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Response of Quality Protein Maize (QPM) hybrids for grain yield in diverse environments

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ABSTRACT

Genotype (G) × environment (E) interaction is very important for the evaluation of cultivars in breeding programmes. Present study was conducted to assess the effect of environment and yield stability of 68 quality protein maize (QPM) hybrids at three test environments [Begusarai (E1), Udaipur (E2) and Karim Nagar (E3)] in randomized block design (RBD). Data was analysed using the additive main effects and multiplicative interaction (AMMI) and genotype main effects and genotype by environment (GGE) biplot methods. The variation in genotypes, environments and genotype × environment interactions (G×E) was highly significant. Maximum variation was explained by G×E interactions (53.84%) and least by differences in environmental conditions (2.36%). Genotype × environment interaction was main source of variation followed by genotypes and environments. Together the two AMMI principal coordinates axes (PCA) explained 100% of phenotypic variation. AMMI Stability value (ASV) was calculated using ASV scores. Among these QPM hybrids, G59 was found to be the most stable with ASV of 0.174. The GGE biplot explained 77.41% of the total variation relative to G and GEI. Superior cross combinations for specific locations were also identified, viz. DQL2053 ×CML161, DQL2028 × CML161, DQL2047 × CML165, DQL2037 × CML161, DQL2042 × CLQRCY40, DQL2032 × CML165, DQL2047 × CML165 and DQL2072 ×CLQRCY40 in E1, DQL2063 × CML161, DQL2057 × CML161, DQL2053 × CML165, DQL2080 × CLQRCY40 and DQL2065 × CLQRCY40 in E2 and DQL2063 × CML161, DQL2039 × CML165, DQL2140 × CML161, DQL2082 × CLQRCY40 and DQL2024 × CML165 in E3.

Key words: Additive main effects and multiplicative interaction (AMMI), Genotype and environment interaction (G×E), GGE biplot, PCA, QPM

Maize (*Zea mays* L.) is an important food crop cultivated in diverse agro-climatic conditions of the world. In India, maize is grown in wide range of environments, extending from extreme sub-arid to sub-humid and humid regions; from sea level to >4000 m above sea level and under irrigated to semi–arid conditions. Normal maize is poor in protein quality due to the deficiency of essential amino acids, viz. lysine and tryptophan.*Opaque-2* mutation in quality protein maize (QPM) doubles the lysine and tryptophan content in the maize kernel. These two amino acids allow the body to digest complete proteins; thereby eliminating wet-malnutrition (Mamatha *et al.* 2017). Therefore, development and release of nutritionally enriched QPM cultivars could have immediate benefits to people. QPM hybrids have been developed worldwide and tested in varying climatic and growing conditions which is roughly grown over 9 million acres (Rugema H 2014). Genotype × Environment (G×E) interaction reduces the association between the phenotype and genotype which in-turn reduces the selection response (Yan and Kang 2003). Further, the existence of G×E complicates the identification process of superior genotypes in yield trials (Yaghotipur and Farshadfar 2007). Multi-environment trials (MET) are routinely used for identification and recommendation of superior stable genotypes in mega-environments. Two powerful statistical tools available for MET analysis are the additive main effects and multiplicative interaction (AMMI) and the genotype main effect and genotype-by-environment interaction (GGE). The AMMI model combines analysis of variance for the genotype and environment main effects with principal components analysis of the G×E interactions (Gauch and Zobel 1996). The GGE integrates the genotypic main effect with the G×E interaction effect (Yan *et al*. 2000). GGE biplot analysis helps in the evaluation of the genotypes in terms of both mean performance and their stability across environments. It provides an easy and comprehensive solution to genotype by environment data analysis (Yan and Tinker 2006). Best performing QPM hybrids can be identified and ranked by assessment of genotype environment interactions and yield

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*Corresponding author e-mail: rk.phagna@gmail.com stability analysis. The objectives of the present study were to identify the QPM hybrids that have both high mean yield and stability across environments and to study the relationships among genotypes and environments.

MATERIALS AND METHODS

Selection of genotypes: Thirty four newly developed QPM inbred lines were selected on the basis of per se performance and crossed with four tester, viz. CML 161, CML 165, HKI 163 and CLQRCY 40 during *kharif* 2013 at experimental farm of ICAR-IIMR, New Delhi. All four testers were sown on two different dates with seven days intervals to ensure the pollen availability.

Multi-location evaluation of crosses: However, crosses only with enough seeds were selected for evaluation in three location testing. A total of 66 hybrids along with two checks (HQPM-1 and HQPM-7) were planted at three locations, viz. Begusarai, Udaipur and Karim Nagar during *rabi* 2013-14 in randomized block design (RBD) with three replications.

HQPM-1 and HQPM-7 are the widely grown AICRP released QPM hybrids with yield potential of 7.5 and 7.2 tons/ha, respectively. The inter row spacing was 0.70 meter with intra row spacing 0.25 meter in a row length of 4 meter. All necessary agronomic and cultural practices were timely followed to ensure good plant stand. The trials were conducted under normal irrigated conditions, and locations were considered as distinct environments due to differences in average rainfall, mean temperature, humidity and soil type. Grain yield (q/ha, at 15% moisture) was subjected to combined analysis of variance. The AMMI and GGE biplot models were computed sequentially to analyse G × E interaction and yield stability of genotypes.

Statistical analysis: The AMMI and GGE analysis was performed using the data from three environments with R software. The AMMI model first fits additive effects for the main effects of genotypes and environments followed by multiplicative effects for G×E interaction by principal component analysis (Balestre *et al.* 2009).

The which-won-where pattern (Gauch and Zobel 1997, Yan 2002), relationships among test environments (Cooper *et al*. 1997) and genotypes (Yan 2001) were visualized using their respective GGE biplots. An average environment coordinate (AEC) was drawn on the genotype focused biplot to visualize the mean and stability of the hybrids (Yan and Kang 2003). The ideal environments and hybrids were identified using the AEC.

RESULTS AND DISCUSSION

Performance of hybrids at individual location: The genotypes, viz. G46, G24, G2, G56, G7, G51, G38 and G42 were the best performing hybrids at Begusarai with 118.16, 117.63, 109.32, 100.46, 98.34, 97.58, 97.57 and 96.45 q/ha yield, respectively. Thirteen genotypes, viz. G22, G16, G24, G18, G23, G26, G30, G44, G9, G10, G68, G37 and G38 at Udaipur whereas eighteen genotypes, viz. G22, G35, G8,G20, G29,G21, G13, G34, G10, G18,G1, G63, G15, G37, G28, G67, G49 and G32 at Karim Nagar recorded grain yield >90 q/ha. Wide range for grain yield was observed at Begusarai (118.16-13.65 q/ha) as well as at Udaipur (133.84-27.43 q/ha) and Karim Nagar (118.08 to 9.98 q/ha). G38 and G24 performed well under both Begusarai and Udaipur whereas G22, G10, G18 and G37 were superior genotypes at both Udaipur and Karim Nagar with G22 the best performing genotype.

Genotypes G22, G24, G18, G16 and G30 were the best genotypes across all three locations as they showed mean yield of 103.42, 98.27, 92.7, 89.79 and 89.69 q/ha which is more than the mean yields of checks HQPM-1 (84.22 q/ha) and HQPM-7 (83.16 q/ha) thus showing 22.79%, 16.68%, 10.06%, 6.61% and 6.49% superiority (over check HQPM-1) and 24.36%,18.16%,11.47%,7.97% and 7.85% yield superiority (over check HQPM-7), respectively.

Combined analysis of variance: The combined analysis of variance of grain yield response of the 68 QPM hybrids evaluated in three test environments (Table 1). The combined analysis of variance showed highly significant effect for environments, genotypes and G×E interactions. Significant G×E interactions revealed that rank of genotypes varied in the three test environments. Of the total variations, 2.36% was accounted for environments and 42.47% and 53.84% were due to genotypes and genotype × environment interactions, respectively. The partitioning of total sum of square (TSS) indicates that the genotype × environment interactions were main source of variation followed by genotypes and environments. Significant and large proportion of genotypic variation indicates the hybrids are diverse in nature.

Additive main effects and multiplicative interaction (AMMI) analysis: AMMI is more suitable in the initial statistical analysis of yield trials which provides estimate of genotype × environment interactions and summarizes the various patterns and relationships among genotypes and environments (Crossa *et al.* 1990). The G×E interaction *vis-a-vis* main effect is well explained by AMMI analysis. The G×E interaction was further partitioned into 2 principal components (IPCA1 and IPCA2). IPCA1 accounted for 60.6% whereas IPCA2 explained 39.4% of variation. Cumulatively, these two principal components were able to explain 100% variation. IPCA scores of genotypes and environments showed both positive and negative values

Table 1 AMMI analysis of variance over 3 environments

Source of variation	Degrees of freedom	SS	MSS	%TSS
Environments	2	5573	2786.36***	2.36%
Replications (Env)	6	113	18.75*	
Genotypes	67	99909	1491.18***	42.47%
Interactions	134	126651	945.15***	53.84%
Residuals	402	2971	7.39	
Total		235217		

*** Significant at 0.001 probability level

Table 2 Mean grain yield (Q/ha), IPCA1 and IPCA2 scores and AMMI stability values of 68 maize hybrids

Crosses	Code	Begusarai	Udaipur	Karim Nagar	Mean	IPCA1	IPCA2	ASV
DQL 2065 × CML 161 (G 1)	G1	58.15	71.82	97.11	75.7	-1.665	-1.002	2.296
DQL 2047 × CML 165 (G2)	G2	109.32	73.41	83.54	88.76	2.101	-1.432	2.543
DQL 2024 × CLQRCY 40	G3	70.45	79.65	53.71	67.94	1.096	1.32	1.716
DQL 2024 × CML 161	G4	49.41	66.55	87.70	67.89	-1.676	-0.726	1.826
DQL 2139 × CLQRCY 40	G5	77.94	68.30	83.43	76.56	0.253	-1.061	1.091
DQL 2026 × CLQRCY 40	G6	69.24	72.58	68.22	70.02	0.406	0.163	0.437
DQL 2042 × CLQRCY 40	G7	98.34	84.11	53.78	78.74	2.741	0.986	2.913
DQL 2140 × CML 161	G8	71.02	73.89	109.02	84.64	-1.483	-1.719	2.27
DQL 2050 × CML 161	G9	52.15	98.03	84.09	78.09	-1.728	1.602	2.357
DQL 2065 × HKI 163	G10	35.13	95.29	101.99	77.47	-3.603	0.955	3.728
DQL 2032 × CML 165	G11	82.54	61.75	81.74	75.34	0.699	-1.549	1.699
DQL 2020 × CLQRCY 40	G12	58.13	68.04	85.75	70.64	-1.067	-0.731	1.293
DQL 2029 × CML 165	G13	51.99	69.58	104.60	75.39	-2.377	-1.372	2.745
DQL 2057 × CML 165	G14	52.38	77.74	45.22	58.45	0.428	2.007	2.052
DQL 2029 × CML 161	G15	73.90	82.35	96.62	84.29	-0.811	-0.602	1.009
DQL 2057 × CML 161	G16	69.84	130.87	68.67	89.79	-0.31	4.239	4.25
DQL 2047 × CML 161	G17	89.34	74.17	83.97	82.49	0.85	-0.937	1.265
DQL 2064 × CML 165	G18	73.50	102.61	101.97	92.7	-1.349	0.584	1.47
DQL 2058 × CLQRCY 40	G19	84.89	85.93	88.42	86.42	0.214	-0.215	0.303
DQL 2026 × CML 165	G20	81.73	51.93	108.11	80.59	-0.508	-3.473	3.51
DQL 2024 × CML 165	G21	76.44	67.03	105.94	83.14	-0.916	-2.182	2.367
DQL 2063 × CML 161	G22	58.34	133.84	118.08	103.42	-3.45	2.374	4.188
DQL 2053 × CML 165	G23	86.68	102.40	64.36	84.48	1.286	2.045	2.416
DQL 2053 × CML 161	G24	117.63	112.95	64.25	98.27	3.05	2.078	3.69
DQL 2022 × CML 165	G25	13.65	27.43	9.98	17.02	0.404	1.024	1.101
DQL 2080 × CLQRCY 40	G26	70.42	101.11	83.54	85.02	-0.624	1.422	1.553
DQL 2083 × CML 161	G27	69.39	86.06	68.37	74.61	0.24	1.104	1.129
DQL 2082 × CML 161	G28	80.42	54.40	93.24	76.02	0.103	-2.564	2.566
DQL 2082 × CLQRCY 40	G29	61.58	80.76	107.10	83.15	-2.052	-0.925	2.251
DQL 2065 × CLQRCY 40	G30	81.18	101.00	86.89	89.69	-0.128	1.007	1.015
DQL 2056 × CML 161	G31	60.56	58.74	55.87	58.39	0.65	-0.027	0.65
DQL 2031 × CML 165	G32	79.50	86.61	90.80	85.64	-0.239	-0.154	0.285
DQL 2022 × CLQRCY 40	G33	60.77	55.66	66.89	61.11	0.166	-0.771	0.789
DQL 2039 × CML 161	G34	76.69	47.69	102.60	75.66	-0.495	-3.393	3.429
DQL 2039 × CML 165	G35	61.95	69.56	117.05	82.86	-2.373	-2.195	3.232
DQL 2052 × CML 161	G36	34.89	83.40	84.17	67.49	-2.603	0.966	2.776
DQL 2066 × CML 161	G37	38.15	93.75	93.66	75.19	-2.995	1.171	3.216
DQL 2047 × CML 165	G38	97.57	90.13	71.59	86.43	1.754	0.585	1.849
DQL 2046 × CML 165	G39	29.75	58.72	72.32	53.6	-2.032	-0.094	2.034
DQL 2026 × CML 161	G40	68.63	82.88	79.80	77.11	-0.323	0.355	0.48
DQL 2063 × CLQRCY 40	G41	62.82	75.51	50.08	62.8	0.858	1.377	1.622
DQL 2072 × CLQRCY 40	G42	96.45	69.10	55.68	73.74	2.722	-0.118	2.724

Contd.

Table 2. (*Concluded*)

Crosses	Code	Begusarai	Udaipur	Karim Nagar	Mean	IPCA1	IPCA2	ASV
DQL 2082 × CML 161	G43	60.64	62.16	59.85	60.89	0.418	0.024	0.419
DQL 2031 × CML 161	G44	78.79	98.65	85.90	87.78	-0.196	0.942	0.963
DQL 2065 × CML 165	G45	66.08	49.64	42.99	52.9	1.726	-0.187	1.737
DQL 2028 × CML 161	G46	118.16	72.85	68.05	86.35	3.401	-0.942	3.529
DQL 2065 × HKI 163	G47	58.10	65.96	73.76	65.94	-0.46	-0.309	0.554
DQL 2080 × CML 165	G48	77.07	81.66	79.48	79.41	0.224	0.089	0.241
DQL 2023 × CML 165	G49	55.09	77.61	91.63	74.78	-1.658	-0.263	1.679
DQL 2063 × CML 165	G50	84.09	84.74	70.24	79.69	1.063	0.581	1.212
DQL 2082 × CML 165	G51	97.58	53.13	63.75	71.49	2.6	-1.653	3.081
DQL 2020 × CML 161	G52	74.61	56.26	71.81	67.56	0.765	-1.283	1.494
DQL 2052 × CML 165	G53	62.75	70.21	79.94	70.97	-0.53	-0.409	0.669
DQL 2025 × CML 165	G54	52.89	79.84	49.79	60.84	0.21	1.927	1.939
DQL 2031 × CLQRCY 40	G55	73.96	67.47	64.72	68.71	0.929	-0.141	0.94
DQL 2037 × CML 161	G56	100.46	58.29	72.20	76.99	2.301	-1.757	2.895
DQL 2054 × CML 165	G57	60.34	67.82	57.63	61.93	0.437	0.535	0.69
DQL 2090 × CML 161	G58	70.24	71.55	58.89	66.89	0.934	0.509	1.064
DQL 2055 × CLQRCY 40	G59	73.89	82.80	83.03	79.91	-0.157	0.075	0.174
DQL 2050 × CML 165	G60	86.06	72.84	66.28	75.06	1.526	-0.116	1.53
DQL 2064 × CML 161	G61	64.36	71.64	55.00	63.67	0.762	0.836	1.131
DQL 2023 × CML 161	G62	71.53	49.99	48.04	56.52	1.81	-0.527	1.885
DQL 2039 × CML 161	G63	59.82	84.85	96.74	80.47	-1.708	-0.105	1.712
DQL 2066 × HKI 163	G64	79.97	70.56	85.16	78.56	0.265	-1.03	1.064
DQL 2055 × CML 165	G65	60.94	67.82	42.65	57.14	1.201	1.231	1.719
DQL 2066 × CML 161	G66	55.56	77.11	52.76	61.81	0.265	1.532	1.554
HQPM-1	G67	78.81	81.47	92.38	84.22	-0.294	-0.576	0.646
HQPM-7	G68	66.03	95.27	88.18	83.16	-1.043	0.893	1.373

(Table 2). Based on IPCA1 scores, QPM genotypes, viz. G46, G24, G7, G42, G51, G56, G2, G62, G38 and G45 showed relatively high positive interaction with the environment whereas genotypes G10, G22, G37, G36, G13, G35, G29, G39, G9 and G63 had high negative interaction. AMMI stability value (ASV) is the distance from zero in a two dimensional scatter plot of IPCA1 scores against IPCA2 (Purchase *et al*. 2000). ASV revealed variations in yield stability among 68 hybrids including checks. G59 was the most stable genotype with the lowest ASV (0.174) and 79.91 q/ha grain yield. Three genotypes, viz. G22, G24 and G18 recorded >90 q/ha with ASV value 4.19, 3.69 and 1.47 respectively. G16 was found to be the most unstable genotype with highest ASV (4.25). G48, G32, G19 and G40 were most stable genotypes (ASV: 0.24, 0.28, 0.30 and 0.48 respectively) with above mean (74.56 q/ha) grain yield. G67 and G44 were high yielding genotypes (84.22 and 87.78) with moderate stability (ASV: 0.65 and 0.96 respectively).

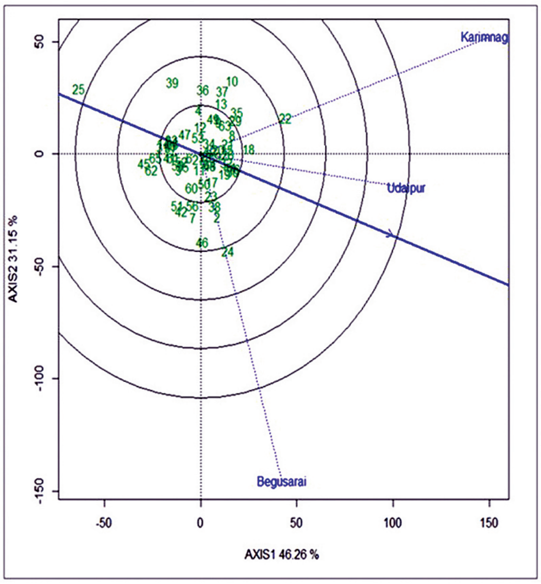
Genotype-Environment Interaction (GGE) biplot analysis: GGE biplot analysis was performed in order to study the relationships among and between environments. The GGE biplot is modification of AMMI analysis which provides graphical display and is considered as an innovative methodology for applied plant breeding (Yan *et al*. 2000). The GGE biplots for grain yield of QPM hybrids evaluated in three environments (Fig 1; A, B and C). The first principal component (PC1) scores were plotted against x-axis and the second principal component (PC2) scores were used in the y-axis. The percentage of variation explained by PC1 and PC2 was 46.26% and 31.15%, respectively. Together both principal components explained 77.41% of the total variation relative to G and GEI. The three test environments showed significant variation and the interrelationships between environments can be predicted from Fig 1 (A). Environment vectors are the lines that connect the test environments to the biplot origin. Similarity between two environments is measured by the cosine of the angle between the vectors of two environments. In the biplot, Udaipur vector forms an acute angle with Karimnagar and Begusarai, thus showing positive correlation. Begusarai forms a right angle with

Karimnagar, depicting no correlation between them. The presence of close associations among test environments suggests that same information about the genotypes could be obtained from fewer test environments, and hence it will reduce testing cost. The length of the environmental vectors is proportional to the standard deviation within the respective environments. It is a measure of the discriminating ability of the environments. So, among the three environments, Karim Nagar was most discriminating. It is good test environment for selecting generally adapted genotypes. It is also the best environment among the test locations for selecting genotypes.The test environment which has a smaller angle with AEA is more representative than other test locations, so Udaipur is more representative than Karimnagar and Begusarai.

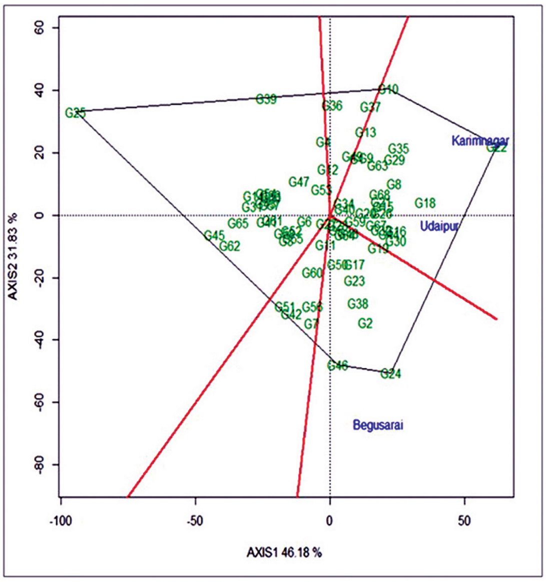
Yan *et al*. (2000) and Yan and Hunt (2001) suggested 'which won where' biplot to identify mega-environments. Fig 1 (B) shows the polygon view of the GGE biplot helpful in visualizing the 'which won where' pattern that showed different winning genotype in different environments. The genotypes which are farthest from the biplot origin are joined with a straight line forming a polygon. These perpendicular lines connecting the biplot origin and each side of the polygon are the equality lines between adjacent genotypes on the polygon. These equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. Genotypes G10, G22, G24, G46 and G25 located at the corner of the polygon are the vertex genotypes with the longest vectors. These genotypes were the most responsive genotypes to environments. Fig 2 shows that G24, G2, G56, G7, G51, G38, G42, G17 and G23 performed best at Begusarai. Performance of G16, G 18, G23 and G30 was best in Udaipur whereas G35, G8 and G29 performed best at Karim Nagar.

High yielding and stable hybrids were identified based on the ranking of genotypes and theirrelationship with the location from the average-environment coordinate (AEC) view of the GGE biplot which is also known as mean vs. stability biplot (Figure 1 C). G22 revealed the highest mean yield as per his biplot on arrow followed by G24, G18, G16, G30 and G44. The arrowed line is the AEC coordinate and it points to greater variability (poor stability) in either direction. Thus, G19 and G30 were identified as the stable genotypes with high mean. Lower ASV scores specify a more stable genotype across environments. These two genotypes also showed low ASV values i.e.0.303 and 1.015 respectively.

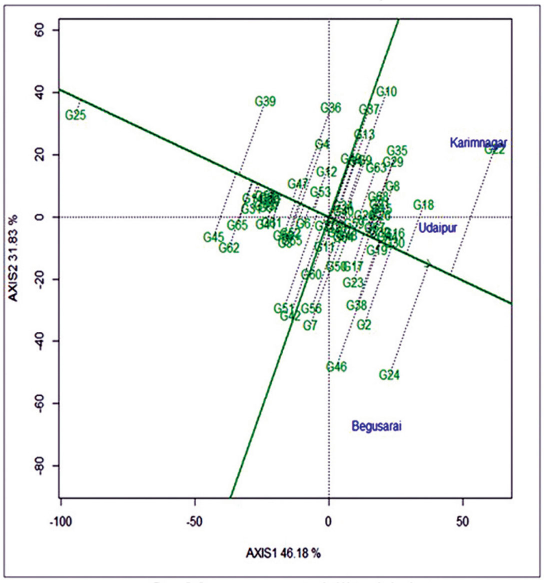
The AMMI model and GGE interaction biplots are important techniques in crop improvement. This study has important implications in determining the appropriate test location for development of cultivars. The most stable genotypes identified in this study could be used in future



A : Discriminative vs. representative biplot



B : Which won where biplot



C : Mean vs. stability biplot

Fig 1 (A) Discrimivative vs. representative biplot showing relationship among environments (B) Which won where biplot indicates superior genotypes in respective environments (C) Mean vs. stability biplot identifies stable genotypes with high mean.

plant breeding programmes directing towards development of superior cultivars suited for an appropriate environment

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