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Identification of promising and stable genotypes of wheat (*Triticum aestivum* L.) for grain yield under varied climatic conditions of north-western Himalayas using joint regression analysis

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Abstract

The present investigation was undertaken to determine the stability of wheat genotypes for grain yield under varied environmental conditions prevalent in north- western Himalayas. A total of 60 genotypes including four checks were evaluated during three cropping seasons (*Rabi* 2019-20 to 2021-22). The stability was estimated using Eberhart and Russell model for six traits viz., days to 50% flowering, days to 75% maturity, flag leaf area (cm^2), tillers per plant, biological yield, and grain yield per plant. The pooled analysis of variance showed differential behavior of genotypes over the environments. The most stable genotypes identified for days to 50% flowering, days to 75% maturity, flag leaf area (cm^2), tillers per plant, biological yield and grain yield per plant was HPW 474. However, the promising and stable genotypes identified specifically for grain yield were HPW 474, HPW 368 and HD 2967. Thus, the genotypes found stable and well adapted to all the types of environments could be exploited as elite gene pool in future breeding programme, where aim is to develop high yielding and stable genotypes over environments or could be further tested in multilocation trials to be released as a cultivar.

Keywords: Grain yield, G×E interactions, wheat genotypes, stability

1. Introduction

Wheat is one of the vital cereal crops after rice to meet the food requirements of the world. It ranks first in terms of acreage while second in terms of production globally. Bread wheat (*Triticum aestivum* L.) is a hexaploid (2n=6x=42; AABBDD genome), self-pollinated and annual cereal crop. It belongs to tribe Triticeae and family Poaceae. It provides over 20% of calories and protein for human nutrition for about 35% of world's population in more than 40 countries. Globally, it occupies 220.89-million-hectare area with the production of 779.2 million tonnes and 3.5 tonnes per ha of productivity (USDA 2020-21), while in India, the wheat crop is grown over 31.35-million-hectare area with total production of 109.59 million tonnes and productivity 34.9 q/ha (Anonymous 2022). India is one of the principal wheat producing and consuming countries in the world. It is grown over a wide range of climatic conditions in India and its importance in Indian agriculture is second only to rice. In Himachal Pradesh, wheat occupies an area of about 0.33 million hectares with total production of 0.57 million tonnes and productivity of 17.12 q/ha (Anonymous 2021).

Grain yield is a quantitative character and therefore, it is influenced by the environmental factors which includes temperature, moisture, soil fertility, sowing time and day length Kumar*et al.*, (2019). Grains per spike contribute positively to yield as reported by Anubhav *et al.*, (2020). These factors are not consistent across the locations and years due to which the yield of wheat does not remain consistent across different environments. Himachal Pradesh is a hilly state and therefore the climatic conditions change very quickly in this region due to change in the altitude and the average grain yield of the crop varies with varying environmental conditions (Devi *et al.*, 2019). Therefore, plant breeders in crop improvement programs aim to develop varieties with well adapted environmental conditions with the aim to improve the agronomic and grain quality traits and to develop desire genotypes which can survive in the wide range of climate, especially with the diverse condition (Kumar *et al.*, 2021). Genotypes often do not perform in similar manner when tested in multiple environments. This phenomenon is due to the presence of genotype by environment interaction (Gauch and Zobel 1997).

A variety's adaptability to diverse environments is usually determined by its interaction with different environments in which it is planted. The genotype x environment (G×E) interactions could be attributed to predictable effects, that may be due to macro-environmental conditions and non- predictable effects, mainly caused by climatic and micro- environmental conditions as reported by Allard and Bradshaw (1964). A variety or genotype is more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown in diverse environments.

Many models have been developed to measure the stability of various parameters. Among those the most widely used model (Eberhart and Russell, 1966) has been followed to interpret the stability statistics in various crops. He suggested that the regression coefficient (b_i) and deviation from regression (S^2_{di}) may be considered as two parameters for measuring the varietal phenotypic stability. The variety with (b_i) value did not significantly differ from unity (b =1) and (S^2_{di}) did not significantly differ from zero could be described as a stable variety. Thus, the present investigation was undertaken to identify the promising and stable genotypes of wheat (*Triticum aestivum* L.) for grain yield under varied climatic conditions of north-western Himalayas using joint regression analysis.

2. Materials and Methods

Experimental site: The experiment was conducted for three consecutive years from *Rabi* 2019-20 to 2021-22 at the Experimental Farm of the Rice and Wheat Research Centre, Malan CSK HPKV, Palampur The experimental site of RWRC, Malan is situated at an elevation of 950 m. above mean sea level with 32.10 N latitude and 76.10 E longitude commanding sub-humid mid-hill conditions in District Kangra of Himachal Pradesh. The annual rainfall of the area is 1800±512 mm. Nearly 80% of the total precipitation is received during the Kharif crop season. The soil in silty clay loam with pH ranging between 5.8 to 6.0.

Plant material and statistical analysis: The experimental material comprised of 60 diverse wheat germplasm lines including four checks *viz*, HPW 251, HS 240, HS 562 and PBW 723 were evaluated using α-RBD design. These genotypes were varying in adaptability and yield potential and therefore, these genotypes were selected based on the yield and contributing traits liketiller count, flag leaf area and biological yield. Each genotype was grown in two rows of one- meter length with 25 x 5 cm spacing. The plot size was kept 1.0 x 0.5 m. The data was recorded on five randomly selected competitive plants in each replication on six quantitative traits viz., days to 50 % flowering, days to 75% maturity,flag leaf area (cm^2), tillers per plant, biological yield per plant (g) and grain yield per plant (g). Data on these traits was subjected to analysis of variance to find significant differences among genotypes for the recorded data. After obtaining the significant differences, data were subjected to stability analysis according to Eberhart and Russel (1966).Data were subjected to stability analysis according to Eberhart and Russell (1966) using OPSTAT software and SPAR 3.0.

3. Results and Discussion

Significance of mean squares: The pooled analysis of variance (Table 1) showed significant differences among the genotypes and environments for all the traits studied,which revealed that there was considerable variation present both among the genotypes and environments. Similar findings for genotypic and environmental variation under different environments were also observed by Gupta *et al.* (2022). The mean sum of squares for G × E interaction were significant for flag leaf area and grain yield per plant while for E+ (G × E), the mean sum of squares was significant for all the traits, indicating differential response of genotypes to different environments. Similar results were also reported by Devi *et al.* (2019). The magnitude of genotypes and environmental variances was observed to be higher than of G × E interaction for all the traits. Further the higher magnitude of mean squares due to environments (linear) as compared to G × E (linear) revealed that the considerable differences in the environments accounted for major part of total variation for most of the traits studied which was mainly due to variation in weather and temperature during different cropping seasons.

Variance due to G× E (linear) was significant for the traits viz., days to 50% flowering, days to 75% maturity, flag leaf area (cm^2), tillers per plant, biological yield per plant and grain yield per plant, which revealed that the major component for differences in stability was due to linear regression and the performance can be predicted with some reliance under different environments for these traits. Similarly, the significant mean squares due to pooled deviation or non-linear component of G ×E interaction suggested that the deviation from linear regression also contributed substantially towards the difference in stability of genotypes.

Table 1. Joint regression analysis of variance for grainyield and related traits over environments

Source of Variation	df	DTF	DTM	FLA	T/P	BY/P	GY/P
Genotype	65	39.08*	24.50*	16.08*	0.322*	11.54*	1.30*
Environment	2	1171.25*	679.84*	2929.23*	9.09*	175.56*	80.40*
G×E	130	1.86	3.24	6.11*	0.15	1.39	0.40*
E+G×E	132	19.58*	13.49*	50.40*	0.29*	4.03*	1.61*
E (linear)	1	2342.50*	1359.68*	5858.45*	18.19*	351.13*	160.80*
G×E (linear)	65	1.93*	4.89*	10.45*	0.25*	1.91*	0.50*
Pooled Deviation	66	1.76*	1.57*	1.75*	0.05	0.85*	0.29*
Pooled Error	390	5.16	3.77	3.73	0.21	1.88	0.34

*Significant at P<0.05;

Note: Days to 50% flowering (DTF), Days to 75% maturity (DTM), Flag Leaf Area (FLA), Tillers per plant (T/P), Biological yield per plant (BY/P), Grain yield per plant

Table 2. Estimates of stability parameters for days to flowering, days to maturity and flag leaf area in wheat

	DTF			DTM			FLA		
Genotype	**Mean**	**b**	**S^2_{di}**	**Mean**	**b**	**S^2_{di}**	**Mean**	**b**	**S^2_{di}**
Agra Local	117.89	1.05	-1.69	162.89	0.65	0.00	21.91	0.87	**3.94***
BRW3273	118.89	1.12	-1.53	161.11	1.67	-0.40	25.83	1.23	**8.44***
DBW107	117.44	0.87	-1.73	159.33	0.91	-1.19	18.08	0.91	**3.63***
DBW179	116.89	1.32	-1.69	164.00	1.24	1.80	22.76	1.02	**3.63***
DBW24	117.56	0.98	-0.94	161.56	2.32	3.68*	19.59	0.57	**7.26***
DBW39	123.44	0.73	-1.66	166.78	0.60	-1.22	23.81	**1.87***	-1.18
Desi Mundla	123.56	1.68	3.31	165.56	1.45	2.90	26.38	1.40	-0.89
FLW16	118.44	1.29	0.88	159.89	0.84	-1.19	24.36	1.01	-1.16
GRU 2010 1817	117.11	0.86	0.77	160.44	1.68	-1.04	24.26	1.69	-0.35
HD2967	120.44	1.28	-0.43	160.56	0.75	-1.05	24.19	1.41	2.00
HD3086	117.78	0.86	-0.51	161.78	0.89	0.77	22.57	0.85	-0.77
HD3237	124.67	1.10	-0.34	164.67	**0.63***	-1.24	23.67	1.34	-0.12
HD3271	122.00	1.10	-1.70	166.11	0.06	-1.24	22.64	1.42	0.72

HI1620	124.00	1.24	-0.41	165.89	1.11	-0.96	22.87	1.04	1.57
HI8173	122.89	1.20	**7.58***	164.33	0.36	-1.23	24.97	1.37	-1.16
HIKK 05	123.00	1.24	2.67	165.67	0.61	0.56	24.43	1.00	-0.37
HPW368	115.56	1.19	-1.71	160.11	0.33	-1.22	21.18	1.19	-0.78
HPW376	113.67	1.17	-0.88	161.22	1.26	**4.80***	19.08	1.12	-0.87
HPW469	110.44	1.55	-1.14	155.33	0.74	0.25	21.04	**1.18***	-1.25
HPW470	110.33	0.88	1.59	159.22	1.01	0.23	20.47	1.28	-1.20
HPW472	116.56	1.05	-1.29	156.78	0.89	0.77	20.10	0.97	-0.13
HPW473	118.11	1.28	-1.69	163.78	0.87	-1.03	24.16	0.67	-1.15
HPW474	117.78	0.81	4.14	160.22	1.81	3.30	21.62	0.82	-0.52
HS295	109.67	1.29	3.93	155.33	0.55	-1.13	18.26	1.15	-1.06
HS627	117.22	**0.501***	-1.75	157.56	1.40	-0.15	19.78	1.11	-1.14
HTW9	117.33	1.23	-0.34	162.00	1.52	-0.01	21.39	0.77	-1.04
HW3631	119.78	0.87	-1.73	160.22	1.02	-1.17	21.66	0.94	-0.94
Kanku	119.67	0.95	-1.32	158.44	**0.693***	-1.24	21.39	1.16	**3.18***
		DTF			**DTM**			**FLA**	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**B**	**S^2_{di}**	**Genotype**	**Mean**
KBRL 79 2	121.00	1.10	-1.70	159.22	0.48	-1.23	15.59	0.84	**5.42***
PBW724	119.44	1.14	-1.71	162.00	1.17	-0.95	22.87	0.69	1.78
PBW725	119.67	0.95	-1.32	158.44	0.87	-1.24	19.44	0.39	-1.03
PBW752	122.22	1.05	-1.72	160.89	0.93	-1.24	18.89	**0.62***	-1.20
PBW756	120.44	0.79	-1.01	161.67	1.36	-0.57	19.39	0.61	-0.69
PBW757	124.44	1.07	-1.76	165.33	0.89	-0.74	22.52	1.20	-0.97
PBW771	123.44	1.07	-1.55	165.00	0.71	0.04	21.09	1.48	-0.95
PBW812	121.78	0.59	-1.75	159.89	0.93	-1.24	19.42	1.27*	-1.24
PBW813	123.11	1.08	-0.84	162.00	1.16	-0.21	21.39	1.47*	-1.26
PW1903	119.89	0.84	-1.59	157.89	0.75	-1.24	21.24	1.29	-0.79
PW1904	119.22	1.12	-1.53	160.44	0.78	-1.20	24.09	1.13	-1.15
PW1905	117.11	1.14	-1.27	161.56	1.21	-1.22	23.93	0.80	-1.00
PW1906	121.56	1.06	-0.32	159.67	0.72	-1.21	22.80	1.50*	-1.24
PW1908	116.89	1.05	-1.72	162.33	1.08	-1.16	26.52	1.02	-0.83
PW1909	116.67	0.88	0.09	161.11	0.85	0.74	20.31	1.39	-1.15
PW1910	120.78	1.07	-1.55	159.00	1.00	-0.41	21.77	1.12	-1.00
PW1911	122.44	1.14	-1.71	160.56	1.19	-0.62	21.50	0.78	-0.71
PW1912	120.89	0.77	-1.37	158.78	**0.51***	-1.23	19.71	0.50	1.20
Sonalika	121.11	0.95	1.96	159.44	1.14	-1.15	17.57	0.64	0.13
Tarmori	114.56	**1.11***	-1.76	161.11	1.95	-0.68	21.21	1.14	-1.04
TL3006	113.22	0.70	1.45	159.00	0.90	-1.19	22.51	0.43	0.15
Unnat PBW 550	118.67	0.75	0.01	155.78	0.88	-1.02	20.09	1.16	**3.51***
WH1105	122.78	0.80	-1.60	161.56	1.92	-0.98	26.61	1.38	1.29

WH1124	124.67	1.10	-1.24	160.44	1.23	-1.23	22.08	0.87	-1.10
WH1127	120.22	0.77	-1.37	159.33	0.61	0.56	21.21	0.96	-0.88
WH1142	121.78	0.87	-1.67	159.44	**2.31***	-1.10	22.07	**0.31***	-1.25
WH1216	120.89	0.98	-0.94	154.89	0.41	-0.09	19.58	0.84	-1.18
WH1264	121.11	0.58	2.26	162.33	1.04	9.436*	22.10	**0.44***	-1.18
WH1270	119.67	0.94	**10.44***	162.11	0.09	**4.22***	18.87	1.20	-0.09
HPW251 (C)	121.89	0.94	18.72	161.00	1.48	**4.72***	18.12	0.64	2.57
HS240 (C)	120.56	0.92	1.13	161.44	0.80	0.21	20.87	0.70	**4.73***
HS562 (C)	118.89	0.30	-1.67	161.56	0.34	**6.28***	21.07	0.68	-0.98
PBW 723(C)	123.67	0.76	-1.45	163.11	0.58	**26.60***	22.10	1.24	**26.65***
Grand Mean	119.66	1.00	-	161.09	1.00	-	21.61	1.00	-
S.E(m) ±	2.89	0.50	-	2.71	0.80	-	2.11	0.68	-

Note: Days to 50% flowering (DTF), Days to 75% maturity (DTM), Flag Leaf Area (FLA), Tillers per plant (T/P), Biological yield per plant (BY/P), Grain yield per plant

Table 3. Estimates of stability parameters for tillers per plant, biological yield per plant and grain yield per plant in wheat

		T/P			**BY/P**			**GY/P**	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**
Agra Local	2.94	1.50	-0.06	15.67	1.11	-0.62	6.16	0.90	0.08
BRW3273	2.99	1.62	-0.03	14.79	0.93	0.67	4.57	**0.39***	-0.11
DBW107	2.61	-0.21	-0.06	13.44	1.94	**3.11***	5.33	1.13	0.16
DBW179	3.72	2.53	-0.05	16.08	1.91	0.28	5.53	1.06	-0.07
DBW24	3.28	1.34	-0.06	13.02	1.61	0.36	4.46	0.74	-0.06
DBW39	3.31	1.51	-0.07	17.22	1.31	-0.40	5.22	1.10	0.03
		T/P			**BY/P**			**GY/P**	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**
Desi Mundla	3.70	**2.95***	-0.07	17.54	**2.48***	-0.61	5.40	1.48	0.01
FLW16	3.16	1.15	-0.06	17.09	1.06	-0.19	5.91	1.73	-0.10
GRU 2010 1817	2.92	0.83	-0.07	14.62	0.99	-0.54	5.57	1.35	-0.08
HD2967	2.72	0.13	-0.07	13.08	0.47	-0.45	5.63	**1.38***	-0.11
HD3086	3.07	0.99	0.03	12.03	0.80	0.38	5.14	1.45	0.17
HD3237	3.16	**2.07***	-0.07	14.61	0.65	-0.55	6.03	1.43	-0.07
HD3271	3.08	1.67	-0.03	13.31	1.47	0.12	4.97	1.16	-0.09
HI1620	2.76	0.35	-0.01	10.80	0.95	-0.33	4.49	1.15	0.11
HI8173	3.02	1.01	0.06	11.68	0.42	0.05	5.09	0.97	-0.07
HIKK 05	2.84	1.16	**0.21***	10.27	0.28	**2.74***	4.54	0.70	**0.63***
HPW368	3.44	**3.37***	-0.07	15.74	1.01	-0.61	6.63	1.66	-0.09
HPW376	2.94	**1.97***	-0.07	15.71	0.95	-0.21	5.46	1.33	-0.11
HPW469	2.93	1.41	-0.06	14.60	0.47	0.04	5.57	0.47	-0.10
HPW470	3.29	**2.54***	-0.07	16.08	0.79	1.77	4.54	1.15	-0.03

HPW472	2.89	0.66	-0.03	12.27	1.62	**1.80***	4.30	1.18	0.07
HPW473	3.12	0.20	-0.07	16.20	1.45	-0.53	5.23	0.27	0.08
HPW474	2.99	0.85	0.06	15.73	0.85	1.69	5.98	0.55	0.03
Desi Mundla	3.70	**2.95***	-0.07	17.54	**2.48***	-0.61	5.40	1.48	0.01
FLW16	3.16	1.15	-0.06	17.09	1.06	-0.19	5.91	1.73	-0.10
GRU 2010 1817	2.92	0.83	-0.07	14.62	0.99	-0.54	5.57	1.35	-0.08
HD2967	2.72	0.13	-0.07	13.08	0.47	-0.45	5.63	**1.38***	-0.11
HD3086	3.07	0.99	0.03	12.03	0.80	0.38	5.14	1.45	0.17
HD3237	3.16	**2.07***	-0.07	14.61	0.65	-0.55	6.03	1.43	-0.07
HD3271	3.08	1.67	-0.03	13.31	1.47	0.12	4.97	1.16	-0.09
HI1620	2.76	0.35	-0.01	10.80	0.95	-0.33	4.49	1.15	0.11
HI8173	3.02	1.01	0.06	11.68	0.42	0.05	5.09	0.97	-0.07
HIKK 05	2.84	1.16	**0.21***	10.27	0.28	**2.74***	4.54	0.70	**0.63***
HPW368	3.44	0.50	-0.07	15.74	1.01	-0.61	6.63	1.66	-0.09
HPW376	2.94	**1.97***	-0.07	15.71	0.95	-0.21	5.46	1.33	-0.11
HPW469	2.93	1.41	-0.06	14.60	0.47	0.04	5.57	0.47	-0.10
HPW470	3.29	**2.54***	-0.07	16.08	0.79	1.77	6.54	1.15	-0.03
HPW472	2.89	0.66	-0.03	12.27	1.62	**1.80***	6.30	1.18	0.07
HPW473	3.12	0.20	-0.07	16.20	1.45	-0.53	7.23	0.27	0.08
HPW474	3.29	0.85	0.06	15.73	0.85	1.69	5.98	0.55	0.03
HS295	2.81	0.24	0.04	12.42	0.03	1.66	6.79	0.39	0.01
HS627	3.16	1.54	-0.05	16.00	1.02	-0.30	5.41	0.86	-0.03
HTW9	2.81	0.64	-0.02	14.71	2.32	-0.53	6.80	1.00	0.07
HW3631	3.46	1.31	-0.05	16.14	0.36	-0.54	6.42	1.19	-0.08
Kanku	3.10	1.01	-0.07	15.76	0.73	-0.55	6.36	1.02	0.12
KBRL 79 2	3.09	0.21	-0.06	15.83	0.68	0.18	5.98	1.60	-0.02
PBW724	2.60	0.61	-0.05	13.18	1.70	1.60	6.40	1.22	-0.06
PBW725	3.02	1.06	-0.05	16.39	2.14	-0.26	8.08	0.29	0.22
PBW752	3.24	0.65	-0.07	14.04	0.99	-0.09	4.99	0.84	-0.09
PBW756	2.83	0.64	-0.02	12.46	0.85	0.30	4.78	0.68	0.31
PBW757	2.73	0.24	-0.05	14.84	1.04	**1.86***	6.11	1.37	0.13
PBW771	2.34	-1.08	-0.04	9.62	0.53	0.75	5.79	0.80	-0.11
PBW812	3.24	1.88	0.01	12.56	1.13	-0.52	5.08	0.44	-0.03
PBW813	3.11	1.04	-0.07	13.19	1.94	0.55	5.18	1.84	0.15
PW1903	3.39	2.24	-0.03	14.32	1.32	0.61	5.01	1.90	0.16
PW1904	2.59	0.13	-0.07	12.10	0.71	1.20	6.83	0.69	**0.51***

		T/P			**BY/P**			**GY/P**	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**
PW1905	2.86	0.67	-0.07	15.42	0.95	-0.62	5.40	0.56	-0.06
PW1906	3.33	1.07	-0.01	14.82	1.15	-0.17	6.84	0.64	0.06

PW1908	3.03	0.09	-0.05	12.19	0.47	0.25	5.27	**1.39***	-0.11
PW1909	2.49	-0.43	-0.02	10.52	-0.08	**2.91***	7.87	1.03	0.06
PW1910	3.50	2.74	-0.01	15.38	1.08	0.75	5.49	1.54	-0.10
PW1911	2.33	-0.30	-0.04	11.21	1.05	-0.62	5.90	1.30	-0.07
PW1912	2.53	-0.09	-0.03	10.82	0.53	-0.60	6.60	**1.18***	-0.11
Sonalika	2.88	1.10	-0.04	11.61	1.04	0.07	5.71	1.35	0.11
Tarmori	2.89	0.99	-0.07	14.34	-0.31	-0.51	5.40	1.20	-0.07
TL3006	2.62	0.21	-0.06	12.27	1.04	-0.39	5.30	**1.23***	0.20
UNNAT PBW 550	3.18	**1.66***	-0.07	12.62	**2.07***	-0.61	6.13	0.86	-0.10
WH1105	3.31	**1.96***	-0.07	13.33	**0.37***	-0.62	5.58	0.48	0.12
WH1124	3.11	1.05	-0.03	12.60	1.63	-0.38	5.34	1.83	-0.05
WH1127	2.69	0.35	-0.01	12.40	-0.25	0.57	7.43	0.88	-0.02
WH1142	3.32	0.98	-0.07	15.70	1.03	-0.18	6.98	0.72	-0.10
WH1216	3.47	3.13	-0.02	17.00	1.25	0.19	6.51	0.17	-0.09
WH1264	2.51	-0.08	0.07	12.69	-0.14	-0.41	5.94	1.10	**1.91***
WH1270	3.18	1.50	**1.20***	10.32	0.92	-0.54	5.82	0.80	**2.38***
HPW251 (C)	2.58	-0.68	-0.07	11.58	0.61	-0.59	4.63	0.00	**1.07***
HS240 (C)	2.70	-0.72	-0.01	11.74	1.22	**2.96***	5.66	0.59	**2.31***
HS562 (C)	3.22	0.37	-0.05	13.56	0.12	0.70	5.73	1.05	**2.43***
PBW 723(C)	2.70	0.88	0.04	12.79	1.11	0.75	6.96	0.31	0.02
Grand Mean	3.01	1.00	-	13.78	1.00	-	5.83	1.00	-
S.E (m) ±	1.14	0.50	-	3.73	0.84	-	1.95	0.63	-

Note: Days to 50% flowering (DTF), Days to 75% maturity (DTM), Flag Leaf Area (FLA), Tillers per plant (T/P), Biological yield per plant (BY/P), Grain yield per plant

Thus, both linear (predictable) and non-linear (unpredictable) components significantly contributed to genotype × environment interactions observed for the traits but with the predominance of the former component suggesting that the performance of genotype across environments could be predicted with greater precision. Similar findings were reported by Devi *et al.,* (2019), Kumar*et al.,* (2021)and Kumar *et al.,* (2022). The non-significance of linear mean square against pooled deviation indicated that the reliable prediction of G× E interaction could not be made for tiller per plant.

***Stability analysis*:** The stability parameters (b &S^2_{di}) for all the traits were recorded (Table 2-3). According to regression model of stability proposed by Eberhart and Russell (1966), b_i is considered as a parameter of response and S^2_{di} indicates instability due to the deviation from zero. However, the significance of the coefficient of regression (b_i) means responsiveness either to favorable environment (bi>1) or poor ones (bi<1). The mean values ranged from 109-131 days with average value of119 days for days to 50% flowering. Genotypes, namely, HS 627 and HS 562 having mean values lower than average (lower days to flowering values are desirable) and regression coefficient greater than unity (b>1), hence these were found stable for favourable environment, while genotype BRW 3273, DBW 179 and FLW16 showed desirable average and regression coefficient less than unity (b<1), therefore, desirable for unfavourable environment. Considering the genotypes showing above average performance, genotypes DBW 24, HPW 472 and HPW 474 were found stable over all the environments for days to 50% flowering.

The mean values ranged from 154-168 days with average value of 37.63 for days to 75% maturity. For this trait,genotype namely, HPW 474 was found stable with above average performance, while, most responsive to favourable conditions (b>1) were HPW 368 and PBW 812.

Genotypes namely, DBW 107, PW 1912 and FLW 16 were found most responsive to unfavorable environment. For flag leaf area, the mean value ranged from 15.58-26.61 cm^2 with an average value of 21.61 cm^2 and genotypes HPW 474 and PBW 724 were found stable under all the types of environments. The genotypes having above average value and responsive to favourable (b>1) conditions were DBW 39 and HPW 469 while for unfavourable environment (b<1), the genotypes having above average performance were BRW 3273 and DBW 24.

Regarding tillers per plant, the mean values ranged from 2.33-3.74 with an average value of 3.01. Genotypes, namely, HPW 368 and HPW 474 were found stable with above average performance under all the types of environments. The most responsive genotypes WH 1142 and HS 562 were observed to perform better under favourable environmental conditions for this trait while PW 1910 and HW3631 were observed toper form better under favourable environmental conditions. The mean values For biological yield per plant, HD 2967, HPW 368 and HPW 474 were found stable and responsive to all the environments. The genotypes having above average value and responsive to favourable (b>1) conditions were WH 1105 and HS 562 while for unfavourable environment (b<1), the genotypes having above average performance were HS 627 and PW 1905.

For the major character i.e., grain yield per plant, the mean value ranged from 4.45-8.07 g with an average value of 5.83 g and only six genotypes, HD 2967, PBW 723, PW 1909, HS 295 and HPW 368 were found stable with bi values approaching to unity and non-significant S^2_{di} values (Table 3). Three genotypes, HD 3237, HPW 470 and HS 627 showed significant bi values (bi> 1) were specifically adapted to most favorable environmental conditions depicting that even a small change in environment may result a large increase in response in these genotypes while for unfavourable environment (b<1), the genotypes having above average performance were BRW 3273 and PW 1906. Similar findings were reported by Kumar *et al.*, (2014), Meena *et al.*, (2014), Kumar *et al.*, (2017), Siddhi *et al.* (2018), Singh *et al.,* (2018), Devi*et al.,* (2019), Kumar *et al.,* (2021) and Kumar *et al.,* (2022).

Conclusion

In the current study, the result concluded that the combined analysis of variance exhibited significant variation due to genotypes, environment and genotype × environment. The genotypes viz., HPW 474, HPW 368 and HD 2967 were found stable across the environment over the years for biological yield and grain yield due to their superior mean performance, regression coefficient (b) near to one with non-significant deviations from regression coefficient. Hence, these genotypes may be included in any breeding programme where objective is to develop high yielding and stable genotypes over environments.

Conflict of interest

The authors declare that there is no conflict of interest.

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Author's contribution

Conceptualization of research (P and VR); Designing of the experiments (P and VR); Contribution of experimental materials (VR); Execution of field experiments and data collection (P, VR and AR); Analysis of data and interpretation (P, DB, VS, AR and VKS); Preparation of the manuscript (P and VR)

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