Fundamental and Applied Agriculture
Vol. 8(1&2), pp. 423–434: 2023
doi: 10.5455/faa.146894

Genetics and Plant Breeding | Original Article

Genotype × environment interaction on grain yield and yield components in bread wheat

Md Nur-E-Alam Siddquie [1*], **Md Aminul Hoque** [2]

[1]On farm Research Division, Bangladesh Agricultural Research Institute, Shyampur, Rajshahi, Bangladesh
[2]Department of Agronomy and Agricultural Extension, University of Rajshahi, Bangladesh

Article Information

Article History
Submitted: 11 Dec 2022
Accepted: 13 Feb 2023
First online: 27 Jun 2023

Academic Editor
A K M Aminul Islam
aminulgpb@bsmrau.edu.bd

**Corresponding Author*
Md Nur-E-Alam Siddquie
nsiddquie@gmail.com

Abstract

Genotype by environment (location) interaction (GEI) is essential for identifying environment-specific and widely adapted genotypes of wheat. The experiment was carried out across five locations (Shyampur and Godagari under Rajshahi district, Nachole at Chapainawabganj, Sapahar at Naogaon and Lalpur at Natore district in north-west Bangladesh) to assess GEI effects on grain yield and its components and to identify high yielding and stable genotypes of wheat for grain yield in the year of 2020-21. Combined analyses of variance for G and GEI were significant for almost all traits. Significant GEI suggested that the performance of genotypes was not consistent across locations, revealing strong influence of environments on the expression of phenotype for all traits. Average over five locations, genotypes G84 (3647 kg ha^{-1}) and G76 (3576 kg ha^{-1}) exhibited maximum values for grain yield and also produced similar tillers m^{-2} (SPM) and grains spike^{-1} (GPS) where difference between them was statistically insignificant thus appeared as leading genotypes for yield and production traits. Again, the genotypes G84 and G76 produced statistically insignificant maximum yield in all locations indicating that they are high yielding and wide adapted genotypes. The genotype G80 produced insignificant yield and other yield traits with G76 and G84 across the locations indicating its wide adaptability. However, G26, G69 and G77 with higher grain yield in Shyampur, G53 and G59 in Godagari, G20 in Lalpur, G3 in Nachole and G8 in Sapahar proved their specific adaptability in particular locations. Among locations, Shyampur and Godagari were identified as highly productive locations in terms of grain yield and positive environmental index. Correlation analysis showed that grain yield had strong positive association with spikes m^{-2} (r = 0.92**), grains spike^{-1} (r = 0.72**) and TGW (r = 0.89**). On the basis of mean grain yield and higher positive phenotypic index for SPM, GPS, TGW and GY, G76, the genotypes G84,G76 and G80 were found as high yielding genotypes and thus could be recommended as important breeding materials in upcoming specific breeding program for drought prone north-west part of Bangladesh.

Keywords: Wheat, genotype, location, correlation coefficient, drought tolerant, combined analysis, grain yield

Cite this article: Siddquie MN, Hoque MA. 2023. Genotype × environment interaction on grain yield and yield components in bread wheat. Fundamental and Applied Agriculture 8(1&2): 423–434. doi: 10.5455/faa.146894

1 Introduction

Wheat is among the world's major food crops in terms of area under cultivation, production volume and the proportion of the global population depend on it as a main diet (Alexandratos and Bruinsma, 2012). It contains about 55% starch that contributes up to 20% of the energy demand of world, about 12.1% protein, as well as some dietary fats, vitamin B, zinc, calcium, and iron (Šramková et al., 2009). Around 95% of the world's wheat crop is hexaploid (Genomic constitution, AABBDD) bread wheat (*Triticum aestivum* L. aestivum,), while the rest are tetraploid (AABB) durum wheat (*Triticum turgidum* L. durum,) and other types of minor economic important wheat (Peng et al., 2011). Present wheat production is about 1.1 million tons from 0.31 million hectare of land area in the year 2021-22 against the annual demand of about 8.5 million tons (Alexandratos and Bruinsma, 2022) in Bangladesh. Thus, the difference between annual wheat production and consumption is about 7.4 million tons. Demand for wheat being a staple food crop, would rise with the increase in population. Now, the climate change especially drought is the biggest issue for wheat production in Bangladesh (Rahman and Miah, 2017). Farmers are looking forward for technological and adaptation measures to continue or in increase wheat production by facing the climate change issues. Wheat production could be increased either by developing high yielding cultivars or growing more area under cultivation. The scope for wheat cultivation on larger area is limited in Bangladesh; however, development of high yielding drought tolerant wheat cultivars with wider adaptability would play significant role.

Cultivars performance largely depends on their genetic makeup (G), environment (E) and their interaction (GEI). Fluctuating response of genotypes across test environments is a usual phenomenon, known as GEI (Akcura et al., 2009; Mohammadi et al., 2012). Yield potential of a cultivar is the result of its performance over locations. Therefore, stability analysis of genotypes is required in the presence of GEI to ascertain high yielding and relatively stable genotypes. For several test environments, the GEI governs the credentials of the most stable genotypes that are suitable for specific environment (Annicchiarico, 2002). Thus, the genotypes possessing genetic homeostasis are essential to increase average yield. Wheat production can boost up through cultivars having broader genetic base and better performance under various agro-climatic conditions. In wheat, genetic improvement is slow process in nature however, the selective process of man can speed it up through appropriate management of environmental factors. Improvement gets complicated when a trait is environment-driven and selection gets more complex (Mohammad et al., 2011). Keeping in view the importance of GEI in reference to its application for identifying stable genotypes, the present experiment was conducted using 14 wheat genotypes. The experiment was carried out across five locations to assess GEI effects on grain yield and its components and to identify high yielding and stable genotypes for grain yield.

2 Materials and Methods

2.1 Experimental sites

The five experimental sites were situated in four different districts of Bangladesh, viz., Shyampur (Field station of on-farm research division, Bangladesh Agricultural Research Institute, Rajshahi) and Godagari under Rajshahi district, Nachole at Chapainawabganj, Sapahar at Naogaon and Lalpur at Natore district. The locations Godagari, Nachole and Sapahar are under AEZ-26. The locations Shyampur and Lalpur are under AEZ-11. The Geo-references of test sites are shown in Table 1. Before seeding of wheat, soil samples were taken from each experimental field and were sent to the laboratory for chemical analysis. The chemical properties of the soil samples were presented in the Table 2. Wheat grows only in winter season in Bangladesh. In Bangladesh, rainfall pattern is uneven round the year and rainfall mostly concentrated in summer and winter is rainless. The rainfall in the wheat growing season in different sites is shown in Table 3.

2.2 Breeding history of planting material

Fourteen wheat genotypes were taken in this trial in 2020-21 wheat growing season for multi-location evaluation across the locations. The pedigrees of these genotypes are presented in Table 4.

2.3 Experimental design

The field trials were laid out in randomized complete block design (RCBD) with three replications. The plot size was 5 m × 1 m with 5 rows. The row length was 5 m long and 20 cm distances from rows and rows, respectively. Within a replication, the genotypes were distributed at random to each of the plots. The seed rate was 12 g m^2 and was sown continuously in rows. Experimental seeds were sown on different locations under non-irrigated conditions. The trial was watered one time at 18-21 days after seeding in different locations for better establishment of crops and then allowed the crops to grow under non-irrigated drought stressed condition. Hand weeding was used to keep the research fields free of weeds and no pest control measures were taken due to absence of pest incidence. Recommended doses of fertilizers and manures were applied at or before during final preparation of the land @ 100-27-50-20-1-4.5-5000 kg ha^{-1} as N-P-K-S-B-Zn-cow dung, respectively. Two third of urea were used as a basal dose and remaining urea was applied at 18-21 days after sowing (after the first irrigation).

2.4 Measurement of traits

The number of spikes m^{-2} (SPM) was counted at physiological maturity of crops. After the central

Table 1. Location, AEZ, and geo-references of experimental sites

Location Name	AEZ	Altitude (m)	Latitude (°) N	Longitude (°) E
Shyampur	11	19	24.368688	88.662078
Godagari	26	36	24.40691	88.43403
Sapahar	26	31	25.108744	88.622367
Nachole	26	34	24.62471	88.421605
Lalpur	11	17	24.261477	89.013842

Table 2. Soil properties of each location of experimental sites

Soil properties	Location				
	Shyampur	Godagari	Nachole	Sapahar	Lalpur
Soil pH	7.6	6.6	5.4	4.8	8.1
Organic matter (%)	1.27 (L)	1.45 (L)	1.59 (L)	1.88 (M)	1.84
Total nitrogen (%)	0.07 (VL)	0.08 (VL)	0.09 (VL)	0.11 (L)	0.14 (L)
P (µg/g soil)	32.0 (H)	14.3 (L)	7.4 (VL)	28.8 (Opt)	9.0 (L)
K(meq/100g soil)	0.28 (M)	0.13 (L)	0.22 (M)	0.14 (L)	0.27 (M)
S (µg/g soil)	24.1(Opt)	64.75(VH)	22.41(M)	26.5(Opt)	24 (Opt)
Zn (µg/g soil)	1.25(M)	1.12 (M)	2.60(VH)	0.86 (L)	0.80 (L)
B (µg/g soil)	0.84 (VH)	0.44(M)	0.28(L)	0.26(L)	0.17 (L)

P = Phosphorus, K = Potassium, Zn = Zinc, S = Sulphur, B =Boron, VL = Very Low, L = Low, M = Medium, H = High, Opt = Optimum and VH = Very High

Table 3. Rainfall (mm) in experimental sites during wheat season of June 2020 - May 2021

Months	Rainfall (mm)				
	Shyampur	Godagari	Nachole	Sapahar	Lalpur
Jun-20	248	326	445	503	132
Jul-20	412	230	292	504	263
Aug-20	144	219	275	227	90
Sep-20	217	236	390	448	255
Oct-20	339	146	95	259	103
Nov-20	0	0	0	0	0
Dec-20	0	0	0	0	0
Jan-21	0	0	0	0	0
Feb-21	0	0	0	0	0
Mar-21	0	2	0	0	0
Apr-21	13	16	20	15	48
May-21	191	136	229	158	168

Table 4. Pedigree of previously selected drought tolerant genotypes of wheat were used in the molecular study

Sl. no.	Code	Variety / Pedigree
1	G3	BARI Gom 30
2	G8	KACHU*2/PANDORA
3	G15	BAJ #1/6/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/KACHU #1
4	G20	SUP152*2/PFUNYE #1
5	G26	SUP152/BAJ #1
6	G53	Sourav
7	G59	BARI Gom 33
8	G69	SUP152/AKURI//SUP152
9	G71	Prodip /BARI Gom 25
10	G76	BARI Gom 26/AKR/3/URES/JUN//KAUZ
11	G77	BARI Gom 26/SW89-5124*2/FASAN
12	G79	SOURAV / CHEN//AE.SQ(TAUS)//BCN/3/2*PASTOR
13	G80	Shatabdi /BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR
14	G84	Bijoy/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1*2/5/WHEAR/SOKOLL

spikes of five randomly chosen plants were harvested, the number of grains per spike (GPS) was counted. Thousand grains were counted randomly from bulk sample and weighed using a sensitive balance to determine thousand grain weight (TGW). Three middle rows from each plot were collected at maturity to determine the grain yield. Plants were threshed to collect grain yield data after several days of sun drying. Grain moisture was taken by grain moisture meter and adjusted the yield at 12% moisture content.

2.5 Statistical analysis

2.5.1 Analysis of variance

Data collected on grain yield and various yield related characters were analyzed statistically across five locations suitable for RCBD using Genstat 17th edition computer software. At the 1% level of probability, the LSD test was used to differentiate means when there were significant differences.

2.5.2 Correlation analysis

Correlations for yield and different morphological characters were calculated using the following formula:

$$r_{xy} = \frac{CoV_{(x,y)}}{\sqrt{V_{(x)}.V_{(y)}}} \quad (1)$$

where r_{xy} = correlation coefficient between x and y; $CoV_{(x,y)}$ = covariance between x and y; $V_{(x)}$ = variance of x; and $V_{(y)}$ = variance of y.

3 Results

3.1 Combined analysis of variance

Combined analysis of variance illustrated that all traits differed significant higher among genotypes, environments (locations) and genotype by environment interactions (GEI) in the present study (Table 5). Significant GEI revealed that the genotypes were not completely stable across diverse environments (locations).

3.2 Mean performances

3.2.1 Number of spikes m^{-2} (SPM)

Combined analysis of variance shown significant differences (P≤0.01) among genotypes, environments (locations), and their genotypes by environments for spike m^{-2} (SPM). Genotypes, environment and GEI contributed 23.45%, 36.99% and 28.10% to the total sum of squares (TSS), respectively (Table 5). The location effects occurred as vital source of variation due to its higher influence (36.99%) to the TSS. Higher involvement due to location concluded that mean performance and ranking of genotypes across locations were mainly influenced by locations followed by their genotypes by environments interaction and genotypes. Similarly, higher contribution due to locations indicated strong effect of locations on the phenotypic appearance of each genotype (Table 5). Spikes m^{-2} ranged from 247 to 297 spikes on average across five locations, with a mean value of 273 spikes and desirable genotypes are selected on the basis of mean performances of genotypes in each location (Table 6). Maximum number of spikes was produced by G76 (297 spikes), G84 (295 spikes) and G80 (294 spikes) as their difference was insignificant, whereas minimum number of spikes were observed for G77 (247 spikes)

Table 5. Combined analysis of variances (ANOVA) for different traits of 14 wheat genotypes on five locations

SOV		Traits			
		SPM	GPS	TGW	GY
Genotype (G) (df=13)	SS	44879.8	949.8	446.1	11612837
	MS	3452.3**	73.1**	34.3**	893295**
	%TSS	23.45	25.37	20.08	21.85
Location (E) (df=4)	SS	70809.2	563.9	548.6	22504513
	MS	17702.3**	141.0**	137.2**	5626128**
	%TSS	36.99	15.06	24.7	42.33
G × E (df=52)	SS	53800.1	1309.1	770.6	15610725
	MS	1034.6**	25.2**	14.8**	300206**
	%TSS	28.1	34.97	34.69	29.37
Residual (df=138)	SS	21531.2	917.9	451.9	3386214
	MS	156	6.7	3.3	24538
Total (df=209)	SS	191425.4	3743.4	2221.1	53158328

SPM = Spikes m^{-2} ; GPS = Grains per spike ; TGW = 1000-grain weight; GY= Grain yield; SS = Sum of Square; MS = Mean of Square; %TSS = Percent of total sum of square (% variation explained), **: Significant at 1% probability level

and G15 (256 spikes) which were statistically insignificant (Table 8). Among locations, spikes m^{-2} ranged from 271 to 327 in Godagari; 227 to 302 in Lalpur; 224 to 299 in Nachole; 199 to 293 in Sapahar and 272 to 303 in Shyampur (Table 6). The mean performance of the genotypes, environments, phenotypic index and environmental index are presented in Table 7. Genotypes G53 (327 spikes), G76 (322 spikes), G59 (318 spikes) and G8 (316 spikes) produced maximum spikes m^{-2} in Godagari; G84 (302 spikes), G76 (301 spikes), G80 (292 spikes) and G8 (291 spikes) in Lalpur; G80 (299 spikes), G84 (294 spikes), G59 (285 spikes), G76 (283 spikes) in Nachole; G84 (293 spikes), G8 (287 spikes), G80 (284 spikes) and G76 (292 spikes) in Sapahar and G26 (303 spikes), G77 (296 spikes), G80, G76 (294 spikes each), G69 (293 spikes), G20 (291 spikes) and G84 (290 spikes) in Shyampur where the difference among all the genotypes in each location were statistically significant (Table 7). From the environmental mean, it was revealed that Godagari and Shyampur were the most favourable environments for SPM due to their positive environmental index. The genotypes G76, G80, G84 and G8 are desirable for SPM due to their positive phenotypic index. At all environments, none of the genotypes fully dominated rest of the genotypes showing location specific performance for spikes m^{-2}. Location Godagari (299 spikes) and Sapahar (248 spikes) were confirmed as highly productive and less productive location in terms of spikes m^{-2}, respectively (Table 9).

3.2.2 Number of grains spike^{-1} (GPS)

Significant differences (P≤0.01) were found across genotypes, environment, and GEI in the combined analysis of variance for GPS. Genotypes and environments accounted for 25.37% and 15.06% of the total variation respectively, whereas the GEI explained 34.97% of it (Table 5). Significant genotypic differences for GPS allow for the option to choose the suitable genotype. However, selection should be environment-specific due to the strong GEI effect (Table 5). GPS had a mean value of 44.5 grains across five locations, ranging from 41.5 to 47.9 grains and the desirable genotypes are selected on the basis of mean performances of genotypes in each location (Table 6). The mean performance of the genotypes, environments, phenotypic index and environmental index are presented in Table 7. From the environmental mean, it was revealed that Godagari and Shyampur were the most favourable environments for GPS due to their positive environmental index. The genotypes G84, G76, G53, G8, G3, G59 and G80 had positive phenotypic index for GPS indicating that they are desirable for overall environments. The highest number of GPS was noticed for G84 (47.9 grains), followed by genotypes G53 (47 grains), G8 (46.6 grains), G3 (45.9 grains), and G76 (45.8 grains) and G59 (45.7 grains), while minimum number of GPS was produced for G77 (39.9 grains) (Table 8). The GPS ranged from 40.1 to 50.1 grains in Godagari; 35.9 to 47.5 grains in Lalpur; 37.1 to 50.9 grains in Nachole; 34.5 to 48.5 grains in Sapahar and 44 to 49.3 grains in Shyampur (Table 6).Overall, G84 showed consistent performance across different environments, as evident from its higher GPS, superiority and stability at all test environments (locations). Moreover, G3, G8, G15, G26, G53, G59, G69, G71, and G77 produced higher GPS in some locations while producing less in others,

Table 6. Descriptive statistics of different traits of 14 wheat genotypes under five environments (locations)

Environments	Parameter	SPM	GPS	TGW	GY
Across 5 environments	Range	247-297	41.5-47.9	41.8-46.6	2887-3647
	Mean	273	44.5	43.8	3232
	DG	G76, G84, G80	G84, G8	G76, G80, G71	G84, G76
Godagari	Range	271-327	40.1-50.1	42-49.1	3340-3853
	Mean	299	46.1	45.4	3634
	DG	G53, G76, G59	G53, G8, G76, G26, G59, G84	G59, G79, G80	G53, G59, G84
Lalpur	Range	227-302	35.9-47.5	38.5-46	2457-3599
	Mean	268	43.6	42.3	3108
	DG	G84, G76, G80	G84, G53, G59	G76, G80, G3	G84, G76, G80
Nachole	Range	224-299	37.1-50.9	41.6-49.4	2300-3600
	Mean	260	43.9	45.5	3056
	DG	G80, G84, G59	G53, G3	G71, G76, G8	G84, G76, G80
Sapahar	Range	199-293	34.5-48.5	37.6-47.1	2002-3575
	Mean	248	42.3	41.6	2779
	DG	G84, G8, G80	G84, G8, G59	G71, G84, G8	G84, G8, G76
Shyampur	Range	272-303	44-49.3	39.9-48.3	3306-3803
	Mean	287	46.7	44.3	3582
	DG	G26, G77, G80, G76	G69, G77, G84, G79, G8, G15, G59	G76, G79, G80	G26, G77, G69

DG=Desirable genotype(s), SPM= Spikes m^{-2}; GPS= Grains $spike^{-1}$; TGW= Thousand grain weight(g) and GY= Grain yield (kg ha^{-1})

showing the specific adaptability of these genotypes to corresponding locations (Table 7).

3.2.3 Thousand grain weight (TGW)

Significant differences (P≤0.01) were found across genotypes, environments, and their genotype by environment interactions (GEI) in the combined analysis of variance for TGW. Generally, genotypes, environment and GEI contributed 20.08%, 24.70% and 34.69% to the total sum of squares (TSS), respectively (Table 5). Effects of the genotype by environment interaction appeared as a significant source of variation due to its greater contribution (34.69%) to the total sum of squares. However, the participation of location (24.07%) was greater than the influence of genotypes (20.08%). Higher contribution due to GEI concluded that mean performance and ranking of genotypes across locations were mainly affected by their interaction with locations. Similar to this, a greater contribution from the location suggested a significant impact of the location on the phenotypic expression of the genotypes (Table 5).

Mean TGW (Table 9) over 14 wheat genotypes showed that the highest TGW was observed in Nachole (45.5 g) and Godagari (45.4 g) where difference between them was statistically insignificant. The smaller TGW and seed was observed in Sapahar (41.6 g) followed by Lalpur (42.3 g) and Shyampur (44.3 g). Location Sapahar (41.6 g) and Nachole (45.5 g) were confirmed as least productive and highly productive location, respectively for of TGW. Based on mean over five environments (Locations), TGW ranged from 41.8 to 46.6 with the mean value of 43.8 g and the desirable genotypes are selected on the basis of mean performances of genotypes in each location (Table 6). The mean performance of the genotypes, environments, phenotypic index and environmental index are presented in Table 7. From the environmental mean, it was revealed that Godagari , Shyampur and Nachole were the most favourable environments for TGW due to their positive environmental index. The genotypes G76, G71, G80, G84, G8 and G3 are desirable for TGW due to their positive phenotypic index. Overall, 6 out of 14 genotypes produced bolder grain than mean TGW (Table 8). The heaviest TGW was observed for genotypes G76 (46.6 g) followed by G80 (45.8 g) and G71 (45.7 g), whereas minimum TGW were observed for genotypes G77 (41.8 g) followed by G53 (42.1 g), G26 (42.3 g), G15 (42.8 g) and G20 (42.9 g). The genotypes G84 (44.9 g), G8 (44.8 g), G3 (44 g), G79 (43.7 g), G69 (43.1 g) and G59 (43 g) produced intermediate TGW in respect of 14 wheat genotypes (Table 8). TGW ranged from 42 to 49.1 g in Godagari; 38.5 to 46 g in Lalpur; 41.6 to 49.4 g in Nachole; 37.6 to 47.1 g in Sapahar and 39.9 to 48.3 g in Shyampur (Table 6). Across all locations, none of the genotypes completely ex-

Table 7. Mean values of Genotype × Environment (Location) interaction for number of spikes m^{-2} (SPM), number of grains $spike^{-1}$ (GPS), thousand grain weight (TGW) and grain yield (GY) traits of 14 wheat genotypes across five environments (locations)

Genotypes	Godagari	Lalpur	Nachole	Sapahar	Shyampur
SPM					
G3	271	253	268	266	282
G8	316	291	259	287	281
G15	310	240	246	200	284
G20	303	278	244	209	291
G26	308	235	243	236	303
G53	327	264	254	241	272
G59	318	255	285	241	276
G69	277	257	242	239	293
G71	288	276	262	253	277
G76	322	301	283	282	294
G77	273	227	242	199	296
G79	280	282	224	246	287
G80	301	292	299	284	294
G84	297	302	294	293	290
CV (%)			4.6		
LSD			20.2		
GPS					
G3	46.3	44.8	48.8	45	44.3
G8	49.7	42.5	46.3	47	47.7
G15	43.5	45.6	44.1	40.7	47.2
G20	46.3	44.3	40.7	38.1	45.9
G26	49.1	42.7	39.3	37.8	47.5
G53	50.1	46.7	50.9	42	45.2
G59	49.1	46.4	39.7	46.7	46.7
G69	44.2	40.6	43.6	38	49.3
G71	41.4	44.2	47.1	44.2	44
G76	49.5	43.8	45.9	44.5	45.6
G77	40.7	35.9	39.3	34.5	49.2
G79	40.1	42.3	37.1	40.5	47.7
G80	46.6	43.7	45	45.2	46.2
G84	48.9	47.5	47	48.5	47.7
CV (%)			5.8		
LSD			4.16		
TGW (g)					
G3	43.1	44.5	46.3	42.2	43.8
G8	46.2	41.4	48.1	44.4	43.7
G15	46.6	39.5	44.4	42.6	41.1
G20	45.5	43.5	43.3	37.8	44.4
G26	46.8	38.5	42.2	39.6	44.4
G53	42	43.8	45.7	39.2	39.9
G59	49.1	40.3	45.3	38.7	41.9
G69	42.2	40.1	47.3	41	44.7
G71	45.2	41	49.4	47.1	46.1
G76	46.4	46	48.1	44.3	48.3
G77	42.5	40.3	45.2	37.6	43.4
G79	48.2	43.4	41.6	38.2	47
G80	46.9	45.7	46.2	43.7	46.4
G84	45.1	44.3	44.5	45.9	45
CV (%)			4.1		
LSD			2.92		
GY (kg/ha)					
G3	3340	3249	3350	3292	3340
G8	3620	3316	3250	3550	3561
G15	3670	2709	3050	2002	3547
G20	3590	3373	2800	2090	3710
G26	3667	2649	2700	2355	3803
G53	3853	2897	2850	2690	3306
G59	3823	3041	2750	2410	3446
G69	3353	2770	3150	2390	3764
G71	3577	3367	3300	3265	3358
G76	3713	3522	3533	3495	3616
G77	3510	2457	2700	1990	3780
G79	3580	3164	2300	2458	3632
G80	3773	3403	3450	3338	3627
G84	3800	3599	3600	3575	3662
CV (%)			4.8		
LSD			252.9		

CV (%)= Percent coefficient of variation and LSD = Least significant difference at 1% level of probability

Table 8. Mean performance of different traits of 14 wheat genotypes under five locations

Genotypes	SPM	GPS	TGW	GY
G3	268	45.9	44	3314
G8	287	46.6	44.8	3459
G15	256	44.2	42.8	2995
G20	265	43.1	42.9	3113
G26	265	43.3	42.3	3035
G53	272	47	42.1	3119
G59	275	45.7	43	3094
G69	262	43.1	43.1	3085
G71	271	44.2	45.7	3373
G76	297	45.8	46.6	3576
G77	247	39.9	41.8	2887
G79	264	41.5	43.7	3027
G80	294	45.3	45.8	3518
G84	295	47.9	44.9	3647
LSD	9	1.86	1.31	113.1

LSD = Least significant difference at 1% level of probability

Table 9. Effect of Environments (locations) on the performance of different traits of 14 wheat genotypes

Environments (locations)	SPM	GPS	TGW	GY
Godagari	299	46.1	45.4	3634
Lalpur	268	43.6	42.3	3108
Nachole	260	43.9	45.5	3056
Sapahar	248	42.3	41.6	2779
Shyampur	287	46.7	44.3	3582
LSD(0.05)	5.4	1.11	0.78	67.6

LSD = Least significant difference at 1% level of probability

Table 10. Correlation among different traits of 14 wheat genotypes across five environments (locations)

Parameters	SPM	GPS	TGW	GY
SPM	1			
GPS	0.76**	1		
TGW	0.80**	0.45ns	1	
GY	0.92**	0.72**	0.89**	1

SPM = spikes m^{-2}; GPS = grains $spike^{-1}$; TGW = thousand grain weight (g) and GY = grain yield (kg/ha); *, **: Significant correlation at 5% and 1% level of probability, where ns = non-significant

ceeded the other genotypes showing location-specific performance for TGW. However, G80, G76 and G71 performed well in most of the locations (Table 7).

3.2.4 Grain Yield (GY)

Significant differences (P≤0.01) were found across genotypes, environments (Locations), and their genotype by environment interactions (GEI) in the combined analysis of variance for GY. Generally, genotypes, environment and GEI contributed 21.85%, 42.33% and 29.37% to the total sum of squares (TSS), respectively (Table 5). The Location effects occurred as vital source of variation due to its higher influence (42.33%) to the TSS. However, the participation of GEI (29.37%) was higher than the effect of genotype (21.85%). Higher involvement due to location concluded that mean performance and ranking of genotypes across locations were mainly affected by locations followed by genotypes by locations interaction and genotypes. Similar to this, a greater contribution from the location suggested a significant impact of the location on the phenotypic expression of the genotypes (Table 5).

Mean GY (Table 9) over 14 wheat genotypes showed that maximum GY was found in Godagari (3634 kg ha^{-1}) and Shyampur (3582 kg ha^{-1}) where there was statistically no difference between them.

The lowest GY was observed in Sapahar (2779 kg ha^{-1}) followed by Nachole (3056 kg ha^{-1}) and Lalpur (3108 kg ha^{-1}). Location Sapahar (2779 kg ha^{-1}) and Godagari (3634 kg ha^{-1}) were established as least productive and highly productive location, respectively for of GY. Grain yield varied from 2887 to 3647 kg ha^{-1} based on the average over five environments (Locations), with a mean value of 3232 kg ha^{-1} and desirable genotypes are selected on the basis of mean performances of genotypes in each location (Table 6). The mean performance of the genotypes, environments, phenotypic index and environmental index are presented in Table 7. From the environmental mean, it was revealed that Godagari and Shyampur were the most favourable environments for GY due to their positive environmental index. The genotypes G84, G76, G80, G71, G8 and G3 also produced positive phenotypic index for GY indicating that they are desirable for overall environments. Six out of 14 genotypes produced more GY than mean GY (Table 8). The highest GY was observed for genotypes G84 (3647 kg ha^{-1}) and G76 (3576 kg ha^{-1}) where difference between them was statistically insignificant. The lowest GY were observed for genotypes G77 (2887 kg ha^{-1}) and G15 (2995 kg ha^{-1}) where difference between them was statistically insignificant. The genotypes G80 (3518 kg ha^{-1}), G8 (3459 kg ha^{-1}) and G3 (44 g) and G71 (3373 kg ha^{-1}), produced intermediate GY and the rest genotypes produced lower GY (Table 8). GY ranged from 3340 to 3853 kg ha^{-1} in Godagari; 2457 to 3599 kg ha^{-1} in Lalpur; 2300 to 3600 kg ha^{-1} in Nachole; 2002 to 3575 kg ha^{-1} in Sapahar and 3306 to 3803 kg ha^{-1} in Shyampur (Table 6). Overall, G84, G80 and G76 showed consistent GY performance across different environments, as evident from its higher GY, superiority and stability at all test environments (Locations). Likewise, G3, G8, G15, G20, G26, G53, G59, G69, G71 and G79 produced higher GY in some environments, while less in the other, indicating the specific suitability of these genotypes to respective environments (Table 7).

3.3 Correlation analysis

Correlation coefficients among spikes m^{-2}, grains spike^{-1}, TGW and grain yield were calculated using mean data of 14 genotypes over five locations. Correlation analysis showed that grain yield had strong positive association with spikes m^{-2} (r = 0.92**), grains spike^{-1} (r = 0.72**) and TGW (r = 0.89**). Positive association of these above-mentioned traits with grain yield (kg ha^{-1}) showed that these characters had major influence to wheat grain yield (Table 10).

Spikes m^{-2} showed strong positive association with grains spike^{-1} (r = 0.76**), TGW (r = 0.80**) and Grain yield (r = 0.92**). Higher number of spikes m^{-2} which increased grains per spike and TGW of wheat showed positive impact on grain yield (Table 10). Grains spike^{-1} had strong positive associations with Grain yield (r =072**) while non-significant relationship with TGW.

Strong positive relationship of thousand grain weight (TGW) with grain yield (r = 0. 89**) suggested that TGW was also a vital contributor towards grain yield besides grains spike^{-1}and spikes m^{-2}. In the present study, spikes m^{-2}, TGW and grains spike^{-1} was identified as direct contributors to grain yield in wheat. Therefore, these traits needs due weightage during selection of high yielding wheat genotypes.

4 Discussion

4.1 G × E (location) interaction

The results of a combined analysis of variance revealed considerable variations in genotypes, environments, and their interactions for spike m^{-2} (SPM), grains spike^{-1} (GPS), thousand grain weight (TGW) and grain yield (GY). Earlier, Dodig et al. (2008); Ali et al. (1997); Shankarrao et al. (2010); Mohammadi et al. (2012); Mehari et al. (2014); Ebrahimnejad and Rameeh (2016); Khan et al. (2010) and Nehe et al. (2019) also stated similar findings in wheat. On the other hand, for tillers m^{-2} and for thousand grain weight (TGW) in wheat, Khan et al. (2010) and Motamedi et al. (2013) revealed non-significant variations among genotypes, environments, and their genotypes by environment interaction. Divergent genotypes used in the study, as well as environmental factors or both, could be the cause of these divisive outcomes. Favorable flowering and pollination conditions produce more spikes m^{-2} and grains spike^{-1} (Ágoston and Pepó, 2005). Genotype G84 showed consistent performance across different environments, as evident from its higher GPS, superiority and stability at all test environments (Locations). These results corroborated those of other researchers, who found that the number of grains spike^{-1} increased wheat crop grain productivity (Sakuma and Schnurbusch, 2019; Wolde et al., 2018). Three crucial traits that directly influence grain yield in wheat are spike m^{-2} (Mian et al., 2020), grains spike^{-1}, and thousand grain weight. As a result, stability of these traits results in stability of grain yield (Dreccer et al., 2008). Yield is directly influenced by the number of effective tillers per plant (spikes m^{-2}). None of the genotypes in the study completely dominated the other genotypes. However, Genotypes G76, G80 and G84 produced highest spikes m^{-2} in most of the locations. Several researchers studied wheat crops and reported that increasing more effective tillers together with other yield-enhancing components boosted wheat crops' grain yield (Abdelkhalik, 2019; Liu et al., 2019). Grain yield was directly improved by an increase in thousand grain weight. In present study, genotypes G80, G76 and G71 performed well in most of the locations in respect of TGW and had yield advantage also. These results supported the statements made by several researchers that TGW increases wheat crop grain production (Bilgrami et al., 2018; Kamaran et al., 2019). In all plant breeding program high yielding line/cultivar development is the essential constituent that governs the crop and its grower's future (Miflin, 2000). The ideal way for plant breeders to maintain high production and effective practices is to subject prospective lines to a wide range of environmental conditions and then choose the stable genotypes with the highest yield (Kaya et al., 2002; Roozeboom et al., 2001; Loffler et al., 2005; Blecha, 2019). In the majority of the locations, genotypes G84, G80, and G76 had the highest spikes m^{-2}, grains spike^{-1}, and grain yield and may be regarded as the highest yielding, most stable genotype for adoption.

4.2 Correlation analysis

According to correlation study, spikes m^{-2}, grains spike^{-1} and TGW were strong positively correlated with grain yield. Ullah et al. (2021) showed that grain spike^{-1} and TGW had a strong correlation with grain yield. Mohsen et al. (2012) also described that grain yield had positively high correlations with above stated characters and they recommended that plant breeders take these characters into account when breeding wheat to improve grain production.

5 Conclusion

All evaluated variables exhibited significant genetic variation among genotypes, indicating there was adequate variation to allow for efficient selection. Likewise, significant genotype × location interactions (GEI) suggested unpredictable performance for almost all traits of genotypes across locations. The GEI occupied a considerable portion of sum of squares demonstrating its greater effects on all characters for phenotypic expression. Significant positive correlations between grain yield with spikes m^{-2}, grains spike^{-1}, and TGW were found using correlation analysis, demonstrating that these characters significantly influenced grain yield in wheat. Genotypes G84, G80 and G76 showed the highest spikes m^{-2}, grains spike^{-1}, TGW and grain yield in most of the locations, and were thus selected as high yielding genotypes.

Acknowledgments

The authors are grateful to PIU-BARC, NATP-2, Bangladesh Agricultural Research Council for providing monetary support for conducting the research

Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

References

Abdelkhalik SAM. 2019. Assessment of some genetic parameters for yield and its components in four bread wheat crosses using six parameter model. Egypt. J. Plant Breed 23:719–36.

Ágoston T, Pepó P. 2005. Effects of genetic and ecological factors on yield formation in winter wheat production. Cereal Research Communications 33:37–40. doi: 10.1556/crc.33.2005.1.8.

Akcura M, Kaya Y, Taner S, et al. 2009. Evaluation of durum wheat genotypes using parametric and nonparametric stability statistics. Turkish Journal of Field Crops 14:111–122.

Alexandratos N, Bruinsma J. 2012. World Agriculture Towards 2030/2050: The 2012 Revision, No. 12-03. Food and Agriculture Organization of the United Nations (FAO), Rome, Italy.

Alexandratos N, Bruinsma J. 2022. Grain and Feed Annual. Global Agricultural Information Network (GAIN). Report No. BG2022-0005. United States Department of Agriculture (USDA).

Ali W, Zada K, Shah P, Haider A, Ayaz S, Malik S. 1997. Correlation and regression analysis of agronomic parameters with grain yield of wheat. Sarhad Journal of Agriculture 13:329–332.

Annicchiarico P. 2002. Genotype × environment interaction: challenges and opportunities for plant breeding and cultivar recommendations. Food and Agriculture Organization of the United Nations (FAO), Rome, Italy.

Bilgrami SS, , Fakheri BA, J VS, Razavi K, Mahdinezhad N, Tavakol E, Ramandi HD, Ghaderian M. 2018. Evaluation of agro-morphological traits related to grain yield of iranian wheat genotypes in drought-stress and normal irrigation conditions. Australian Journal of Crop Science 12:738–748. doi: 10.21475/ajcs.18.12.05.pne878.

Blecha S. 2019. Addressing the Challenges Facing Wheat Production: Nebraska and International Breeding Efforts. PhD Thesis, University of Nebraska, USA.

Dodig D, Zoric M, Knezevic D, King SR, Surlan-Momirovic G. 2008. Genotype×environment interaction for wheat yield in different drought stress conditions and agronomic traits suitable for selection. Australian Journal of Agricultural Research 59:536. doi: 10.1071/ar07281.

Dreccer MF, Chapman SC, Ogbonnaya FC, Borgognone MG, Trethowan RM. 2008. Crop and environmental attributes underpinning genotype by environment interaction in synthetic-derived bread wheat evaluated in Mexico and Australia. Australian Journal of Agricultural Research 59:447. doi: 10.1071/ar07220.

Ebrahimnejad S, Rameeh V. 2016. Correlation and factor analysis of grain yield and some important component characters in spring bread wheat genotypes. Cercetari Agronomice in Moldova 49:5–15. doi: 10.1515/cerce-2016-0001.

Kamaran S, Khan TM, Bakhsh A, Hussain N, Mahpara S, Manan A, Chattha WS, Jilani TA, Sherani J, Iqbal M. 2019. Assessment of morphological and molecular marker based genetic diversity among advanced upland cotton genotypes. Pakistan Journal of Agricultural Sciences 56.

Kaya Y, Palta C, Taner S. 2002. Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turkish Journal of Agriculture and Forestry 26:275–279.

Khan N, Syeed S, Masood A, Nazar R, Iqbal N. 2010. Application of salicylic acid increases contents of nutrients and antioxidative metabolism in mungbean and alleviates adverse effects of salinity stress. International Journal of Plant Biology 1:e1. doi: 10.4081/pb.2010.e1.

Liu C, Khodaee M, Lopes MS, Sansaloni C, Dreisigacker S, Sukumaran S, Reynolds M. 2019. Multi-environment QTL analysis using an updated genetic map of a widely distributed seri × babax spring wheat population. Molecular Breeding 39. doi: 10.1007/s11032-019-1040-1.

Loffler CM, Wei J, Fast T, Gogerty J, Langton S, Bergman M, Merrill B, Cooper M. 2005. Classification of maize environments using crop simulation and geographic information systems. Crop Science 45:1708–1716. doi: 10.2135/cropsci2004.0370.

Mehari M, Tesfay M, Yirga H, Mesele A, Abebe T, Amare B, Workineh A. 2014. Pattern analysis of multi-environment grain yield trial of bread wheat genotypes in South Tigray, Ethiopia. International Journal of Plant Breeding and Genetics 9:22–27. doi: 10.3923/ijpbg.2015.22.27.

Mian MAK, Begum AA, Saha RR. 2020. Functional relationship between grain yield and spikes per square meter of wheat as influenced by seed rate under late sown condition. Bangladesh Agronomy Journal 22:105–113. doi: 10.3329/baj.v22i1.44942.

Miflin B. 2000. Crop improvement in the 21st century. Journal of Experimental Botany 51:1–8. doi: 10.1093/jexbot/51.342.1.

Mohammad F, Abdalla O, Rajaram S, Yaljarouka A, Khan NU, Khan AZ, Khalil SK, Khalil IH, Ahmad I, Jadoon SA. 2011. Additive main effect and multiplicative analysis of synthetic-derived bread wheat under varying moisture regimes. Pakistan Journal of Botany 43:1205–1210.

Mohammadi M, Karimizadeh R, Sabaghnia N, Shefazadeh MK. 2012. Genotype × environment interaction and yield stability analysis of new improved bread wheat genotypes. Turkish Journal of Field Crops 17:67–73.

Mohsen AA, Hegazy SRA, Taha MH. 2012. Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat genotypes. Journal of Plant Breeding and Crop Science 4:9–16.

Motamedi M, Safari P, Motamamedi C. 2013. Additive main effect and multiplication interaction analysis of grain yield in bread wheat genotypes across environments. International Journal of Biosciences (IJB) 3:218–225. doi: 10.12692/ijb/3.8.218-225.

Nehe A, Akin B, Sanal T, Evlice AK, Unsal R, Dinçer N, Demir L, Geren H, Sevim I, Orhan Ş, Yaktubay S, Ezici A, Guzman C, Morgounov A. 2019. Genotype x environment interaction and genetic gain for grain yield and grain quality traits in turkish spring wheat released between 1964 and 2010. PLOS ONE 14:e0219432. doi: 10.1371/journal.pone.0219432.

Peng JH, Sun D, Nevo E. 2011. Domestication evolution, genetics and genomics in wheat. Molecular Breeding 28:281–301. doi: 10.1007/s11032-011-9608-4.

Rahman MM, Miah MG. 2017. Wheat production in North West region of Bangladesh. Bangladesh Journal of Administration and Management 27.

Roozeboom K, Bowden R, Brooks L. 2001. Kansas performance tests with winter wheat varieties. volume 879. Agriculture Experimentation Station Report Progress.

Sakuma S, Schnurbusch T. 2019. Of floral fortune: tinkering with the grain yield potential of cereal crops. New Phytologist 225:1873–1882. doi: 10.1111/nph.16189.

Shankarrao BS, Mukherjee S, Pal AK, De DK. 2010. Estimation of variability for yield parameters in bread wheat (*Triticum aestivum* L.) grown in Gangetic West Bengal. Electronic Journal of Plant Breeding 1:764–768.

Šramková Z, Gregová E, Šturdík E. 2009. Chemical composition and nutritional quality of wheat grain. Acta chimica slovaca 2:115–138.

Ullah MI, Mahpara S, Bibi R, Shah RU, Ullah R, Abbas S, Ullah MI, Hassan AM, El-Shehawi AM, Brestic M, Zivcak M, Khan MI. 2021. Grain yield and correlated traits of bread wheat lines: Implications for yield improvement. Saudi Journal of Biological Sciences 28:5714–5719. doi: 10.1016/j.sjbs.2021.06.006.

Wolde GM, Mascher M, Schnurbusch T. 2018. Genetic modification of spikelet arrangement in wheat increases grain number without significantly affecting grain weight. Molecular Genetics and Genomics 294:457–468. doi: 10.1007/s00438-018-1523-5.

The Official Journal of the **Farm to Fork Foundation**
ISSN: 2518–2021 (print)
ISSN: 2415–4474 (electronic)
http://www.f2ffoundation.org/faa