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Research Article

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. 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; Trethowan *et al.*, 2018). 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. 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).

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; Kumar *et* *al.* 2021. 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 grain yield and related traits over environments

Source of Variation	df	DTF	DTM	FLA	T/P	BY/P	GY/P
Genotype	65	39.08*	24.507*	16.082*	0.322*	11.545*	1.306*
Environment	2	1171.25*	679.841*	2929.23*	9.096*	175.565*	80.4*
G×E	130	1.862	3.246	6.118*	0.154	1.395	0.403*
E+G×E	132	19.58*	13.498*	50.408*	0.29*	4.034*	1.615*
E (linear)	1	2342.50*	1359.68*	5858.45*	18.192*	351.131*	160.801*
G×E (linear)	65	1.931*	4.897*	10.458*	0.251*	1.919*	0.502*
Pooled Deviation	66	1.765*	1.571*	1.751*	0.057	0.858*	0.299*
Pooled Error	390	5.165	3.776	3.736	0.218	1.885	0.34

*Significant at P<0.05;

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	117.889	1.051	-1.694	162.889	0.647	0.004	21.911	0.871	**3.944***
BRW3273	118.889	1.121	-1.531	161.111	1.673	-0.404	25.833	1.234	**8.445***
DBW107	117.444	0.866	-1.729	159.333	0.905	-1.187	18.078	0.910	**3.639***
DBW179	116.889	1.322	-1.688	164.000	1.241	1.804	22.756	1.024	**3.632***
DBW24	117.556	0.976	-0.939	161.556	2.315	3.689*	19.589	0.573	**7.260***
DBW39	123.444	0.732	-1.656	166.778	0.600	-1.216	23.811	**1.870***	-1.177
Desi Mundla	123.556	1.678	3.313	165.556	1.448	2.904	26.378	1.402	-0.891
FLW16	118.444	1.287	0.879	159.889	0.839	-1.192	24.356	1.009	-1.164
GRU 2010 1817	117.111	0.858	0.767	160.444	1.679	-1.044	24.256	1.689	-0.353
HD2967	120.444	1.284	-0.430	160.556	0.746	-1.053	24.189	1.405	2.004
HD3086	117.778	0.861	-0.509	161.778	0.891	0.766	22.567	0.853	-0.766
HD3237	124.667	1.102	-0.343	164.667	**0.633***	-1.237	23.667	1.339	-0.120
HD3271	122.000	1.096	-1.699	166.111	0.060	-1.241	22.644	1.420	0.715
HI1620	124.000	1.239	-0.408	165.889	1.106	-0.962	22.867	1.039	1.566

HI8173	122.889	1.204	**7.582***	164.333	0.360	-1.232	24.967	1.374	-1.157
HIKK 05	123.000	1.244	2.671	165.667	0.614	0.563	24.433	1.002	-0.372
HPW368	115.556	1.188	-1.708	160.111	0.333	-1.220	21.178	1.190	-0.779
HPW376	113.667	1.169	-0.875	161.222	1.262	4.805*	19.078	1.119	-0.865
HPW469	110.444	1.547	-1.141	155.333	0.738	0.250	21.044	**1.181***	-1.254
HPW470	110.333	0.879	1.588	159.222	1.007	0.225	20.467	1.275	-1.199
HPW472	116.556	1.046	-1.292	156.778	0.891	0.766	20.100	0.970	-0.128
HPW473	118.111	1.276	-1.693	163.778	0.866	-1.025	24.156	0.671	-1.148
HPW474	117.778	0.812	4.139	160.222	1.808	3.301	21.622	0.823	-0.518
HS295	109.667	1.287	3.926	155.333	0.546	-1.134	18.256	1.151	-1.063
HS627	117.222	**0.501***	-1.750	157.556	1.397	-0.146	19.778	1.111	-1.138
HTW9	117.333	1.225	-0.337	162.000	1.520	-0.008	21.389	0.766	-1.042
HW3631	119.778	0.866	-1.729	160.222	1.019	-1.169	21.656	0.943	-0.936
Kanku	119.667	0.954	-1.317	158.444	**0.693***	-1.239	21.389	1.162	**3.181***
		DTF			**DTM**			**FLA**	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**B**	**S^2_{di}**	**Genotype**	**Mean**
KBRL 79 2	121.000	1.096	-1.699	159.222	0.480	-1.225	15.589	0.837	**5.422***
PBW724	119.444	1.139	-1.706	162.000	1.166	-0.945	22.867	0.686	1.775
PBW725	119.667	0.954	-1.317	158.444	0.872	-1.241	19.444	0.391	-1.028
PBW752	122.222	1.048	-1.715	160.889	0.932	-1.241	18.889	**0.627***	-1.200
PBW756	120.444	0.794	-1.005	161.667	1.364	-0.570	19.389	0.609	-0.689
PBW757	124.444	1.072	-1.760	165.333	0.893	-0.739	22.522	1.195	-0.968
PBW771	123.444	1.070	-1.554	165.000	0.707	0.039	21.089	1.477	-0.952
PBW812	121.778	0.592	-1.746	159.889	0.932	-1.241	19.422	1.273*	-1.241
PBW813	123.111	1.078	-0.839	162.000	1.160	-0.210	21.389	1.477*	-1.255
PW1903	119.889	0.842	-1.594	157.889	0.753	-1.240	21.244	1.293	-0.786
PW1904	119.222	1.121	-1.531	160.444	0.779	-1.199	24.089	1.130	-1.153
PW1905	117.111	1.137	-1.266	161.556	1.205	-1.218	23.933	0.802	-0.998
PW1906	121.556	1.056	-0.321	159.667	0.720	-1.205	22.800	1.500*	-1.243
PW1908	116.889	1.048	-1.715	162.333	1.079	-1.160	26.522	1.022	-0.826
PW1909	116.667	0.882	0.086	161.111	0.854	0.737	20.311	1.385	-1.151
PW1910	120.778	1.070	-1.554	159.000	1.004	-0.405	21.767	1.115	-0.998
PW1911	122.444	1.139	-1.706	160.556	1.193	-0.620	21.500	0.784	-0.705
PW1912	120.889	0.772	-1.365	158.778	0.513*	-1.231	19.711	0.501	1.197
Sonalika	121.111	0.946	1.964	159.444	1.139	-1.150	17.567	0.641	0.134
Tarmori	114.556	1.118*	-1.760	161.111	1.946	-0.677	21.211	1.141	-1.042
TL3006	113.222	0.697	1.454	159.000	0.899	-1.185	22.511	0.425	0.153
Unnat PBW 550	118.667	0.745	0.011	155.778	0.879	-1.015	20.089	1.159	3.512*
WH1105	122.778	0.796	-1.602	161.556	1.919	-0.983	26.611	1.377	1.290
WH1124	124.667	1.099	-1.243	160.444	1.232	-1.233	22.078	0.873	-1.099

WH1127	120.222	0.772	-1.365	159.333	0.614	0.563	21.211	0.956	-0.879
WH1142	121.778	0.869	-1.673	159.444	2.311*	-1.100	22.067	0.312*	-1.250
WH1216	120.889	0.976	-0.939	154.889	0.405	-0.089	19.578	0.842	-1.180
WH1264	121.111	0.582	2.260	162.333	1.035	9.436*	22.100	0.447*	-1.180
WH1270	119.667	0.938	10.440*	162.111	0.090	4.221*	18.867	1.196	-0.092
HPW251 (C)	121.889	0.938	18.721	161.000	1.475	4.725*	18.122	0.639	2.573
HS240 (C)	120.556	0.922	1.126	161.444	0.798	0.212	20.867	0.704	4.730*
HS562 (C)	118.889	0.295	-1.673	161.556	0.336	6.289*	21.067	0.676	-0.983
PBW 723(C)	123.667	0.756	-1.454	163.111	0.579	26.605*	22.100	1.236	26.653*
Grand Mean	119.660	1.00	-	161.090	1.00	-	21.61	1.00	-
S.E (m) ±	2.89	0.50	-	2.71	0.80	-	2.11	0.68	-

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	2.944	1.497	-0.058	15.667	1.113	-0.617	6.156	0.904	0.075
BRW3273	2.989	1.621	-0.029	14.789	0.929	0.669	4.567	**0.394***	-0.112
DBW107	2.611	-0.213	-0.064	13.444	1.942	**3.114***	5.333	1.127	0.155
DBW179	3.722	2.533	-0.054	16.078	1.910	0.276	5.533	1.058	-0.072
DBW24	3.278	1.341	-0.059	13.022	1.607	0.357	4.456	0.739	-0.058
DBW39	3.311	1.505	-0.072	17.222	1.313	-0.397	5.222	1.099	0.026

		T/P			BY/P			GY/P	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**
Desi Mundla	3.700	**2.959***	-0.071	17.544	**2.482***	-0.614	5.400	1.476	0.008
FLW16	3.156	1.149	-0.058	17.089	1.063	-0.192	5.911	1.733	-0.103
GRU 2010 1817	2.922	0.829	-0.072	14.622	0.988	-0.541	5.567	1.354	-0.084
HD2967	2.722	0.131	-0.072	13.078	0.471	-0.449	5.633	**1.388***	-0.112
HD3086	3.067	0.992	0.032	12.033	0.800	0.382	5.144	1.449	0.172
HD3237	3.156	**2.075***	-0.072	14.611	0.646	-0.553	6.033	1.425	-0.071
HD3271	3.078	1.672	-0.029	13.311	1.467	0.121	4.967	1.160	-0.092
HI1620	2.756	0.348	-0.014	10.800	0.947	-0.329	4.489	1.146	0.111
HI8173	3.022	1.007	0.057	11.678	0.423	0.049	5.089	0.971	-0.068
HIKK 05	2.844	1.160	**0.217***	10.267	0.276	**2.749***	4.544	0.699	**0.638***
HPW368	3.444	**3.374***	-0.071	15.744	1.012	-0.606	6.633	1.658	-0.090
HPW376	2.944	**1.972***	-0.072	15.711	0.951	-0.212	5.456	1.331	-0.107
HPW469	2.933	1.408	-0.059	14.600	0.466	0.039	5.567	0.466	-0.101
HPW470	3.289	**2.545***	-0.070	16.078	0.787	1.772	4.544	1.150	-0.032
HPW472	2.889	0.662	-0.033	12.267	1.623	**1.800***	4.300	1.183	0.072
HPW473	3.122	0.204	-0.070	16.200	1.445	-0.534	5.233	0.266	0.077
HPW474	2.989	0.852	0.059	15.733	0.851	1.686	5.978	0.552	0.033

Desi Mundla	3.700	**2.959***	-0.071	17.544	**2.482***	-0.614	5.400	1.476	0.008
FLW16	3.156	1.149	-0.058	17.089	1.063	-0.192	5.911	1.733	-0.103
GRU 2010 1817	2.922	0.829	-0.072	14.622	0.988	-0.541	5.567	1.354	-0.084
HD2967	2.722	0.131	-0.072	13.078	0.471	-0.449	5.633	**1.388***	-0.112
HD3086	3.067	0.992	0.032	12.033	0.800	0.382	5.144	1.449	0.172
HD3237	3.156	**2.075***	-0.072	14.611	0.646	-0.553	6.033	1.425	-0.071
HD3271	3.078	1.672	-0.029	13.311	1.467	0.121	4.967	1.160	-0.092
HI1620	2.756	0.348	-0.014	10.800	0.947	-0.329	4.489	1.146	0.111
HI8173	3.022	1.007	0.057	11.678	0.423	0.049	5.089	0.971	-0.068
HIKK 05	2.844	1.160	**0.217***	10.267	0.276	**2.749***	4.544	0.699	**0.638***
HPW368	3.444	0.502	-0.071	15.744	1.012	-0.606	6.633	1.658	-0.090
HPW376	2.944	**1.972***	-0.072	15.711	0.951	-0.212	5.456	1.331	-0.107
HPW469	2.933	1.408	-0.059	14.600	0.466	0.039	5.567	0.466	-0.101
HPW470	3.289	**2.545***	-0.070	16.078	0.787	1.772	6.544	1.150	-0.032
HPW472	2.889	0.662	-0.033	12.267	1.623	**1.800***	6.300	1.183	0.072
HPW473	3.122	0.204	-0.070	16.200	1.445	-0.534	7.233	0.266	0.077
HPW474	3.290	0.852	0.059	15.733	0.851	1.686	5.978	0.552	0.033
HS295	2.811	0.239	0.039	12.422	0.027	1.663	6.789	0.392	0.014
HS627	3.156	1.539	-0.053	16.000	1.015	-0.303	5.411	0.862	-0.025
HTW9	2.811	0.635	-0.023	14.711	2.317	-0.525	6.800	1.000	0.073
HW3631	3.456	1.307	-0.045	16.144	0.356	-0.539	6.422	1.188	-0.083
Kanku	3.100	1.009	-0.071	15.756	0.733	-0.550	6.356	1.015	0.118
KBRL 79 2	3.089	0.213	-0.064	15.833	0.684	0.179	5.978	1.596	-0.022
PBW724	2.600	0.613	-0.050	13.178	1.700	1.601	6.400	1.217	-0.060
PBW725	3.022	1.055	-0.054	16.389	2.141	-0.260	8.078	0.294	0.224
PBW752	3.244	0.652	-0.069	14.044	0.988	-0.087	4.989	0.837	-0.088
PBW756	2.833	0.636	-0.022	12.456	0.847	0.296	4.778	0.683	0.312
PBW757	2.733	0.243	-0.047	14.844	1.035	**1.864***	6.111	1.370	0.131
PBW771	2.344	-1.075	-0.035	9.622	0.526	0.748	5.789	0.801	-0.110
PBW812	3.244	1.875	0.012	12.556	1.130	-0.518	5.078	0.439	-0.028
PBW813	3.111	1.036	-0.072	13.189	1.941	0.553	5.178	1.843	0.149
PW1903	3.389	2.242	-0.033	14.322	1.317	0.606	5.011	1.895	0.161
PW1904	2.589	0.134	-0.068	12.100	0.706	1.197	6.833	0.693	**0.519***

		T/P			BY/P			GY/P	
Genotype	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**	**b**	**S^2_{di}**	**Genotype**	**Mean**
PW1905	2.856	0.671	-0.069	15.422	0.949	-0.618	5.400	0.562	-0.056
PW1906	3.333	1.074	-0.008	14.822	1.152	-0.169	6.844	0.643	0.056
PW1908	3.033	0.088	-0.046	12.189	0.466	0.251	5.267	1.391*	-0.111
PW1909	2.489	-0.429	-0.020	10.522	-0.084	2.916*	7.867	1.027	0.056
PW1910	3.500	2.739	-0.005	15.378	1.082	0.753	5.489	1.542	-0.103
PW1911	2.333	-0.299	-0.035	11.211	1.048	-0.620	5.900	1.299	-0.069

PW1912	2.533	-0.091	-0.028	10.822	0.526	-0.604	6.600	1.180*	-0.112
Sonalika	2.878	1.104	-0.039	11.611	1.038	0.068	5.711	1.347	0.112
Tarmori	2.889	0.987	-0.072	14.344	-0.308	-0.512	5.400	1.195	-0.074
TL3006	2.622	0.213	-0.064	12.267	1.036	-0.394	5.300	1.233*	0.198
UNNAT PBW 550	3.178	1.661*	-0.072	12.622	2.079*	-0.614	6.133	0.858	-0.095
WH1105	3.311	1.969*	-0.071	13.333	0.371*	-0.620	5.578	0.482	0.123
WH1124	3.111	1.051	-0.025	12.600	1.633	-0.375	5.344	1.829	-0.051
WH1127	2.689	0.348	-0.014	12.400	-0.245	0.569	7.433	0.876	-0.024
WH1142	3.322	0.982	-0.069	15.700	1.034	-0.179	6.978	0.721	-0.102
WH1216	3.467	3.126	-0.019	17.000	1.249	0.190	6.511	0.173	-0.091
WH1264	2.511	-0.075	0.069	12.689	-0.136	-0.407	5.944	1.102	1.917*
WH1270	3.178	1.495	1.205*	10.322	0.917	-0.538	5.822	0.804	2.383*
HPW251 (C)	2.578	-0.676	-0.071	11.578	0.605	-0.594	4.633	0.002	1.070*
HS240 (C)	2.700	-0.715	-0.011	11.744	1.216	2.964*	5.656	0.594	2.316*
HS562 (C)	3.220	0.371	-0.054	13.556	0.116	0.696	5.733	1.050	2.437*
PBW 723(C)	2.700	0.876	0.042	12.789	1.106	0.749	6.956	0.313	0.024
Grand Mean	3.010	1.0	-	13.777	1.0	-	5.830	1.0	-
S.E (m) ±	1.14	0.50	-	3.73	0.84	-	1.95	0.63	-

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 of 119 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 to perform 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.,* (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.

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Author Contributions

All authors contributed equally for preparing the final version of the manuscript.

Conflict of Interest

Authors declare no conflict of interest.

Ethical Approval

The article doesn't contain any study involving ethical approval.

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