



# Article Genotype by Environment Interaction Analysis for Grain Yield of Wheat (*Triticum aestivum* (L.) em.Thell) Genotypes

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Abstract: Genotype environment interaction and stability performance were investigated on grain yield per plot in eight environments during Rabi (here, rabi means that a crop has been grown in Rabi season: crops that are sown in winter and harvested in spring in the Indian subcontinent) 2019–2020 and 2020–2021 using 100 diverse wheat genotypes. Research was conducted at Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana in India. The analysis of variance revealed that genotype, environment and their interaction had a highly significant effect on the yield as reflected in Eberhart and Russel model and The Eberhart and Russell model indicated the suitability of the genotypes WH 1142, PBW 661, PBW 475 and DBW 17 with high mean, bi > 1 and non-significant deviation from regression to favorable environment, whereas the genotypes UP 2660 and DBW 88 with high mean, bi < 1 and non-significant deviation from regression were found suitable for poor environment. The Additive Main Effects and Multipicative Interaction (AMMI) analysis of variance for grain yield per plot across the environments showed that 26.41% of the total variation was attributed to genotypic effects, 70.22% to environmental effects and 3.37% to genotype  $\times$  environment interaction effects. AMMI biplot study indicated the genotypes PBW 750, DPW 621-50, WH 542, PBW 486, PBW 661 and WH 1192 stable across the environments as they did not exert strong interactive forces; hence, they were selected as potential candidates for possible release in the study areas. Furthermore, the which-won-where model indicated the adaptation of genotypes PBW 706, PBW 769, DBW 116, WH 1157, WH 789 and WH1186 to first mega-environment and genotypes DBW 16, WH 1152, WH 1105 and PBW 503 in the second. 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; Eberhart and Russel model; GGE biplot; grain yield; stability; wheat

## 1. Introduction

Wheat is a staple food crop of many countries across the globe, including India, which plays an important role in nutritional as well as food security. Additionally, it is an industrial crop because the grain, along with stalk and chaff, serves as industrial raw materials, which are also used as mulch, construction material and animal bedding. It contains good nutrition profile with 12.1% protein, 1.8% lipids, 1.8% ash, 2.0% reducing sugars, 6.7% pentosans, 59.2% starch and 70% total carbohydrates and provides 314 Kcal/100 g of food [1]. In India, wheat was cultivated over 31.45 million hectares with a record production of



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**Copyright:** © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). 107.6 million tons during 2019–2020 [2]. It can be grown not only in tropical and subtropical zones but also in temperate zone and the cold tracts of the far north, even beyond the 600 North, Central Zone and Peninsular Zone due to its versatile genotype, which has wide adaptation to diverse agro-ecological conditions. There are many constraints in the breeding of wheat. Among them, droughts and high temperatures are the most important limiting factors for crop production in the world [3]. Yield instability in wheat under heat and moisture stress can be caused by accelerated phasic development, increase in respiration [4], reduction in photosynthesis [5] and inhibition of starch synthesis in developing kernels, which affects both grain setting and grain filling. With looming negative climate change impacts on crop productivity, there is a need to develop high buffering wheat genotypes that adapt to diverse environmental conditions—more productive and with more stable yield in changing climate conditions.

For the development of stable varieties, there must be a presence of large genetic diversity in the populations under study. From these populations, one can identify genotypes showing wide stability under different environmental conditions. This is performed by understanding the interaction of genotype with the environment [6]. Genotype  $\times$  Environment Interaction (GEI) is a phenomenon related to the inconsistent performance under diverse environmental conditions, and it plays an important role in the performance of genotypes under different environments [7].  $G \times E$  interaction reduces the efficiency of selection and accuracy of varietal recommendation [8]. Due to this interaction of the genotype  $\times$  environment, it is necessary to study the genotype in the environment interaction before introducing new high-yielding genotypes with high stability in different environments. To reveal patterns of  $G \times E$  Interaction, several statistical methods have been developed, which are usually divided into two groups, parametric and non-parametric. The parametric methods themselves are divided into two groups: univariate and multivariate. Univariate methods include stability factor [9], a regression-based approach [10–13], whereas multivariate methods include the AMMI (Additive Main Effects and Multipicative Interaction) model [14] and Genotypic Main Effect plus Geotype by environment (GGE) biplot analysis [15]. Eberhart and Russell (1966) suggested that regression coefficient 'b' and deviation from regression coefficient 'S<sup>2</sup>d' might predict stable genotype. A cultivar with b = 1 and  $S^2d = 0$  might be stable across divergent environmental conditions [16]. In addition, additive main effects and multiplicative interaction (AMMI) analysis has been proved as a useful analytic approach for linear and non-linear response of genotypes over the environmental conditions [17], which combines ANOVA (with additive parameters) and principal component analysis (with multiplicative parameters) into a single analysis [18] and interprets multi-environment data structure in breeding programs [19]. It is also an effective tool to diagnose genotype environment interaction patterns graphically [20]. Furthermore, the GGE (genotype plus genotype by environment interaction) biplot procedure is an effective tool based on principal component analysis (PCA) to fully explore multi-environment trials (METs) by partitioning G + GE into principal components through singular value decomposition of environmentally centered yield data [21]. So, for the breeders to develop a variety suitable for different environments, the analysis of the stability of genotypes is the most important tool. In this study, 100 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  $\times$  environment interaction and stability parameters.

#### 2. Material and Methods

#### 2.1. Field Experimentation

The field experiment was conducted in four environments viz. irrigated, rainfed, timely sown and terminal heat stress during two consecutive years of Rabi (here, Rabi means a crop that has been grown in the Rabi season: crops that are sown in winter and harvested in spring in the Indian subcontinent) 2019–2020 and 2020–2021 at Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India. The field, in timely

sowing conditions, was sown in the third week of November (18 November) to provide normal temperature to wheat crop in the reproductive and ripening stage. In the field of terminal heat stress, sowing was delayed by a month (4th week of December; 22 December) to provide higher temperature to wheat crop in the reproductive and ripening stage, which causes heat stress. Table 1 represents codes used for different production environments.

	Timely Sown (18 November)		Late Sown (22 December)	
	Irrigated	Rainfed	Irrigated	Rainfed
2019–2020	E1	E2	E3	E4
2020-2021	E5	E6	E7	E8

Table 1. Codes used for production environments during 2019–2020 and 2020–2021.

#### 2.2. Plant Materials

The research was conducted with 100 wheat genotypes (Table 2) at research area, Wheat and Barley section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar, India. The 100 wheat genotypes included in the experiment were chosen on the basis of previous yield data, and the samples include both old cultivars that were previously widely cultivated and newly bred genotypes having great importance for today's wheat production.

Table 2. List of 100 bread wheat genotypes used in the present study.

Serial No.	Name of Genotype	Serial No.	Name of Genotype	Serial No.	Name of Genotype	Serial No.	Name of Genotype
1	WH1182	26	PBW693	51	WH1184	76	WH789
2	PBW725	27	WH1188	52	WH1021	77	PBW750
3	WH1061	28	WH714	53	PBW503	78	DPW621-50
4	PBW729	29	PBW698	54	WH1158	79	WH542
5	PBW560	30	WH1062	55	WH1164	80	PBW486
6	PBW728	31	WH1105	56	WH1129	81	WH147
7	PBW721	32	DBW88	57	UP2902	82	WH1120
8	WH1139	33	PBW527	58	WH1166	83	PBW769
9	UP2565	34	PBW676	59	WH711	84	PB934
10	DBW136	35	WH283	60	WH1181	85	WH1192
11	WH1025	36	WH1138	61	DBW90	86	HD3086
12	WH1152	37	WH1153	62	WH1140	87	PBW163
13	PBW752	38	WH1175	63	WH1132	88	PBW712
14	PBW475	39	WH1235	64	PBW158	89	DBW129
15	PBW621	40	DBW233	65	PBW502	90	WH1124
16	PBW730	41	PBW528	66	UP2338	91	WH1264
17	WH1136	42	PBW88	67	DBW17	92	PBW762
18	WH730	43	PBW706	68	PBW123	93	WH1142
19	PBW343	44	WH1063	69	UP2906	94	WH1186
20	DBW116	45	WH1157	70	PBW681	95	DBW95
21	HD2967	46	PBW550	71	PBW677	96	PBW540
22	WH1151	47	UP2473	72	PBW763	97	PBW542
23	UP2660	48	UP2865	73	WH1123	98	PBW661
24	PBW695	49	PBW726	74	WH1080	99	WH1131
25	PBW709	50	C306	75	DBW16	100	PB533

#### 2.3. Experimental Design and Layout

The experiment was laid out in a Randomized Block Design (RBD) with 3 rows of 2 m length each, in two replications. A row to row distance of 20 cm was maintained for both dates of sowing. The observations were recorded on five randomly selected competitive plants from each genotype in each replication.

#### 2.4. Statistical Analysis

The combined analysis of variance of yield data over all environments, using genotype– environment interaction data for stability analysis using the Eberhart and Russell model (Tables 3 and 4), AMMI model and GGE biplot analysis was performed with the help of INDOSTAT 8.1, Hyderabad, India and PB tools developed at IRRI, Philippines.

**Table 3.** Data collected from separate trials were analyzed as combined over the environments using the following ANOVA outline:.

Source	Df	MSS	F
Total	(ger-1)		
Treatment	(ge-1)		
Genotypes	(g-1)	MS1	MS1/MS3
Environment	(e-1)	MS2	MS2/MS3
Genotype Environment	(g-1)(e-1)	MS3	MS3/Mse
IPCA1	(G + E-1-2n)	MS4	MS4/Mse
IPCA2	(G + E-1-2n)		
Residual			
Blocks	(r-1)		
Error	(r-1)(ge-1)	Mse	

Here, Df = degree of freedom; MSS = mean sum of squares; g = genotypes; e = environment; ge = genotype by environment, Mse = mean squared error; r = replication.

Table 4. Analysis of variance for stability based on Eberhart and Russell model.

Source of Variation	Df	MS	F Value
Genotype (G)	(g-1)	MS1	MS1/MS3
Environment (E)	(n-1)	MS2	MS2/MS3
G  imes E	(g-1) (n-1)		
Environment (linear)	1		
Genotype × Environment (linear)	(g-1)	MS3	MS3/MS4
Pooled Deviation	g (n-2)		
Genotype 1	(n-2)		
Genotype 2	(n-2)		
Pooled error	n(g-1)(r-1)	MS4	
Total	(ng-1)		

The AMMI model equation is:

$$Y_{ij} = \mu + g_i + e_j + \Sigma \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

where

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

 $\mu = general mean$ 

gi = ith genotypic effect

ej = jth location effect

 $\lambda_n$  = eigen value of the Principal Component Axis n

 $\alpha_{in}\gamma_{jn}$  = ith genotype, jth environment Principle component analysis (PCA) scores for the PCA axis

 $\theta_{ij} = residual$ 

n = number of PCA axes retained in the model.

The equation for Eberhart and Russell model is:

$$Y_{ij} = \mu_i + \beta_i I_j + S_{ij}$$

where

 $Y_{ii}$  = Mean of the ith variety at the jth environment

 $\mu_i$  = Mean of ith variety over all environments

 $\beta_i$  = The regression coefficient that measures the response of ith variety to varying environments

 $S_{ii}$  = The deviation from regression of the ith variety at the jth environment

 $I_j$  = The environmental index obtained by subtracting the grand mean from the mean of all varieties at the jth environment

Simultaneous study of the genotype plus genotype–environment interaction was performed using GGE biplot, where GGE biplot used principal component consisting of a set of elite lines scores multiplied by environment scores, which gives a two-dimensional biplot.

#### 3. Results

#### 3.1. Eberhart and Russell Model

The genotype–environment interaction component (GEI) was elaborated by using the joint regression model of stability analysis [11]. The mean grain yield per plot among the genotypes ranged from 394.30 to 841.60, with an overall population mean of 576.27. PBW 729 gave the maximum grain yield per plant (841.6), whereas minimum grain yield per plot was observed in DBW 90 (394.3) (Table 5). Considering Eberhart and Russell's model of analysis, significant differences were revealed by a pooled analysis of variance for both the main effects, genotypes and environments, as well as for interaction effects (Table 6). No genotype had  $b_i = 1$  and  $S^2 di = 0$ ; however, some genotypes, HD 3086, DBW 16, PBW 527, PBW 528, PBW 502 and PBW 503, had bi values near to one, showing that most of these genotypes almost produced similar grain yield per plot under all the environments (Table 5). Genotypes WH 1142 ( $\mu$  = 622, bi = 1.158\*\*, S<sup>2</sup>di = -1135.98), PBW 661 ( $\mu$  = 609.50, bi =  $1.13^{**}$ ,  $S^2$ di = -1299.38), PBW 475 ( $\mu = 810.80$ , bi =  $1.11^*$ ,  $S^2$ di = -1056.61) and DBW 17 ( $\mu = 606.70$ , bi = 1.10<sup>\*</sup>, S<sup>2</sup>di = -1431.94) were observed to be stable in a rich (E5) environment (Table 5), whereas for genotypes UP 2660 ( $\mu$  = 594.10, bi = 0.99\*\*, S<sup>2</sup>di = 341.71) and DBW 88 ( $\mu$  = 664.10, bi = 0.97\*, S<sup>2</sup>di = 44.95), high means with lower b<sub>i</sub> values were detected. The lower values of b<sub>i</sub> indicate that these genotypes show more resistance to the unfavorable (E4) environment. The performance was unpredictable for the genotypes WH 1182, PBW 677, WH 1061, PBW 729, PBW 560, PBW 728 and PBW 721, as these genotypes had significant deviations from regression.

**Table 5.** Stability parameters as per Eberhart and Russell, 1966 model for grain yield per plot of 100 wheat genotypes tested across the environments.

S. No	Genotypes		Grain Yield per Pl	ot
		Mean	b <sub>i</sub>	S2di
1	C 306	521.30	0.788	-1431.7637
2	HD 2967	668.40	0.968	700.1297
3	HD 3086	591.10	1.002	-1423.8511
4	DBW 16	562.30	1.008	-1431.7638

S. No	Genotypes		Grain Yield per Pl	ot
		Mean	b <sub>i</sub>	S2di
5	DBW 17	606.70	1.108 **	-1431.9366
6	DBW 88	664.10	0.965 **	44.9539
7	DBW 90	394.30	0.897	155.1777
8	DBW 95	415.10	0.990	-265.7533
9	DBW 116	551.80	1.008	703.1385
10	DBW 129	538.50	0.977	-1378.6330
11	DBW 136	776.30	0.965	-245.7541
12	DBW 233	655.10	0.945	44.9539
13	DPW 621-50	688.50	1.002	-1423.8439
14	PB 533	482.10	1.109 *	-1208.4167
15	PB 934	498.50	1.002	-1423.8433
16	PBW 88	511.60	0.965	44.9544
17	PBW 123	543.20	0.957	-1207.4127
18	PBW 158	622.30	1.008	-1431.7640
19	PBW 163	545.00	1.002	-1423.8487
20	PBW 343	396.50	0.767 *	-472.6532
21	PBW 475	810.80	1.105 **	1056.6122
22	PBW 486	595.90	1.002	-1423.8325
23	PBW 502	599.60	1.007	-1432.1440
24	PBW 503	528.70	1.008	-1431.8938
25	PBW 527	656.50	0.965	54.0440
26	PBW 528	691.80	0.966	36.5229
27	PBW 540	454.00	1.039	-858.3855
28	PBW 542	569.50	1.130 **	-1299.3752
29	PBW 550	396.20	0.924	-411.0996
30	PBW 560	482.40	1.092	7855.5913 ***
31	PBW 621	408.10	0.823	659.4150
32	PBW 661	609.50	1.130 **	-1299.3753
33	PBW 676	616.10	0.965	44.9540
34	PBW 677	550.70	1.008	-1431.9195
35	PBW 681	614.60	1.008	-1432.0705
36	PBW 693	659.60	0.965	44.9539
37	PBW 695	710.70	0.935	40.9461
38	PBW 698	589.60	0.932	44.9541
39	PBW 706	398.80	0.806 *	-706.5090
40	PBW 709	702.70	0.965	41.7894
41	PBW 712	562.50	1.002	-1423.8435
42	PBW 721	582.10	1.104	8679.9017 ***
43	PBW 725	517.40	1.061	7269.3556 ***
44	PBW 726	704.90	0.986	-1093.2270

Table 5. Cont.

S. No	Genotypes		Grain Yield per Pl	ot
		Mean	b <sub>i</sub>	S2di
45	PBW 728	491.60	1.104	8679.9020 ***
46	PBW 729	841.60	1.104	8679.9007 ***
47	PBW 730	512.10	1.101	484.4683
48	PBW 750	735.10	1.060	2215.0743 *
49	PBW 752	708.50	1.002	-1423.8440
50	PBW 762	560.90	0.875	198.7622
51	PBW 763	601.60	0.978	-1372.5130
52	PBW 769	549.10	1.002	-1423.8500
53	UP 2338	669.40	1.008	-1431.4475
54	UP 2473	534.60	0.965	44.9543
55	UP 2565	708.80	0.965	-245.7539
56	UP 2660	594.10	0.987 **	341.7076
57	UP 2865	528.20	0.965	42.4225
58	UP 2902	588.30	1.008	-1431.7639
59	UP 2906	524.60	1.008	-1432.0702
60	WH 147	522.90	1.002	-1423.8077
61	WH 283	689.60	0.965	44.9538
62	WH 542	636.50	1.002	-1423.8437
63	WH 711	475.20	1.008	-1431.9700
64	WH 714	542.20	0.965	43.0552
65	WH 730	661.10	1.101	484.4678
66	WH 789	503.90	1.005	-1431.1050
67	WH 1021	582.20	1.008	-1432.0206
68	WH 1025	644.20	1.012	-695.7495
69	WH 1061	478.80	1.053	6991.1393 ***
70	WH 1062	572.10	0.965	44.9542
71	WH 1063	432.80	0.623 *	1789.4185 *
72	WH 1080	556.40	1.008	-1431.4750
73	WH 1105	567.50	0.965	50.8702
74	WH 1120	530.00	1.002	-1423.8434
75	WH 1123	545.80	1.008	-1431.7638
76	WH 1124	751.20	1.047	-1279.7099
77	WH 1129	571.10	1.007	-1432.2321
78	WH 1131	509.00	1.130 **	-1299.5106
79	WH 1132	618.30	1.008	-1431.7640
80	WH 1136	498.60	1.101	484.4683
81	WH 1138	532.70	0.966	338.6289
82	WH 1139	535.90	1.035	388.8467
83	WH 1140	568.10	1.007	-1432.1681
84	WH 1142	622.00	1.158 **	-1135.9830

Table 5. Cont.

S. No	Genotypes		Grain Yield per Pl	ot
		Mean	b <sub>i</sub>	S2di
85	WH 1151	772.40	1.008	700.1294
86	WH 1152	651.50	1.060	2199.6990 *
87	WH 1153	674.60	0.965	44.9539
88	WH 1157	409.60	0.965	44.9547
89	WH 1158	471.80	0.983	-1389.8129
90	WH 1164	467.50	0.997	-1405.2532
91	WH 1166	545.40	1.008	-1431.3627
92	WH 1175	589.60	0.965	44.9541
93	WH 1181	697.30	1.008	-1431.7643
94	WH 1182	791.60	1.104	8679.9009 ***
95	WH 1184	507.30	1.008	-1431.7637
96	WH 1186	459.20	1.028	-746.4416
97	WH 1188	518.50	0.965	55.5269
98	WH 1192	444.70	1.002	-1423.8488
99	WH 1235	579.60	0.965	44.9542
100	WH 1264	504.80	1.092	-882.0992
	MEAN	576.30		
	STANDARD ERROR		0.10	

Table 5. Cont.

\*, \*\* and \*\*\* = significance at 0.05, 0.01 and 0.001 level.

**Table 6.** Pooled analysis of variance of 100 genotypes across eight environmental conditions for grain yield per plot in wheat (Eberhart and Russell, 1966 model).

Source	DF	Grain Yield per Plot (g)
Genotype (Gen.)	99	77,289.410 ***
Environment (Env.)	7	2,906,548.000 ***
Gen. $\times$ Env.	693	1410.637 ***
Env. + (Gen. $\times$ Env.)	700	30,462.010 ***
Env. (Linear)	1	20,345,830.000 ***
Env. $\times$ Gen. (Linear)	99	1112.672 **
Pooled Deviation	600	1445.695 **
Pooled Error	792	891.864
Total	799	36,264.150

\*\* and \*\*\* = significance at 0.01 and 0.001 level.

### 3.2. Environmental Indices

The environment index reveals the suitability of an environment at a particular location. Estimates of environment index can provide the basis for identifying the favorable environment for the expression of maximum potential of the genotype. The positive values of environment indices conclude the favorable environment for genotypes. As indicated by the environment index, E5 (260.03) showed highest yield and was found to be most favorable production environment (Table 7).

Trait	Environmental Index						Moon		
IIall	E1	E2	E3	<b>E4</b>	E5	E6	E7	<b>E8</b>	Wiedii
GYP	225.028	-23.472	-144.559	-199.442	260.028	70.524	-68.416	-119.691	576.27

Table 7. Environmental indices for grain yield per plot across the environment in 100 wheat genotypes.

## 3.3. AMMI Biplot Analysis

 $G \times E$  interaction study in multi-environment trials was also carried out by AMMI model to increase the reliability of the multi-location trial analysis. The results of the analysis of variance of the AMMI model revealed that grain yield is significantly (p < 0.001) affected by environment, genotype and genotype–environment interaction, which explained 70.22%, 26.41% and 3.37% of the occurred variation, respectively. Furthermore, it showed that two PC with significant differences cumulatively captured 93.14% of total GEI as the first principal component of AMMI, explaining 80.52% of the genotype–environment interaction, whereas the second principal component explained 12.62% of the genotype–environment interaction (Table 8).

**Table 8.** Pooled analysis of variance for grain yield per plot of 100 wheat genotypes across different environments using AMMI model.

Source	Degree of Freedom	Grain Yield Per Plot	% Explained
Trials	799	36,264.17 ***	
Genotypes	99	77,289.54 ***	26.41
Environments	7	2,906,549.42 ***	70.22
$G \times E$ interaction	693	1410.62 ***	3.37
PCA I	105	7496.20 ***	80.52
PCA II	103	1197.47 *	12.62
PCA III	101	443.23	4.58
Pooled error	800	935.70	

\* and \*\*\* = significance at 0.05 and 0.001 level.

## 3.4. The AMMI 1 Model

The AMMI biplot has the main effect as grain yield per plot in the abscissa and the IPCA1 as the ordinate where the genotypes or environments that lie on the same vertical line have the same yield, and those that lie on the same horizontal line have the same interaction pattern. In the AMMI 1 biplot, the elite wheat genotypes PBW 750, DPW 621-50, WH 542, PBW 486, PBW 661 and WH 1192 are relatively stable genotypes in yield that are broadly adapted lines (Figure 1).

The wheat genotypes HD 2967, WH 1151, UP 2660, PBW 676, WH 1182, PBW 729, WH 1061, PBW 560, PBW 725 and PBW 721 are relatively unstable in yield because these lines are far from the origin and can be specifically adapted to particular environment. Especially, genotypes HD 2967, WH 1151, UP 2660 and PBW 676 were likely to perform better in the E6 environment, whereas the genotypes WH 1182 and PBW 729 were identified as specially adapted to environments E1 and E5, respectively. E8 was the most responsive environment for genotypes WH 1061, PBW 560, PBW 725 and PBW 721 (Figure 1).

## 3.5. The AMMI2 Model

In AMMI2 biplot, the Interaction Principal Component Axes 1(IPCA1) and Interaction Principal Component Axes 2 (IPCA2) scores are reported as the representation of the stability of the lines across the environment; that is, the lines with the least PC scores have high stability and vice versa, i.e., the more IPCA scores that approximate to zero, the more stable the genotypes are across all the locations. The environments E1 and E5 had comparatively short spokes, and they did not exert strong interactive forces, while environments E2, E3, E4, E6, E7 and E8 had long spoke exert strong interaction (Figure 2). Similarly, genotypes WH 1158, WH 1164 and PBW 726 were near the origin, so they were non-sensitive to environmental interactive forces, while genotypes PBW 706, WH 1063, PBW 343 and PBW 762 were away from the zero line, so they were the most responsive. In this case, the best-adapted genotype with respect to site E4 was WH 1063, whereas the genotypes WH 1152, PBW 752 and PBW 475 were tightly grouped in the sites E1, E2 and E5.



**Figure 1.** AMMI (Additive Main Effects and Multipicative Interaction) 1 biplot for grain yield per plot of 100 wheat genotypes and 8 environments using genotypic and Environmental scores.



**Figure 2.** AMMI 2 biplot for grain yield per plot showing interaction of IPCA (Interaction Principal Component Axes) 2 against IPCA 1 scores of 100 wheat genotypes in 8 environments.

## 3.6. GGE Biplot Analysis Which-Won-Where Model

GGE biplot analysis, the most effective way of summarizing the genotype and genotypeenvironment interaction of the dataset was used to identify the best line of each environment and assess the stability of the lines. The most attractive feature of GGE biplots is the polygon view, which addresses the 'which-won-where' pattern of multi environment data, in which there is a graphical representation of crossover GE interaction, mega-environment differentiation and specific genotype adaptation. The polygon is drawn by joining the genotypes located farthest from the origin, such that all other genotypes are included within the polygon. A genotype located at the edge is called a vertex genotype, and vertex genotypes were the most responsive. In this biplot, genotypes DPW 621-50, DBW 16, PBW 88 and PBW 706 were the most responsive genotypes. The equality line divides the graph into six sectors, and eight environments were retained in two sectors and partitioned into two mega-environments, one with E1, E2, E3, E4 and E5, and the second with E6, E7 and E8 (Figure 3). In the first mega-environment, the genotypes PBW 706, PBW 769, DBW 116, WH 1157, WH 789 and WH1186 were the winning genotypes, and genotypes DBW 16, WH 1152, WH 1105 and PBW 503 were those in the second (Figure 3).



**Figure 3.** Polygon view of GGE (genotype plus genotype by environment interaction) biplot (whichwon-where model) showing 20 elite wheat lines in irrigated and drought environment.

## 4. Discussion

A major goal of plant breeding programs is to increase stability and stabilize crop yield over a range of environments. The most appropriate methods include identifying desirable cultivars with high productivity genetic potential and testing wide adaptability to most conditions by multi-condition experiments in target environments. The results of pooled analysis of variance for stability as devised by Eberhart and Russell [11] and the AMMI model showed that variance due to genotypes and environments was significant for grain yield per plot, indicating that the performances of genotypes as well as the environments were different; the genotypes also had differential responses to the changes in the environmental conditions. Similar results were reported by Dhiwar et al. [22] and Attia et al. [23]. In this study, the four genotypes WH 1142, PBW 661, PBW 475 and DBW 17 had regression coefficients of 1.158, 1.13, 1.11 and 1.10 and were observed to be stable in the rich (E5) environment. According to the E-R model, a slope of >1.0 with high mean and non-significant squared deviation are suitable for a favorable environment [24]. Suresh and Munjal [25] found four genotypes, namely HD 3059, WH 1105, HTW 66 and WH 1124, with bi values significantly greater than 1 and with higher average productivity than the overall mean; these conditions are suitable for high input and timely sowing conditions.

It is interesting to note that no genotype was stable for grain yield; however, some genotypes, HD 3086, DBW 16, PBW 527, PBW 528, PBW 502 and PBW 503, almost produced a similar grain yield per plot under all the environments. Similar results were reported by Kumar et al. [26], who observed that the genotypes LOK-1, NI-5439 and HUW-468 were found stable across the environments with high mean value, bi values close to 1 and non-significant deviation from regression. In this study, genotypes UP 2660 and DBW 88 were determined to be suitable for unfavorable environments, as genotypes with less than unity regression value and non-significant squared deviation indicate suitability for a poor environment [27]. The performance was unpredictable for genotypes WH 1182, PBW 677, WH 1061, PBW 729, PBW 560, PBW 728 and PBW 721 with significant squared deviation. For the genotypes exhibiting non-significant deviations from regression (S<sup>2</sup>di), their performance can be predicted well, as the genotypes are within the range of minimum deviation from regression [28].

The AMMI model explains the genotype–environment interaction [29], which is used for reliable yield estimates [30], and provides a base of better use for other models [19]. AMMI revealed that a major part of the variation in yield is explained by environment, which indicates that the environments were diverse. The results are line with the findings of Ljubičić et al. [31] and Hanif et al. [32].

The AMMI1 biplot analysis revealed variation due to the main effect (grain yield) and the interaction effect [33]. Genotypes and environments with IPCA1 scores close to zero were characterized with low interaction effects, being considered stable [34]. In this study, the wheat genotypes PBW 750, DPW 621-50, WH 542, PBW 486, PBW 661 and WH 1192 were identified as stable genotypes in yield, and the genotypes HD 2967, WH 1151, UP 2660, PBW 676, WH 1182, PBW 729, WH 1061, PBW 560, PBW 725 and PBW 721 were unstable. Similar to this research, Dabi et al. [35] also identified high-yielding and stable genotypes ETBW 9080, ETBW 9172, ETBW 9646, ETBW 9396, ETBW 9452, ETBW 9136 and ETBW 9139, inferring little interaction with the environment. Genotypes HD 2967, WH 1151, UP 2660 and PBW 676 far from the IPCA origin appeared to be adapted to a timely sown rainfed environment, whereas the genotypes WH 1182 and PBW 729 were specially adapted to a timely sown irrigated environment. Additionally, Bishwas et al. [36] identified the high-responsive genotypes of wheat in irrigated and heat-stressed environments. Especially, NL 1179 was specifically adapted to a terminal heat-stressed environment.

An AMMI2 biplot was devised using genotypic and environmental scores (IPCA1 versus IPCA2 scores), providing a good explanation of the data pattern to interpret genotypic behaviors across different environments [37]. The IPCA 1 and IPCA 2 scores delineated the stability of the lines across the environment—that is, the lines with the least PC scores do not show an association with any environment, whereas a lower PC score means genotypes show specific adaptation to a particular environment [38]. In the present study, genotypes WH 1158, WH 1164 and PBW 726 were highly stable, while the genotypes PBW 706, WH 1063, PBW 343 and PBW 762 were the most responsive. According to the AMMI2 biplot, timely sown irrigated environment was determined as the most favorable environment, with the least interactive forces, and WH 1025 was highly adapted to this environment. Similarly, Attia et al. [23] concluded East Barrani as most favorable environment for all cultivars according to AMMI2 bi-plot and Sakha 94 was the superior cultivar in this environment. Similar results were further confirmed by Verma and Singh [17] while analyzing the stability of wheat genotypes by AMMI in the Peninsular Zone of India. Therefore, the above-mentioned genotypes were found most stable for grain yield and can be incorporated as breeding stocks in any future breeding programs aiming to produce high yielding lines of bread wheat.

The GGE biplot is a data visualization tool that allows an evaluation of environments due to the discriminative ability and representativeness of the GGE view, which is an advantage over the AMMI biplot analysis [39]. The GGE biplot analysis is the most effective way for a precise and useful interpretation of genotype-environment interactions as well as interrelationships among various test environments and genotypes and identifies the best line of each environment [40]. Genotypes and environments were analyzed together through the which-won-where model of the GGE-biplot. The vectors were connected furthest from the origin of the biplot, and a polygon was obtained. In this biplot, genotypes DPW 621-50, DBW 16, PBW 88 and PBW 706 were the most responsive genotypes, with crossover GE interaction, mega-environment differentiation and specific genotype adaptation [41]. These vertex genotypes were the most responsive, located at the greatest distance from the biplot origin [40]. The graph was then divided into six sectors, and eight environments were retained in two sectors and partitioned into two mega-environments, probably due to latitudinal and longitudinal differences [42]. Variation in the genotypic performance within environments indicated the strong influence of environments and the existence of a mega-environment [40,43,44].

## 5. Conclusions

This study indicated that genotype, environment and their interaction have a significant effect on the yield stability as per the Eberhart and Russell model, AMMI and GGE biplot. Further analysis of stability through the Eberhart and Russell model concluded that elite wheat genotypes WH 1142, PBW 661, PBW 475 and DBW 17 were specifically adapted to a timely sown irrigated environment during *Rabi* 2020–2021, whereas UP 2660 and DBW 88 were specifically adapted to late sown rainfed environment during *Rabi* 2019–2020. In this experiment, PBW 750, DPW 621-50, WH 542, PBW 486, PBW 661 and WH 1192 were found to be the most stable and high-yielding genotypes across all the test environments as per AMMI biplot. All in all, these genotypes can be used as high-yielding lines, which are stable too, and for farmers, WH 1142, PBW 661, PBW 475 and DBW 17 can be used for high yield with adaptability in a timely sown irrigated environment. These genotypes need to be further tested in heat- and drought-stressed environments to ensure their performance over the years.

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