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STABILITY ANALYSIS FOR YIELD AND RELATED TRAITS OVER FOUR ENVIRONMENTS IN WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

This Experiment was conducted with seventeen genotypes of wheat for ten quantitative traits in two date of sowing during *Rabi*-2016-17 *viz.*, 18th Nov. (normal sown as E_1) and 18th Dec. (Late sown as E_2) and again in *Rabi*-2017-18 sown on 20th Nov. (normal sown as E_3) and 20th Dec. (late sown as E_4) at Agriculture research farm, Institute of Agricultural Sciences, Banaras Hindu university, Varanasi. The significant variations due to genotypes against pooled error revealed the presence of genetic variability for all the traits under study. The component G × E interaction being highly significant indicated that genotypes interacted considerably to environmental conditions in different environments. For yield per plant the genotypes, HUW 234 exhibited at par value with the population mean, bi near to unity and non-significant deviation from regression line(S^2di), showing that genotype was stable under all environments. However, none of the genotypes were found to show stable performance as per days to 50% flowering, grain filling duration seeds/plants and 1000 grain weight.

Key words: Wheat, stability analysis, four environment, G × E interaction

Introduction

Globally Wheat (*Triticum* spp.) is a most consumed cereal crop. In India wheat improvement in its productivity leading to green revolution has played a pivotal role in making the country self-sufficient in food. Global demand for wheat by the year 2020 is forecasted to be around 950 million tones. This target will be achieved only if global wheat production is increased by 2.5 % per annum.

In India during 2018-2019 area under wheat cultivation was 29.55 mha million ha with the production of 101.20 million tones with an average productivity of 34.24 q/ha (Annual report IIWBR, 2018-19) the highest ever recorded in India. Terminal heat stress has been a prevalent problem in NEPZ zone where the present experiment was conducted for years and tends to get worse with the changing climatic conditions. Furthermore, the estimates shows that in India alone, more than 13.5 million ha of wheat growing area is heat stressed (Joshi *et al.*, 2007) and With every degree rise in temp there is 3-4% loss of yield (Wardlaw *et al.*, 1989). It is known that genotypes, environment and their interaction (G × E) have influence on the phenotype of the various traits in wheat. Some genotypes may perform well in certain environments, but, fail in several others. The basic differences between genotypes and in their yield stability is the wide occurrence of Genotype × Environment (GE) interactions. The quality of Wheat grains is affected by environmental conditions such as temperature, humidity during grain filling, duration of grain filling, sowing time, date etc. As in NEPZ rice-wheat cultivation is in practice the late harvest of rice has lead to delay in the sowing of wheat. Hence, adversely affecting the yield of wheat, as the grain filling duration coincides with the rise in temperature and heat waves. To overcome the stress and unfavorable conditions studies are required to identify stable and heat tolerant genotypes which can perform significantly even on exposure to high temperature and which could perform consistently better over a wide range of environments. The present experiment was conducted for normal and late sown condition for two years *i.e Rabi* 2016-17 and *Rabi* 2017-2018. To test the stability of the

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Table 1: Analysis of variance for stability in wheat

	DF	DFL	DM	GFD	SPP	PH	SL	AL	SPS	YPP	1000 GW
Rep within Env.	4	1.665	1.956	1.621	1.295	6.679	0.462	0.355	3.907	0.061	1.895
Genotypes	16	55.484***	17.201***	33.984***	11.253***	491.163***	1.677***	1.202***	101.995***	22.27***	22.82***
Env.+(Gen.* Env.)	51	96.109***	139.181***	14.815*	3.632*	24.985	1.737***	0.301*	64.17**	20.061***	9.759*
Environments	3	1518.719***	2282.059***	104.161***	29.593***	189.17***	20.011***	1.144***	574.262***	211.404***	66.223***
Gen.* Env.	48	7.196	5.251	9.231	2.009	14.724	0.595*	0.249*	32.289	8.102	6.23
Environments (Lin.)	1	4556.158***	6846.178***	312.482***	88.778***	567.511***	60.034***	3.432***	1722.785***	634.213***	198.668***
Gen.* Env.(Lin.)	16	9.087	6.417	10.639	2.169	7.662	1.182***	0.439**	39.105	12.163*	7.587
Pooled Deviation	34	5.883***	4.394***	8.025***	1.816***	17.181***	0.284*	0.144*	27.182***	5.714***	5.225***
Pooled Error	64	0.658	0.737	1.137	0.376	1.763	0.162	0.087	2.983	0.345	0.791
Total	67	86.408	110.052	19.393	5.452	136.311	1.723	0.516	73.203	20.588	12.878

*,** and *** indicates significant at 5% , 1% and 0.01% against pooled error respectively.

genotypes and to estimate genotype × environment (GE) interaction Eberhart and Russell (1966) model was used. The stability of varieties was defined by high mean yield and regression coefficient (bi = 1.0) and deviations from regression as small as possible ($S^2di = 0$).

Materials and Methods

Seventeen genotypes of wheat including two checks were evaluated in RBD with 2 replications during *Rabi* 2016-17 at two dates *i.e* 18th November (normal sown as E_1) and 18th December (late sown as E_2) and in *Rabi* 2017-18 at two dates 20th November (normal sown as E_3) and 20th December (late sown as E_4). Each genotype was sown in two rows of 2 m length with row to row distance of 22.5 cm. Recommended cultivation practice was followed to raise a healthy crop. The experiment was conducted in Agriculture Research Farm, Institute of Agricultural sciences Banaras Hindu University, Varanasi, Uttar Pradesh. Data were recorded on 10 traits *viz* days to 50% flowering (DFL), days to maturity (DM), grain filling duration (GFD), spike/plant (SPP), plant height (PH in cm), spike length (SL in cm), awn length (AL in cm), seeds/spike (SPS), yield/plant (YPP in gm) and 1000 grain weight (GW in gm). The data were collected and analyzed for analysis of variance and stability analysis. All analysis was performed using the statistical software INDOSTAT. Data from the four environments were subjected to stability analysis using the Eberhart and Russell (1966) model. As per the model, three parameters *viz*., overall mean performance of each genotype across the environments, the regression of each genotype on the environmental index (bi) and squared deviation from the regression (S^2di) were estimated.

Genotypes that proved to be stable for most stability analysis or at least for the yield was then selected as the best. Stability values were estimated from the quadratic mean of the regression and the deviation from the regression coefficient (Eberhart and Russell, 1966). To identify a stable genotype which had higher or equal mean grain yield than population mean and regression coefficient as 1 or at par equity and showing small deviation from the regression was considered stable for grain yield.

Result and Discussion

Stability analysis as per Eberhart and Russell (1966) model showed highly significant ($p<0.01$) differences among seventeen genotypes for all the ten characters *viz*. days to 50% flowering days to maturity, grain filling duration, spike/ plant, plant height, spike length, awn length, seeds/spike, yield/plant and 1000 grain weight studied over different environments. The studies on estimate of stability parameters revealed that none of the genotype was stable for all the characters. This reveals not only the amount of variability that existed among environments but also the presence of genetic variability among the genotypes. It was emphasized that both linear (bi) and non-linear (s^2di) components of GE interactions are necessary for judging the stability of a genotype. A regression coefficient (bi) approximating 1 coupled with an s^2di of zero indicates average stability. Regression values above 1 describe

Table 2: mean, regression and deviation from regression from the mean

	DFL			DM			GFD			SPP			PH		
	Mean	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**
HD2733	83.75	0.895	21.5742***	114.5	0.89	0.898	30.75	0.392	14.7942***	10.3375	1.145	-0.0773	79.4663	0.468	20.1405***
K1006	79.75	0.939	9.7317***	111	1.035	1.6068	31.25	0.688	17.6037***	9.905	0.737	1.2049*	85.5375	0.585	-0.1083
K0307	79.875	0.792*	-0.1019	111.9	1.094	3.0969*	32	1.755	12.2674***	10	0.868	-0.3113	94.8663	1.111	-0.6123
DBW 39	79.5	1.099	7.3093***	111	0.935	1.5009	31.5	-0.09	7.7608**	9.0125	1.988	2.1481**	85.9213	1.293	6.0564*
PHS 1106	75.375	0.985	4.6993**	115.4	0.908	3.5532**	40	1.319	17.5883***	5.9	1.292	0.223	89.4638	1.691	16.8225***
UP 2847	79.125	0.914	2.5934*	112.8	1.127	1.8909*	33.625	1.59	6.4466**	7.3213	1.799	0.0462	93.135	1.153	7.4335*
UP 2871	77.75	1.185	2.1777*	112.8	1.095	0.9833	35	0.771	-0.8822	7.67	0.745	-0.1182	89.8663	0.805	3.3205
RWP 2015	75.125	1.017	3.8027**	109.1	0.958	-0.6863	34	0.497	1.066	7.1788	0.601	1.2840*	99.8738	1.583	27.7495***
CG 1505	77	1.114	-0.1476	111.3	1.114	4.5389**	34.25	1.022	1.859	6.4413	-0.517*	0.1635	111.7338	1.883	9.2223**
CG 1507	78.375	1.126	1.0035	109.5	0.908	0.2495	31.125	0.434	4.6986**	6.3963	0.161	0.32	110.0338	0.951	61.7028***
PBW 343	89.5	1.309	3.9388**	116.5	1.128	12.6026***	27	0.661	4.0709*	11.8038	1.445	4.7968***	78.8013	1.303	13.3330**
LOK 1	79	1.296	4.9591***	110.5	0.948	1.8501*	31.5	-0.086	21.5172***	8.955	1.422	0.0719	73.8913	0.25	0.717
HUW 234	77.5	0.941	-0.6341	109.8	1.189	6.8042***	32.25	2.408*	0.1794	8.8788	1.674	-0.0145	79.4975	0.351	55.7215***
HUW 510	77.625	1.139	0.6308	111.1	1.074	-0.1295	33.5	0.849	-0.5377	9.4375	1.012	5.4998***	80.8788	1.018	32.3873***
NW 1014	76.5	0.7	12.8218***	111.5	1.05	6.2237***	35	2.551*	-0.7033	8.8	1.402	3.0426***	78.8413	1.309	3.6474
HD 2967	85.5	0.831	8.4907***	113.5	0.718	8.4096***	28	0.78	8.9923***	10.8875	0.214	4.0266***	84	0.658	-0.0536
DBW 14	77.375	0.718	4.9707***	110.5	0.829	7.5586***	33.125	1.458	-0.1057	9.4125	1.01	1.2562*	77.6875	0.587	-0.2902
pop mean	79.331			111.912			32.581			8.726			87.853		

genotypes with higher sensitivity to environmental change (below average stability) and greater specificity of adaptability to high yielding environments. A regression coefficient below 1.0 provides a measurement of greater resistance to environmental change (above average stability), and thus increases the specificity of adaptability to low yielding environments (Wachira *et al.,* 2002).

The analysis of variance is given in Table 1. Environmental variances were significant for all characters. G × E interaction was significant for only spike length and awn length. G × E (Linear) was found to be significant for spike length , awn length and yield per plant (YPP) indicating that the variation in the performance of genotype is due to the regression of genotypes in environments and hence making its the performance predictable in nature also signifying that there is unit change in environmental index for each unit change in the environmental conditions. Siddhi *et al*., (2018), Krupal *et al.,* (2018), Singh B. *et al*., (2017) has similar findings which are in agreement with the present study.

Variance due to Environment + (Genotype × Environment) was found to be highly significant for all the characters except for plant height. The ANOVA revealed that the mean sum of square due to environment (Linear) was significant for the entire trait tested against pooled error, hence predicting that value for all the characters under study could be attributed to linear regression. Mean square due to pooled deviation was found to be significant for all the characters indicating greater role of non-predictable components in genotype × environment interaction. Thus both linear and non-linear components were useful for determining the stability. Similar results were obtained by Madhu *et al*., 2018, Polat *et al.*, 2016, Pansuriya *et al*., 2014, hence, in agreement with the present study.

Linear regression for the average grain yield of a single genotype against the population mean in each environment resulted in regression coefficients ranging from -0.003 to 1.939 for grain yield. As per the Fig. 1. Only genotype no. 13 (HUW234) showed stable performance. This large variation in regression coefficients indicates different responses of genotypes to

Cont Table 2….

	SL			AL			SPS			YPP			1000 GW		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
HD2733	14.3	1.005	0.3931 *	5.1975	-0.101	0.1085	55.675	0.595	10.2750 *	14.2188	1.888	9.4211 ***	38.2938	1.734*	-0.7386
K1006	14.9038	1.565	0.2989	5.4013	2.949*	-0.0744	51.1463	0.827	-0.9285	10.5438	1.509	9.8404 ***	35.7688	0.298	2.4642 *
K0307	15.685	1.609	0.183	6.5363	1.131	-0.0474	47.5125	0.806	2.6191	10.5938	1.117	2.6452 ***	35.4725	1.513	4.0271 **
DBW 39	15.23	0.537	-0.0952	5.2875	0.964	-0.0532	54.45	1.317	7.8594 *	9.3138	0.795	0.7740 *	37.7275	1.719*	-0.6213
PHS 1106	15.5888	0.871	-0.1034	5.73	0.13	0.2052	55.9913	1.466	3.0517	8.7213	0.672	1.7348 **	39.8913	-0.286	37.2554 ***
UP 2847	15.7375	1.44	-0.0038	5.2863	-1.636	0.0145	60.5425	1.085	17.9145 **	9.37	0.372**	-0.2335	41.3575	1.944*	-0.4837
UP 2871	16.705	0.308*	-0.1526	6.3188	2.905	-0.0373	55.3325	0.8	91.4839 ***	11.025	1.13	0.8607 *	40.6913	0.853	-0.6615
RWP 2015	16.6375	0.184*	-0.1306	6.5538	0.532	0.008	47.1	0.838	4.5638	9.8363	0.253	1.5863 **	39.4063	0.854	0.474
CG1505	16.3375	1.229	0.0375	5.1138	0.977	0.1265	53.5838	1.37	95.9195 ***	10.2163	0.942	1.9331 **	44.4888	2.309	8.7422 ***
CG1507	15.4338	0.843	-0.1261	5.9813	2.041	-0.0626	51.6838	1.145	8.8173 *	10.6713	-0.003*	1.2702 *	44.1625	1.642	1.0651
PBW 343	15.3713	0.066	0.5254 *	5.3225	1.68	-0.0835	52.3575	1.163	16.4815 **	13.605	1.186	14.5146 ***	38.5363	1.209	1.8607 *
LOK 1	16.7963	1.76	0.3296	6.94	2.481	0.2260 *	49.4338	1.214	40.3103 ***	11.105	0.738	0.1264	40.7738	-0.196	7.1220 ***
HUW 234	15.2675	2.139*	0.0245	6.0725	0.619	0.082	56.7663	-0.013	80.6418 ***	11.87	1.009	0.0166	40.875	1.4	2.0507 *
HUW 510	15.77	0.739	0.2765	6.3375	3.123	0.2019	46.65	0.491	16.5375 **	14.0163	1.238	23.4259 ***	40.5188	1.37	7.7708 ***
NW 1014	15.775	0.56	0.2526	5.8813	-0.017	0.0159	46.1338	0.213**	-2.6363	12.3725	0.415	13.0682 ***	40.2225	-0.17	2.0635 *
HD 2967	15.645	1.078	0.1691	5.6675	-0.701	0.0806	63.665	2.842	19.6717 **	17.4125	1.939	9.4220 ***	39.335	0.478	-0.3102
DBW 14	15.7638	1.066	-0.1013	5.8738	2.185	-0.0114	47.5	0.838	-2.1116	14.95	1.802	1.1509 *	38.9475	0.328	2.1889 *
pop mean	15.703			5.853			52.678			11.738			39.792		

environmental conditions (Table 2 and Fig. 1). For DFL, GFD, SPS and 1000GW none of the genotypes were found to show a stable response (Table 2). For DM, genotype HUW 510 have regression coefficient (bi) value close to unity (1.074) with small deviation from regression -0.1295 and near average yield of 111.1 than the population mean of 111.91 and thus possessed fair stability and wider adaptation over different environment. For SPP, genotype HD 2733 showed high mean yield, a regression coefficient near to the unity (1.145) and small deviations from regression (-0.0773) considering it stable. For PH genotype K0307 was found to have above mean value and near unity regression coefficient (1.111) with small deviation from the regression coefficient t (-0.6123. For spike length genotype DBW 14 showed above mean spike length (15.7638) near equity regression value (1.066) and a small deviation from the regression deviation (-0.1013). For awn length genotype K0307 showed above average length (6.5363) near equity regression coefficient (1.131) and a small S2di (-0.0474). For yield per plant HUW 234 showed near mean value of yield with near equity regression value (1.009) and a small deviation from the s2di (0.0166). Rest of the genotypes for different trait showed poor stability for different environment hence selection for them would not be effective to generate a genotype or utilized in crossing programmme to generate a new stable genotype. Similar findings reported by Banerjee *et al.,* 2006, Mut *et al.,* 2010, Kant *et al.,* 2014 and Kashte 2013 which where in agreement with the result obtained in the present findings.

Conclusion

Only genotype HUW 234 showed at par grain yield with the population mean having near equity regression coefficient and near zero deviation from the regression coefficient value. Hence, in terms of yield per plant HUW 234 can be considered the most stable compared to other genotypes. Therefore, it could be included in the hybridization program to converge the stability characteristics of grain yield for the development of stable cultivar adapted to a wide range of environments. Thus any generalization regarding stability of

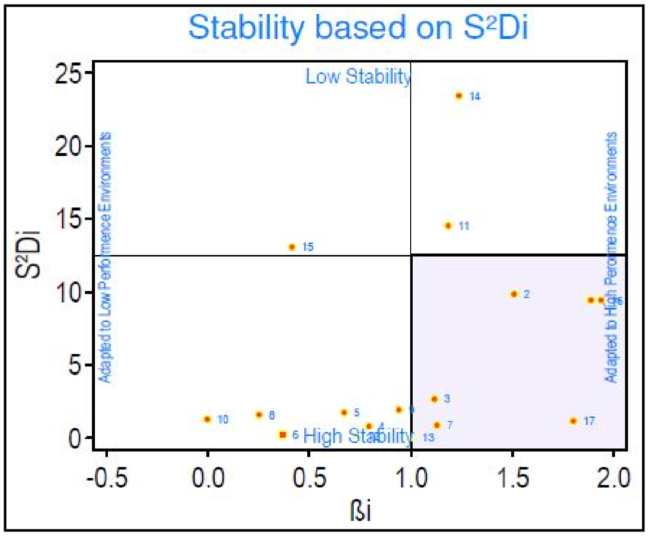

Fig. 1: Quadratic regression and deviation from regression for yield per plant

genotypes for all characters it is too difficult since the genotypes may not simultaneously exhibit uniform responsiveness and stability for all the characters.

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