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Yield Stability Analysis of Wheat Genotypes at Irrigated, Heat Stress and Drought Condition

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ABSTRACT

Wheat (*Triticumaestivum*) is the largest food crop to cover the earth's surface and the second largest crop after maize in terms of the production in the world. Demand of wheat is rising and it is expected that by 2050 the requirement of wheat would be 60% higher than the present year. Food security is the major challenge faced by human race in the 21st century. The uncertainty in environmental condition will cause a reduction of 7% in the global crop yield. The cultivation of wheat will be most affected because wheat is vulnerable to high temperature, drought and heat stress. Environmental influences are considered as the measurement criteria for genetic stability. Sensitivity of a crop genotype to the environmental factors gives rise to genotype-Environment Interaction (GEI). Breeders' objective is to develop varieties that give high productivity under available environmental conditions. From this study GEI of the 20 wheat genotypes evaluated was found to be significant for grain yield. Significant variance for Genotype, environments and genotype by environments interaction is shown by AMMI analysis for the additive main effect and multiplicative interaction effect. The AMMI gives top model fitness while conducting a study of genotype with the environment interaction of 20 wheat genotypes in six different environments. The consideration of stability and mean grain yield is most important for multi-environment adaption trial. GGE showed that genotypes 14(NL1325), 5(NL1244) and 15(NL1326) were winning genotypes or best genotypes for irrigated, drought and heat stress condition respectively. Similarly 11(BL4708), 13(NL1260), 10(BL4707), 2(NL1202), 4(NL1211) are good performing genotypes in normal condition and can be recommended where normal sowing area. Genotype 15(NL1326) is winning genotypes for Heat stress condition and 9(BL4699) also perform better at such environmental condition and can be recommend for late sown area. Genotype 5(NL1244) is best for Drought condition, also 16(NL1327) has high yield but lower stability. So Genotype 5(NL1244) can be recommended at rain fed or water stress proned area. As per the ASV and AMM1 biplot NL1202, RR21, Gautam, Bhrikuti and NL1253, the genotypes of bread wheat were stable genotypes. These are coupled with higher mean grain yield. Besides, the genotype BL4708 has highest mean yield with good stability. So this six genotypes can be recommend as stable genotypes in normal, Drought and heat stress condition.

Keywords: Wheat, Heat stress, Drought, Stability, Genotypes

INTRODUCTION

Triticum aestivum, commonly known as wheat, is a cereal grass placed in family *poaceae*. Wheat has high importance among cereal crop in Nepal after rice and maize and is ranked at 3rd position both in order of area and productivity according to Wheat Atlas. Apart from yield potential, quality traits possessed by wheat seeds should be high temperature tolerance and drought tolerance. Wheat is a mesophytic plant so for cultivation of wheat temperature range is relatively narrow and ranges from 10-15°C while sowing and 21-26°C during the ripening period though there are varieties of wheat that can even grow at 35°C.With every passing year, there is change in rainfall patterns, increase in Carbon dioxide and other greenhouse gases concentration along with decrease in annual precipitation [1]. The period 1980 to 2015 has been the warmest period of the 1400 year duration; global temperature has risen to about 0.85°C during this period. This climate change will have lethal effects on the natural systems. In many regions of the world there is alteration in the precipitation patterns and snow is melting. One of the consequences of climate change will be the reduced crop yield and it is believed to be the major risk in the realm of agriculture [2]. Among all the crops, wheat production will be highly reduced due to rise in temperature. If the global temperature rise just 1°C it would lead to fall in global wheat yield. World' s total wheat production is 701 million tons. Reduction in wheat yield is estimated to be from 4.1-6.4 percent that makes about 42 million tons of wheat. Heat stress adversely affects osmotic adjustments, seed germination, seedling emergence and rate of photosynthesis. Wheat plant exposure to high temperature after anthesis caused reduction in rate of grain filling. Heat stress before anthesis also resulted in reduction of yield Heat stress destroys thylakoid membranes and causes generation of reactive oxygen species that inactivate the chloroplast enzymes. Due to reduction in photosynthesis wheat plants show poor growth and in turn their yield decreases [3]. The trend of rise in world population is explosive. If the population keeps on increasing in this manner then feeding the population in the face of environmental stresses would be a frightening problem.

Along with heat stress climate change would come with other problems one of them is drought. Drought negatively affects the plant development, growth, morphology and physiology. It reduces the number of spikes per m2, number of grains per spike and the time period in which the wheat completes its cycle [4]. Drought is a period of dry weather that can extend from months to years and area under drought does not receive normal amount of rain. Temperature rise of 1°C increases evapotranspiration to about 3-5%.Main limiting factor for wheat cultivation in Nepal is lack of water for wheat cultivation and genetic makeup [5]. Water requirement of wheat crop is estimated to be 266.8-500 mm which is much higher as compared to water requirement of other crops including maize [6]. Wheat yield is strongly influenced by the availability of water. By 2050, there is utter need for increasing crop yield from 50% to meet the necessities of rapidly growing population. Agriculturists are striving for development of wheat varieties that can withstand heat and water stress.

Among the factors that affect food security worldwide, drought is listed at the top. Drought negatively affects the plant development, growth, morphology and physiology. It reduces the number of spikes per m^2, number of grains per spike and the time period in which the wheat completes its cycle [4]. Effect of water stress on plant depends on several factors including severity and time period of stress, developmental stage of plant and genetics of the cultivar. Water stress not only affects morphological characters but also physiological characters. Under drought plants close their stomata to prevent the loss of water through evaporation due to which turgor pressure drops [7]. When a plant is exposed to long duration of water stress, stomata die because starch in the guard and mesophyll cells denature. In turn, diffusion of carbon dioxide in the leaf is reduced due to which photosynthetic activity falls. In plants that are negatively influence by water stress increase in protein synthesis was observed. Drought and heat stress if combined significantly reduce the yield of wheat. To confront the ever-rising demand of wheat there is need for marker assisted selection and screening of heat and drought tolerant varieties and germplasms of wheat.

A good seed and good field produces high yield. It highlights the importance of both genotype and environment in attaining high productivity and yield. Breeding of just these well adapted commercial high yielding varieties narrowed down the wheat diversity in some of countries [8]. In 21st century, to deal with food scarcity there is need for seeds that can adapt to the environmental challenges coming ahead [9]. All the similar individuals in a population behave similarly to the stress conditions. That’s why Stability of genotypes is crucial for improvement, breeding, survival and adaptability to get a high quality and quantity produce that would be enough to feed people in the era of population explosion [10]. To achieve these aims selection of wheat genotypes is important that can tolerate major environmental stresses like heat and drought is crucial.

Environmental influences are considered as the measurement criteria for genetic stability. Sensitivity of a crop genotype to the environmental factors gives rise to genotype-Environment Interaction (GEI). Breeders’ objective is to develop varieties that give high productivity under available environmental conditions. Same genotype of a crop (wheat) grown under varying environmental conditions give rise to different productivity. This alteration in yield is the result of genotype-Environment Interaction. This interaction brings difficulties and laborious tasks of testing for breeders. This testing is done by alternating the environmental conditions provided. In case of wheat, the major limiting factors are Heat and water stress; therefore, to analyse the stability of a genotype it is inevitable to test it in multi-environments by varying favourable and unfavorable conditions for wheat growth [11].Wheat production can take a leap via Crop Management Research (CMR), genetic gain in yield potential, genetic gains in tolerance to biotic and abiotic stresses and synergistic effects by combining all these factors [12].

MATERIALS AND METHODOLOGY

The field experiment was conducted at Bhairahawa, Rupandehi, Nepal. Geographic location of the research site is 27°30' N and 83°27' E and at the altitude of 79 meters above the sea level. This site has a humid sub-tropical climate where summers are hot and winters are cold with total annual rainfall as 1725.3 mm. The agro-metrological information (**Figure 1**) was collected from National Wheat Research Program (NWRP), Bhairahawa, which is the nearest meteorological station from the research sites.

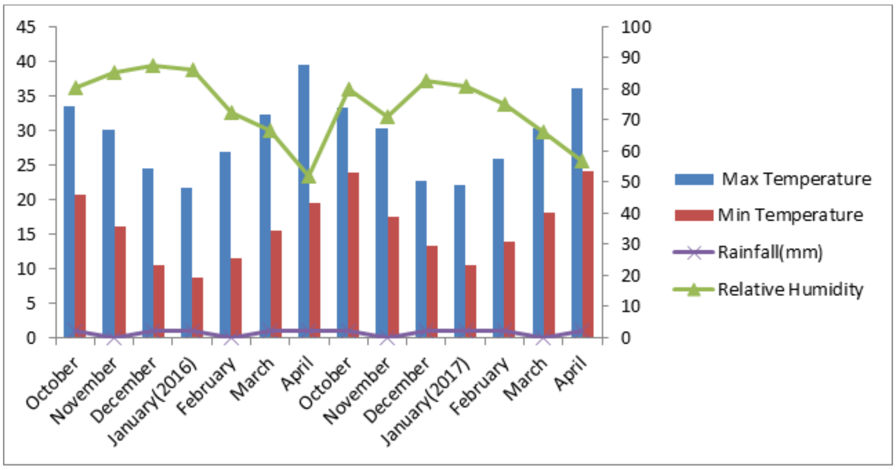

Figure 1: Agro-metrological data (2016-2018) of research site.

A set of 20 wheat genotypes were obtained from National Wheat Research Program (NWRP), Bhairahawa, Nepal. There were 4 Bhairahawa lines (BL), 13 Nepal lines (NL) and 3 commercial varieties. Bhrikuti, RR21 and Gautam were used as the standard check variety which was released as variety of Nepal. The complete sets of genotype with their entry names are presented in the **Table 1**.

Table 1: List of genotypes used for the field experiment.

S. No	Genotypes	Source	Origin	Parentage	Released year
1	BL4335	NWRP,Bhairahawa	Nepal	n.d	n.d
2	NL1202	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
3	NL1207	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
4	NL1211	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
5	NL1244	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
6	NL1247	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
7	NL1253	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
8	NL1254	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
9	BL4699	NWRP,Bhairahawa	Nepal	n.d	n.d
10	BL4707	NWRP,Bhairahawa	Nepal	n.d	n.d
11	BL4708	NWRP,Bhairahawa	Nepal	n.d	n.d
12	BL4307	NWRP,Bhairahawa	Nepal	n.d	n.d
13	NL1260	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
14	NL1325	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
15	NL1326	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
16	NL1327	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
17	NL1328	NWRP,Bhairahawa	CIMMYT, Mexico	n.d	n.d
18	BHRIKUTI	NWRP,Bhairahawa	CIMMYT, Mexico	CMT/COC75/3/ PLO//FURY/ANA75	1994
19	RR21	NWRP,Bhairahawa	CIMMYT, Mexico	1154-388/AN/3/ YT54/NIOB/RL64	1971
20	GAUTAM	NWRP,Bhairahawa	Nepal	SIDDHARTH/ NING8319/NL297	2004

The field experiment was conducted following Alpha Lattice design (**Figure 2**) with five blocks and the block size of 4 plots, replicated twice, irrigated as normal condition, drought as water stress and heat stress condition as late season. In each replication there were 5 blocks consisting of 4 plots. Each genotype was planted in a plot size of 10m² (4m×2.5m). Each plot was provided with rows with spacing of 25 cm between rows and there was continuous sowing as in line sowing method. There was gap of 0.5 meter in each plot and 1 meter gap between two replication (**Table 2**).

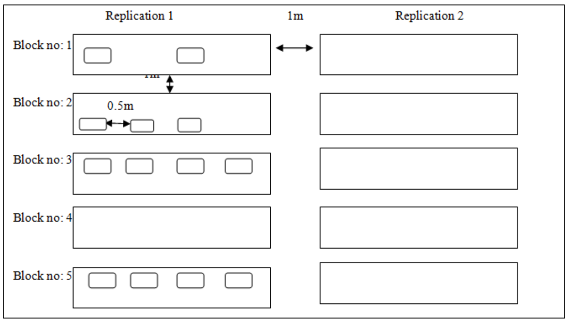

Figure 2: Experiment layout of the field in alpha lattice design.

Table 2: Indication of Year*environments and environments.

No.	Year*Environment	Envt.	Envt.
1	2017_irrigated	A	1
2	2018_irrigated	B	2
3	2017_Rainfed	C	3
4	2018_Rainfed	D	4
5	2017_Heat_Stress	E	5
6	2018_Heat_Stress	F	6

Stability analysis by statistical method

Research data is very valuable and expensive. To fully understand and correlate all these factors and to derive conclusions there is need for statistical analysis. The most important among these are ANOVA, AMMI model and GGE biplot. Data entry and processing was carried out using Microsoft Office Excel 2010. Analysis of variance of all the parameters and calculation of means was done by using R3.5.0 a software package for alpha lattice design by ADEL-R (CIMMYT Mexico). An individual year-environment considered as a unique and random environment while a genotypic effect was analyzed as fixed. The BLUPs data and combined analysis of all environment was done by META-R (CIMMYT, Mexico).Stability measurement were performed on grain yield under six environments (two seasons and three environments which compose six environments) i.e. AMMI and stability by using R softwear GEAR (version4.0, CIMMYT, Mexico).The combination of 2 tests ANOVA and Principal component analysis (PCA) is known as Additive Main Effect and Multiplicative Interaction (AMMI). Application of AMMI leads to the identification and screening of genotypes that are least affected by GEI i.e., having stability and adaptability features. AMMI makes use of ANOVA first for the calculation of Environment and Genotype additive effect that is of major concern and later AMMI utilizes PCA to analyze residual from ANOVA. PCA calculates the genotype score and environmental score, the product of these 2 will give the yield of the crop under study. This test provides reliable and least error prone estimates of genotype performance.

The equation of AMMI model is as stated below:

Where Y_{ger} is the observed yield of genotype g in environment e for replicate r. The additive parameters are: µ the grand mean, αg the deviation of genotype g from the grand mean, β_e the deviation of environment e. The multiplicative parameters are: λ_n the singular value for interaction principal component axis (IPCA) n, γ_{gn} the genotype eigenvector for axis n, and δ_{en} the environment eigenvector. The eigenvectors are scaled as unit vectors and are unit less, whereas λ has unit of yield. A convenient scaling for the multiplicative parameters is $\lambda^{0.5}$ γg and $\lambda^{0.5}$ δ_e, termed the “genotype IPCA scores” and “environment IPCA scores” because their product gives the expected interaction value directly without need of a further multiplication by singular value. There are at most min (G-1,E-1) axes, but usually the number of axes N retained in the model is smaller, producing a reduced model denoted AMMI1 or AMMI2 if retaining 1 or 2 IPCAs, and so on. A reduced model leaves residuals, ρ_{ge}. Finally, if the experiment is replicated, there is also the error term ϵ_{ger}.

Furthermore, to determine the stability of genotypes in positions using PCA columns (main component axis) and ASV (AMMI stability value) the AMMI analysis too is used on the basis of relative contribution of IPCA1 to IPCA2 to the sum of interaction of square the ASV was also calculated for each of the genotype. Measurement of quantitative stability is essential to quantify and rank genotypes as per their yield stability, though the AMMI model has no such provision to measure quantitative stability. Therefore the given equation was proposed by Purchase (1997).

Those genotypes that have less ASV were taken as widely adapted genotypes. Likewise, the IPCA2 score close to zero showed greater stability, whereas higher values showed more sensitivity and less stability in genotypes.

For the determination of effect of environment (E), genotype (G) and GE interaction GEAR software is used. To get the biplot the first two components obtained from the principal components were used by GGE biplot software (Gabriel 1971). Given below is the basic model for a GGE biplot.

Where Y_{ij} = the mean yield of genotype i(=1,2,… ,n) in environment j(=1,2,…m), μ is the the grand mean, β j is the main effect of environment j, ($\mu + \beta$ j) being the mean yield of environment j, λl is the singular value (SV) of lth principal component (PC), the square of which is the sum of squares explained by PCl=(l=1,2,…,k with k $\leq$ min (m,n) and k=2 for a two-dimensional biplot), ξ_{il} is the eigenvector of genotype i for PCl, η_{lj} is the eigenvector of environment j for PCl, ε_{ij} is the residual associated with genotype i in environment j.

We need to partition the SVs into the genotype and environment eigenvector in order to generate a biplot which we can used during the visual analysis of MET data due to which the above model can be expressed in the form of

Where for for genotype i and environment j the PCI scores are g_{il} and e_{lj} respectively. The genotype i presented as a point defined by all g_{il} values, and environment j is presented as a point defined by all e_{lj} values (l=1 and 2 for a two-dimensional biplot) in a biplot.

If there were the data's that are environment-standardized, to generate the GGE biplot the common formulae would be as follows

Where Sj is the standard deviation in environment j, i=1,2, … .,k, gi1 and e1j are PC1 scores for genotype i and environment j, respectively. In the present study we used environment standardized model.

RESULTS

The AMMI analysis can be used to diagnose whether a specific sub-case provides a more appropriate analysis.

AMMI has no specific experimental design requirements, except for a two way data structure. "Although the AMMI analysis of performance tests does not use data on environmental factors, these factors such as rainfall, the daily average, maximum and minimum temperatures, as well as height and amplitude, nitrogen fertilizers; irrigation and the clay content are often related to the statistical data of the AMMI.

The results of AMMI model for grain yield are presented in **Table 3**. As it can be seen from the table, the mean square of the three IPCA were highly significant (p<0.001). AMMI multiplicative component further partitioned the GE interaction into five interaction principal component axes (IPCAs). However, only the first three axes showed significant contribution to the GEI in the AMMI model. The remaining two principal components contributed insignificant portion of the variation. The AMMI biplot, which accounted for 93.57% of the G x E interaction, provides the interaction principal component scores of the 1st and 2nd IPCA with 44 degrees of freedom. The first PC axis (PC1) score explained 59.88% of the variation in GEI, while the second PC axes accounted for 33.68% of the variability. Many researchers witnessed that the best accurate AMMI model prediction can be made using the first two IPCA. Therefore, the dataset obtained from the interaction of 20 genotypes tested at 6 environments was best predicted by the first two IPCAs. On the other hand, the IPCA scores of a genotype in the AMMI analysis are reported as indication of the stability of a genotype across environments. Accordingly, the closer the IPCA scores are to zero (origin), the more stable the genotypes are across all their testing environments.

Table 3: The analysis of variance for grain yield using AMMI model.

Source of variation	df	SS	MSS	F-value	Explain (%)
Genoypes	19	6464748	340250	4.71***	3.6
Env	5	1.62E+08	32357379	276.75***	90.2
Env*Gen	95	11107135	116917	1.6208**	6.19
PC1	23	6433114	279700.6	5.86***	59.88385
PC2	21	3619187	172342.2	3.61185***	33.68988
PC3	19	378975.5	19946.08	0.41802	3.52776
Residual	120	8656291	72136		

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components. The greater the IPCA scores (positive or negative) as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype is across environments sampled. AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes.

The AMMI analysis for the IPCA1 captured 59.88% and the IPCA2 explained 33.69% and the two IPCs cumulatively captured 93.57% of the sum of square the GEI of bread wheat genotypes. When the IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot the more stable is the genotype and the reverse is true.

In AMMI biplot (**Figure 3**), the environmental scores are joined to the origin by sidelines. Environments A,B,C,D,E and F are connected to origin. The genotypes occurring close to the origin on the plot tend to have similar in yield in all environments, while genotype far apart may either differ in yield or show a different pattern of response over environments. Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield. Those genotypes that are clustered closer to the center tend to be stable and those plotted far apart are unstable in yield. Hence the genotype near the origin is not sensitive to environments and those distant from the origin are sensitive and have large interaction. According, genotype 5,16,12,8,3,14,5 and 17 were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The 18,19,20,2 and 7 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments. The rest of the bread wheat genotypes (4,10,11,13,9,6) were unstable and were located distant from the origin. Genotypes 5,16 are positively interact at 3 and 4 envt. The genotype 1,9 positively interact at 5 and 6. Similarly genotypes 14 and 10 were positively interacting with 1 and 2 environment.

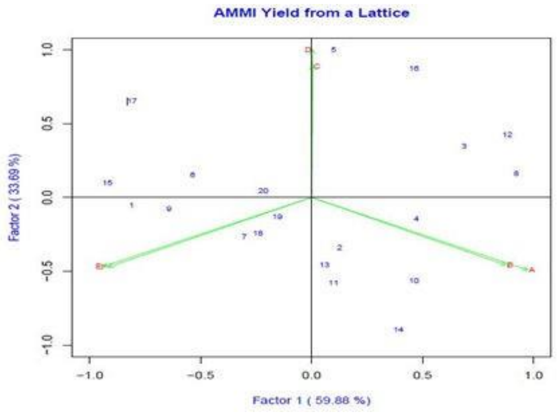

Figure 3: AMMI Biplot showing interaction of 20 genotypes with six different environments.

AMMI stability value (ASV)

The difference in stability measurement of the two principal components can be compensated by proportional difference between the IPCAs (1:2) then determined by Pythagoras theorem in effect of AMMI stability value. Purchase, (1997) noted that AMMI stability value (ASV) does not for quantitative stability measure by rather quantify and rank genotypes according to their yield stability. The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability (**Table 4**).

Table 4: AMMI-estimates per Genotypes (yield (kg/ha) across years and environments).

E.N.	Genotypes	Gy	ASV	YSI	rASV	Rysi	DIM1	DIM2
18	Bhrikuti	2426	5.73	6	4	2	-0.24336	-0.24259
1	BL4335	2251	18.12	24	15	9	-0.8125	-0.05381
9	BL4699	2356	14.9	17	12	5	-0.64389	-0.07532
10	BL4707	2258	13.47	17	10	7	0.459376	-0.5649
11	BL4708	2439	10.06	7	6	1	0.097059	-0.58125
20	GAUTAM	2106	5.31	16	3	13	-0.21836	0.045807
2	NL1202	2386	4.32	5	1	4	0.125025	-0.33909
3	NL1207	1961	14.84	30	11	19	0.687692	0.34761
4	NL1211	2252	10.54	16	8	8	0.471302	-0.14636
5	NL1244	2068	18.04	28	14	14	0.099435	1
6	NL1247	2040	13.42	25	9	16	-0.53692	0.152168
7	NL1253	2285	7.11	11	5	6	-0.30453	-0.26906
8	NL1254	2055	20.68	34	19	15	0.921694	0.162884
13	NL1260	2131	10.19	19	7	12	0.056077	-0.45926
12	NL1307	1965	19.19	35	17	18	0.880484	0.42508
14	NL1325	2199	20.79	31	20	11	0.389781	-0.89709
15	NL1326	2244	17.75	23	13	10	-0.92121	0.099591
16	NL1327	2389	19.39	21	18	3	0.45944	0.871779

17	NL1328	1889	18.87	36	16	20	-0.8104	0.655195
19	RR21	2011	5.15	19	2	17	-0.1562	-0.13137

The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability. Considering the first interaction principal component (IPCA1) the genotypes NL1326, were the most stable genotype with IPCA1 value (-0.921) followed by BL4335, NL1328 and BL4699 with IPCA1 value of (-0.8125, -0.810, -0.644). When the second interaction principal component (IPCA2) was considered NL1325 was the most stable genotype with interaction principal component value (-0.87) followed by the genotype BL4708 and BL4708 with the IPCA2 value (-0.581 and -0.565). The two principal components have their own extremis, but calculating the AMMI stability value (ASV) is a balanced measure of stability. Based on ASV genotype NL1202 was the most stable with an ASV value of 4.32 followed by the genotype RR21,Gautam Bhrikuti and NL1253 with ASV value of 5.15, 5.31, 5.73 and 7.11 in grain yield respectively and the genotype NL1325, NL1254, NL1327 and NL1328 were the most unstable with ASV value of 20.79,20.68,9.39 and 18.87 in grain yield respectively.

GGE biplot analysis

Which-won-where model: To explicitly display the 'which-won-where' pattern and sensitivity degree between the variety and environment, polygon view of a GGE biplot based on the IPCA1 and IPCA2 values was displayed in **Figure 4**. Yan and Kang explained that the polygon view of a biplot was the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot. From this polygon view of biplot, test environments and genotypes fell into 3 and 8 sectors respectively. 5 of the sector in the polygon had no test environments. A, B, C and D, E and F are in one sector each suggesting repeatable performance of genotypes in this environments.

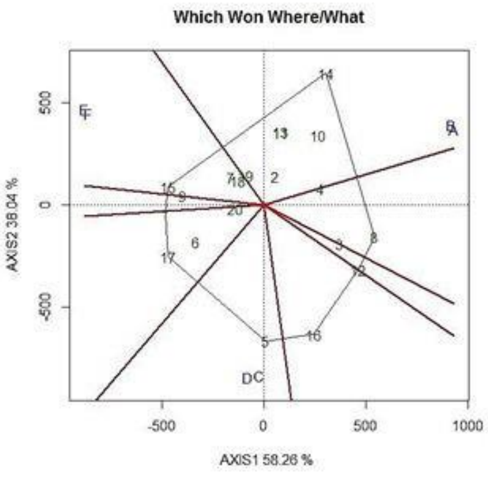

Figure 4: Which-won-where for genotypes and environments. The Polygon view of genotype environment interaction for wheat-barley disomic addition lines over six test environments.

In this study, this 'which won where' feature of the biplot identified wining genotypes; 14 for instance was the winning/ corner genotype in locations A and B. Similarly, 5 was the vertex/winning genotype in location C and D. And 15 is winning genotypes for E and F environment. They were also the most responsive genotypes which also showed specific adaptation [13]. They show lower or decreased stability. According to the findings of Yan and Tinker, the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction. These genotypes are referred to as vertex genotypes characterized by having the longest distance from the origin of the biplot in their directions. On the other hand, the result also showed some genotypes which fall in sectors where there were no locations at all; these genotypes are poorly adapted to six of the testing locations (3,8,12,16,6,17). From this study, Genotypes 2,7,18,19,20 and 4 are most stable genotype as they are nearer to point of origin.

Mean vs stabilty model: Performance and stability of genotypes were visualized graphically through the GGE biplot. This can be evaluated by average environment coordination (AEC) method [14]. In **Figure 5**, the line with single arrowhead is the AEC (average environment coordinate) abscissa. AEC abscissa passes through the biplot origin and marker for average environment and points towards higher mean values. The average environment has average PC1 and PC2 scores across environments [15]. The perpendicular lines to the AEC passing through the biplot origin are referred to as AEC ordinate. Greater the absolute length of the projection of a genotype indicates more instability. Furthermore, the average yield of genotypes is approximated by the projections of their markers to the AE Cabscissa [15].

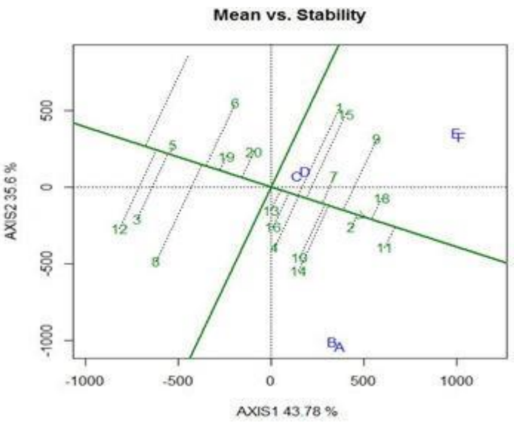

Figure 5: Mean *vs*. stability of 20 different genotypes.

The greater the absolute length of the projection of a cultivar, the less stable it is. An ideal genotype should have the highest mean performance and absolute stable(less absolute length of projection). Based on this, Entries 11(BL4708), 18 (Bhrikuti) and 2(NL1202) were the most stable with an above average performance, as they are closed to arrow. In contrast, entries

8(NL1254), 17NL1328), 1(BL4335), 15(NL1326), 14(NL1325) were the least stable genotypes. However, entries 5(NL1244), 19(RR21) and 20 (Gautam) were the lower yielding as compare to mean yield but very stable genotypes. Entries 17(NL1328), 12(NL1307), 8(NL1254) and 6(NL247) were not only low yielding but also among the least stable genotypes.

Ranking genotypes

In the biplot, an ideal genotypes is located at near the arrow of the center of concentric circle.it is the location with longest vector of all the genotypes and with near zero ordinates ATC axis projection. In view of this, Genotypes 15(NL1326) and 9(BL4699) were the most ideal genotype. The genotypes 15(NL1326) and 9(BL4699) could be used as a reference for genotype evaluation. They could also have the greatest commercial success because they showed the highest stability. Other desirable genotypes included 1 (BL4335)and 7 (NL1253) (**Figure 6**) and this could be included in further testing in stress and non-stress environments.

15>9>1>7>18>19>20>6>17>2>16>11>4>10>14>3>5>8>12 >16

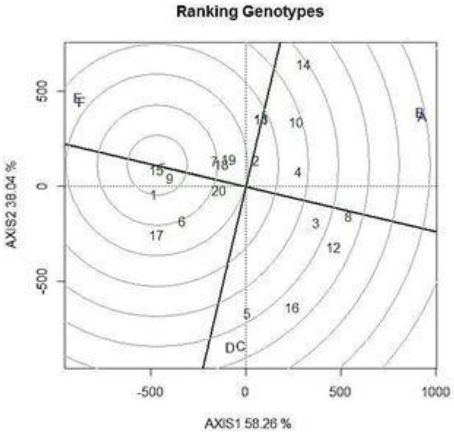

Figure 6: The comparison method ranks the genotypes to an ideal genotype.

DISCUSSIONS

AMMI analysis

Crossa et al. indicated that the AMMI model can be used to analyse GEI and identify superior grnotypes [15]. Furthermore, he stressed that it can be used in selecting the best test environments for assessing the genotype. Fan et al. demonstrated that the GGE biplot methodology was a useful the limited resources available for wheat breeding programs.

Annicchiarico (1997) stated that the AMMI analysis seems to be particularly useful in describing the adaptive responses of small grain cereals tested in a wide range of environments. At the same time, the researcher explained that joint regression and AMMI analysis are more likely to be performed in the same way and to provide similar results for small grain cereals in areas where cold stress is limited.

From the results of the combined analysis of variance, the genotypes contributed 3.6% of the total variation in the sum of squares for grain yield, while E and G × E sources of variation accounted for 90.02% and 6.19% of the total variation respectively. This result is consistent with the findings of Fakorede and Adeyemo (1986), Badu-Apraku et al. and Mohammadi et al. who reported that the largest proportion of total variation in multi-environment trials is attributed to environments, whereas G and G × E sources of variation are relatively smaller. The significant mean square for location showed that genetic effects were influenced by the environments, which is a consequence of environmental diversity. Similar observations were reported by Butron et al. in which they indicated that G x E effects for grain yield were mainly due to environmental yield limiting factors such as the mean minimum temperature and relative humidity. The observed Significant G x E mean square for grain yield suggested that the locations for which the Genotypes were tested comprise of a number of special environments. Hence, Genotypes selected should be specifically adapted to the different environments.

Ammi stability value (ASV)

In ASV method, a genotype with least ASV score revealed the most stable. Genotypes NL1202 is the most stable followed by RR21, Gautam, Bhrikuti and NL1253.Similarly, NL1327 and NL1328 were most unstable. This was in agreement with Farshadfar who has used ASV as one method of evaluating grain yield stability of bread wheat varieties. Similar reports were also observed in Fereny who has studied adaptability and stability pattern of spring wheat using ASV and other stability parameters. In general, analysis using this AMMI model had been exploited in the variety evaluation of barley, wheat. The Genotypes with lower ASV values is considered more stable and genotypes with higher ASV are unstable. The significant mean square for location showed that genetic effects were influenced by the environments, which is a consequence of environmental diversity. Similar observations were reported by Butron et al. in which they indicated that G x E effects for grain yield were mainly due to environmental yield limiting factors such as the mean minimum temperature and relative humidity [14]. The observed Significant G x E mean square for grain yield suggested that the locations for which the Genotypes were tested comprise of a number of special environments. Hence, Genotypes selected should be specifically adapted to the different environments.

Yield stability index (YSI)

Stability is not the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability: rank-sum, modified rank-sum and the statistics yield stability In this regard, ASV takes into account both IPCA1 and IPCA2 and justifies most of the variation in the GEI. The least YSI is considered as the most stable with high yield mean. It was applied to identify high yielding stable genotypes in cereal crops like maize and durum wheat. By using these measures, suitable wheat genotype can be identified for varying existing environmental conditions. Based on YSI the most stable genotype with high grain yield is genotype NL1202 with the value YSI 5 followed by Bhrikuti and BL4708 with YSI value 6 and 7 respectively. While most unstable genotypes are NL128 with YSI value of 36 followed by NL1307 and NL1254 with YSI value of 35 and 34 respectively.

The genotype x environment interaction (GEI) has been an important and challenging issue among plant breeders, geneticists, and agronomists engaged in performance testing. The GEI reduces association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters that are sensitive to environmental fluctuations. Such traits are less amenable to selection. Both yield and stability of performance should be considered simultaneously to reduce the effect of GEI and useful for selecting genotypes in a more precise and refined way. Genotype NL1202 was the most stable with an ASV value of 4.32 followed by the genotype RR21, Gautam Bhrikuti and NL1253 with ASV value of 5.15,5.31,5.73 and 7.11 in grain yield respectively and the genotype NL1325,NL1254,NL1327 and NL1328 were the most unstable. Genotypes 5,16 are positively interact at 3 and 4 envt. The genotype 1, 9 positively interact at 5 and 6. Similarly genotypes 14 and 10 were positively interacting with 1 and 2 environment.

GGE biplot analysis

Which won where: The GGE biplot is an invaluable statistical tool for examining the performance of genotypes tested in different environments. The polygon view of the GGE biplot (**Figure 5**) indicated the best genotype in each environment. The “ which-won-where ” view of the GGE biplot is an effective visual tool in mega-environment analysis. The term mega-environment analysis defines the partition of a crop growing region into different target zones. It consists of an irregular polygon and lines drawn from the biplot origin. With this biplot, vertex genotypes located farthest away from the biplot origin in various directions with straight line and as a result rest of the genotypes placed inside the polygon. The rays in **Figure 6** are lines that intersect perpendicularly sides of the polygon or their extensions. Eight rays divide the biplot into eight sectors.

Yan and Kang explained that the polygon view of a biplot was the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot. The genotypes at vertex are the most responsive genotypes which also showed specific adaptation [13]. They show lower or decreased stability. According to the findings of Yan and Tinker, the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction. These genotypes are referred to as vertex genotypes characterized by having the longest distance from the origin of the biplot in their directions. The genotypes nearer to origin are most stable genotypes.

Mean vs stabilty model

Mohammadi and Amri also evaluated total entries of crop in six environments. The genotypes were also grouped into either high yielding or low yielding by the average tester coordinates(ATC).The line passing through the origin represents stability of genotypes. The vertical dark line is a performance line which passes through the origin of the biplot and helps to determine mean performance of a genotype with the right side from the origin showing increasing mean grain yield performance. The average yield of the cultivars is approximated by the projections of their markers on the average-tester axis.

Ranking genotypes

Through the genotype ranking, the genotype which had the highest grain yield and absolutely stable in performance across test environments was also identified (**Figure 6**). The ideal genotype basically has the highest average value of all genotypes and is absolutely stable (PCA scores near zero) in that it does not exhibit any genotype by environment interaction hence broad adaptation.

CONCLUSION

The differential ranking of genotypes showed the presence of the genotypes by location interaction for grain yield. After carrying out this study we have to the conclusion that the significant GEI in grain yield among the genotypes obtained differential response of the genotypes across the testing sites that are subjected to the different climatic condition and environmental factors. Thus for the all kind of location that are included in this trial, to pin point one superior genotype is a tough. This shows that a certain genotype most likely to rank differently in amount of grain yield in different location due to existence of either genetic diversity or differences in locations. Hence for assessing adaptability/ stability of performance and range of adaptation it very crucial to test newly developed genotypes under numerous environments and should be analyzed using GGE and AMMI.

Thus on the basis of overall mean grain yield and stability of this multi-Environment varieties 2(NL1202), 7(NL1253), 18(Bhrikuti), 19(RR21), 20(Gautam) could be grown to farmers in all areas as it is stable variety. Likewise, genotypes 14(NL1325), 5(NL1244), 15(NL1326) could be recommended for release to irrigated, Rainfed and heat stress environments respectively. Similarly 2,10,11,13(NL1202,BL4707,BL4708,NL1260) were good for Irrigated condition likewise genotypes 7(NL1253), 18(Bhrikuti), 19(RR21), 9(BL4699), 15(NL1326) good for heat stress environments.

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