

STABILITY ANALYSIS OF ADVANCE WHEAT LINES FOR YIELD ACROSS VARYING LOCATIONS THROUGH STABILITY INDICES

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Abstract

In present era of climate change, it's a big challenge for the breeders to minimize the yield losses specifically caused by the G x E interactions. The basic intention of present study was the assessment of stability in performance of diverse wheat genetic material in various parts of the country. In the study, 30 diverse advance wheat genotypes were sown at 6 locations namely Islamabad, Chakwal, Pirsabak, Bahawalpur, Tandojam and Faisalabad. By Pooled Analysis of variance (ANOVA), highly significant differences were obtained for the main effects of genotypes, environments and genotype x environment interaction ($p < 0.01$). Average yield performance across the environments was found to be varying in between 2.58 to 5.29 t/ha while in a comparison of genotypes' average it ranged from 4.73 t/ha (G1) to 3.482 t/ha (G30). Based on the stability parameters, five genotypes (G13, G16, G19, G20 & G23) were referred to as better yielding and more stable as these were having above average yield, regression coefficient near to unity and deviation from regression around zero. It is evident from heat map that some genotypes exhibited higher yield in certain set of environmental conditions as compared to others because of significant affection between genotype and environment. In GGE bi plot about 65 % variability was explained by two components (PC1 39.1% and PC2 25.2%). Here in this study the genotype G21 was best in terms of yield and stability for the environments. In order to figure out environment specific genotypes its vivid how efficiently the genotypes performed for specific environments so highest yielding genotype can be picked from a sector for accompanying environment.

Keywords: *Adaptability, GGE Biplot, Principal Component Analysis, GxE Interaction, Heat Map*

Introduction

Wheat (*Triticum aestivum* L.), belonging to the family Poaceae is most influential cereal crop. It is staple food of most of the countries around the globe including Pakistan and is consumed by nearly 40% of the world Population (Curtis and Halford 2014). More than 50% of world population depends on wheat grains to fulfill half of their dietary and protein requirements. About 60 % of the daily calories and 28 % of world edible dry matter is provided by the wheat (Chakmak, 2008 ;Ladha et al. 2016).

Wheat is one of the most important crops in Pakistan as it contributes 1.6% to the GDP and 8.9% added in agricultural value (GoP, 2019). During 2019-20, globally it was cultivated on an area of about 215M hectares with 772.64 MT production (USDA, 2020). Major producing countries include European Union being at the top followed by India, Russia, United States, Canada & Australia (USDA 2020). Pakistan ranked 8th in global wheat production with 25.7MT from an area of 9 MH (USDA 2020) but in terms of average yield per unit area Pakistan stands at 60th position (GoP 2019). An increase of 3.13% was observed in current year's wheat production in Pakistan as compared to the previous year production (24.3 MT).

Main objective of most of the breeding programs is to attain high yield. Yield is not a simple factor but is the result of the performance of complex contributing characters. Yield being a quantitative feature, is affected by the environmental factors on large (Arain et al., 2011; Pirttioja et al. 2015). Stability in performance of different high yielding wheat genotypes is determined by their good genetic potential and adaptability to the growing environment (Ali et al., 2008; Miah and Uddin, 2016).

Considering the rapidly changing climatic conditions, presence of genetic diversity is of immense importance (Bharanwalet al., 2013). A wider range of variability enables to get better performance due to the presence of genotypes possessing the alleles which are well suited to changing environments (Khan et al., 2007; Zeb et al., 2009; Sajjad et al., 2018). Being controlled by the process of natural selection in wider range of climates only the fittest will

prosper and the undesired will be ruled out thus helping the development of superior populations (Arain et al., 2011; Kalimullah et al., 2012).

While considering the commercial significance of a crop, the stability in the genetic structure is pivotal in diverse environments (Wu, 2000). Similar performance in changing environments reveals the ability of a genotype to over bridge the environmental masks so the cultivation of stable genotypes is required to ensure sustainable production (Riaz et al., 2013). As Pakistan is characterized by diverse environments in various parts of the country so adaptability and acclimatization of a variety is essential for its better survival and spread throughout the country (Ali et al., 2017). In present era of climate change, it's a big challenge for the breeders to minimize the yield losses specifically caused by the G x E interactions (Rauf et al., 2018). This can be achieved by improving the various morphological and physiological plant characters that may pose a significant positive effect towards plant's adaptability such as light interception, day/night cycle, maturity duration and growth rate without suppressing the yield (Ahsan et al., 2020).

A wide range of varieties have been developed as a result of various crop improvement programs that are superior in major yield contributing traits maintaining the food quality limits. However, field performance is determined by the expression of genetic potential relative to the environment because of significant G x E contribution (Janjua et al., 2014). Thus development of broad range varieties keeping in view the existing instability of climatic factors is a dire need of the time.

The basic intention of present study was the assessment of stability in performance of diverse wheat genetic material in various parts of the country. It will enable to evaluate and figure out the best suitable genotype for each region as well as the identification of stable genotypes that can be planted for higher yield all around the country. It will facilitate in terms of commercial cultivation in farmer field and their exploitation as parents in further crop improvement programs to attain desirable combinations.

Materials and Methods

Experimental:

In present study 30 diverse advance wheat genotypes (Table 1) were sown at 6 locations namely Islamabad (33.670N, 73.126E) (two trials), Chakwal (32.933N, 72.863E), Pirsabak (34.031N, 72.035E), Bahawalpur (29.354° N, 71.691° E), Tandojam (25.428N, 68.530E) and Faisalabad (31.450N, 73.135E), as shown in Fig 1. The experiment was carried out following standard field operations. A total of 7.5m² plot size was maintained keeping 30cm row to row distance among 6 rows in a plot where each row was of 5m. Similar agronomic practices were maintained according to the standards at all the locations in order to minimize the differences due to farm operations. Data for the yield and maturity duration were recorded at all the locations which was subjected to statistical analysis to reveal the results..

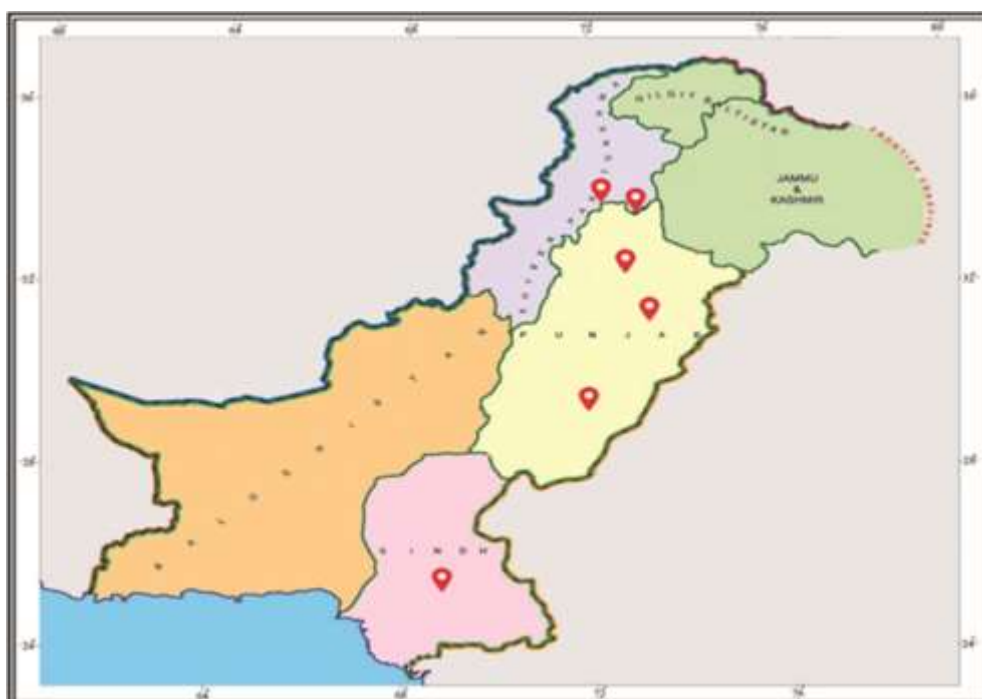


Figure 1: Experimental Locations for the Stability Studies

Table 1: List of 30 advance wheat lines with parentage and pedigree used in study

Geno type	Parentage	Pedigree
G1	SHORTENEDSR26TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARD	CMSS08Y01115T-099M-099Y-099M-099NJ-14WGY-0B
G2	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/QUAIU/5/BORL14	CMSS11B00520S-099M-099NJ-099NJ-31WGY-0M
G3	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07/4/MUTUS*2/TECUE #1	CMSS12B00028S-099M-0SY-23M-0WGY
G4	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI	CMSA10M00159T-050Y-099ZTM-099NJ-099NJ-5WGY-0B
G5	INIA CHURRINCHE/KIRITATI*2//KFA/2*KACHU	CMSS12Y01129T-099TOPM-099Y-099M-0SY-25M-0WGY
G6	MUTUS/ROLF07//MUCUY	CMSS12B00083S-099M-0SY-1M-0WGY
G7	KACHU//WBLL1*2/BRAMBLING/3/KACHU/KIRITATI	CMSS12Y00241S-099Y-099M-0SY-9M-0WGY
G8	NADI#2//TRCH/HUIRIVIS #1/3/NADI#1	CMSS12Y00880T-099TOPM-099Y-099M-0SY-17M-0WGY
G9	PRL/2*PASTOR*2//MISR2, EGY/3/2*BECARD//ND643/2*WBLL1	CMSS12Y00645T-099TOPM-099Y-099M-0SY-9M-0WGY
G10	BECARD/QUAIU #1//ONIX/KBIRD	CMSS12B00280S-099M-0SY-6M-0WGY
G11	BORL14//BECARD/QUAIU #1	CMSS12Y00070S-099Y-099M-0SY-9M-0WGY
G12	WBLL1*2/BRAMBLING//CHYAK*2/3/KINGBIRD #1//INQALAB 91*2/TUKURU	CMSS12B00929T-099TOPY-099M-0SY-13M-0WGY
G13	WBLL1//PUB94.15.1.12/WBLL1/3/MUCUY	PTSS14Y00345S-0B-099Y-099B-29Y-0B
G14	D67.2/PARANA 66.270//AE.SQUARROSA (465)/3/2*MUCUY	PTSS14B00002T-099Y-099B-5Y-020Y
G15	PAVLOVKA/V15.89C//NAVJ07/3/ROLF07/4/MUCUY	PTSS14Y00314S-0B-099Y-099B-23Y-020Y
G16	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA(784)/6/2*MUCUY	PTSS14B00005T-099Y-099B-19Y-020Y
G17	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/6/VILLA JUAREZ F2009/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR/4/WBLL1*2/BRAMBLING/7/T RAP#1/BOW/3/VEE/PJN//2*	CMSS13B01913T-099TOPY-099M-099Y-9M-0RGY
G18	Mairaj 08/T.DICOCCON CI9309/AE.SQUARROSA (409)/3/MILAN/S87230//BAV92/4/2*MILAN/S87230//BAV92//NARC 2011	NRBW012 011-0ID-0K -050ID-0K-050ID-050ID
G19	KOKILA/3/MUTUS*2//ND643/2*WBLL1/8/PSN/BOW//SERI/3/MILAN/4/ATILIA/5/KAUZ*2/CHE N//BCN/3/MILAN/6/WBLL1*2/SHAMA/7/IWA 8600211//2*PBW343*2/KUKUNA	CMSS13B01939T-099TOPY-099M-099Y-16M-0WGY
G20	MAYIL	CMSS08Y01129T-099M-099Y-3M-0Y-5M-0Y
G21	VILLAJUAREZF2009/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//3*PASTOR/4/WBLL1*2/BRAMBLING/5/WBLL1*2/BRAMBLING//QUAIU	CMSS13B00898S-099M-099Y-17M-0WGY

G22	PAURAQ//RL6043/4*NAC/3/2*QUAIU #1/SOLALA//QUAIU #2	CMSS13Y01652T-099TOPM-099Y-099M- 099Y-3M-0WGY
G23	VILLA JUAREZ F2009/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR/4/WBLL1*2/BRAMBLING/5/ WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WB LL1*2/4/KIRITATI/2*TRCH	CMSS13Y00894S-099Y-099M-099Y-34M- 0WGY
G24	PAURAQ//AG/5*NAC/3/2*QUAIU #1/SOLALA//QUAIU #2	CMSS13Y01654T-099TOPM-099Y-099M- 099Y-23M-0WGY
G25	MANKU//MUTUS*2/TECUE #1	CMSS13B00893S-099M-099Y-29M-0WGY
G26	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAY ON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOC CON PI94624/AE.SQUARROSA (409)//BCN/4/BL 1496/MILAN/3/CROC_1/AE.SQUARROSA (205)//KAUZ/7/FRNCLN/3/ND643//2*PRL/2*PAS TOR/4/FRANCOLIN #1	CMSS13B01010S-099M-099Y-26M-0WGY
G27	SHAKTI/7/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/ KRONSTAD F2004/5/MUNAL/6/MUNAL #1/8/MP4010/MUNAL #1	CMSS13B01842T-099TOPY-099M-099Y-29M- 0WGY
G28	REH/HARE//2*BCN/3/CROC_1/AE.SQUARROS A(213)//PGO/4/HUITES/5/T.SPELTAPI348599/6/ REH/HARE//2*BCN/3/CROC_1/AE.SQUARROS A(213)//PGO/4/HUITES/7/QUAIU/8/KFA/2*KAC HU	CMSS12Y01444S-099Y-099M-099Y-33M- 0WGY
G29	ZINCOL/VALI	CMSS12B01234S-099M-099Y-29M-0WGY
G30	LOCAL CHECK	Pakistan 13

Statistical and stability analyses:

Pooled Analysis of variance (ANOVA) was performed to test the significance of genotypes over locations for yield. As GGE model is based on both the ANOVA and PCA so to get clear picture of acclimatization of genotypes in respective environments a biplot was developed between genotype x environment means (X-axis) and respective PCA values (Y-axis). Towards total G X E interaction, the role of each genotype and environment was graphically portrayed as recommended by Zobel et al., (1988). GGE model was executed based on the equation:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^K \lambda_k \delta_{ik} \beta_{jk} + \varepsilon_{ij}$$

Here, Y_{ij} indicates the yield of i^{th} genotype in j^{th} -environment; μ represents grand mean; g_i and e_j are the effects of the i^{th} genotype and j^{th} environment respectively; λ_k is the eigen value of the PCA for axis k. Then δ_{ik} is the PCA score of genotypes for axis k and β_{jk} is the PCA score of environments for axis k expressed as unit vector times the $\sqrt{\lambda_k}$ while ε_{ij} is the residual term.

Results And Discussion

Mean performance of Genotypes and Environments

Pooled analysis of variance of 30 wheat genotypes tested over 7 locations for yield (t/ha) was computed and highly significant differences were obtained for the main effects of genotypes, environments and genotype x environment interaction ($p < 0.01$). Out of the total variance, major portion was contributed by environment as it shares about half of the total variance i.e. 46.24%. Whereas genotype x environment contributed 22.36% and in case of genotype the contribution was only 7% to the total variability observed in the study (Table 2).

Table 2: Pooled Analysis of Variance of 30 wheat genotypes over 7 locations for Yield

Source	DF	SS	MS	F	Variance Component %
Replication	2	0.569	0.2844		0.067
Genotype	29	60.237	2.0772**	4.18	7.042
Environment	6	395.549	65.924**	132.64	46.242
Genotype*Environment	174	191.276	1.0993**	2.21	22.362
Error	418	207.748	0.497		24.287
Total	629	855.38			
CV 16.74		Grand Mean 4.2121 (t/ha)			
**Significant at 0.01 Probability level					

It revealed that variation in yield performance was highly affected by environmental conditions as compared to G x E interaction and genotypic differences. The highly significant effect showed by environment and its highest contribution towards expressed variability, indicates the major differences in the environmental conditions and location attributes such as altitude, temperature and rainfall. It has also been reported in the literature that the portion of environmental variation is larger than the genotypic differences in case of wheat germplasm (Mohammadi et al., 2012; Matlala et al., 2019; Mohamdi&Amri, 2013). Parallel to the previous results as narrated by Fan et al. (2007) and Mitrovia et al. (2012) in maize, the variance due to G x E interactions was higher than genotypic values as portrayed in Table 2 for this study. This marked G x E interaction effect in the result revealed that a significant difference in yield performance over the environments was due to the differential response of a genotype towards changing climatic conditions. Hence it's clear that development of new varieties can't be same throughout the country but it would be different for the varying ecological zones of the state due to dominating effect of G x E interactions over the genotypic effect. So it's very important to get a deep insight towards the yield performance, environmental adaptability and stability of wheat genotypes towards changing climatic conditions.

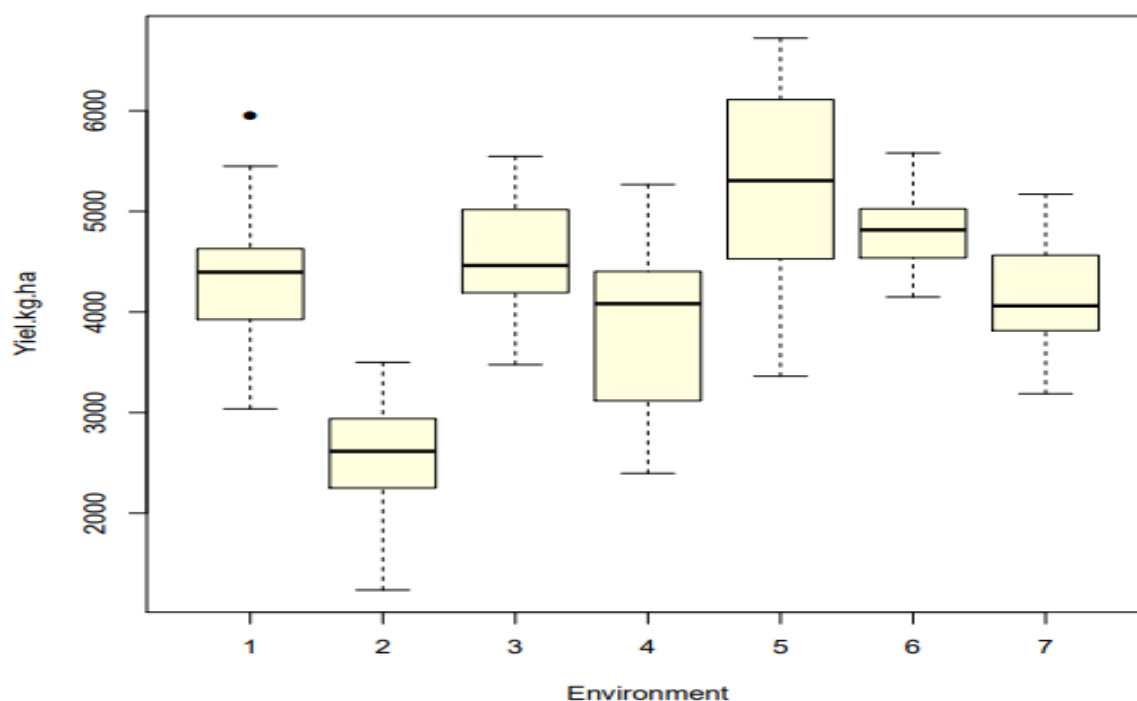


Figure 2: Average yield of wheat genotypes in 7 locations

Average yield performance across the environments was found to be varying in between 2.58 to 5.29 t/ha (Fig 2). Among the 7 changing conditions, E5 was found to be favoring the higher yield on average while E2 designated as the lower yielding environment as most of the genotypes yielded the lowest in this set of conditions. Other 5 environments were observed as to be average yielding as their yield was lying around 4 tons/ha (Fig 2).

In a comparison of genotypes' average grain yield, maximum yield was observed in case of genotype G1 with a value of 4.73 t/ha while minimum was in case of genotype G30 with 3.482 t/ha with a grand mean of 4.212 t/ha. While considering the performance of genotypes in certain environment the maximum average grain yield was noted in a range of 10 t/ha to 5 t/ha for genotype labelled as G22 in E5 and G2 in E4 & E5. In case of minimum average yield of genotypes in each environment, it ranged in between 1.021 t/ha to 3.059 t/ha for the genotypes G30 and G28 respectively both in E2. The yield amplitude was different in each case as maximum amplitude was noted in genotype G22 and minimum in case of G2. The trend of amplitude was same as highest average yield because at both places highest position was occupied by genotype G22 and lowest was taken by G2. Highest yield amplitude value revealed that highest yielding genotype G22 was not stable over the environments while genotype G2 was regarded as stable in yield over the wider conditions due to having the lowest amplitude value (Fig 3).

In terms of mean performance of genotypes for yield in respective environment, the genotype G1 occupied the 1st position in 3 sets of conditions as E1, E2 and E4 along with being ranked at the top in overall average performance. In case of the rest 4 environments 4 different high, yielding varieties as G14, G22, G29 and G7 got the title of highest yielding genotypes in E3, E5, E6 and E7 respectively. The stats summary depicted that yield is not only the genetic potential of the genotype but largely being affected by environment interactions. As in each environment the performance of most of the genotypes was having significant differences thus selection and development of a new variety should be for the specific area to attain the higher

yield. In highest yielding environment the best performing genotype was G22 and in lowest yielding environment the highest yield was attained by G1. This type of differential response of genotypes towards the environments depicted that the G x E interaction was of crossover type.

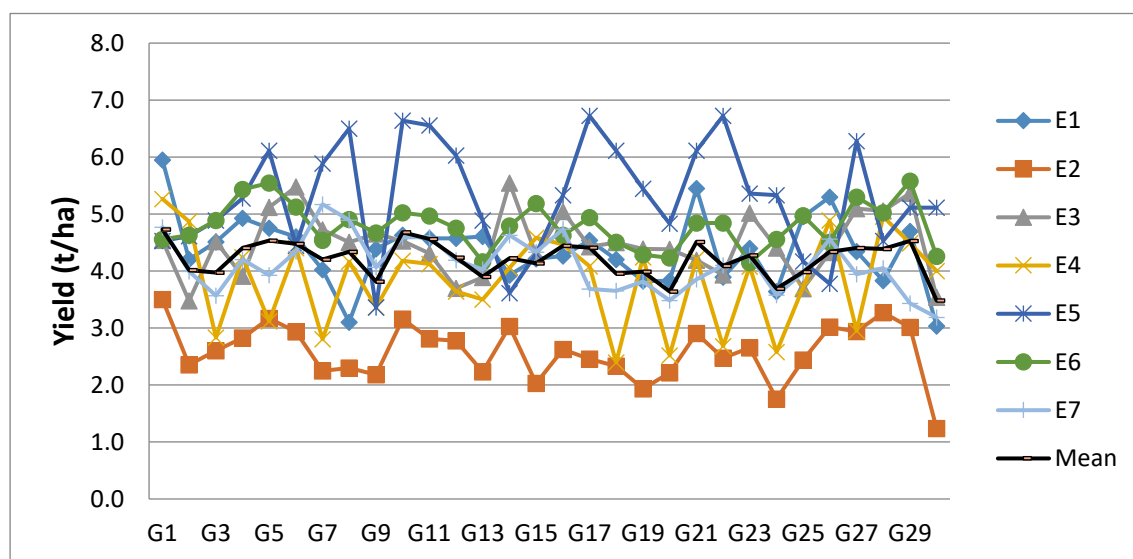


Figure 3: Mean Performance of Genotypes across the 7 locations

Stability Analysis of Genotypes

According to the stability parameters based on joint regression of genotypes over the changing environments as expressed in table 3, it is evident that regression coefficient (b_i) and standard deviation (s^2d_i) values were not persistent to evaluate the genotypic performance over the wider environmental conditions. In terms of regression coefficient, almost all the genotypes showed b_i values around the unity but in terms of standard deviation, it valued about 0 with minor variations. This revealed that all the genotypes showed an average performance in terms of yield over the changing set of conditions of environmental variables. As regression coefficient of unity is designated to indicate the average performance of genotypes in varying environments.

It has been reported that those genotypes show better stability to the changing environments which have higher yield, regression coefficient about 1 and standard deviation not deviating from zero. Based on the stability parameters five genotypes (G13, G16, G19, G20 & G23) were referred to as better yielding and more stable as these were having above average yield, regression coefficient not varying from unity and deviation from regression not different from zero. Five genotypes (G5, G15, G21, G27 & G29) were found to have b_i value not deviating from 1 and deviation from regression coefficient more than zero so designated to be well adaptable to the wider climatic conditions. While five genotypes namely G7, G9, G18, G20 & G30 were categorized as not only the low yielders but also the poorly adaptable.

Table 3: Separate stability statistics values of the 30 genotypes tested across 7 Locations

Gen	Yi	CVi	bi	s2di	Wi2	Di	StabVar	YSi	Si(1)	Si(2)	Si(3)	Si(6)	TOP	NPi(1)	NPi(2)	NPi(3)	NPi(4)
1	1	2	4	3	28	26	28	6.5	30	30	30	30	1	30	30	30	30
2	21	10	2	2	21	23	21	21.5	12.5	16	13	5	22.5	9.5	7	7	8
3	24	18	1	1	8	10	8	20	11	11	5	7	22.5	17	15	8	9
4	11	8	1	1	6	7	6	9	14.5	13	19	20	10	14	21	19	20
5	4	20	1	1	17	18	17	3.5	19.5	21	27	29	3.5	15.5	27	28	28
6	7	4	2	1	13	13	13	8	6	8	20	18	10	5	19	21	19
7	18	25	3	3	24	24	24	23.5	21	22	21	22	10	18.5	10	14	14
8	14	26	3	3	26	30	26	16	26	26	24	21	10	25.5	22	22	22
9	27	15	3	3	25	25	25	30	17	18	8	8	22.5	18.5	13	10	10
10	2	13	1	1	7	9	7	1	1	1	4	13	10	1.5	24	24	24
11	3	19	1	1	9	8	9	2	4	3	11	14	22.5	4	12	17	16
12	16	17	1	1	10	11	10	13	9	9	7	10	22.5	13	17	12	12
13	26	12	1	1	1	1	1	23.5	6	7	6	4	22.5	6	4	3	3
14	17	5	4	3	30	29	30	18.5	29	28	25	25	10	28	20	25	25
15	19	16	1	2	18	21	18	18.5	24	24	23	23	22.5	25.5	14	16	17
16	8	6	1	1	2	4	2	6.5	18	17	12	17	22.5	21	18	20	21
17	9	24	4	1	19	12	19	10	10	10	15	12	10	7	11	15	15
18	25	28	4	2	22	22	22	28	12.5	12	10	6	22.5	11.5	6	6	6
19	22	21	1	1	5	5	5	17	8	5	9	11	22.5	8	3	4	4
20	29	22	1	1	4	6	4	27	2	2	1	1	22.5	3	1	1	1
21	6	14	1	1	12	14	12	3.5	16	15	16	19	10	15.5	23	18	18
22	20	29	4	3	27	28	27	25	22	20	18	16	10	21	16	13	13
23	15	7	1	1	3	3	3	12	3	4	14	9	22.5	1.5	8	9	7
24	28	27	4	1	11	2	11	26	6	6	3	3	22.5	9.5	2	2	2
25	23	11	1	1	15	17	15	21.5	14.5	14	17	15	22.5	11.5	9	11	11
26	13	3	4	3	29	27	29	15	27.5	29	28	27	3.5	29	29	26	26
27	10	23	3	2	20	20	20	11	19.5	23	22	24	22.5	24	25	23	23
28	12	1	4	1	23	16	23	14	27.5	27	26	26	3.5	27	28	27	27
29	5	9	1	2	14	19	14	5	25	25	29	28	3.5	21	26	29	29
30	30	30	3	1	16	15	16	29	23	19	2	2	22.5	23	5	5	5

Phenotypic stability parameters (σ_i^2 , W_i and P) determine the contribution of each genotype towards the sum of squares of G x E interaction effect. Based on lowest values of these parameters along with the CV_i values, different genotypes at both the extremes were identified as G3, G13, G19, G20 & G25 (low yielding) and G4, G10, G11, G12 & G23 (high yielding) which were relatively stable across the environments. It indicates the lesser differential response of these genotypes towards the changing meteorological factors which also reflects the nominal contribution to the interaction effects regardless of yield potential. It has been found that selection based on the stability parameters as P, σ_i^2, W_i results into favoring the average performing genotypes rather than the highest yielding ones. It also has been reported that the genotypes with average performance were more stable over the locations as compared to those which yield higher.

Thus stability parameters were found to be more reliable in devising results (type I stability) keeping in view if these were having the additive type of genetic inheritance. It has been reflected from the stability parameters that the genotype with highest yield (G1) couldn't show significant stability but two other wheat genotypes (G10 & G11) found to exhibit static stability along with higher yield in contrast to the findings that the high yielding are less stable.

It is evident from heat map that some genotypes exhibited higher yield in certain set of environmental conditions as compared to others because of significant affection between genotype and environment. Genotypes which project darker color in the heat map (Fig 4) were designated to express higher yield for that condition. It clearly portrays the overall performance of all the genotypes in comparison to each other in all the environments. The intensity of color indicates the degree of the expression of that in genotype in corresponding environmental conditions. The white color in the map exhibits the poor performance of that line. Its obvious that a genotype showing white for one environment is performing much better in other environment thus indicating the effect of G x E interaction. The performance was found to be largely controlled by the prevailing conditions where its tested in contrast to the genetic potential of that genotype thus

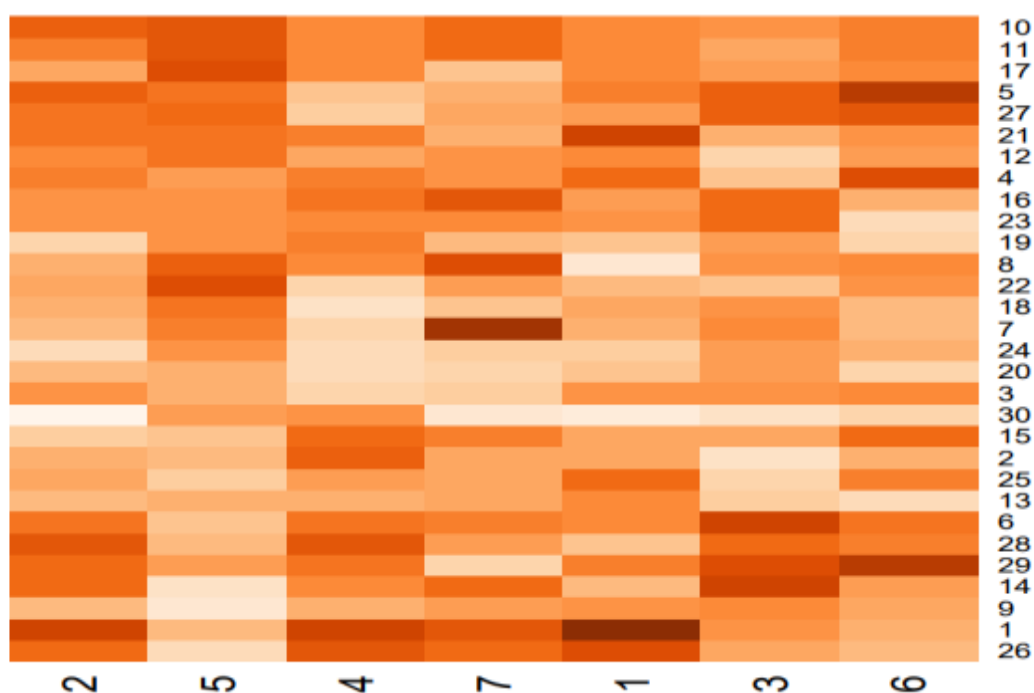


Figure 4: G x E Heat Map among 30 genotypes and 7 locations

emphasizing the importance of G x E relationship. In the heat genotypes were ranked from top to bottom at the right side with respect to their relative stability across the location as G10 was found to perform average in yield but this was almost constant in all cases while G1 and G26 were high yielding for E1, E2, E4 & E7 environments but in E5, E3 and E6 these couldn't get the higher position.

GGE bi plot provides much obvious picture to clarify the yield stability and adaptability. In the bi plot (Fig 5) about 65 % variability was explained by two components (PC1 39.1% and PC2 25.2%). Yield and stability could be explained for each genotype by their position with respect to PC1 and PC2 axis by using so called average coordinates of the environment (ACE) method (Yan.2001; Yan and Hunt,2001). Here PC1 axis was allocated for yield so the genotypes with higher PC1 values were considered to be more productive in terms of yield. While PC2 axis was the projection of stability index that was characterized by stability genotypes associated with PC2 values. Average values of PC1 and PC2 for all environments indicate the average environment. Two lines pass from the circle in x and y direction, the line which passes the origin of circle is referred to as average environment axis (AEA) while the other perpendicular to it is named as average ordinate environment (AOE). The line helps to rank the genotypes in terms of yield performance as AOE divides the genotype into two groups. Genotypes spotted on right (below) to the AOE were having more than average yield while those are at left (above) were producing less than mean yield. To figure out rank among the high yielder, AEA provides projection of the position as arrow icon indicates the direction of yield increase. In present study highest yield was for genotype G1. Stability was linked with the distance of genotype in GGE bi plot from x axis. Closer to the AEA axis more the stability so among high yielders, genotype G21, G29, and G4 were found to have more stability. Whereas the most stable in all the conditions was G23.

Rankings of genotypes as per GGE means vs stability was also executed on a graph indicating the "ideal genotype" (Fig 6). In multi-locations trial the ideal genotypes is one which gets the highest position in

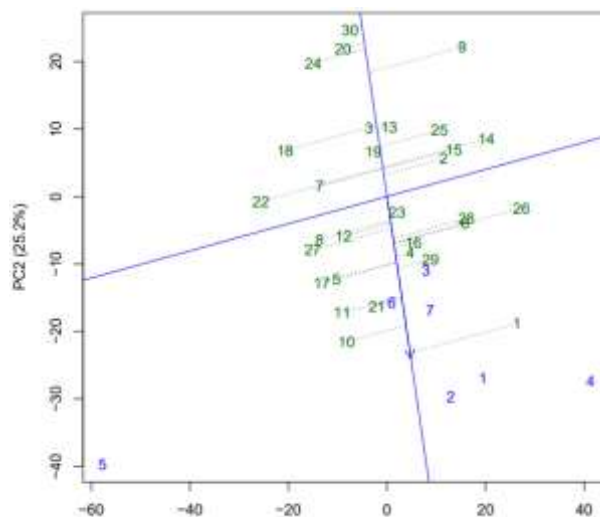


Figure 6: GGE biplot showing "Mean vs Stability"

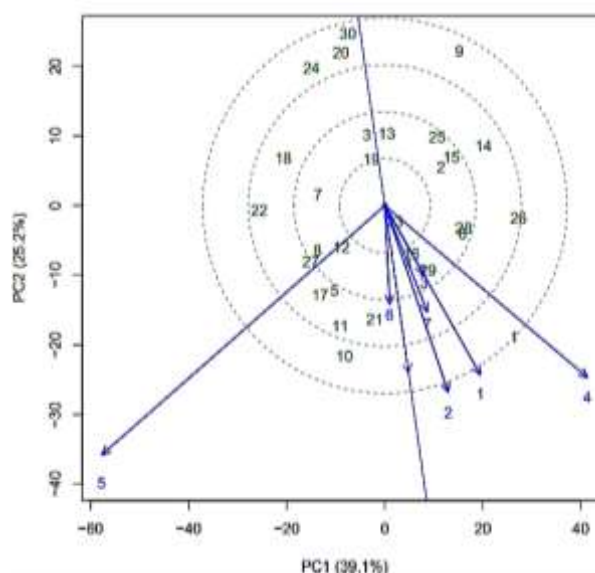


Figure 5: GGE biplot showing "Ideal Genotype"

all the environments under observation and maintains stable performance (Yan and Kang, 2003). In real experiments it's not possible to attain an ideal genotype so similarly couldn't find such in this study. However, the best title can be awarded to one which lies nearest to the ideal one. Ideal one in graph is one which lies towards the arrow sign of line passing through origin (indicating high yield) and sticking to the line (indicating more stable). Here in this case the genotype G21 was best in terms of yield and stability for the environments.

In order to evaluate the performance of genotypes as per certain environment to point out the environment specific genotypes "Which Won Where" plot was executed based on GGE biplot values (Yan et al., 2000; Yan and Hunt, 2001). Among the scattered genotypes around the origin, those lying at the extremes were linked with each thus developing a shape of polygon (Fig 7). Lines originating from the center were perpendicular to the sides of the Polygon that subdivided it into several sectors. Each sector was having specific set of genotypes along with the environments. Environments in a sector may be regarded as mega environments for the genotypes accompanying it in that sector. In the graph, seven sectors were identified where two sectors were main including the environments along with genotypes in same sector. Group 1 was characterized by the presence of 8 genotypes (1, 29, 4, 16, 28, 6, 23 & 26) with environment 1, 2, 3, 4, 7. A genotype closer to certain environment indicates the stronger relation to that condition while performance level is directly proportional to the distance from the origin.

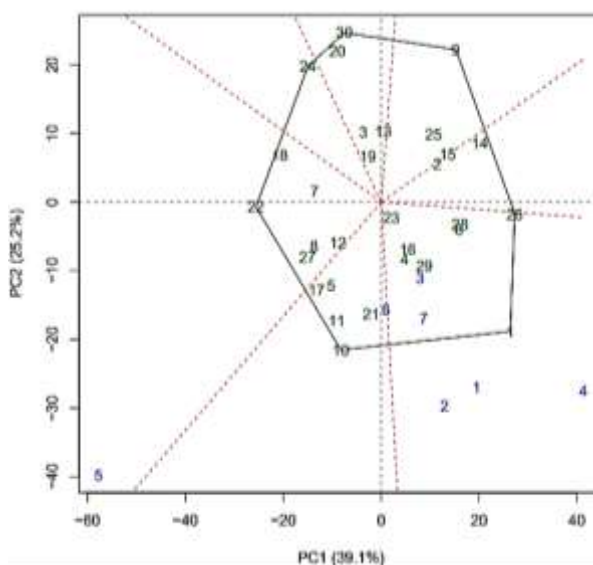


Figure 7: GGE biplot showing "Which won Where"

So these genotypes would yield higher in aforementioned environments with some lesser yield in E 3 and E7 as compared to E1, E2 and E4 which also has been certified by the mean performance of genotypes as illustrated in fig 3. The second group was containing E6 with G10, G21, G11, G5 and G17 while third group was comprised of E5 and G27, G8, G12, G22, G8 and G17. So in order to figure out environment specific genotypes its vivid how efficiently the genotypes performed for specific environments so highest yielding genotype can be picked from a sector for accompanying environment.

CONCLUSION

In the study average yield was observed to demonstrate higher range value across the environments as it ranged between 2.58 to 5.29 t/ha for the 7 environments while just considering the genotypes neglecting the environmental factor it ranged 3.482 to 4.73 t/ha for 30 genotypes. Highest yielding genotypes were not found to maintain stable performance over the changing locations rather some average better performing

genotypes in terms of yield were also found to have stability in performance. stability parameters (σ_i^2 , W_i and P) lead towards the selection of average performing stable genotypes rather than the highest yielding unstable ones. Fives genotypes (G13, G16, G19, G20 & G23) were referred to as better yielding and more stable based on stability parameters. Specific GxE effect was also observable from the heat map which indicated the performance of each genotype in each environment. Overall on the basis of biplot, the genotype G21 was granted the best position in terms of yield and stability for the environments. Selection for individual environment is quite easy and efficient by “Which Won Where” biplot in order to figure out the area based genotypes. By such stability studies, objective based results can be withdrawn at a time with much higher efficiency rather we want to select overall stable one or to evaluate the best for each region. This may also help to further develop crop improvement program with wider prospective and higher effectiveness. These results will give a clear picture to the researcher to proceed ahead in the desired dimension with complete information of the genetic potential and environmental influence.

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Conflict of Interest

“The authors declare no conflict of interest”

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