Indian J. Genet., (2023); 83(1) : 59-68
doi: 10.31742/ISGPB.83.1.8
ISSN: 0975-6906
www.ijgpb.org

RESEARCH ARTICLE

Dissection of genotype × environment interaction for green cob yield using AMMI and GGE biplot with MTSI for selection of elite genotype of sweet corn (*Zea mays* conva. Saccharata var. rugosa)

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Abstract

Contemporary sweet corn differed from other types of maize due to the presence of a mutated version of one or more modest alleles in the endosperm which participates in starch synthesis. In the present study, 45 sweet corn genotypes were evaluated under three environments, namely, Anand (E_1), Godhra (E_2) and Sansoli (E_3) in Gujarat during *rabi* 2020-21. Data on 14 characters were subjected to joint analysis of variance. After observing significant G × E interaction except for days to 50% tasseling and silking, the phenotypic stability of sweet corn genotypes for green cob yield was analyzed using multivariate techniques like AMMI and GGE biplots. Which-won-where biplot identifies 1820231/T1 and 1820228/T2 genotypes suitable for Godhra and Anand, respectively. At the same time, discriminativeness and representativeness decipher Anand as highly interactive environment for green cob yield. Y × WAASB biplot identify best genotypes with higher mean performance with excellent stability from the fourth quadrant. Multi-trait stability index identified seven genotypes *viz.,* 1820162/T1 (G28), 1820194/T2 (G37), I-07-34-3-1 (G19), 1820164/20 (G3), I-07-62-22-5 (G24), 1820192/C4-20 (G16) and 1820214/C1-20 (G30) with higher phenotypic stability and mean performance for all interactive traits.

Keywords: Sweet corn, AMMI, GGE biplot, MTSI, green cob yield, stability.

Introduction

Maize production has surpassed rice production as the world's most produced cereal, it also surpassed wheat in the year 1996 and 1997 (Fischer et al. 2014). Asia is the world's second-largest maize producer with 31% share of worldwide maize production from around 34% of the total harvested area. The current decade has seen impressive growth in maize production with significant increases in all sub-regions, including Southeast Asia (10.8%), Southern Asia (27.3%) and East Asia (30.6%), resulting in an overall 27.7% increase in maize production in Asia between 2010 and 2016 (FAOSTAT 2018). Economically, normal maize yields low returns per unit area, the growers are rapidly switching to sweet corn production, which yields higher returns and stimulates the economy.

Sweet corn has a sizeable commercial potential as well as a lot of genetic variability and area of improvement regarding the nutritional value and yield potential. Sweet corn originated from a naturally occurring recessive gene mutation that drives sugar to starch conversion inside the endosperm. Therefore, it is harvested early (dough stage), cooked, and consumed as a vegetable rather than a grain. Sweet corn does not store well since the maturation process involves converting sugar to starch. It must be consumed

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How to cite this article: Patel R., Parmar D.J., Kumar S., Patel D. A., Memon J., Patel M.B. and Patel J.K. 2023. Dissection of genotype × environment interaction for green cob yield using AMMI and GGE biplot with MTSI for selection of elite genotype of sweet corn (*Zea mays* conva. Saccharata var. rugosa). Indian J. Genet. Plant Breed., **83**(1): 59-68.

Source of support: Nil

Conflict of interest: None.

Received: Aug. 2022 **Revised:** Dec. 2022 **Accepted:** Jan. 2023

fresh, canned or frozen before the kernels turn tough and starchy. Sweet corn is high in thiamine, pantothenic acid, ascorbic acid, phosphorus, manganese, folate and dietary fiber. Numerous health benefits are connected with eating this scrumptious vegetable. It was quickly adopted as a popular vegetable in the United States, Canada and Australia. In India and other Asian countries, it is gaining popularity due to its higher economic benefits (Najeeb et al. 2011).

Sweet corn is harvested and consumed at the dough stage when sugar content is highest in its kernels so "Green cob yield" is one of the most important characteristics to selecting high-yielding cultivars. In India, sweet corn production is facing low average output due to complex G × E interaction (GEI), changing climatic conditions and lack of high-yielding cultivars. It is critical to pick genotypes based on yield stability rather than average performance in a variety of environments (Islam et al. 2015). GEI hampers the crop's ability to achieve full genetic gain. Thus, plant breeding initiatives focus on boosting green cob yield in a certain macro environment or across a broad range of growth circumstances. A complete understanding of G × E interaction in any crop is essential before plant breeders can reliably decide on ideotype design, ideal parental combination, compatible environment and best crop management practice (Xavier et al. 2018).

A few researchers have conducted studies on stability performance for green cob yield using a different set of sweet corn genotypes at diverse agro-climatic zones. Several statistical models are available to evaluate and select stable genotypes but among all statistical packages, Additive Main effect and Multiplicative Interaction Model (AMMI) is widely used because this model have ability to extract additive effects using analysis of variance (ANOVA) and multiplicative effects through principal component analysis (PCA) which results in great changes in the ranking of the genotypes over the environments (Ajay et al. 2021). For a long time, researchers have used the GT (genotype trait) biplot technique in plant breeding. This strategy, however, does not provide accurate results for breeders to determine suitable cultivars for recommendation (Kendal 2019). Finally, the GYT (genotype yield trait) biplot technique was developed to address the shortcomings of the GT biplot model, allowing more efficient genotype selection based on overall superiority across yield-trait combinations and trait profiles, facilitating genotype evaluation and recommendation (Yan and Fregeau-Reid 2018). The multi-trait stability index (MTSI) was also used to select high-performing stable genotypes in multi-environment trail based on several traits using both a fixed-effect and a mixed-effect model (Olivoto et al. 2019a). It offers a one-of-a-kind selection procedure for fine-tuning stability and mean performance by considering several traits based on the positive or negative selection difference required for a given attribute (Olivoto et al. 2019b).

With this background knowledge, the aim of the present study was to identify stable sweet corn genotypes for breeding purposes through GEI (genotype-environment interaction) analysis of green cob yield in addition to breeding these genotypes may be introduced across a wide range of environments in western India.

Materials and methods

Planting material and experimental design

A total of 45 sweet corn genotypes were used in this study (Table 1). The field experiment was conducted at three different locations *viz.,* Anand (E_1), Godhra (E_2) and Sansoli (E_3) in 2020-21 in *rabi* season. Among all environments, E_2 (Godhra) is popular maize growing area while E_1 (Anand) and E_3 (Sansoli) are non-conventional maize cultivation area and adopting maize for cultivation but all these locations are new for sweet corn cultivation. The meteorological data with respect to sun shine days which ranged from 4.9 to 10 days; there was no rainfall except 3 days (3–10 mm); maximum temperature ranged from 24.1-36.6°C and minimum temperature ranged from 7.9-24.7°C with mean range of 16-27.2°C, respectively and relative humidity ranged from 38.5 to 70.4% was recorded during the seasons across the locations.

The experiment was performed in a completely randomized block design with two replications at each location. Genotypes were sown at 60 × 30 cm spacing with a single row of 6 m length of plot having 20 plants of each genotype. Standard agronomic practices were adopted during the experiment. Pendimethalin 30% EC was applied immediately after sowing as a pre-emergence herbicide to control the initial weed problem.

Trait phenotyping

The morphological observations like plant height (PH cm), ear height (EH cm), ears per plant (EPP), ear length (EL cm), ear girth (EG cm), number of kernel rows per ear (KRP), number of kernels per row (KPR), number of kernels per ear (NKE) and green cob yield (GCY g) were recorded on five randomly selected competitive plants ofeach genotype in each replication for various characters as per descriptors in maize (IBPGR 1991). The phenological characters *viz.,* days to 50% tasseling (TA) and silking (SI) were recorded on a plot basis. Protein content (Pro), (A.O.A.C. 1980), total soluble sugar (TSS) and β-carotene (Car) (Sathya et al. 2017) were measured in bulked self-pollinated seeds of five randomly plants of each genotype in every replication. For this the seeds (30g) were cleaned, oven dried, powdered and stored in sealed plastic bags for analysis. Sugar content was measured at the dough stage from selfed cob of three randomly selected plants.

Statistical analysis

The data of green cob yield and its related traits under three test environments were analyzed through pooled analysis of variance by assuming genotypes as fixed and environments as random factors (Peterson 1939).

AMMI analysis

The data of green cob yield were subjected to AMMI analysis (Gauch 1988). Regular ANOVA explained the additive main effects of genotype and environments and PCA revealed a non-additive portion. The location-wise stable genotypes identified by AMMI analysis were assessed for significance using the Gauch (1968) F-test approach (Vargas and Crossa 2000). The main effect of means *vs* the first principal component axis (PCA I) and between the first two principal component axes were used to create AMMI biplots. The AMMI stability values (ASV) and yield stability index (YSI) were also used to rank genotypes and was calculated using R package 'metan' (Atta et al. 2009).

GGE biplots

The site regression (SREG) genotype × genotype × environment interaction (GGE) biplot models are characterized as a powerful tool for successful analysis and interpretation of multi-environment data structure (Samonte et al., 2005). The GGE analysis showed that the variation explained by the first two components best fit for further developing GGE biplots. All the biplots in the study were created with environment-centered data without scaling through the symmetrical method of singular value partitioning (SVP) while the mean *vs.* stability biplot was constructed using row metric preserving method of SVP using R package 'metan'.

Multi-trait stability index

Singular value decomposition of matrix of BLUPSs was used to measure the stability. The weighted average of absolute scores from the SVD was used to determine the stability of each genotype and simultaneous selection for mean performance and stability was done using the WAASBY index. The multi-trait stability index (MTSI) was performed by Olivoto et al. (2019a). 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. These selected and non-selected genotypes were shown graphically by plotting MTSI scores.

The studied genotypes were classified into four unique groups by constructing GCY × WAAS biplot, allowing the joint interpretation of stability and mean performance in different environments. This biplot with four quadrants was constructed with green cob yield on the x-axis and WAASB values on y-axis.

Results and discussion

ANOVA and mean performance

Pooled ANOVA showed significant differences among genotypes and indicated that studied genotypes are completely different for all the traits under study (Table 2). It suggested that variation towards total variability (G+E+GEI) was the highest for KRP (46.25%) followed by EG (40.35%), NKE (39.54%), EPP (39.11%) and GCY (27.50%), where genotypes had a maximum variation for β-carotene (98.42%) followed by protein (97.63%) and TSS (97.08%). These quality parameters showed a minimum total variation of 1.50, 2.35 and 2.91% for β-carotene, protein and TSS, respectively. Ear height (40.32%), plant height (35.17%) and green cob yield (13.49%) shared maximum variation for environment towards total variation than other characters. Combined ANOVA indicates ample variability for traits under study, and the maximum portion of this variability was explained by genotype (Table 2). Here, green cob yield showed significant GEI indicated the necessity of stability analysis for sweet corn genotypes over environments. Williams (2017) found similar results while evaluating sweet corn genotypes for adoption in processing. Mean green cob yield was 98.37 g/plant over the environment with a range of 17.31 (E_3) to 174.45 g/plant (E_2) (Table 3). The mean over environments of the other characters studied are given in Supplementary Table S1 and also displayed in Fig. 1. Abe and Adelegan (2019) also reported results for plant height, ear height, days to tasseling (55.2 days), days to silking (57.8 days) and cob length (15.7 cm) which are close to present study and suggested the presence of the significant amount of genetic variability among the traits under study.

Table 1. List of the sweet corn genotypes studied

Genotypes with code	Origin/source
1. I-07-62-42-2, 18. I-07-33-04, 19. I-07-34-3-1, 20. I-07-36-1-4, 21. I-07-36-2, 22. I-07-37-6-1, 23. I-07-40-4-2, 24. I-07-62-22-5 and 45. I-07-62-3-2	AAU, Godhra
1820161/20-5, 3.1820164/20, 4.1820168/T1, 5.1820213/9-20, 6.1820215/C1-20, 7.1820228/T2, 8.11820211/T2, 9.1820211/T1, 10. 1820200/C1-20, 11. 1820198/C1-20, 12. 1820197/T2, 13. 1820197/T1, 14. 1820167/C4-20, 15. 1820194/T1, 16. 1820192/C4-20, 17. 1820229/T2, 25. 1820162/T3, 26. 1820166/T2, 27. 1820162/T2, 28. 1820162/T1, 29. 1820212/T2, 30. 1820214/C1-20, 31. 1820228/T1, 32. 1820229/T1, 33. 1820230/T1, 34. 1820230/T2, 35. 1820231/T1, 36. 1820199/20-5, 37. 1820194/T2, 38. 1820196/T2, 39. 1820193/T2, 40. 1820195/20, 41. 1820166/T1, 42. 1820231/T3, 43. 1820196/T1 and 44. 1820212/T1	IIMR, Ludhiana

Table 2. Combined analysis of variance for all the traits studied along with their contribution towards total variation among 45 sweet corn genotypes in three test environments in *rabi* 2020-21

Source of variation	Environment (df: 2)		Genotype (df: 44)		GEI (df: 88)		Residual (df: 132)
Trait	Mean Squares	% (G + E+GEI)	Mean Squares	% (G + E + GEI)	Mean Squares	% (G + E + GEI)	Mean Squares
TA	200.95**	7.76	101.18**	86.04	3.64	6.19	4.19
SI	183.1**	7.29	95.94**	84.13	4.88	8.56	5.03
PH	51088.17**	35.17	2596.34**	39.32	841.81**	25.50	142.69
EH	30019.39**	40.32	1158.67**	34.24	430.35**	25.43	40.74
EPP	0.07	0.69	0.28**	60.18	0.09**	39.11	0.04
EL	43.22**	4.52	31.25**	72.06	5.07**	23.40	1.46
EG	4.84*	1.16	11.01**	58.47	3.80**	40.35	1.06
KRP	6.87**	0.63	26.24**	53.11	11.43**	46.25	0.88
KPR	36.01**	0.81	140.15**	69.83	29.45**	29.34	4.04
NKE	15800.03**	0.93	45751.1**	59.51	15201.24**	39.54	2240.18
Protein	0.01	0.00	9.14**	97.63	0.11	2.35	0.45
B-carotene	4.06*	0.06	266.71**	98.42	2.04**	1.50	1.26
TSS	0.0005	0.00	1.68**	97.08	0.02**	2.91	0.01
GCY	32273.77**	13.49	6411.34**	58.99	1494.87**	27.50	237.51

Df = degree of freedom, TA = Days to 50% tasseling, SI = Days to 50% silking, PH = Plant height, EH = Ear height, EPP = Ears per plant, EL = Ear length, EG = Ear girth, KRP = Number of kernel rows per ear, KPR = Number of kernels per row, NKE = Number of kernels per ear, Protein = Protein content, TSS = Total soluble sugars, Carotene = β-carotene content, GCY = Green cob yield; ** significant at 1%

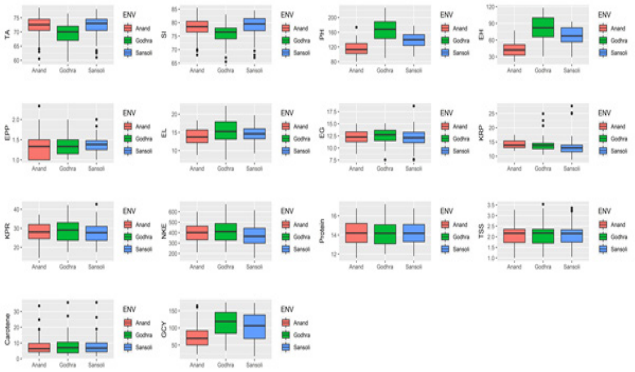

Fig. 1. Box plots showing mean performance of the studied traits across all three environments during rabi 2020-21: TA= Days to 50% tasseling, B) SI: Days to 50% silking, PH= Plant height, EH= Ear height, EPP= Ears per plant, EL= Ear length, EG= Ear girth, KRP= number of kernel rows per ear, KPR= Number of kernels per row, NKE= number of kernels per ear, Protein= Protein content, TSS= Total soluble sugars, Carotene= β-carotene content, and GCY= Green cob yield.

GEI analysis

The AMMI analysis for green cob yield revealed that a significant additive portion of the total sum of squares contributed by the genotypic effect (58.99%) followed by GEI effect (27.50%) and environment effect (13.49%) (Table 2). Thus, the result indicated that the performance of green cob yield is influenced by the environment, genotype, and their interaction (GEI). AMMI partitioned GEI effect into two interactive principal components (IPCA I and IPCA II) with 79.00 and 21.00% of GEI sum of squares (Supplementary Table S2). Yan et al. (2001) suggested that significant GEI effects reduce the gain for quantitative traits like green cob yield. Significant GEI effect and principal interactive component indicated the need to identify specific environments and genotypes.

AMMI biplot

Different biplots visualized the stability of genotype, green cob yield potential, and association of test environment. AMMI I biplot was developed by depicting mean green cob yield on the abscissa, representing main effects while ordinates depicting by IPCA I scores indicated multiplicative or GEI effects (Ebdon and Gauch 2002). AMMI I biplot (mean green cob yield *vs.* IPCA I) revealed a relationship between genotype and environment (Fig. 2A). In the AMMI I biplot, E_1 placed far from the origin with the longest vector represents strong interaction. On the other hand, E_3 was closer to the origin with the shortest vector indicating poor interaction force. E_2 and E_3 placed on the right-hand side of the grand mean line in the biplot suggested that both these locations are favorable for sweet corn to harvest high green cob yield while E_1 was declared as poor environment as placed opposite to E_2 and E_3 (Fig. 2A). Shinde et al. (2002) and Mebratu et al. (2019) also explained similar results. Genotype 1820198/C1-20 (G11) followed by 1820197/T1 (G13), 1820192/4-20 (G16), 1820168/T1 (G4) and I-07-36-2 (G21) showed higher green cob yield than overall mean performance (Fig. 2A). Genotypes *viz.,* I-07-33-04 (G18) followed by 1820162/T1 (G28), 1820162/T3 (G25) and 1820193/T2 (G39) placed near to origin are broadly adopted to all the environments with

Table 3. Mean of quantitative traits of sweet corn genotypes in different environments

Traits	E_1:Anand	E_2: Godhra	E_3: Sansoli	Mean over environment
TA	71.74	69.30	72.01	71.02
SI	78.00	75.73	78.37	77.37
PH	114.56	162.20	137.71	138.16
EH	43.54	79.52	67.00	63.35
EPP	1.39	1.34	1.40	1.38
EL	13.79	15.18	14.54	14.50
EG	12.28	12.43	11.98	12.23
KRP	14.17	14.21	13.71	14.03
KPR	27.90	28.84	27.63	28.12
NKE	396.68	406.83	375.59	393.03
Protein	14.20	14.18	14.19	14.19
Car	8.47	8.78	8.87	8.71
TSS	2.12	2.12	2.12	2.12
GCY	77.10	113.40	104.62	98.37

TA = Days to 50% tasseling, SI = Days to 50% silking, PH = Plant height, EH = Ear height, EPP = Ears per plant, EL = Ear length, EG = Ear girth, KRP = Number of kernel rows per ear, KPR = Number of kernels per row, NKE = Number of kernels per ear, Protein = Protein content, TSS = Total soluble sugars, Carotene = β-carotene content and GCY = Green cob yield

Table 4. Mean green cob yield (g/plant), IPCA I and IPCA II score, AMMI stability value (ASV), rank of ASV, Yield stability index (YSI) and rank of YSI of 45 sweet corn genotypes tested across three environments during *Rabi* 2020-21

Genotype*	Mean	IPCA I	IPCA II	ASV	rASV	YSI	rYSI
1	47.37	-2.7437	0.5210	10.313	34	77	43
2	82.39	0.4509	0.7166	1.838	3	34	31
3	65.93	-0.4142	0.2866	1.581	1	39	38
4	150.48	-1.5594	-0.8938	5.922	20	24	4
5	68.03	-4.4283	-1.1257	16.662	44	81	37
6	75.24	-2.6322	1.4022	9.980	33	67	34
7	132.96	-4.3465	-0.0625	16.317	43	50	7
8	45.89	-1.4153	-0.9145	5.391	18	62	44
9	124.42	-2.8851	1.6941	10.962	37	49	12
10	132.63	3.2990	-0.0842	12.385	40	48	8
11	157.74	-1.8662	0.8017	7.051	25	26	1
12	63.27	-0.5383	1.4447	2.484	5	44	39
13	157.62	-0.4306	-0.0676	1.618	2	4	2
14	70.52	-2.2264	-0.3198	8.364	31	66	35
15	61.45	-3.3579	-1.4524	12.689	41	81	40
16	152.19	-1.0094	-0.0464	3.790	11	14	3
17	83.20	2.0939	1.2474	7.959	30	60	30
18	99.39	0.9305	2.8571	4.513	15	35	20
19	89.85	-1.7837	-0.6096	6.724	24	52	28
20	70.19	2.0639	-0.0295	7.748	26	62	36
21	144.69	-1.4603	1.9743	5.827	19	24	5
22	124.12	0.0399	-5.1847	5.187	16	29	13
23	104.69	1.7337	0.3678	6.519	23	42	19
24	119.28	2.0582	-0.7196	7.760	27	42	15
25	95.01	-0.7472	-2.1143	3.513	8	31	23

26	113.63	2.8064	-0.4932	10.547	35	52	17
27	108.78	2.0939	0.7148	7.893	28	46	18
28	96.55	0.8152	-1.2164	3.293	6	27	21
29	77.90	-1.1990	-2.7934	5.298	17	49	32
30	132.11	-0.7118	-2.0519	3.369	7	16	9
31	113.93	4.3276	-0.9010	16.271	42	58	16
32	90.33	3.0195	-0.8530	11.367	38	63	25
33	57.33	1.0731	0.0079	4.028	12	53	41
34	89.89	0.2184	3.6202	3.712	9	36	27
35	124.56	5.3277	-0.5196	20.007	45	56	11
36	89.89	1.7056	0.1824	6.405	22	48	26
37	77.02	1.9365	-3.0743	7.893	29	62	33
38	29.17	-2.2803	0.8251	8.600	32	77	45
39	94.60	-0.5512	-0.9989	2.298	4	28	24
40	48.53	-2.8448	0.2546	10.682	36	78	42
41	96.31	1.5475	2.2744	6.239	21	43	22
42	120.10	0.7664	2.8660	4.061	13	27	14
43	133.20	3.0887	-0.0686	11.595	39	45	6
44	83.53	-0.9856	0.5378	3.739	10	39	29
45	130.92	1.0208	1.9983	4.322	14	24	10
Anand	77.10	-12.2589	0.9234	-	-	-	-
Godhra	113.40	7.2426	7.1654	-	-	-	-
Sansoli	104.62	5.0163	-8.0888	-	-	-	-

*See Table 1

Table 5. Selection differential for mean of the traits and WAASBY index for 11 traits of 45 sweet corn genotypes across three environments during *rabi* 2020-21

Trait*	Factor	Mean performance			WAASBY		
		Overall (X_0)	Selected genotype (X_s)	SD (%)	Overall (X_0)	Selected genotype (X_s)	SD (%)
PH	FA 1	138.157	143.788	5.631	57.455	67.515	10.059
EH	FA 1	63.353	69.192	5.839	56.826	69.287	12.461
Car	FA 1	8.705	8.985	0.279	34.863	30.851	–4.011
GCY	FA 1	98.373	104.703	6.330	57.087	63.211	6.124
EL	FA 2	14.503	14.654	0.150	62.880	62.644	–0.236
KPR	FA 2	28.123	30.589	2.466	53.983	66.998	13.014
TSS	FA 2	2.120	2.139	0.019	60.553	62.586	2.033
EG	FA 3	12.232	12.684	0.452	58.367	66.056	7.689
KRP	FA 3	14.030	15.877	1.847	45.307	60.710	15.403
NKE	FA 3	393.033	478.725	85.692	57.138	79.242	22.104
EPP	FA 4	1.377	1.512	0.135	44.382	53.588	9.205

FA1= Factor 1, FA2= Factor 2, FA3= Factor 3, FA4= Factor 4, PH= Plant height, EH= Ear height, Car.= β-carotene, GCY= Green cob yield, EL= Ear length, KPR= Number of kernels per row, TSS= Total soluble sugars, EG= Ear girth, KRP= Number of kernel rows per ear, NKE= Number of kernels per ear, EPP= Ears per plant X_0 = Mean of the original population, X_s = Mean of the selected genotypes and SD= Selection differential.

near to average mean green cob yield production (Fig. 2A) according to Ebdon and Gauch (2002).

For the detailed exploration of the AMMI biplot, AMMI II biplot was constructed using IPCA I and IPCA II (Fig. 2B). In this plot, the polygon view of the dotted line connected the vertex genotypes, which showed maximum grain yield in a specific environment. The perpendicular projection from the genotype to the environmental vector revealed the amount of interaction with the particular environment. This biplot showed that E_1 is a highly interactive environment for 1820228/T2 (G7) and 1820213/9-20 (G5), contributing mainly to the GEI. The Genotype 1820231/T1 (G35) exceptionally

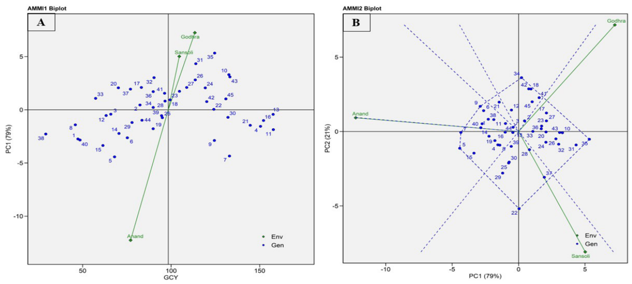

Fig. 2. A. AMMI I biplot (green cob vs IPCA I) of 45 sweet corn genotypes (Blue text) and three environments (Green text) for green cob yield evaluated during *rabi* 2020-21 and **B.** AMMI II biplot (IPCA I vs IPCA II) for green cob yield of 45 sweet corn genotypes evaluated across three environments during *rabi* 2020-21.

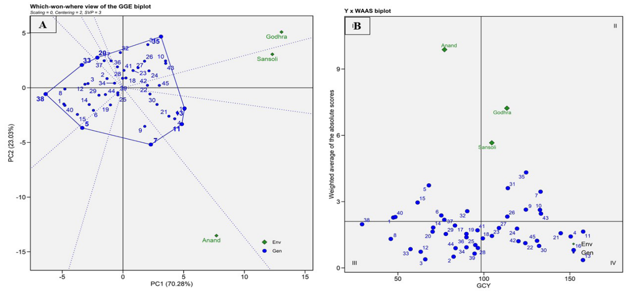

Fig. 3.A. Which-won-where view of 45 genotypes of sweet corn (blue text) evaluated across three environments (green text) during *rabi* 2020-21and **B.** Green cob yield × WAASB biplot based on combined interpretation of productivity (GCY) and stability (WAASB) for 45 sweet corn genotypes evaluated across three environments during *rabi* 2020-21.

performed well in E_2 while I-07-37-6-1 (G22) performed well in E_3 (Fig. 2B). The present results are in accordance with Elayaraja et al. (2022) who identified some stable genotypes of sugarcane for the sucrose percentage.

According to AMMI stability value, genotypes 1820164/20 (G3), 1820197/T1 (G13), 1820161/20-5 (G2) and 1820193/T2 (G39) had low ASV value indicating higher stability while 1820231/T1 (G35), 1820213/9-20 (G5), 1820228/T2 (G7) and 1820228/T1 (G31) had higher ASV value indicating higher interaction with environments (Table 4). YSI integrates green cob yield and stability across environments. The lower YSI index represents higher stability and higher productivity of genotypes (Mohammadi et al. 2010). According to YSI index, 1820198/C1-20 [G11 (rYSI=1)], 1820197/T1 [G13 (rYSI=2)], 1820192/4-20 [G16 (rYSI=3)] and 1820168/T1 [G4 (rYSI=4)] were detected as the best genotype for higher stability with greater yield while genotype 1820196/T2 [G38 (rYSI=45)], 11820211/T2 [G8 (rYSI=44)], I-07-62-42-2 [G1 (rYSI=43)] and 1820195/20 [G40 (rYSI=42)] with poor production efficiency with lower stability (Table 4). Similar results were recorded by Wardofa et al. (2019) in wheat with high performance and greater stability.

GGE biplots

Which won where and what?

Which-won where pattern analysis facilitates the identification of the most appropriate genotype for a given environment. The outermost genotypes are joined to form a polygon in this biplot (Fig. 3A). Polygon is also further divided into seven different sectors using rays (dotted lines) that start from the origin of plot and pass perpendicular to the sides of the polygon. This division helps to recommend genotypes for a particular sector (Gauch 2013). The biplot showed environments E_1: Anand, E_2: Godhra and E_3: Sansoli falling under separate mega-environments. Biplot showed that 1820231/T1 (G35) is a high-yielding vertex genotype for E_2 environment while 1820228/T2 (G7) is a high-yielding vertex genotype for E_1 environment (Fig. 3A). E_3 (Sansoli) environment didn't contain any vertex genotype. Genotypes namely, 1820213/9-20 (G5), 1820196/T2 (G38), 1820230/T1 (G33), I-07-36-1-4 (G20) and 1820198/C1-20 (G11) also were vertex genotypes but no environment falls in their sector indicating that they are low green cob yielding genotypes at few or all locations. Nzuve et al. (2013) analyzed genotype x environment interaction in maize hybrids and reported similar results concerning grain yield and developed which won where through biplot and found three mega-environments for a superior yield of four varieties.

Mean green cob yield vs stability

The 2-D visualization of green cob yield vs stability based on PCA I and PCA II scores were developed according to reports of Yan et al. (2001). This plot is perfect for genotype evaluation as it was developed through row metric preserving method (Supplementary Fig. 1A). An average environment coordination view was plotted to visualize the stability of the genotypes. A small perpendicular line indicated highly stable genotypes to the AEC axis. Higher mean green cob yield across the environment pointed by AEC abscissa. Genotype namely, 1820168/T1 (G4), 1820161/20-5 (G2), 1820198/C1-20 (G11), I-07-37-6-1 (G22), 1820230/T2 (G34), 1820193/T2 (G39) and 1820197/T1 (G13) were highly stable with low to good yielding ability. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses was carried out by Alwala et al. (2010) to identify stable and high-yielding maize hybrids.

Discriminativeness vs representativeness

The cosine angle between environmental vectors explains the association between two environments (Yan, 2002). A perfect 90° angle between two environments indicates no correlation, acute angle suggests a positive correlation and obtuse angle indicates a negative correlation. A positive correlation among all environments was recorded. In contrast, the longest vector of E_1 (Anand) indicates that it is most discriminative environment. On the biplot, the length of the environment's vector is proportional to

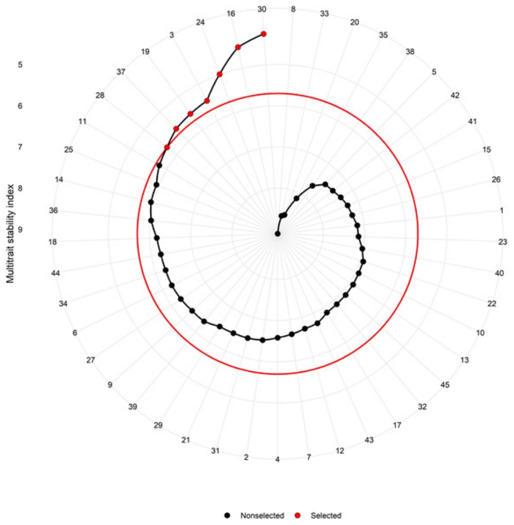

Fig. 4. Genotype ranking and selected genotypes among 45 sweet corn genotypes for multi trait stability index (MTSI) considering 15% selection intensity.

the standard deviation within that same environment and gives information regarding the environment's discriminating ability (Sserumaga et al. 2016; Samyuktha et al. 2020). The average environment axis is required to assess the representativeness of the environment. The discrimination and representativeness view of the GGE biplot has been studied in several crops (Reddy et al. 2022; Kottawa-Arachchi et al. 2022) to show the discriminating ability and representativeness of the test environments. A higher angle between AEA and the environmental vector indicates lower representativeness and vice versa. In the view of representativeness, E_3 is highly representative environment. The present results indicated that widely adopted genotypes were selected from E_3 (Sansoli), while specifically adapted genotypes were selected from the E_1 (Anand) environment.

Y × WAASB biplot

Y × WAASB biplot was constructed using green cob yield on X-axes and WAAS value on y-axes (Fig. 3B). This plot divides genotypes into four quadrants, allowing simultaneous genotype selection with a high mean performance of included traits and its stability. According to biplot (Fig 3B), six genotypes along with E_1 (Anand) fall in first quadrant, 6 genotypes along with E_2 and E_3 were in the second quadrant. At the same time, the third quadrant had 17 genotypes and the rest fell in the fourth quadrant. First quadrant showed greater instability of genotypes with low productivity and environment with high discrimination ability, the second quadrant included genotypes with poor stability and higher green cob yield above the grand mean. It also suggested giving special attention to the environment for higher green cob yield. The third quadrant contains genotypes with greater stability (due to low WAAS value) but lower productivity and the fourth quadrant indicates the genotypes with greater stability with more incredible performance for green cob yield as earlier observed by Singamsetti et al. (2021).

Multi-trait stability index (MTSI)

The primary purpose of any breeding strategy is to select high-performing genotypes with desired features. The majority of plant breeders used traditional stability indices based on first-degree statistics. The choice of a stable genotype based on mean, regression and departure from regression parameters may not be enough to offer a straightforward interpretation of mean performance and trait stability. As a result, the MTSI approach is a sophisticated quantitative genetic tool for the exploitation of appropriate variations in all crop species (Olivoto et al. 2019b). It utilized the mean performance and stability of the genotype for multiple traits.

MTSI included all traits except TA, SI and protein because their p-value for likelihood ratio also found non-significant. The WAASBY values generated using a Pearson's correlation matrix and the retrieved high magnitude relationships were combined as a common factor. Exploratory factor analysis using 11 characters resulting from four PCs cumulatively explained 73.08% of the variation (Supplementary Table S3). Communality, an indication of shared variance among traits, ranged from 0.283 (Carotene content) to -0.923 (KRP) with an average value of 0.73 after varimax rotation. Eleven traits were grouped in the four factors by extracting WAASBY value from each character given in Table 5. PH, EH, carotene content and GCY were grouped in the FA1. EL, KPR and TSS were in FA2. EG, KRP and NKE are harbored by FA3. FA4 had only one trait *i.e.,* EPP (Table 5). The selection differential for mean performance was positive with a range of 0.35 (EPP) to 85.69 (NKE), while the selection differential for WAASBY index was negative for EL and carotene (Table 5). The selection performed in Fig. 4 was used to calculate the mean of the selected genotypes (X_S), which was higher than the mean of the original population for mean performance. It also showed a positive selection differential with a range of 0.35 (EPP) to 85.69 (NKE). While for the WAASBY index X_S is lower for the carotene and EL (also showed negative value for selection differential), which suggested rejection of these two characters for simultaneous selection for yield and stability. A similar approach was adopted to evaluate the relative effects of drought and saline stress on seed germination in sweet sorghum (Patanè et al. 2013) and cowpea (Murillo-Amador et al. 2002).

The selection of stable genotypes with greater mean performance for various traits is most important in stability analysis (Yue et al. 2021). It was performed using genotype-ideotype Euclidian distance-based scores. Scores for 45 genotypes, along with ideotype estimated in first four factors, were obtained through exploratory factor analysis (Supplementary Table S4). MTSI help to select genotype having higher stability with a higher mean performance of all measured traits. Lower MTSI-valued genotypes were selected with 15% selection intensity. According to Fig. 4, 1820214/C1-20 [G30 (MTSI=4.24)], 1820192/4-20 [G16 (MTSI=4.48)], I-07-62-22-5 [G24 (MTSI=4.99)], 1820164/20 [G3 (MTSI=5.45)], I-07-34-3-1 [G19 (MTSI=5.51)], 1820194/T2 [G37 (MTSI=5.56)] and 1820162/T1 [G28 (MTSI=5.70)] were selected with maximum stability and high mean performance of analyzed traits (all traits which were significant for G × E). The red circle in Fig. 4 indicated the cutoff point with an MTSI value of 5.70 of G28. Genotype 11820211/T2 (G8) had a higher MTSI value (MTSI=9.10) followed by 1820230/T1 [G33 (MTSI=8.66)], I-07-36-1-4 [G20 (MTSI=8.62)] and 1820231/T1 [G35 (MTSI=8.31)], these genotypes were recognized as an unstable genotype with the poor performance for traits under study. These findings were comparable to that of Koundinya et al. (2021), who used MTSI to evaluate genotype-environment interactions, including leaf area index, yield per plant, harvest index, dry matter and starch yield per plant in 25 cassava genotypes.

In the mean vs stability' biplot, the majority of genotypes identified by MTSI were shown to be closer to the AEC (Supplementary Fig. 1A). Among these selected genotypes, 1820192/C4-20 (G16) and 1820214/C1-20 (G30) had the lowest MTSI value and fell in the fourth quadrant of Y × WAAS biplot, near to origin in which-won where biplot and also found near to origin in AMMI II biplot. These results support 1820192/C4-20 (G16) and 1820214/C1-20 (G30) for using as a genitor for future breeding and pre-breeding programs to develop new cultivars. Furthermore, MTSI also help to focus on the selected trait to attain stability with great performance through factor analysis as suggested by Koundinya et al. (2021) in cassava, Sellami et al. (2021) in lentil and Memon et al. (2023) in castor. In the present investigation, genotypes 1820192/4-20 (G16) and 1820214/C1-20 (G30) sowed lower WAASBY value for the traits belonging to FA1 and FA4 because they had higher relative contributions of 39.101 and 29.903% for 1820192/C4-20 (G16) and 32.00 and 31.63 for 1820214/C1-20 (G30).

Supplementary materials

Supplementary Fig. 1 and Supplementary Tables S1 to S4 are provided which can be accessed online www.isgpb.org

Authors' contribution

Conceptualization of research (DAP, RP, JM); Designing of the experiments (DAP, SK, MBP, JK); Contribution of experimental materials (MBP, JKP); Execution of field/lab experiments and data collection (RP, JM); Analysis of data and interpretation (RP, JM, DJP); Preparation of the manuscript (RP, JM, SK).

Acknowledgement

Anand Agricultural University is greatly acknowledged to provide necessary facilities. ICAR-IIMR, Ludhiana (Punjab) is also acknowledged to provide seed material for the present study.

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Supplemental Table S1. Mean over environments of 45 sweet corn maize genotypes for different characters over environment (E_1: Anand, E_2: Godhra, E_3: Sansoli)

Name of genotype (Genotype code)	TA	SI	PH	EH	EPP	EL	KPR	EG	KRP	NKE	Pro	TSS	Car	GCY
I-07-62-42-2(G1)	69.00	75.50	132.48	55.40	1.28	12.80	25.00	10.88	12.22	307.49	15.31	2.33	3.04	47.37
1820161/20-5(G2)	62.33	68.17	153.43	58.27	1.58	16.81	29.48	11.34	13.14	388.46	16.74	1.63	2.51	82.39
1820164/20(G3)	67.17	73.50	129.65	65.67	1.33	15.05	30.85	12.46	15.82	490.66	16.76	1.75	6.49	65.93
1820168/T1(G4)	69.00	75.67	157.82	68.25	1.15	17.23	31.32	14.71	12.97	405.01	15.50	1.92	3.20	150.48
1820213/9-20(G5)	71.50	78.17	125.66	64.35	1.17	14.98	29.00	11.06	12.65	371.61	12.05	1.05	4.78	68.03
1820215/C1-20 (G6)	69.17	76.00	140.74	53.72	1.68	14.02	28.97	10.75	13.34	389.91	12.65	2.49	8.51	75.24
1820228/T2(G7)	60.83	68.67	149.43	60.58	1.72	17.07	34.13	12.90	13.70	467.22	13.29	2.12	5.11	132.96
11820211/T2(G8)	76.50	82.50	116.78	64.69	1.25	14.30	23.02	11.46	12.57	290.04	16.10	1.70	3.34	45.89
1820211/T1 (G9)	74.33	81.00	171.68	75.03	1.30	16.52	31.37	11.92	13.13	412.40	13.85	1.77	6.89	124.42
1820200/C1-20 (G10)	69.67	75.67	134.61	74.50	1.25	17.72	33.13	11.70	12.58	417.35	12.75	1.70	6.28	132.63
1820198/C1-20(G11)	64.33	71.00	164.11	76.06	1.39	18.70	36.49	13.16	13.71	499.27	14.25	2.14	16.72	157.74
1820197/T2 (G12)	73.83	79.33	113.60	44.41	1.41	14.52	28.60	9.96	12.28	347.35	14.17	1.64	18.82	63.27
1820197/T1(G13)	72.50	79.00	162.41	76.19	1.20	18.71	39.34	13.73	13.65	536.29	13.85	1.26	35.06	157.62
1820167/C4-20 (G14)	64.67	70.50	157.44	81.22	1.33	10.01	20.05	13.04	13.80	281.66	13.95	3.38	14.34	70.52
1820194/T1 (G15)	63.00	69.67	113.66	55.28	1.50	8.86	24.46	10.96	12.83	313.10	13.26	3.22	8.18	61.45
1820192/4-20(G16)	71.67	78.50	147.17	71.26	1.58	15.80	35.63	12.95	14.32	507.56	14.95	2.48	7.00	152.19
1820229/T2 (G17)	76.33	82.00	122.88	53.01	1.33	13.90	23.57	12.04	13.79	329.64	14.90	1.59	3.55	83.20
I-07-33-04(G18)	71.67	78.83	165.74	76.97	1.41	14.98	30.33	12.61	13.21	403.40	11.79	2.23	26.08	99.39
I-07-34-3-1(G19)	71.67	77.67	129.15	57.82	2.11	12.70	28.96	11.00	13.11	374.14	12.19	1.77	17.13	89.85
I-07-36-1-4(G20)	72.67	78.50	99.39	43.06	1.36	10.98	21.35	9.18	11.68	226.56	12.38	2.12	2.17	70.19
I-07-36-2(G21)	70.67	77.50	150.63	78.39	1.36	17.95	33.20	12.83	13.96	462.74	13.07	2.15	3.24	144.69
I-07-37-6-1(G22)	63.33	69.67	135.64	53.12	1.68	15.10	22.74	15.29	20.71	446.99	12.47	2.29	4.33	124.12
I-07-40-4-2 (G23)	69.83	76.83	141.52	55.78	1.17	13.78	26.12	13.32	13.31	347.44	13.94	3.18	6.05	104.69
I-07-62-22-5(G24)	63.17	69.17	162.02	82.13	1.39	15.39	32.18	14.25	16.93	544.44	15.10	2.23	6.94	119.28
1820162/T3(G25)	70.83	77.67	142.17	78.06	1.42	13.80	25.42	13.39	15.59	390.12	12.89	2.44	2.67	95.01
1820166/T2 (G26)	71.50	78.00	145.64	86.33	1.33	15.35	31.47	13.00	14.65	460.18	15.35	2.18	6.73	113.63
1820162/T2 (G27)	72.33	78.83	145.16	60.05	1.32	13.87	22.57	13.53	13.03	299.14	13.83	2.16	4.56	108.78
1820162/T1(G28)	73.50	80.17	142.68	72.66	1.25	14.51	33.41	12.61	16.03	544.71	15.55	1.54	5.46	96.55
1820212/T2 (G29)	75.00	80.67	173.95	79.73	1.41	13.55	26.21	11.92	13.74	360.38	14.73	2.32	9.24	77.90
1820214/C1-20(G30)	72.50	78.83	148.66	71.10	1.83	13.61	24.46	13.08	15.21	371.92	15.08	2.53	4.89	132.11
1820228/T1(G31)	72.00	78.83	124.21	61.00	1.36	12.78	25.64	12.05	15.63	401.21	15.04	3.25	5.56	113.93
1820229/T1 (G32)	74.33	80.33	102.81	45.37	1.25	12.99	24.23	11.63	20.98	501.03	15.74	1.97	9.02	90.33
1820230/T1(G33)	73.50	79.83	113.88	44.62	1.00	12.38	24.02	12.55	14.36	346.09	14.96	2.04	2.91	57.33
1820230/T2 (G34)	74.33	79.50	141.83	68.67	1.35	17.50	36.89	12.66	14.08	527.27	14.19	1.48	9.21	89.89
1820231/T1(G35)	76.83	83.00	114.07	35.18	1.29	11.06	21.47	8.93	11.85	254.66	13.93	1.09	9.46	124.56
1820199/20-5 (G36)	68.67	74.67	133.68	58.23	1.61	15.66	29.21	11.11	11.69	342.12	13.55	2.22	5.05	89.89
1820194/T2(G37)	76.67	83.50	147.21	63.71	1.08	15.52	28.64	12.45	19.72	517.65	13.44	2.67	14.99	77.02
1820196/T2(G38)	75.33	81.17	114.56	56.28	1.24	10.70	18.63	9.75	12.56	226.56	15.34	2.25	3.33	29.17
1820193/T2(G39)	72.67	78.83	99.77	34.75	1.75	12.31	27.22	11.33	12.61	343.65	14.21	2.16	15.48	94.60
1820195/20(G40)	75.00	81.33	95.91	34.59	1.43	11.83	22.68	11.86	13.79	314.34	15.26	2.23	18.18	48.53
1820166/T1 (G41)	73.17	78.83	177.72	82.58	1.27	15.30	25.10	12.82	13.31	334.98	14.00	2.06	4.45	96.31
1820231/T3 (G42)	72.67	79.83	129.87	64.18	1.19	15.61	26.29	12.75	12.44	330.85	12.75	1.44	12.99	120.10
1820196/T1 (G43)	73.50	80.17	139.18	76.48	1.08	16.12	30.65	13.67	13.68	418.67	13.55	2.68	10.89	133.20

1820212/T1 (G44)	70.33	77.00	149.70	51.02	1.28	16.69	33.22	12.06	13.28	441.28	14.67	2.45	7.94	83.53
I-07-62-3-2 (G45)	72.33	77.50	156.81	81.18	1.30	13.66	28.86	13.87	13.76	398.98	15.11	2.11	9.03	130.92
Mean	71.02	77.37	138.16	63.35	1.38	14.50	28.12	12.23	14.03	393.03	14.19	2.12	8.71	98.37
Min	60.83	68.17	95.91	34.59	1.00	8.86	18.63	8.93	11.68	226.56	11.79	1.05	2.17	29.17
Max	76.83	83.50	177.72	86.33	2.11	18.71	39.34	15.29	20.98	544.71	16.76	3.38	35.06	157.74

Supplemental Table S2. Analysis of variance based on AMMI model of green cob yield per plant for 45 sweet corn genotypes across three environments in Rabi-2020-21

Source	df	MS	Total Explained variation (%)	GEI Contributed (%)
Environment	2	32273.76**	13.49	-
Genotype	44	6411.34**	58.99	-
GEI	88	1494.86**	27.50	-
IPCA I	45	2308.38**	-	79.00
IPCA II	43	343.51**	-	21.00
Residual	132	237.50	-	00.00
Total	357	1814.86	-	-

Df= Degrees of freedom, **SS=** Sum of squares, **MS=** Mean sum of squares, **GEI=** Genotype by environmental interaction, **IPCA=** Interactive principal component analysis, * significant at 5%, ** significant at 1%

Supplementary Table S3. Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities and uniqueness obtained in the factor analysis of the 11 variables studied in 45 sweet corn genotypes across three environments during rabi 2020-21

VAR	FA1	FA2	FA3	FA4	Communality	Uniqueness
PH	–0.836	0.022	–0.127	0.097	0.724	0.276
EH	–0.840	–0.056	–0.173	–0.120	0.753	0.247
EPP	0.039	–0.025	0.019	0.936	0.879	0.121
EL	–0.363	0.734	–0.223	–0.217	0.767	0.233
EG	–0.504	0.262	–0.613	–0.304	0.791	0.209
KRP	0.070	–0.081	–0.955	–0.003	0.923	0.077
KPR	–0.492	0.698	–0.090	0.241	0.796	0.204
NKE	–0.318	0.553	–0.652	0.167	0.859	0.141
TSS	–0.323	–0.772	–0.118	0.051	0.717	0.283
Car	–0.487	0.189	0.094	–0.039	0.283	0.717
GCY	–0.510	0.432	–0.310	–0.074	0.548	0.452
Eigenvalue	4.143	1.507	1.284	1.105	-	-
Variance (%)	37.664	13.703	11.677	10.044	-	-
Accumulated (%)	37.664	51.367	63.044	73.088	-	-

FA= Factor analysis, PH= Plant height, EH= Ear height, EPP= Ears per plant, EL= Ear length, EG= Ear girth, KRP= Number of kernel rows per ear, KPR= Number of kernels per row, NKE= Number of kernels per ear, TSS= Total soluble sugars, Car.= β-carotene and GCY= Green cob yield.

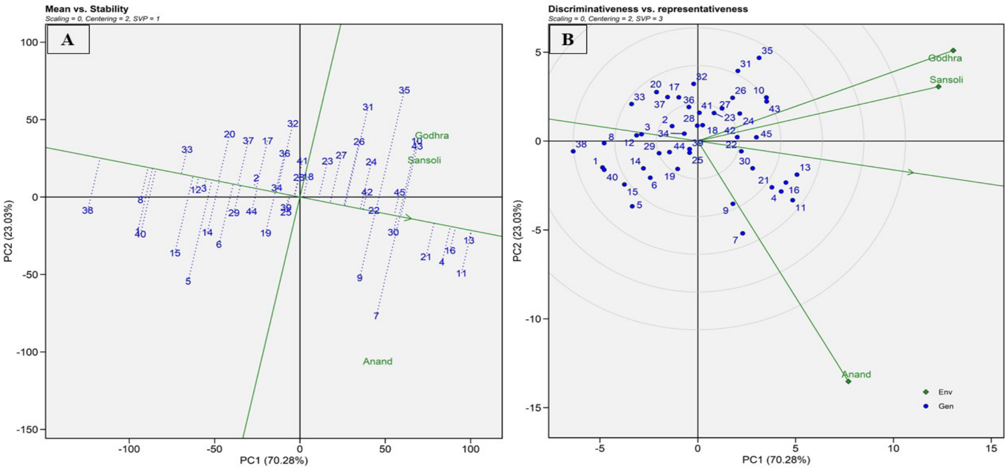
Supplementary Table S4. Genotype-ideotype (ID) scores, MTSI values for the 45 sweet corn genotypes for the first four factors along with relative contribution of each factor towards the MTSI

Genotype code	FA1		FA2		FA3		FA4		MTSI
	Score	RC %	Score	RC %	Score	RC %	Score	RC %	
G1	–4.284	38.346	–1.247	11.162	–2.307	20.650	3.334	29.842	7.166
G2	–4.103	34.616	0.601	5.070	–3.167	26.719	3.982	33.595	6.502
G3	–4.120	30.892	0.092	0.690	–4.669	35.008	4.456	33.411	5.457
G4	–5.867	49.298	0.268	2.252	–3.257	27.367	2.509	21.082	6.585
G5	–3.595	34.349	0.737	7.042	–3.156	30.155	2.978	28.454	7.442
G6	–4.334	36.030	–0.586	4.872	–3.024	25.139	4.085	33.960	6.253
G7	–3.949	33.441	0.635	5.377	–3.830	32.433	3.395	28.749	6.647

G8	−3.187	43.426	−0.282	3.842	−3.049	41.545	0.821	11.187	9.108
G9	−5.607	46.690	−0.317	2.640	−3.005	25.023	3.08	25.647	6.316
G10	−4.146	36.622	0.691	6.104	−3.328	29.397	3.156	27.877	6.921
G11	−6.288	44.457	0.882	6.236	−3.802	26.881	3.172	22.426	5.792
G12	−3.872	35.429	0.112	1.025	−2.412	22.070	4.533	41.477	6.713
G13	−5.789	41.323	2.089	14.912	−3.471	24.777	2.66	18.988	6.9
G14	−5.756	37.145	−2.694	17.385	−3.274	21.128	3.772	24.342	5.941
G15	−4.925	36.974	−2.653	19.917	−1.042	7.823	4.7	35.285	7.276
G16	−5.862	39.101	0.179	1.194	−4.468	29.803	4.483	29.903	4.481
G17	−3.131	28.793	−0.170	1.563	−3.764	34.615	3.809	35.029	6.853
G18	−6.309	47.440	−1.030	7.745	−2.985	22.445	2.975	22.370	6.175
G19	−4.003	29.846	0.176	1.312	−3.388	25.261	5.845	43.580	5.511
G20	−2.972	34.944	−1.088	12.792	−2.230	26.220	2.215	26.044	8.621
G21	−5.235	44.376	0.13	1.102	−3.850	32.635	2.582	21.887	6.469
G22	−3.503	24.139	−1.874	12.913	−6.587	45.390	2.548	17.558	6.925
G23	−5.283	41.786	−1.769	13.992	−3.807	30.112	1.784	14.111	7.145
G24	−5.676	38.772	−0.541	3.637	−5.005	33.649	3.561	23.941	4.992
G25	−4.927	35.193	−1.714	12.243	−3.797	27.121	3.562	25.443	5.937
G26	−4.737	47.177	0.062	0.617	−2.562	25.515	2.68	26.691	7.243
G27	−4.708	38.489	−0.670	5.477	−3.602	29.447	3.252	26.586	6.276
G28	−4.642	35.907	−0.248	1.918	−4.374	33.834	3.664	28.342	5.704
G29	−4.895	53.613	−1.344	8.101	−2.976	17.937	3.376	20.348	6.454
G30	−5.180	32.007	−1.126	6.957	−4.759	29.406	5.119	31.630	4.249
G31	−4.286	33.764	−1.515	11.935	−3.244	25.555	3.649	28.746	6.474
G32	−2.365	18.779	−0.713	5.661	−5.668	45.006	3.848	30.554	6.877
G33	−2.972	34.554	−0.391	4.546	−4.183	48.634	1.055	12.266	8.665
G34	−4.445	33.041	1.301	9.671	−3.979	29.577	3.728	27.711	6.252
G35	−2.522	28.760	0.35	3.991	−2.471	28.179	3.426	39.069	8.135
G36	−3.826	31.111	−0.207	1.683	−3.049	24.793	5.216	42.413	6.023
G37	−4.483	30.397	−1.128	7.648	−5.646	38.283	3.491	23.671	5.568
G38	−3.363	31.448	−1.579	14.765	−2.678	25.042	3.074	28.745	7.668
G39	−3.638	31.596	0.01	0.087	−3.223	27.992	4.643	40.325	6.332
G40	−3.184	30.344	−0.222	2.116	−3.172	30.230	3.915	37.311	7.021
G41	−4.438	38.950	−1.532	13.446	−2.992	26.259	2.432	21.345	7.34
G42	−4.259	42.031	0.476	4.727	−2.405	23.734	2.99	29.508	7.41
G43	−5.259	45.037	−0.375	3.211	−3.863	33.082	2.18	18.669	6.732
G44	−5.135	43.658	−0.017	0.145	−3.397	28.881	3.213	27.317	6.232
G45	−5.210	45.518	0.604	5.277	−2.835	24.768	2.797	24.436	6.888

FA= Factor analysis, RC= Relative contribution, MTSI= Multi-trait stability index

Genotypes in bold were selected as per lower MTSI value with 15% selection intensity that computed based on the genotype-ideotype distance considering the multiple variable



Supplementary Fig.1. A) Average environment coordination (AEC) view of the GGE-biplot based on environment-focused scaling, genotype focused singular value partitioning for the mean performance and stability of 45 sweet corn genotypes (blue text) and three environments (green text) during rabi 2020-21 and B) GGE biplot view of the discriminativeness and representativeness developed through environment focused centering and symmetrical method of singular value partitioning of 45 sweet corn genotypes (blue text) evaluated across three environments (green text) during rabi-2020-21