Original Research Article

Genotype × Environment Interaction for Grain Yield and Component Traits in Wheat (*Triticum aestivum* L.) for Varietal Recommendations in Meghalaya state of India

Abstract

The study aims to evaluate the stability of fifteen wheat (*Triticum aestivum* L.) genotypes under varying sowing dates to identify genotypes with superior grain yield and stability in the North Eastern Region of India. The study also seeks to assess G×E using the Eberhart and Russell model and the AMMI model, to recommend suitable genotypes for cultivation in this region.This is a two-year field study conducted during the rabi seasons of 2017-18 and 2018-19.Fifteen genotypes were sown on six different dates including E_1 (27th Oct. 2017-18), E_2 (6th Nov. 2017-18), E_3 (16th Nov. 2017-18), E_4 (27th Oct. 2018-19), E_5 (6th Nov. 2018-19), and E_6 (16th Nov. 2018-19) to evaluate the stability of these genotypes.This experiment was performed in Randomized Block Design (RBD) with three replications.All genotypes exhibited significant differences across the studied environments. The genotype-environment interaction was significant for most traits except days to 50% crop emergence, test weight, and harvest index.RAJ-3765 and HD-2985 were identified as high-yielding and stable genotypes across all environments, while HD-3118 and HD-2733 performed well in favorable conditions. The AMMI analysis revealed that HD-2985 and RAJ-3765 were the most stable, and WR-544 was the poorest performer.Genotypes RAJ-3765 and HD-2985 showed superior stability and yield across diverse environments, making them suitable for broader cultivation in Meghalaya. HD-2733 and HD-3118 were better suited for favorable environments, while WR-544 was the least adapted. These findings suggest the potential for expanding wheat cultivation in the region using these stable genotypes.

Key words: Wheat, stability analysis, genotype-environment interaction, AMMI, GGE biplot

1. Introduction

Wheat is the second most important food grain crop after rice in India. The development of stable and high - yielding genotypes combined with resistance to diverse abiotic and biotic factors will be necessary to meet the demand for food grain in the nation. Multi-location trial is a key solution for selecting a stable and best - performing genotypes in different environments [3, 12 and 31]. The grain yield and its related traits were determined by the genotypic potential (G), environmental effect (E) and the genotype x environment interaction (GEI) [35].

Cultivation of wheat (*Gehun*) in Meghalaya is new to farmers though it is widely cultivated in North western part of the country. Wheat crop has central acreage in West Garo Hills district of Meghalaya where it is grown as rainfed crop after rice harvest with very low productivity (1.92 t $ha^{-}1$ as compare to 3.4 t ha^{-1} of national average as reported in The Handbook on Area, Production and Yield of Principal Crops in Meghalaya [1]. Among the NEH region, Tripura, Manipur and Meghalaya have large scope of wheat during the *rabi* season as there is availability of large plain areas in between the hills and meager irrigation facilities which can be made available near the Dams and river.

Since genotypes are extremely influenced by the locations and environments therefore performance associated to stability of genotypes is a pre-requisite and should be carried out in varied environments over years in a different location [17]. Stability is the capacity of a genotype to maintain the uniformity of the trait at high or low performance in different environment [5]. For developing good performance genotypes that are phenotypically stable and a large number of genotypes are needed for identifying the desirable traits which would be useful for screening the ideal plant type [34]. A phenotype of a genotype is the outcome of interaction among the genotypes and the environments (G × E) which assists in finding a stable genotype across the environments with wider adaptability [4]. There are genotypes which depicts abnormally in different environments while the other genotypes shows similar trait over a wide range of environments [13]. Hence to overcome this limitation, several quantitative methods for stability analysis were evolved out of which regression coefficient [11], the environmental variance [21] are widely accepted. Now-a-days, the AMMI model of biplot method is mainly used for stability testing. It provides suitable statistical analysis using G x E interactions for grain yield and its related traits [26]. The present analysis used regression co-efficient analysis and Additive Main effects and Multiplicative Interaction model (AMMI). The AMMI biplot approach has been used for the identification of stable genotypes in multi-environment trials of wheat and barley [18, 32]. In this present study, both the Eberhart and Russell method as well as AMMI model analysis were performed for the comparison of the results to find the appropriate high grain yield and stable genotypes. It is very challenging for the breeders to develop a variety that has good and stable performance throughout varied environmental conditions for specific recommendations in a new niche.

2. Materials and methods

2.1 Collection and planting of the germplasm

The experimental material consists of 15 genotypes of *Triticum aestivum* collected from ICAR-IIW&BR, Karnal (Table 1). These were sown at experimental farm of CPGS-AS, Umiam, Meghalaya. The genotypes were sown in RBD design with three replications. The row to row and plant to plant spacing of 20 cm × 5 cm respectively. Six different environments as different date of sowing were created considering receipt of different temperature, humidity and precipitates as differs in the date of sowing.Experimental soil was clay loam with a moderately acidic pH of 5.8. Meteorological conditions included temperatures ranging from 4-12°C (minimum) to 17-27°C (maximum). Relative humidity varied from 18-76% in the evening to 61-93% in the morning. The annual rainfall was 66.2 mm in the 2017-18 *rabi* season and 92.5 mm in the 2018-19 *rabi* season.

2.2*Statistical analysis*

After taking the morphological and yield data of 13 important traits for two years, the analysis was done using statistical software (GENES and GEA-R). Eberhart and Russell [11] method was used to study both the linear (β_l) and non- linear ($\sigma^2 d_l$) parameters of phenotypic stability. The stability analysis was done using the linear regression model suggested by Eberhart and Russell [11]. AMMI model analysis of Gauch [16] was also done for yield related traits in *Triticum aestivum* to check the genotype - environment interaction and stability.

3. Results and discussion

3.1 Pooled ANOVA for the 15 genotypes of Triticum aestivum **L.**

The pooled analyses of variance for 15 elite genotypes for 13 important characters were carried out (Table 2). The MSS due to genotypes and environment were highly significant showing sufficient variability among genotypes chosen and environments created. The G x E interaction components also showed significant mean sum of squares tested against pooled error mean sum of squares for all the traits except 50% plant emergence, test weight and harvest index indicating that the environment over the different date of sowings in two years widely influenced on the performance of genotypes for the traits under study.

Table 1. Collection of different accessions of wheat

Sl. No.	Treatment	Name of genotype	Sl. No.	Treatment	Name of genotype
1	V1	SONALIKA	9	V9	HD-2643
2	V2	DBW-39	10	V10	HD-2967
3	V3	DBW-71	11	V11	NW-2036
4	V4	DBW-107	12	V12	NW-1014
5	V5	DBW-14	13	V13	HI-1563
6	V6	HD-2985	14	V14	RAJ-3765
7	V7	HD-2733	15	V15	WR-544
8	V8	HD-3118			

GXE interaction showed the yield response of genotypes studied under variable environments. Highly significant E+(G×E) for all the traits against pooled error indicated distinct nature of environments and G x E interactions in the phenotypic expression. It was stated that number of years and environments for an experiment should be given more focus rather than multi locations [29]. Also, GEI must be considered for selection of good performing genotypes [28]. GEI is studied by statisticians for non - additive, quantitative genetics of GEI magnitude and by plant breeders for selection of good performing genotypes [14].

Highly significant genotype x environment component was noticed for all the traits except 50% plant emergence, test weight and harvest index indicating that all the genotypes interacted considerably well with the environmental conditions (Table 2). The non-significant mean sum of squares due to 50% plant emergence, test weight and harvest index revealed that the different environment did not have significant role in altering the performance of varied genotypes. Similar result was also reported by Admassu *et al*. [2]. The G x E (linear) component was significant for plant height, 50% heading, heading to maturity, number of panicles, panicle length, number of grains per panicle, grain weight per plant and grain yield per plant. This revealed that the performance of genotypes for these traits was predictable in nature and linear components will be responsible for the G × E interaction. However, G x E (linear) component was non-significant for 50% emergence, test weight, biological yield and harvest index indicating that the performance of these traits was unpredictable and non-linear components were largely responsible for their varied performance. Singh et al. [28], Ullah et al. [32], and Lal et al. [19] also noticed same reason for non-significance of some of the traits studied in mungbean. Highly significant values were seen in the environment (linear) variance for all the traits indicating additive environmental variance. The pooled deviation was significant for all the traits except 50% plant emergence, test weight, grain weight and harvest index. This is due to the deviation in the linear graph for the performance of the respective significant traits to the environment confirming the role of some other unpredictable components of G × E interaction.

3.2 Stability analysis using Eberhart and Russell model

In accordance with Kumawat et al., 2023 [38], The regression coefficient (b_i), squared deviation from regression (S^2di) and mean performance for traits under studiedwere presented in Table 3. The mean performance of the plant height from the stability analysis ranged from 81.81 cm to 100.90 cm with an average value of 95.22 cm over the environment. Out of the 15 genotypes studied four genotypes *viz.*, Sonalika, DBW-39, DBW-71 and HD-2967 were considered as desirable and stable based on their performances according to Eberhart and Russell model. It was also reported that genotypes with $b_i = 0$ has no reaction towards the environmental factors considering it to be stable, and genotypes showing average response to the environmental factors possess $b_i = 1$ according to static concept [7]. But, according to dynamic concept proposed by Eberhart and Russell [11], the genotypes is stable if it shows high mean performances, regression coefficient equal to 1 ($b_i = 1$) and deviation from regression (S^2di) as low as possible. Four genotypes have $b_i > 1$ indicating its adaptability to the favourable environment while the remaining genotypes with $b_i < 1$ were least affected by the environment. Similarly, the range for panicle length varies from 6.97 cm to 8.47 cm with average value of 7.81 cm. The genotypes with $b_i > 1$ for the panicle length was shown by 15 genotypes out of which only one genotype RAJ-3765 was found to be stable and desirable for panicle length. The high performing and stable genotypes were HD-2643 and DBW-107 for the characters 50% heading and heading to maturity, respectively. Likewise, the highly adapted and stable genotypes were HD-2643 for 50% physiological maturity, HD-3118 for number of panicle per plant, DBW-71, HD-2967, NW-2036 and HD-3118 for number of grains per panicle.

Grain yield ranged from 2.71 to 3.98 t ha^{-1}with population mean of 3.33 t ha^{-1}. Almost all the genotypes showed consistent performance in its characteristic with S^2di = 0, out of which HD-2985 and RAJ-3765 genotype were phenotypically stable for grain yield (t ha^{-1}) while HD-2733 and HD-3118 showed better adaptation to the above average environment with $b_i > 1$ and S^2di = 0. The two genotypes were also good for grain weight per plant. The genotype NW-1014 showed better adaptation to below average environment with S^2di=0. Deviation from regression (S^2di) is characterized as stability parameter while b_i is considered as response parameter since the variability due to the unpredictable factor of any genotype is related to S^2di while the reaction of any genotype towards environmental factor is related to b_i [9]. Again, for the biological yield, the mean performances ranged from 6.63 to 10.96 with population mean of 9.04. Here, out of 15 genotypes, seven genotypes had b_i> 1 with significant values showing its adaptability towards environmental conditions thereby making it unstable. However, b_i = 1 and S^2di = 0, RAJ-3765 genotype was found to be stable and good for biological yield. The value for harvesting index ranged from 34.47 to 41.19 and population mean of 37.14.

"The overall results obtained from the analysis of stability parameters for six different date of sowing covering two different years indicated that different genotypes were stable for different traits. However, the genotypes stable for grain yield (t ha^{-1}) showed stable and good performance in some of yield components trait also. The location for each year can be considered as macro-environments" [11]. "Two-year data was studied rather than different multi-locations since regression in macro environments is more appropriate to study the difference in the values of the traits" [6]. "Based on different traits different stable and high yielding genotypes should be considered for selection. The performance of these genotypes will remain unchanged regardless of distinctive environmental conditions. Further, it was also reported that stability analysis will be helpful in combating diseases, stress factors and identifying quality traits" [7].

Table 2. Pooled analysis of variance of fifteen genotypes for two years trial of wheat

Source of variation	D.F.	50% crop emergence	Plant height	50% Heading	Heading to maturity	50% physiological maturity	Number of panicle	Panicle length	Number of grains per panicle	Test weight	Grain weight per plant	Grain yield per plant	Biological yield	Harvest index
Environment	5	3.13**	197.52**	213.91**	978.56**	616.35**	17.98**	16.56**	311.28**	7.98**	51.32**	1.65**	5.37*	367.95**
Genotypes	14	0.72*	442.35**	511.50**	78.26**	371.63**	2.15**	4.91**	150.83**	386.69**	12.28**	2.38**	20.85**	70.21**
G x E	70	0.51	28.90**	22.83**	34.07**	30.96**	0.85**	1.05**	20.57**	0.00	1.70**	0.47**	2.38**	22.83
E + (G x E)	75	0.68**	40.15**	35.57**	97.04**	69.98**	2.00**	2.09**	39.95**	0.53**	5.01**	0.55**	2.58**	45.83**
E (linear)	1	15.62**	987.60**	1069.57**	4892.80**	3081.78**	89.89**	82.78**	1556.41**	39.88**	256.62**	8.23**	26.85**	1839.75**
G x E (linear)	14	0.28	8.84**	34.98**	61.45**	29.31**	3.14**	1.50**	20.32*	0.02	6.45**	0.44**	0.57	30.26
Pooled deviation	60	0.52	31.66**	18.47**	25.41**	29.28**	0.26**	0.88**	19.26**	0.00	0.48	0.44**	2.65**	19.57
Pooled error	**168**	0.38	1.65	7.65	12.82	5.00	0.12	0.10	9.36	0.04	0.42	0.18	0.78	19.04

Table 3. Stability parameters for morphological traits across environments

Genotypes	**50% emergence**			**Plant height (cm)**			**50%heading**			**Heading to maturity**		
	bi	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**
SONALIKA	1.17	-0.04	7.44	1.10	-0.20	98.76	0.21	-2.16	71.78	0.51	-1.36	54.69
DBW-39	0.99	0.30*	7.61	0.86	0.49	100.90	0.79	3.51	77.94	0.86	6.97*	51.56
DBW-71	0.58	0.14	7.72	0.85	0.10	95.54	0.91	-1.03	72.11	1.06	2.07	55.50
DBW-107	0.76	0.02	7.44	1.80	13.94**	96.83	1.06	-1.65	72.67	1.05	-1.00	56.56
DBW-14	0.90	0.01	7.50	0.70	0.53	81.81	1.03	3.76*	66.33	0.79	-2.78	56.39
HD-2985	0.72	0.01	7.61	1.40	3.42**	94.54	1.17	2.80	70.89	0.90	10.09*	58.56
HD-2733	0.80	-0.05	7.61	1.32	6.63**	99.68	1.55	8.22**	80.44	1.25	2.42	56.06
HD-3118	1.53	0.14	7.64	0.68	17.71**	99.46	1.22	20.77**	73.22	1.35	4.42	55.72
HD-2643	0.43	0.07	7.00	1.34	25.63**	92.05	0.93	0.04	76.83	1.59	1.26	57.33
HD-2967	1.87	-0.12	7.44	1.11	-0.04	96.59	0.48	1.72	82.94	1.36	-0.04	53.89
NW-2036	0.52	0.15	7.39	0.73	2.67**	98.17	1.78	-0.86	74.89	1.58	7.97*	57.83
NW-1014	2.02	0.00	7.11	0.94	-0.33	94.32	0.70	4.89*	75.22	0.53	13.00**	53.50
HI-1563	0.23	-0.02	7.67	0.28	23.73**	95.04	1.23	6.38**	70.11	1.03	4.39	59.17
RAJ-3765	1.42	0.13	7.58	0.90	1.29*	96.80	-0.57	2.98	77.17	-0.03	17.55**	55.28
WR-544	1.06	-0.08	7.44	0.99	54.46**	87.84	2.52	4.70*	61.83	1.17	-2.06	58.39
Mean **C.D. at 0.05**			**7.48** **0.99**			**95.22** **2.07**			**73.63** **4.45**			**56.03** **5.77**

Genotypes	**Days to 50% Physiological maturity**			**Number of panicle per plant**			**Panicle length (cm)**			**No. of grains per panicle**			**Test weight (g)**		
	bi	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**	**bi**	**S^2di**	**MEAN**
SONALIKA	0.78	0.31	126.47	2.26	0.07*	3.88	1.55	0.20**	8.08	0.87	-2.80	35.63	0.98	-0.01	46.88
DBW-39	0.58	7.43**	129.50	0.65	0.00	2.85	0.13	0.43**	7.44	1.51	1.93	36.50	0.84	-0.01	40.34
DBW-71	1.17	8.87**	127.61	0.09	0.00	3.33	1.93	0.49**	7.79	0.83	-1.32	40.02	1.02	-0.01	48.88
DBW-107	0.97	4.17**	129.22	0.84	-0.01	3.30	1.24	0.14**	8.39	1.88	9.02**	37.78	1.10	-0.01	52.39
DBW-14	0.99	6.98**	122.72	0.73	-0.00	3.72	0.46	0.47**	7.13	0.24	8.22**	30.37	1.10	-0.01	52.43
HD-2985	1.23	13.47**	129.44	2.12	0.03	3.48	1.34	0.11**	8.31	0.59	23.54**	39.05	1.10	-0.01	52.91
HD-2733	0.70	8.60**	136.50	0.20	0.00	3.48	0.67	0.33**	7.20	0.71	-1.85	35.76	1.04	-0.01	49.88
HD-3118	1.29	4.38**	128.94	0.92	-0.01	3.80	0.78	0.02	8.43	1.38	-0.45	39.60	1.09	-0.01	51.71
HD-2643	1.92	-0.75	134.17	2.19	0.13**	3.96	0.91	0.74**	7.84	0.57	12.88**	32.75	1.00	-0.01	47.72
HD-2967	1.22	14.14**	136.83	1.08	-0.00	2.93	1.69	0.40**	8.00	1.19	-2.02	37.30	0.94	-0.01	44.56
NW-2036	1.21	12.52**	132.72	1.60	0.44**	3.64	1.07	0.20**	7.52	0.95	-2.33	37.53	0.82	-0.01	39.33
NW-1014	0.71	6.52**	128.72	0.77	0.05*	3.01	0.85	-0.02	7.28	1.05	-2.32	32.68	0.94	-0.01	45.00
HI-1563	1.15	-0.69	129.28	0.85	-0.00	3.17	0.21	0.40**	8.31	0.80	2.33	39.37	0.88	-0.01	42.05
RAJ-3765	0.40	22.01**	132.44	0.46	-0.03	3.25	1.31	0.00	8.47	1.63	2.85	39.61	1.10	-0.01	52.91
WR-544	0.70	13.44**	120.22	0.20	0.00	3.25	0.85	-0.03	6.97	0.80	1.79	37.44	1.05	-0.01	50.16
Mean			**129.65**			**3.40**			**7.81**			**36.76**			**47.81**
C.D. at 0.05			**3.60**			**0.55**			**0.51**			**4.93**			**0.32**

Genotypes	**Grain weight per plant (g)**			**Grains yield(t ha^{-1})**			**Biological yield (t ha^{-1})**			**Harvest index**		
	Bi	**S^{2}di**	**MEAN**	**bi**	**S^{2}di**	**MEAN**	**bi**	**S^{2}di**	**MEAN**	**bi**	**S^{2}di**	**MEAN**
SONALIKA	1.52	0.10	5.31	1.56	0.01	3.07	-0.03	0.74**	8.61	1.78	-1.80	35.81
DBW-39	0.78	-0.03	3.69	2.59	0.10*	2.94	1.05	0.81**	8.24	1.40	5.36	35.82
DBW-71	0.24	0.03	5.35	1.08	0.03	3.09	2.24	0.09	8.81	1.04	-2.70	35.49
DBW-107	1.55	-0.09	5.48	2.10	0.10*	3.22	0.54	0.99**	9.35	1.53	-5.89	34.47
DBW-14	0.36	0.24*	4.82	0.44	0.00	2.98	0.47	0.30	7.80	0.94	-3.90	38.37
HD-2985	1.05	0.03	5.77	1.16	0.03	3.98	0.75	0.57*	10.88	1.28	-2.90	36.82
HD-2733	1.33	0.00	5.14	1.94	0.30**	3.95	1.55	1.53**	10.96	1.56	-4.08	36.32
HD-3118	1.41	-0.13	6.48	1.65	-0.02	3.43	0.72	0.33	9.31	1.10	-1.18	36.87
HD-2643	1.91	0.06	5.11	1.54	0.16**	3.20	1.56	0.98**	9.12	1.03	-2.07	35.46
HD-2967	1.10	-0.11	4.15	0.80	0.00	3.18	1.18	0.54*	8.69	0.47	-1.09	37.00
NW-2036	1.23	0.34**	4.48	-0.03	0.05	3.53	0.87	0.70**	9.39	1.00	-3.94	37.68
NW-1014	0.73	-0.05	3.81	0.59	0.07	3.62	1.31	0.24	8.94	0.33	-1.26	40.47
HI-1563	0.67	0.05	4.49	-0.19	0.42**	3.49	0.47	1.11**	9.73	1.01	4.89	35.89
RAJ-3765	1.04	-0.08	5.64	1.15	0.00	3.54	0.89	-0.10	9.08	-0.02	2.52	39.19
WR-544	0.01	-0.06	3.72	-1.07	0.02	2.71	1.42	0.43*	6.63	0.54	20.58**	41.49
Mean			**4.90**			**3.33**			**9.04**			**37.14**
C.D. at 0.05			**1.04**			**0.68**			**1.42**			**7.03**

Table 4: ANOVA table for AMMI model in fifteen genotypes of wheat

Source of variation	DF	50% Plant emergence		Plant height (cm)		50% Heading		Heading to Maturity		50% Physiological maturity		No. of panicles per plant		Panicle length (cm)	
		MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained
ENV	5	3.13**	25.52	197.52**	10.73	213.91**	10.88	978.56**	58.43	616.36**	29.49	17.98**	50.01	16.56**	36.74
GEN	14	0.72	16.50	442.35**	67.29	511.50**	72.86	78.26**	13.08	371.63**	49.78	2.15**	16.75	4.91**	30.50
G × E	70	0.51	57.98	28.90**	21.98	22.83**	16.26	34.07**	28.48	30.96**	20.73	0.85**	33.24	1.05**	32.76
PC1	18	0.96**	48.84	80.68**	71.77	49.83**	56.13	55.14**	41.62	45.83**	38.07	2.66**	80.24	2.62**	63.97
PC2	16	0.67	30.18	34.80**	27.52	31.84**	31.88	41.41**	27.78	44.34**	32.73	0.73**	19.66	1.65**	35.79
Residuals	180	0.43	0.00	2.57	0.00	9.20	0.00	14.63	0.00	5.04	0.00	0.13	0.00	0.11	0.00

Source of variation	DF	Number of grains per panicle		Test weight (g)		Grain Weight		Grain yield (t ha^{-1})		Biological yield (t ha^{-1})		Harvest Index	
		MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained	MS	% Explained
ENV	5	311.28**	30.47	7.98	0.73	51.32**	46.83	1.65**	11.08	5.37*	5.53	367.95**	41.62
GEN	14	150.83**	41.34	386.69**	99.26	12.29**	31.39	2.38**	44.85	20.85**	60.11	70.21**	22.24
G × E	70	20.57**	28.19	0.01	0.01	1.70**	21.78	0.47*	44.07	2.38	34.37	22.83	36.15
PC1	18	47.28**	59.09	0.02	99.96	5.54**	83.59	0.82**	45.10	4.85**	52.30	38.90*	43.82
PC2	16	36.63**	40.70	0.00	0.04	0.82	11.02	0.57**	27.82	4.04**	38.72	29.78	29.82
Residuals	180	9.56	0.00	4.38	0.00	0.52	0.00	0.32	0.00	1.80	0.00	20.11	0.00

3.3 Additive Main Effects and Multiplicative Interaction Model (AMMI) Analysis

The AMMI model analysis is used extensively because of its ability to clarify multiple environmental impacts, reveals G × E interaction and depicts accurate trait estimation [10, 15, 37]. The AMMI analysis of variance (Table 4) of the 15 genotypes showed that the environmental and genotypic effect were highly significant for all the traits except test weight and 50% plant emergence in which either genotype or environment only is significant. Non-significant effect of G × E interaction was observed 50% plant emergence, test weight, biological yield and harvesting index indicating similar response of genotypes across different environments for these traits. Significant effect in plant height, days to 50% heading, heading to maturity, 50% physiological maturity, number of panicles per plant, panicle length, number of grains per panicle, grain weight and grain yield (t ha^{-1}) depicted divergent performance caused due to varied environmental effect. Therefore, precision analysis of the significant traits must be carried out for efficient selection and development of genotypes.

AMMI model analysis represents effectively the G x E interaction patterns since both additive and multiplicative components are involved in this analysis. Earlier in wheat, AMMI model analysis was used to reduce G x E interaction for selection of high grain yield and stable genotype over the environment. The interaction effect can be analyzed using principal component analysis (IPCA) i.e., PCA1 and PCA2 of AMMI ANOVA depicted 72.92 % in grain yield (Fig. 1), 99.79% in number of grains per panicle (Fig. 2), 96.55% in number of days for heading to maturity, 99.90% in number of panicles per plant and 94.61% in grain weight per plant (Fig.4) of G × E interaction sum of squares.

"The genotypes can be differentiated based on its performance over the years using AMMI biplot analysis" [23]. "It is also helpful in the selection of stable genotypes that has wide range of adaptability in different environments because G × E interaction affects the genetic gain of the crop thereby making it important for plant breeding programme [8]. Though low G × E interaction for the studied characters confirms stability performance of the genotypes in different environments but sometimes high G × E interaction may also be beneficial in some conditions" [24]. The biplot of the first AMMI interaction (IPCA1) against means of the genotypes and environment explains the relationship between them for the concern trait.

The AMMI biplot of the grain yield represented five genotypes viz.,HD-2985, HD-2733, HD-3118, NW-2036, NW-1014, HI-1563 and RAJ-3765, as the most promising and high yielding while, the other eight genotypes viz., were unpredictable and not suitable for any environments (Fig. 1). [39] Similarly PCA 1 was also plotted against PCA 2 since PCA 2 plays an important role in explaining the G × E interaction. The AMMI 2 and GGE biplot interaction showed seven vertex genotypes that are joined together to form a polygonal view depicting which-won-where pattern and all other genotypes within the polygon. The segmented lines perpendicular to the sides of polygon cleave the biplots into different sectors inclusive of both genotypes and environments. The vertex genotype located in a particular sector is the most suitable and high yielding genotypes of that environment. Environment 1 and 4 consist of one high yielding genotype HD-2733 while the genotype HD-2985 was high yielding in 3 and 6 environments. The genotype HI-1563 was high yielding and high performance in environment 5 means 6th Nov sowing in 2018-19. Here the date of sowings *i.e.,* 27thOctober, 6th Nov and 16th Nov of 2017-18 represents the environment 1, 2 and 3, and 27th Nov, 6th Nov and 16th Nov of 2018-19 represents environment 4, 5 and 6, respectively. Though, the genotypes HD-2733 and HI-1563 were identified as the high yielding but they were highly unstable in nature. Therefore, their performances are very unpredictable and cannot be considered for wider cultivationcommercially.However, they were highly adapted specifically in the favourable environment.

However, three genotypes can be considered ideal for grain yield as observed in the AMMI biplot forming both vertices as well as nearer to biplot origin. The genotypes that were nearer to the PCA origin were found to be stable in the respective environment. For number of grains per panicle, eight most stable and high yielding genotypes were identified along with five low yielding stable genotypes. Since these genotypes had PCA 1 values near to zero therefore they had negligible interactions across environments. Genotypes with higher PCA values showed high interaction with the environment and were thus unstable. Environment 1 and 4 consist of genotypes DBW-107 and RAJ-3765 as high number of grains per panicles while the genotype HD-2985 was having higher number of grains per panicles in 2, 3, 5 and 6 environments (Fig. 2). The different interactions observed may be due to different environments and different genetic constitution of the genotypes. From the AMMI 2 biplot of number of days for heading to maturity, six genotypes were observed far away from the biplot origin. These genotypes were either the lowest or high number of days for heading to maturity in some or all the environments (Fig. 3). While, the vertex of polygon for a particular sector is the highest yielding genotype for the particular environment falling in that sector [36, 22]. According to Sood *et al*. [30], the genotypes located in the vertex within a sector of AMMI biplot is the high yielding genotype. Here, four best genotypes for heading to maturity were identified for environment 1, 4 and 5 with two vertex genotypes. For environment 3 and 6, there were one vertex genotype and four other genotypes with less mean which may be a desirable one for such trait.

The polygonal view of AMMI biplot depicts seven vertices with four promising genotypes (Sonalika, HD-2985, HD-2643 and NW-2036) possessing highest number of panicles per plant in environment 1 and 5 whereas HD-3118 and DBW-14 genotypes in environment 3, 4 and 6. In the character days to heading to maturity and 50% physiological maturity, the genotype RAJ-3765 was located farthest from the biplot origin and are therefore unstable in nature. Grain yield, number of panicles, grains per panicle, number of days for heading to maturity and 50% physiological maturity are the economical characters of the crop.

As per AMMI biplot analysis, five genotypes (HD-2985, HD-2733, HD-3118, NW-2036, NW-1014, HI-1563 and RAJ-3765) for higher grain yield, three genotypes (HD-2985, HD-3118 and RAJ-3765) for grain weight per plant, five genotypes (HD-2985, HD-3118, HD-2967, NW-2036 and RAJ-3765) for number of grains per panicle, four genotypes (HD-2643, NW-2036, HI-1563 and WR-544) for number of days for heading to maturity, four genotypes (HD-2985, HD-3118, HD-2643 and NW-2036) for number of panicles per plant and four genotypes (HD-2733, HD-2643, HD-2967 and RAJ-3764) for days to 50% physiological maturity were promising, high yielding stable genotypes best suited to the testing environments adopted. This may be promoted for stable varietal development programme since a genotype is said to be successful only when it is able to express its economical traits while maintaining the stability making the selection procedure more reliable and accurate [20]. The affinity of AMMI model along with Eberhart and Russell method is highly recommended in stability analysis for obtaining superior genotypes [25].

For the testing environments, the first sowing date (E1) 27th Oct., 2017-18 and (E4) 27th Oct., 2018-19, the second sowing date (E2) 6th Nov., 2017-18 and (E5) 6th Nov., 2018-19, likewise the third sowing date (E3) 16th Nov., 2017-18 and (E6) 16th Nov., 2018-19 create three different mega environment and pairwise they were close to each other indicating equal efficiency in differentiating varied genotypes.

4. Conclusion: the present investigation on wheat was to identify genotypes having high economical yield that can perform consistently over the different sowing dates as environments and for identification of suitable productive environment in Meghalaya condition. The genotype HD-2985 and RAJ-3765 were found to be high yielding and stable genotypes across the testing environment and genotype HD-2733 and HD-3118 were identified high yielding specifically adapted genotypes in the rich and favourable testing environment. From the present study, it could be inferred that identification of stable genotypes using both the analytical model showed almost similar results. However, AMMI & GGE biplot showed its superiority in identification of more desirable genotypes visually and delineation of the mega environment for testing of genotypes for their varied response to environment.

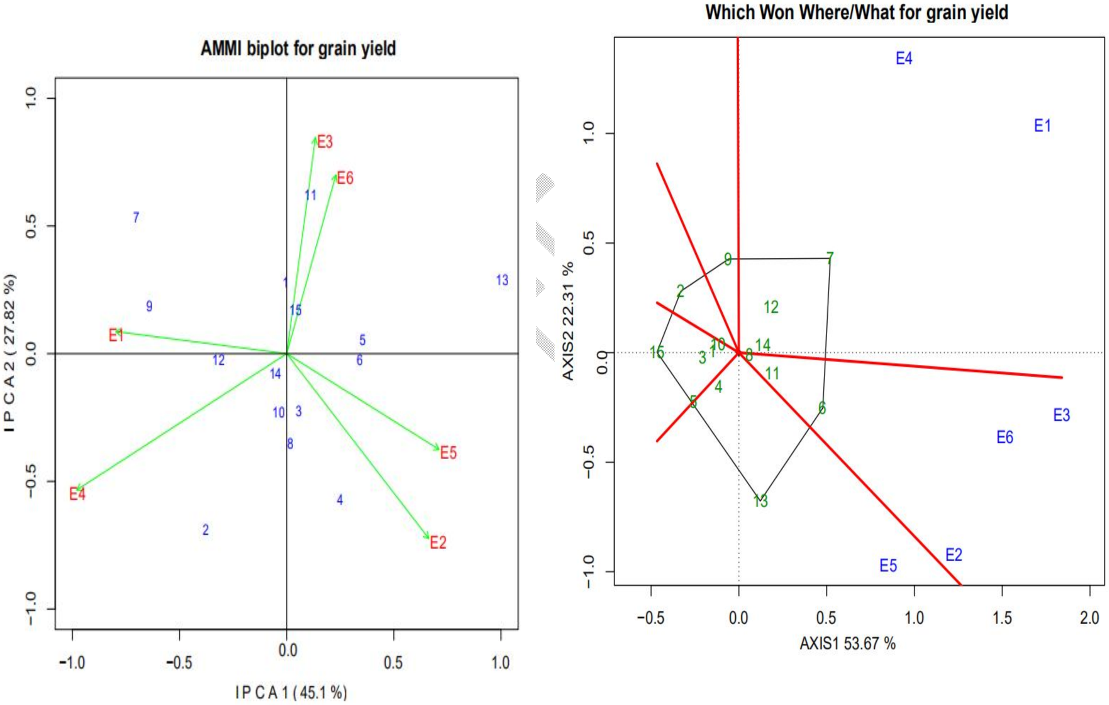


Fig. 1. AMMI 2 and GGE biplot for grain yield of the 15 genotypes of wheat for six environments.

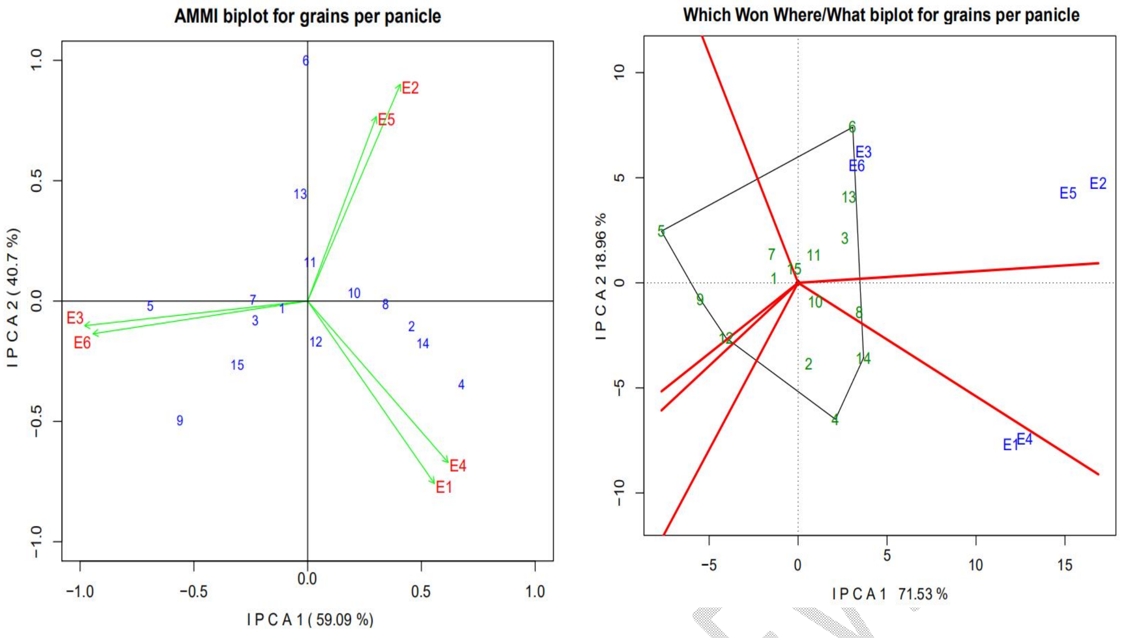


Fig. 2. AMMI 2 and GGE biplot for number of grains per panicle of the 15 genotypes of wheat for six environments.

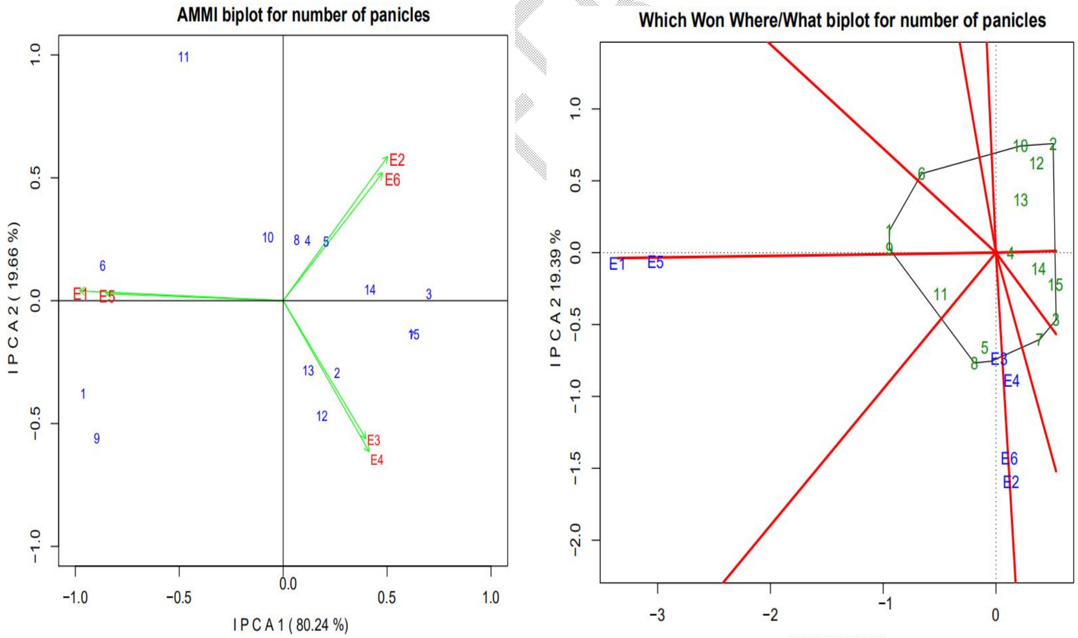
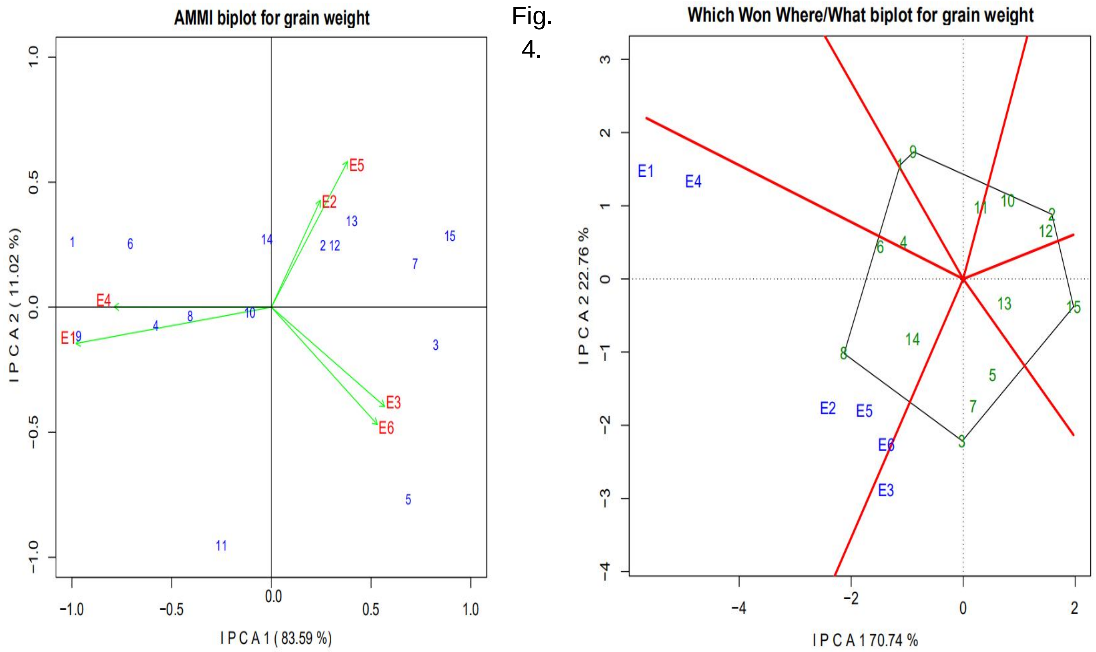


Fig. 3. AMMI 2 and GGE biplot for number of panicles per plant of the 15 genotypes of wheat for six environments.

Fig. 4.



AMMI 2 and GGE biplot for grain weight of the 15 genotypes of wheat for six environments.

Disclaimer (Artificial intelligence): Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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