resources, Methodology, Writing - review & editing. **P.H. Zaidi:** Supervision, Resources, Methodology, Writing - review & editing. **K. Seetharam:** Conceptualization, Writing - review & editing, Methodology. **M.T. Vinayan:** Conceptualization, Writing - review & editing, Methodology. **Munnesh Kumar:** Writing - review & editing. **Saurav Singla:** Data curation, Formal analysis, Visualization, Software. **Kumari Shikha:** Writing - review & editing. **Kartik Madankar:** Data curation, Formal analysis, Visualization, Software.

Declaration of Competing Interest

The authors report no declarations of interest.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.fcr.2021.108224.

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