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AMMI Analysis for Genotype × Environment Interactions for Yield and Yield attributing traits in bread wheat (*Triticum aestivum*. L)

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ABSTRACT

Wheat production is affected by emerging problems like climate change, terminal heat stress, and over-utilization of resources. To obtain consistent yield, variety should be adaptable and stable in various production conditions. The ideal time of sowing of wheat is before 15 Nov in Indian sub contientent as delay in sowing will effect the yield because of terminal heat stress so to tackle this problem more adaptable and late sown varities should be identified so by the present study will able to identify which genotypes are highly adaptable in late sown condition. The experiment was carried out at B.A.U, Ranchi 2019-20 with three dates of sowing i.e. timely sowing (E1), late sowing (E2), very late sowing (E3) using twenty-eight genotypes including advanced breeding lines, local land races and released varieties, grown in RBD with two replications. The AMMI analysis of variance revealed that genotype, environment, and their interaction had a highly significant effect on the yield and yield-attributing traits. The Additive Main Effects and Multiplicative Interaction (AMMI) analysis of variance for grain yield per plant across the environments showed that 65.49 % of the total variation was attributed to genotypic effects, 11.07% to environmental effects and 23.42% to genotype-environment interaction effects. The genotypes which has stable yield in all the three environment timely, late and very late are DBW-273, UP-2981, RAJ-4529, HI-1621, DBW-252, WR-544, DBW-14, WH-1235, PBW-773. AMMI models revealed stable and high-yielding genotypes suitable for specific environments, thus DBW-136, DBW-14, DBW-252, WR-544 for Environment 1, DBW-273, UP-2981 for Environment 2, RAJ-4529, HI-1621 for Environment 3. Overall environment E1 followed by E2 and E3 were suitable for most of the traits. These genotypes could be utilized in breeding programs to improve grain yield in bread wheat and may be used as stable breeding material for commercial cultivation.

Keywords: *AMMI biplot analysis; grain yield; stability; G × E interaction; Yield;wheat*

1. Introduction

Wheat is a key staple food crop in many countries around the world, including India, where it plays a crucial role in both nutrition and food security. Moreover, it is an important industrial crop, as the grain, along with the stalk and chaff, is used as raw material in various industries and serves purposes such as mulch, construction material, and animal bedding. It has a strong nutritional profile, consisting of 12.1% protein, 1.8% lipids, 1.8% ash, 2.0% reducing sugars, 6.7% pentosans, 59.2% starch, and 70% total carbohydrates, offering 314 Kcal per 100 grams of food (31) . Wheat is grown mainly in two seasons in the world viz. winter and spring. Winter wheat is grown in cold countries like Europe, U.S.A., Australia, the Russian federation etc. While spring wheat is grown in Asia and apart of U.S.A. spring wheat matures in 120-130 days while winter wheat takes 240-300 days for maturity. Due to this reason productivity of winter wheat is higher in comparison to spring wheat . There are several challenges in wheat breeding, with droughts and high temperatures being the most significant factors that limit crop production globally (3) .

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Yield instability in wheat under heat and moisture stress can result from accelerated developmental phases, increased respiration (32) , reduced photosynthesis (33), and inhibited starch synthesis in developing kernels, all of which impact both grain setting and grain filling. Given the impending negative impacts of climate change on crop productivity, it is crucial to develop wheat genotypes with high resilience that can adapt to varying environmental conditions, ensuring higher productivity and more stable yields in the face of climate shifts.

To develop stable varieties, it's essential to have significant genetic diversity within the populations being studied. By analyzing these populations, genotypes that exhibit broad stability across various environmental conditions can be identified. This is achieved by understanding the interaction between genotype and environment. The presence of Genotype × Environment interaction in any genetical study simply leads to over estimation of genetical and statistical parameters. Thus, it vitiates the estimation of variance and co-variance and related statistics, heritability, selection differential, degree of dominance, genetic advance, and response to selection, variance components, divergence analysis and so forth. The phenotypic (P) value measured on a suitable scale is not equal to the genotypic value(G) when the genotype is grown in more than one environment(E) therefore, P= G + E + (G×E). Genotype × environment (G×E) interaction decreases the effectiveness of selection and the precision of varietal recommendations (5). Several statistical methods have been developed to identify

patterns of genotype × environment (G×E) interaction, typically categorized into two groups: parametric and non-parametric. Parametric methods are further divided into univariate and multivariate approaches. Univariate methods include the stability factor D. Lewis,1984. Univariate methods encompass the stability factor, a regression-based approach, while multivariate methods include the AMMI (Additive Main Effects and Multiplicative Interaction) model (8), and Genotypic Main Effect plus Genotype-by-Environment (GGE) biplot analysis (30), (34) proposed that the regression coefficient 'b' and the deviation from the regression coefficient 'S^2d' could be used to predict stable genotypes. A cultivar with b = 1 and S^2d = 0 is likely to be stable across a range of different environmental conditions (2) . Additionally, Additive Main Effects and Multiplicative Interaction (AMMI) analysis has proven to be a valuable method for examining both linear and non-linear genotype responses to environmental conditions (28) . This approach combines ANOVA (with additive parameters) and principal component analysis (with multiplicative parameters) (8) into a single analysis, helping to interpret multi-environment data in breeding programs. It is also a useful tool for graphically diagnosing genotype-environment interaction patterns. In this study, 28 wheat genotypes were evaluated for grain yield across different environments to identify stable genotypes for general and specific adaptation in different sowing conditions and to estimate genotype-environment interaction and stability parameters.

2. Material and Methods

2.1 Field Experimentation

The present experiment was conducted at of BAU experimental area Kanke, Ranchi during *rabi*-2019. Birsa Agricultural University (BAU), Kanke is located at an elevation of 634 meters above mean sea level with 85°18'48.3"East longitude and 23°25'47.3"North latitude. The experimental material for the present study comprised of twenty-eight wheat genotypes (Table 1) cultivars and along with four check varieties which are K-307, BG-3, DBW-14, WR-544 are used in this experiments.

Table 1: List of genotypes with codes

Code	Genotypes	Code	Genotypes
G1	WR-544	G15	MACS-6696
G2	DBW-114	G16	WH-1239
G3	HD-2932	G17	NI-5439
G4	DBW-110	G18	K-1317
G5	MP-1331	G19	RIL-5138
G6	NIAW-3170	G20	RW-5
G7	DBW-273	G21	PB-773
G8	HI-1628	G22	UP-2981
G9	HI-1621	G23	RAJ-4529
G10	HD-237	G24	M-516
G11	DBW-252	G25	LBP-2017-2
G12	PB-773	G26	RWP-2018-31
G13	DBW-233	G27	BG-3
G14	K-307	G28	WH-1235

2.2 Experimental design and field layout

These 28 wheat genotypes were sown during Rabi 2019 on three different date of sowing (Table 2) in Randomized Block Design (RBD) with two replications having a plot size of 0.6m x 4m. In E1(Timely sown), E2(Late sown), E3(Very late sown) and every sowing is done with a gap period of fifteen days.

Table 2: Description of environments

Environment	Date of sowing
1) Environment 1	27/11/2019
2) Environment 2	12/12/2019
3) Environment 3	27/12/2019

2.3 Statistical Analysis

The combined analysis of variance of yield data overall environments, using genotype-environment interaction data for stability analysis using the AMMI model and GGE biplot analysis was performed by R software.

AMMI MODEL

The data compared the performance of AMMI analysis with ANOVA approach and regression approach and found that ANOVA fails to detect a significant interaction component and regression approach accounts only a small portion of the interaction sum of squares only when the pattern fits a specific regression model (8). The AMMI model for T genotypes and S environment is given as

$$Y_{ij} = \mu + gi + ej + \sum_{n}^{n-1} \lambda_n \alpha_{in} y_{jn} + \theta_{ij}$$

$$\theta_{ij} \sim N(0,\sigma^2) ; i = 1,2...T; j=1,2,...,S$$

Where,

Y_{ij}= mean yield of the ith genotype in the jth environment

μ=general mean gi is the ith genotypic effect

e_j=jth location effect

λn=eigen value of the PCA axis n

α_{in} and γ_{jn}= i^{th} genotype j^{th} environment PCA scores for the PCA axis n

θ_{ij}= residual

n = number of PCA axes retained in the model

Ordinarily the number n is judged on the basis of empirical consideration of F-test of significance (Gauch 1988). The residual combines the PCA scores from the N-n' discarded axes, where N= min (G-1, E-1). The number of PCA axes to be retained is determined by testing the mean square of each axis with the estimate of residual through F-statistic (8). The mean sum of squares of each PCA axis is equal to the ratio of square of the corresponding eigen value and the degree of freedom of each axis obtained as G+E-1-2n.The member of AMMI family with 1 PCA axis (while relegating all higher axes to the residual) is denoted AMMI I, while AMMI II retains2 PCA axes and so on. In general, AMMI N denotes the AMMI model with IPCA axes 1 to N, AMMI 0 has no IPCA axes and is identically ANOVA. The full model with minimum (G-1, E-1) Interaction Principal Component Axis, is denoted by AMMI E. The equation, except that it deletes the residual and error and that it stipulates a specific AMMI model rather than the entire AMMI family.

The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as subcases when these are better for particular data sets (8). Secondly, AMMI clarifies the G x E interaction. AMMI summarizes patterns and relationships of genotypes and environments (Zobel et al. 1988). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increase the number of replicates by a factor of two to five (9). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments, or to improve efficiency in selecting the best genotypes.

The AMMI model combines the analysis of variance for the genotypes and environments main effects with principal components analysis of the genotype x environment interaction. It has proven useful for understanding complex G x E interaction.

The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments. AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters

Steps in Computation

Environment-wise analysis and pooled analysis of variance were conducted as per normal procedure. If genotypes, environments and G x E interaction are significant, the analysis may proceed further for AMMI analysis.

Table 3: Analysis of variance for stability-AMMI model

source	d.f	MSS	F
Total	(ger-1)		
treatment	(ge-1)		
genotypes	(g-1)	MS1	MS1/MS3
Environment	(e-1)	MS2	MS2/MS3
G x E	(g-1) (e-1)	MS3	MS3/MSE
IPCA1	(G+E-1-2n)	MS4	MS4/MSE
IPCA2	(G+E-1-2n)		
Residual			
Error	(r-1) (ge-1)	MSE	

If IPCA mean sum of square are significant and residual mean is non significant, the step may be conducted for development of biplot. The AMMI biplot is developed by placing both genotypes and environment mean value on X-axis and the respective IPCA axis eigen vector on Y axis.

Interpretation of biplots

In biplot displacements along the X-axis indicate differences in main (additive) effects, whereas displacement along the ordinate (Y-axis) indicate differences in interaction effects. For the points of different kinds, the AMMI model equation provides the expected yield value. The biplot has another important interpretation. The main effect for genotypes reflects breeding advances. Similarly the main effects of environment reflect overall comparison of environments.

From the values of mean and IPCA1, the genotypes are classified into four distinct class:

Class 1: Genotypes with high mean and positive IPCA1

Class 2: Genotypes with high mean and negative IPCA1

Class 3: Genotypes with low mean and negative IPCA1

Class 4: Genotypes with low mean and positive IPCA1

In AMMI II interaction biplot between IPAC1 and IPAC2, the environment scores are joined to the origin by site lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. The genotypes occurring close together on the plot will tend to have similar yield in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments.

Hence, the genotypes near origin are not sensitive to environmental interaction and those distant from origins are sensitive and have large interaction. Genotypes and environment that fall in same sectors interact positively in contrast; if they fall in opposite sectors interact negatively. If they fall into adjacent sectors, interaction is somewhat more complex.

3. Result and Discussion

3.1 Pooled analysis of variance as per AMMI model

The combined analysis of variance as per AMMI model Table-4.6 showed that mean sum of squares due to genotypes × environments interaction were highly significant ($P < 0.01$) for maximum characters evaluated under present investigation. Therefore considerable amount of variation was present among all the genotype as well as environments. AMMI analysis was performed only for yield and yield attributing traits. In Table:4 it has shows highly significant differences were observed for genotypes, environments and G × E interaction for different characters like 1000 seed weight, grain yield per plant, biological yield and harvest index at 1% and 5% levels of significance. For characters like no of grains per spike and no of effective tillers Significant difference was observed for Genotype and environment and for spike length Significant difference was observed for genotype only. The mean sum of squares attributed by genotypes were highest was highest for spike length (93.72%) followed by 1000 seed weight (91.39), grain yield per plant (65.49), no of effective tillers (65.09), no of grains per spike (37.85), harvest index (28.39) and biological yield (28.27). The mean sum of squares attributed by environment were highest were highest for no of grains per spike (51.47) followed by biological yield (49.65), harvest index (26.99), no of effective tillers (15.76), grain yield per plant (11.07), 1000 seed weight (5.09) and spike length (0.35). The highest mean sum of squares for G × E interaction was contributed by Harvest index (44.61) followed by grain yield per plant (23.47), biological yield (22.06), no of effective tillers (19.14), no of grains per spike (10.54), spike length (5.91) and 1000 seed weight (3.51). G × E interaction was partitioned among the two interaction principal component axis (IPCA). The IPCA1 and IPCA2 partitioned the interaction effect into different values for different traits like for grain yield per plant IPCA1 Score (78.88) and IPCA2 score (21.11), spike length IPCA1 Score (65.90) and IPCA2 score (34.09), 1000 seed weight IPCA1 Score (72.90) and IPCA2 score (27.09), no of effective tillers IPCA1 Score (78.44) and IPCA2 score (21.55), no of grains per spike IPCA1 Score (83.86) and IPCA2 score (16.13), biological yield IPCA1 Score (77.11) and IPCA2 score (22.88), harvest index IPCA1 Score (62.80) and IPCA2 score (37.19).

Table 4: AMMI analysis for yield and yield attributing traits in wheat (Triticum aestivum L.) across different environments (E_1, E_2 & E_3)

SOURCE	DF	Spike length(cm) MSS	% Explained	1000-seed Weight(g) MSS	% Explained	No. of grains/ spike	% Explained	No. of Effective tillers	% Explained
Genotypes	27	11.86**	93.72	164.09**	91.39	162.54**	37.98	5.00**	65.09
Environments	2	0.60	0.35	123.39**	5.09	1619.25**	51.47	16.37*	15.76
G×E Interaction	54	0.37	5.91	3.15*	3.51	16.64	10.54	0.73	19.14
IPCAI	28	0.47	65.90	4.43**	72.90	26.91**	83.86	1.11**	78.44
IPCAII	26	0.26	34.09	1.77	27.09	5.57	16.13	0.32	21.55
Residual	84	0.63	0	2.01	0	12.08	0	0.53	0

SOURCE	DF	Biological yield (g/plant) MSS	% Explained	Harvest Index (%) MSS	% Explained	Grain yield / plant(g) MSS	% Explained
Genotypes	27	26.66**	28.27	77.69**	28.39	8.77**	65.49
Environments	2	632.11**	49.65	997.13**	26.99	20.02**	11.07
G×E Interaction	54	10.40*	22.06	61.04**	44.61	1.59**	23.42
IPCAI	28	15.47**	77.11	73.94**	62.80	2.38**	78.88
IPCAII	26	4.94	22.88	47.16**	37.19	0.68	21.11
Residual	84	6.74	0	19.10	0	0.52	0

***= significant at 1%, *= significant at 5%*

3.2 AMMI biplot analysis

Spike length (cm)

AMMI1 biplot (IPCAI vs. Mean)

Genotypes HD-2932 (G3) had the highest positive IPCAI values and UP- 2981 (G22) had the highest negative IPCAI value, indicating the least stability of these genotypes for spike length. The genotypes NI- 5439 (G17), K- 1317 (G18), K-307 (G14), MACS-6696 (G15) , MP- 1331 (G5), LBP- 2017-2 (G25), HD-3237 (G10) and NIAW- 3170 (G6) scored near zero IPCA1 score. Out of which HD-2932 (G3) and BG- 3 (G27) had the highest spike length and DBW- 14 (G2) and PBW- 773 (G21) had the lowest spike length and were regarded as the most stable genotypes (Fig 1). A result similar to the present findings has also been reported earlier by (14), (21).

AMMI2 biplot (IPCAI vs. IPCAII)

AMMI2 biplot for spike length represented the IPCAI and IPCAII scores of the genotype and G × E interactions and explained 65.9% and 34.1% of the total variation. Environments E3 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 and E1 had the shortest spoke and did not exert strong interactive environmental forces. The best adapted genotypes with respect to the site Environment E1 were MP- 1331 (G5), RIL- 5138 (G19) and UP- 2981 (G22) whereas, genotypes K-307 (G14), LBP- 2017-2 (G25), NIAW-3170 (G6) and MACS-6696 (G15) were to environment E2. Genotypes WH-1235 (G28), BG- 3 (G27), HD-2932 (G3) and NI-5439 (G17) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were K-307 (G14), K- 1317 (G18), NI- 5439 (G17), HD-3237 (G10), LBP- 2017-2 (G25), NIAW- 3170 (G6) and MACS-6696 (G15) with higher spike length and Environment E2 was least interactive environment (Fig 2). A result similar to the present findings has also been reported earlier by (15), (26).

1000 seed weight (g)

AMMI1 biplot (IPCAI vs. Mean)

Genotypes BG- 3 (G27) had the highest positive IPCAI values and DBW- 273 (G7) had the highest negative IPCAI value, indicating the least stability of these genotypes for 1000 seed weight. The genotypes M- 516 (G24), WH-1235 (G28), WH- 1239 (G16), DBW -233 (G13), DBW -252 (G11), DBW -110 (G4) and HI- 1621 (G9) scored near zero IPCA1 score. Out of which DBW -110 (G4) had the highest 1000 seed weight and M- 516 (G24), WH-1235 (G28) had the lowest 1000 seed weight and were regarded as the most stable genotypes (Fig 3). A similar result also been reported by (27), (7).

AMMI2 biplot (IPCAI vs. IPCAII)

AMMI2 biplot for 1000 seed weight represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 72.9% and 27.1% of the total variation (Fig.8). Environments E1 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 followed by E3 had the shortest spoke and did not exert strong interactive environmental forces. The best-adapted genotypes with respect to the site Environment E1 were MP- 1331 (G5), K- 1317 (G18) and DBW- 14 (G2) whereas, genotypes DBW -110 (G4), RWP-2018-31 (G26) and DBW- 273 (G7) were to environment E2. Genotypes HI- 1621 (G9), HD-3237 (G10), DBW- 136 (G12), RIL-5138 (G19) and RW-5 (G20) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were M- 516 (G24), HI- 1621 (G9), WH-1235 (G28), WH- 1239 (G16) and RWP-2018-31 (G26) with higher 1000 seed weight and Environments E2 and E3 was least interactive environment (Fig 4). Same trend has also been observed by (28), (12).

Number of grains per spike

AMMI1 biplot (IPCAI vs. Mean)

Genotypes RW-5 (G20), NI-5439 (G17) and MP-1331 (G5) had the highest positive IPCAI values and MP- 1331 (G5) and DBW-273 (G7) had the highest negative IPCAI value, indicating the least stability of these genotypes for no of grains per pike. The genotypes RAJ- 4529 (G23), M- 516 (G24), DBW -252 (G11) and HD-3237 (G10) scored near zero IPCA1 score. Out of which HD-3237 (G10) had the highest no of grains per spike and RAJ- 4529 (G23), M- 516 (G24) had the lowest grains per spike and were regarded as the most stable genotypes (Fig 5). The findings are in confirmatory to that of (10), (4)

AMMI2 biplot (IPCAI vs. IPCII)

AMMI2 biplot for no of grains per spike represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 83.86% and 16.14% of the total variation. Environments E1 and E3 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 had the shortest spoke and did not exert strong interactive environmental forces. The best-adapted genotypes with respect to the site Environment E1 were NI- 5439 (G17) whereas, genotypes HD-3237 (G10) were to environment E2. Genotypes HI- 1621 (G9), DBW -252 (G11) and K-307 (G14) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were HD-3237 (G10), DBW -252 (G11), K-307 (G14), M- 516 (G24), RAJ- 4529 (G23) and LBP- 2017-2 (G25) with higher no of grains per spike and Environment E2 was least interactive environment (Fig 6). A result similar to the present findings has also been reported earlier by (19).

Number of effective tillers per plant

AMMI1 biplot (IPCAI vs. Mean)

Genotypes DBW- 273 (G7), DBW- 14 (G2) and MP- 1331 (G5) had the highest positive IPCAI values and PBW- 773 (G21) had the highest negative IPCAI value, indicating the least stability of these genotypes for no of effective tillers per plant.

The genotypes PBW- 773 (G21), RIL- 5138 (G19), MACS-6696 (G15), DBW -110 (G4) and DBW- 14 (G2) scored near zero IPCA1 score. Out of which DBW- 14 (G2) and DBW -110 (G4) had the highest no of effective tillers per plant and PBW- 773 (G21), RAJ- 4529 (G23) had the lowest no of effective tillers per plant and were regarded as the most stable genotypes (Fig 7). The findings are confirmatory to that of (22), (6)

AMMI2 biplot (IPCAI vs. IPCII)

AMMI2 biplot for no of effective tillers per plant represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 78.45% and 21.55% of the total variation (Fig.16). Environments E1 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 and E3 had the shortest spoke and did not exert strong interactive environmental forces. The best adapted genotypes concerning the site Environment E1 were K-307 (G14), RAJ- 4529 (G23) and HI-1628 (G8) whereas, genotypes LBP- 2017-2 (G25) were to environment E2. Genotypes M- 516 (G24), WH-1235 (G28), DBW- 14 (G2) and PBW- 773 (G21) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were RIL- 5138 (G19), MACS-6696 (G15), DBW -110 (G4), PBW- 773 (G21), DBW- 14 (G2) and WH-1235 (G28) with higher no of effective tillers per plant and Environment E3 was least interactive environment (Fig 8). Similar results was observed by (12), (15).

Biological yield (g/plant)

AMMI1 biplot (IPCAI vs. Mean)

Genotypes HD-3237 (G10) and WH- 1239 (G16) had the highest positive IPCAI values and DBW- 273 (G7) and WH-1235 (G28) had the highest negative IPCAI value, indicating the least stability of these genotypes for biological yield. The genotypes UP- 2981 (G22), RIL- 5138 (G19), HI- 1621 (G9), K-307 (G14), HI-1628 (G8) and BG- 3 (G27) scored near zero IPCA1 score. Out of which HI-1628 (G8) and BG- 3 (G27) had the highest biological yield and UP- 2981 (G22) and RIL- 5138 (G19) had the lower biological yield and were regarded as the most stable genotypes (Fig 9).

AMMI2 biplot (IPCAI vs. IPCII)

AMMI2 biplot for biological yield represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 77.12% and 22.82% of the total variation (Fig.22). Environments E1 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 and E3 had the shortest spoke and did not exert strong interactive environmental forces. The best-adapted genotypes with respect to the site Environment E1 were DBW -252 (G11) and NI- 5439 (G17) whereas, genotypes RIL- 5138 (G19) and DBW- 136 (G12) were to environment E2. Genotypes M- 516 (G24), DBW -110 (G4) and PBW- 773 (G21) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were RIL- 5138 (G19), HI- 1621 (G9), BG- 3 (G27), HI-1628 (G8) and UP- 2981 (G22) with higher biological yield and Environment E2 and E3 was least interactive environment (Fig 10) Similar results was also observed by (1), (23).

Harvest index (%)

AMMI1 biplot (IPCAI vs. Mean)

Genotypes HD-2932 (G3) and NIAW- 3170 (G6) had the highest positive IPCAI values and RW-5 (G20) and DBW -110 (G4) had the highest negative IPCAI value, indicating the least stability of these genotypes for harvest index.

The genotypes PBW- 773 (G21), RAJ- 4529 (G23), DBW- 136 (G12), HD-2932 (G3), DBW- 14 (G2) and K- 1317 (G18) scored near zero IPCA1 score. Out of which K- 1317 (G18) and DBW- 14 (G2) had the highest harvest index and PBW- 773 (G21) and RAJ-4529 (G23) had the lower harvest index and were regarded as the most stable genotypes (Fig 11) The same trend has also been observed by (17), (12).

AMMI2 biplot (IPCAI vs. IPCII)

AMMI2 biplot for harvest index represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 62.8% and 37.2% of the total variation (Fig.24). Environments E3 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 and E1 had the shortest spoke and did not exert strong interactive environmental forces. . The best-adapted genotypes with respect to the site Environment E1 were RW-5 (G20), HI-1628 (G8), and BG- 3 (G27) whereas, genotypes PBW- 773 (G21) and DBW- 14 (G2) were to environment E2. Genotypes NI- 5439 (G17) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were PBW- 773 (G21), DBW- 14 (G2), HD-2932 (G3), K- 1317 (G18), DBW- 136 (G12) and RAJ-4529 (G23) with higher harvest index and Environment E2 was least interactive environment (Fig 12) The same trend has also been observed by (4), (31).

Grain yield per plant (g)

AMMI1 biplot (IPCAI vs. Mean)

Genotypes LBP- 2017-2 (G25) and M- 516 (G24) had the highest positive IPCAI values and K-1317(G18) and WR-544 (G1) had the highest negative IPCAI value, indicating the least stability of these genotypes for grain yield. The genotypes DBW- 136 (G12) and HI- 1621 (G9) scored near zero IPCA1 score. Out of which HI- 1621 (G9) had the highest grain yield per plant and DBW-136 (G12) had the lower grain yield per plant and were regarded as the most stable genotypes (Fig 13). A result similar to the present findings has also been reported earlier by (26), and (16).

AMMI1 biplot (IPCAI vs. Mean)

AMMI2 biplot grain yield per plant represented the IPCAI and IPCAII scores of the genotype and G×E interactions and explained 78.8% and 21.12% of the total variation (Fig.26). Environments E1 had the longest spokes and exerted strong G × E interaction. In contrast, Environment E2 and E3 had the shortest spoke and did not exert strong interactive environmental forces. The best-adapted genotypes with respect to the site Environment E1 were DBW- 136 (G12), DBW- 14 (G2), DBW -252 (G11), and WR-544 (G1) whereas, genotypes DBW-273 (G7) and UP- 2981 (G22) were to environment E2. Genotypes RAJ- 4529 (G23) and HI- 1621 (G9) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were DBW -252 (G11), WR-544 (G1), DBW- 14 (G2), WH-1235 (G28) and PBW- 773 (G21) with higher grain yield per plant and Environment E2 and E3 was least interactive environment (Fig 14). Similar results was observed by (26), (15).

Conclusion

This study indicated that genotype, environment, and their interaction have a significant effect on the yield stability as per the AMMI model the best-adapted genotypes with respect to the site Environment E1 were DBW- 136 (G12), DBW- 14 (G2), DBW -252 (G11) and WR-544 (G1) whereas, genotypes DBW- 273

(G7) and UP- 2981 (G22) were to environment E2. Genotypes RAJ- 4529 (G23) and HI- 1621 (G9) were well adapted in E3. In conclusion, it was found that stable genotypes for this trait were DBW -252 (G11), WR-544 (G1), DBW- 14 (G2), WH-1235 (G28) and PBW- 773 (G21) with higher grain yield per plant and Environment E2 and E3 was the least interactive environment. All in all, these genotypes can be used as high-yielding lines, which are stable too, and for farmers, DBW -252 (G11), WR-544 (G1), DBW- 14 (G2), WH-1235 (G28) and PBW- 773 (G21) can be used for high yield with adaptability in a timely sown irrigated environment, whereas genotypes RAJ- 4529 (G23) and HI- 1621 (G9) were adapted to late-sown rainfed environment. These genotypes need to be further tested in heat- and drought-stressed environments to ensure their performance over the years.

Future Scope of Study

AMMI analysis revealed about the stability of genotypes according to the environment specifically which will be helpful for varietal recommendation according to the environment and sowing times without loss of yield. As the world is facing climate change problem so we need more adaptable genotypes which is highly adaptable to different environment. Genotypes which were identified superior for grain yield and other desirable traits can be further utilized in crop improvement.

Compliance with Ethical Standards

Conlict of interest: The authors declare that they have no conlict of interest.

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AMMI biplot display for yield and yield contributing traits of wheat (Triticum aestivum L.) genotypes for environments (E_1, E2 & E_3) Spike length (cm)

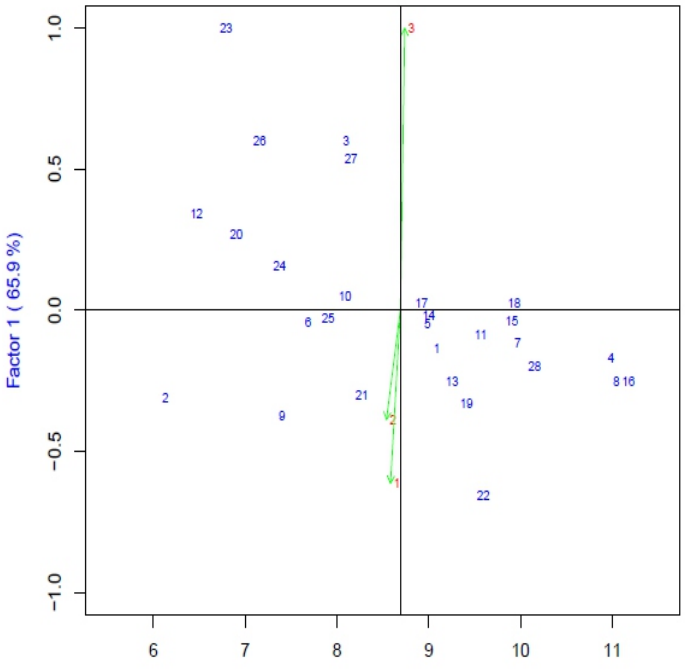

Fig- 1: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for spike length in three environments

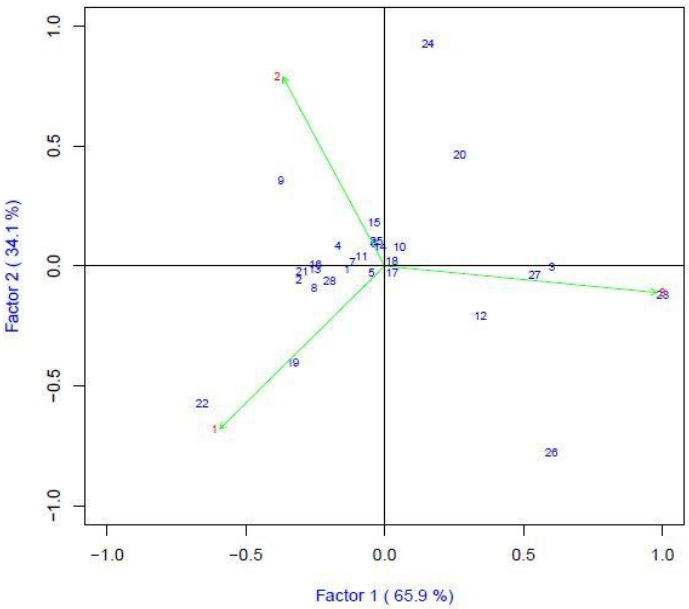

Fig- 2: AMMI2 biplot display (IPCAI vs. IPCAII) of wheat genotypes for spike length in three environments.

1000 seed weight (g/plant)

AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat

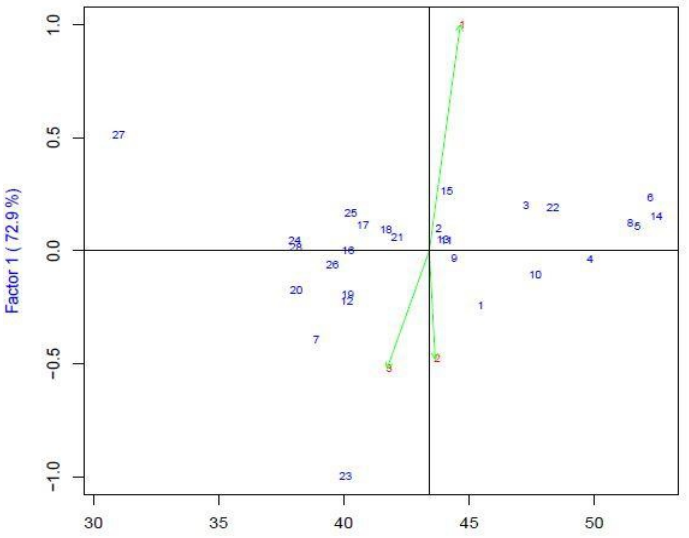

Fig- 3: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for 1000 seed weight in three environments

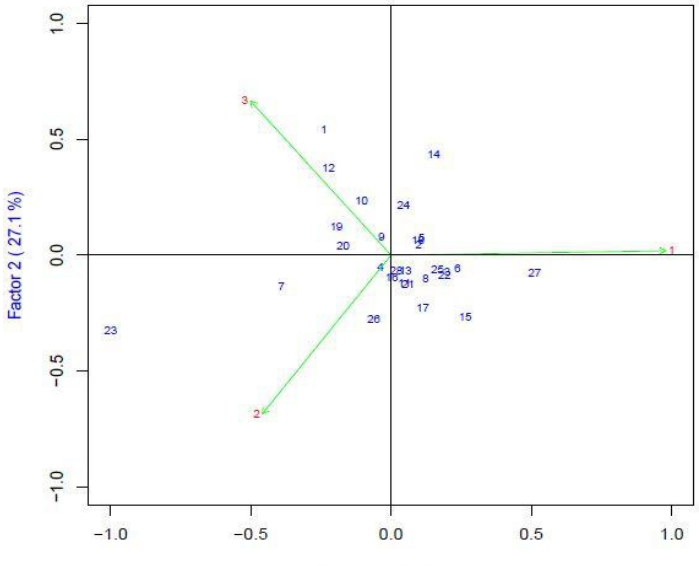

Fig- 4: AMMI2 biplot display (IPCAI vs. IPCAII) of wheat genotypes for 1000 seed weight in three environments.

No grains per spike

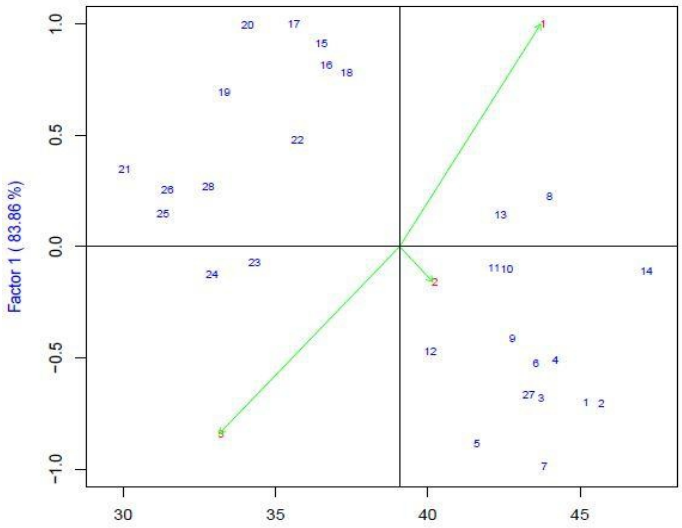

Fig- 5: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for No of grains per spike in three environments

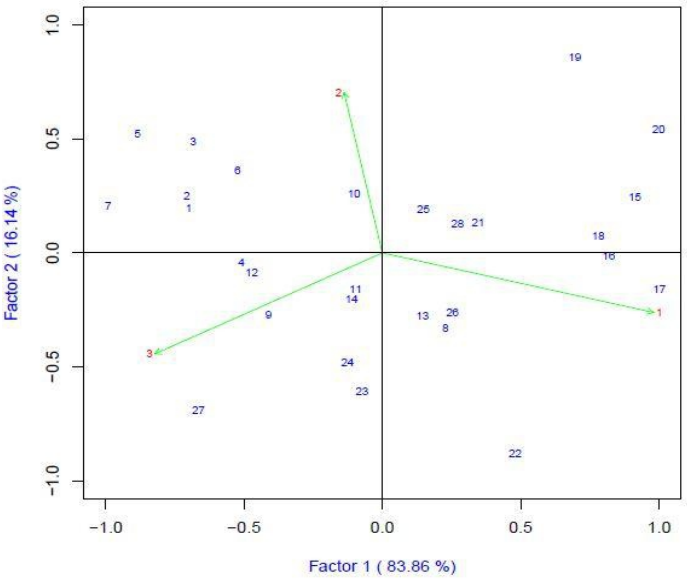

Fig- 6: AMMI1 biplot display (IPCAI vs. IPCAII) of wheat genotypes for No of grains per spike in three environments

No effective tillers per plant

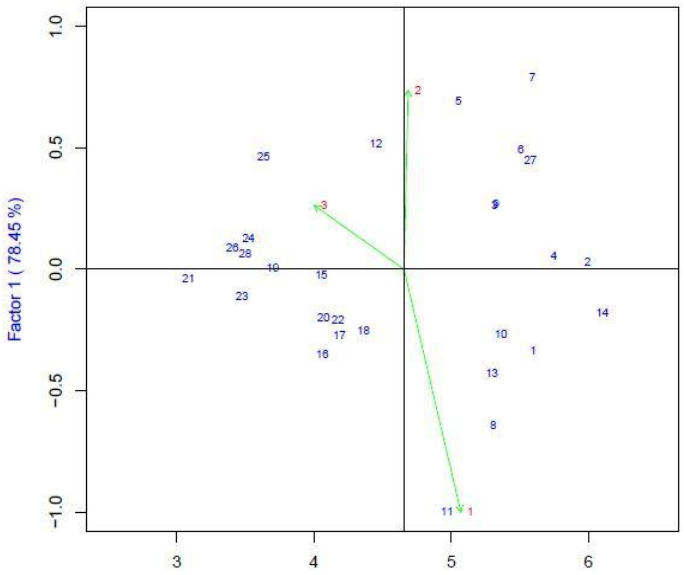

Fig- 7: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for No of effective tillers per plant in three environments

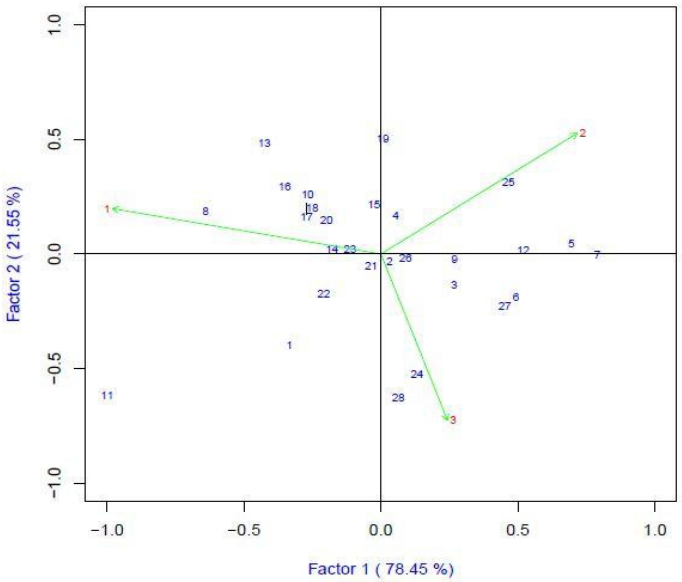

Fig- 8: AMMI1 biplot display (IPCAI vs. IPCAII) of wheat genotypes for No of effective tillers per plant in three environments

Biological yield

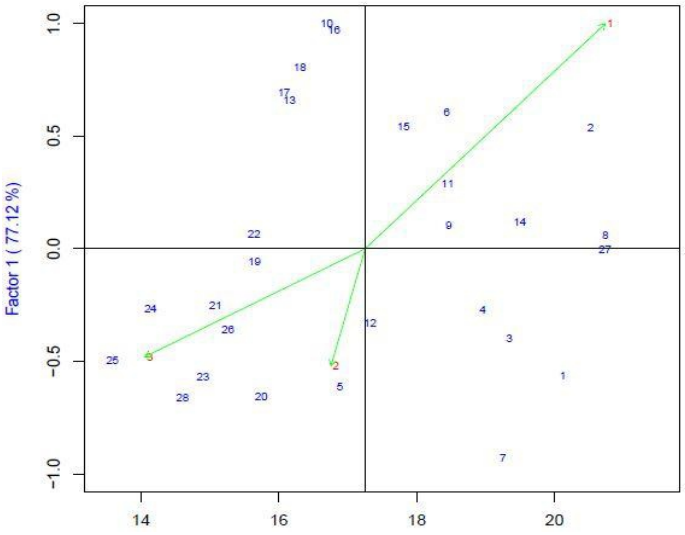

Fig- 9: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for Biological yield in three environments

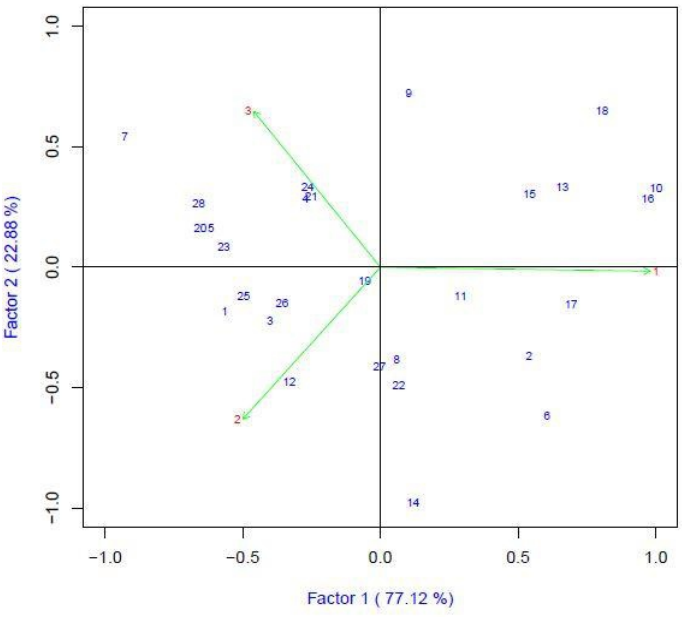

Fig- 10: AMMI1 biplot display (IPCAI vs. IPCAII) of wheat genotypes for Biological yield in three environments

Harvest index (%)

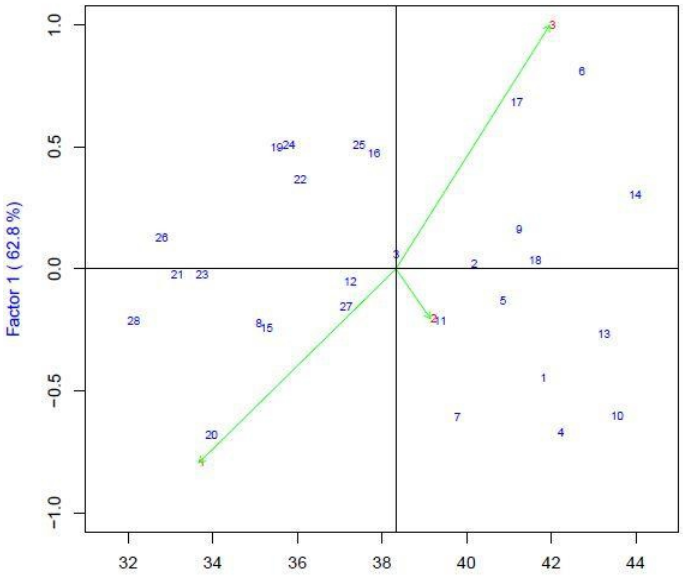

Fig- 11: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for Harvest index in three environments

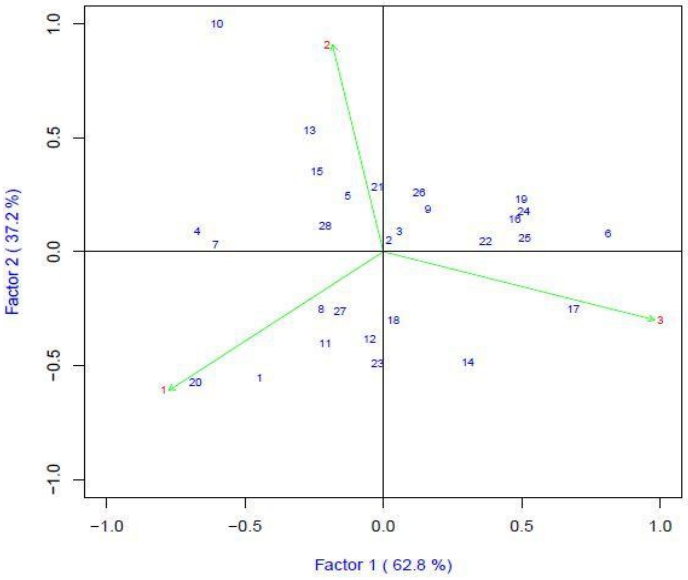

Fig- 12 AMMI1 biplot display (IPCAI vs. IPCAII) of wheat genotypes for Harvest index in three environments

Grain yield per plant

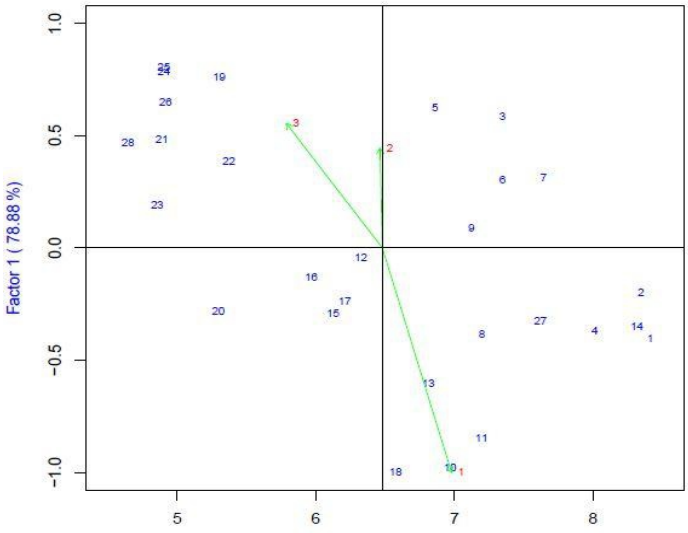

Fig- 13: AMMI1 biplot display (mean/main effects vs. IPCAI) of wheat genotypes for grain yield per plant in three environments

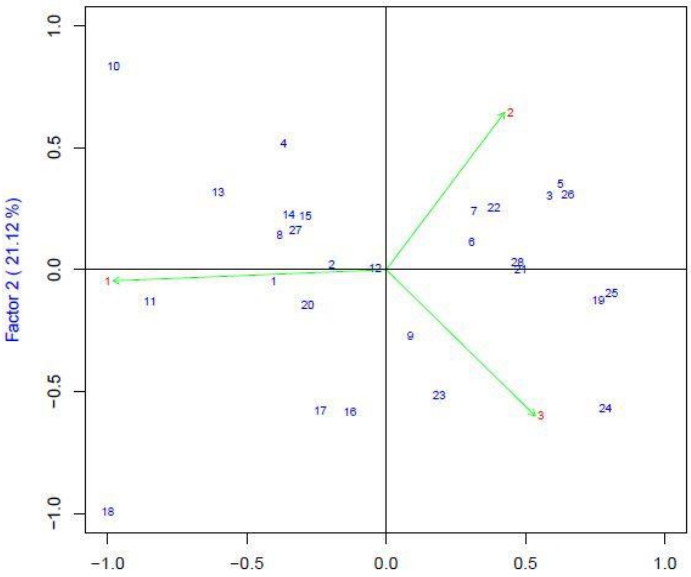

Fig- 14: AMMI1 biplot display (IPCAI vs. IPCAII) of wheat genotypes for grain yield per plant in three environments

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