



STABILITY ANALYSIS FOR YIELD, YIELD COMPONENT AND QUALITY TRAITS IN WHEAT (*TRITICUM AESTIVUM* L.) UNDER TEMPERATE CONDITIONS IN KASHMIR VALLEY

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Abstract

A field experiment was conducted during *Rabi* season of 2012-2013 at four random locations namely Experimental Farm, Division of Genetics and Plant Breeding, Shalimar, Srinagar; Experimental Farm, Mountain Research Centre for Field Crops, Khudwani; Experimental Farm, Dry land (Karewa) Agriculture Research Station, Budgam and Experimental Farm, Organic Farming Research Centre, Wadura, SKUAST-Kashmir to estimate stability parameter for yield and other component traits. The experimenting material was comprised of 22 wheat genotypes (obtained from CIMMYT, Mexico) along with two checks (Shalimar wheat 1 and SKW 355). These genotypes were grown in randomized complete block design with three replications over four different environments and observations were recorded for different quantitative traits *i.e.*, plant height (cm), no. of effective tillers meter⁻¹, days to 50% heading (days), days to 50% maturity (days), no. of spikelets spike⁻¹, spike length (cm), no. of grains spike⁻¹, 1000 grain weight, grain yield plot⁻¹ (gm), harvest index and protein content (%). Genotypes CMT 1162, CMT 198, CMT 1006, CMT 125, CMT 1193 were average in stability across all the environments for various yield and yield related traits.

Key words : Wheat, stability analysis, grain yield, spike length.

Introduction

Wheat occupies the foremost position among the cereal crops of the world in terms of production, consumption, storage qualities & adaptation and has been ultimately linked with the development of both agriculture and civilizations. It is one of the most leading sources of vegetable proteins and end use quality of wheat is determined on protein content present in its grain (Kamaluddin, 2011). Wheat grains are highly nutritive as they are rich in energy, carbohydrates, dietary fiber, fat, protein, thiamine, riboflavin, niacin, pantothenic acid, vitamin B6, folate, calcium, iron, magnesium, phosphorus, potassium, zinc and manganese (Acharya *et al.*, 2011). In Jammu and Kashmir, wheat ranks third position both in area and productivity after rice and maize and occupies an area of 0.32 million hectares with a total production of 0.52 million tonnes and a productivity of 16.25 q ha⁻¹ (Anonymous, 2010).

Plant breeders aim to develop new wheat cultivars that consistently have high yield in a variety of

environments. A variety or genotype is considered to be more adaptive or stable, if it has a high mean yield with low degree of fluctuation in yielding ability grown over diverse climatic conditions. The concept of stability has been defined in several ways and several biometrical methods including uni-variate and multivariate ones have been developed to assess stability (Lin *et al.*, 1986; Becker and Leon, 1988; Crossa, 1990). The method to measure stability was previously proposed (Finlay and Wilkinson, 1963) and was later improved (Eberhart and Russell, 1966). The stability of varieties was defined by high mean yield, regression coefficient ($b_i = 1.0$) and deviations from regression as small as possible ($s^2_{di} = 0$).

Stable wheat production is a major concern in Hilly areas that are affected by different environmental factors. Growing adapted cultivars with high yield stability is an effective strategy for reducing environmental effects on wheat production in such areas. To develop suitable cultivars, evaluation of improved genotypes is a critical phase in wheat breeding programs, because great numbers of genotypes need to be evaluated across locations.

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Therefore, the aim of this study is to screen wheat genotypes for their stability of yield, yield components and quality traits under different environmental conditions of Kashmir valley.

Materials and Methods

The experimental material for the study comprised of 24 diverse wheat (*Triticum aestivum* L.) genotypes including two checks SW-355 and SW-1 were evaluated in a Randomized Complete Block Design (RCBD) with three replications at four random locations namely Experimental Farm, Division of Genetics & Plant Breeding, Shalimar, Srinagar; Experimental Farm, Mountain Research Centre for Field Crops, Khudwani; Experimental Farm, Dry land (Karewa) Agriculture Research Station, Budgam and Experimental Farm, Organic Farming Research Centre, Wadura, SKUAST-Kashmir during *rabi* 2012-13. The material was procured from CIMMYT; Maxico and maintained at Faculty of Agriculture, Wadura Campus, SKUAST of Kashmir. Each entry was sown in five rows of 4m length with 25 cm and 15 cm spacing between rows and plants, respectively. The experimental fields were well prepared and all the recommended package of practices was adopted to raise a good crop. Observations were recorded on ten randomly selected competitive plants from each experimental plot in each replication for all traits *viz.* plant height (cm), no. of effective tillers meter⁻¹, no. of grains spike⁻¹, spike length (cm), no. of spikelets spike⁻¹. The data for days to 50% heading (days), days to 50% maturity (days) and yield was recorded on whole plot basis and for 1000 grain weight, data was recorded by weighing two random sun-dried samples of 1000 seeds in each experimental plot. Protein content (%) was determined using nuclear resonance machine. Stability analysis of different genotypes across the environments was worked out as per the method given by Eberhart and Russel (1966).

Results and Discussion

The perusal of analysis of variance (table 1) showed that the genotypes were differed significantly for all traits showing presence of diversity among the wheat genotypes studied. Similarly, environments in which genotypes were grown also differed significantly for all traits except grains spike⁻¹ and protein content (%). Mean squares arising due to G × E interaction revealed that the variance ratio is highly significant for most of the traits except spikelet spike⁻¹, harvest index and protein content showing that most of the characters of the genotypes under study were having significant differential response

to the changing environment. Similar findings were also reported by Sabaghnia *et al.* (2014) and Khan *et al.* (2012).

Mean squares due to environment + (genotype × environment) were significant for all the traits except for no. of effective tillers meter⁻¹, days to 50% heading, days to 50% maturity, spikelet spike⁻¹, no. of grains spike⁻¹, 1000 grain weight, harvest index, grain yield plot⁻¹ and protein content. Partitioning of this variation in to linear and non linear components revealed that the mean squares due to environment (linear) were significant for almost all the characters except spike lets spike⁻¹, grains spike⁻¹, harvest index and protein content. The significant mean squares confirm that the environments were random and different and they exercised influence on the expression of the trait and this variation could have arisen due to the linear response of the regression of the cultivar to the environment. The mean squares due to G × E (linear) were significant for all the characters except days to 50% heading, days to 50% maturity, no. of spikelets spike⁻¹, grains spike⁻¹, 1000 grain weight, harvest index and protein content (%) exhibiting that the nature of the genotype could be predicted over the environments more precisely and accurately since the G × E interaction was the result of the linear function of the environmental components. However, mean squares due to G × E (linear) were non-significant for days to 50% heading, days to 50% maturity, no. of spikelets spike⁻¹, grains spike⁻¹, 1000 grain weight, harvest index and protein content (%) indicating possible absence of genetic differences among the genotypes for their regression on environmental index making difficult the prediction for the performance of these traits. Mean square due to pooled deviation was non-significant for all the characters except no. of effective tillers meter⁻¹, days to 50% heading, no. of grains spike⁻¹, grain yield plot⁻¹ and harvest index showing that the prediction of stability of the genotypes could be reliable.

The stability parameters analyzed for the traits under study are presented in table 2. Mean plant height across the environment ranged from 96.80 cm (CMT 1007) to 122.00 cm (SKW 355) with general mean of 109.20 cm. Genotype CMT 125 was found well adapted to all the environments. Mean of no. of effective tillers meter⁻¹ over locations ranged from 141.7 (CMT 1007) to 159.5 (SKW 355) with average mean of 151.0. Genotypes CMT 1162, CMT 198 and CMT 125 were found stable and average responsive for days to 50% heading. The mean value for days to 50% maturity ranged from 220.2 days (CMT 1202) to 244.5 days (CMT 1142) with a population mean of 235.7 days. Genotypes CMT 1162,

Table 1 : List of wheat genotypes used in study.

S. no.	Code of the genotypes	Pedigree	Origin
1	CMT 1162	MUNAL \neq 1	CIMMYT
2	CMT 198	BAV92/3/OASIS/SKAUZ//4*BCN/4/PASTOR	-do-
3	CMT 1137	PFAU/MILAN/3/SKAUZ/KS94U215//SKAUZ	-do-
4	CMT 1007	KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ	-do-
5	CMT 1006	PBW343*2/KUKUNA//PBW343*2/KUKUNA	-do-
6	CMT 1138	OTUS//PRL/2*PASTOR	-do-
7	CMT 1027	C80.1/3*BATAVIA//2*WBL1/3/KRONSTAD	-do-
8	CMT 1173	CROC_1/AE.SQURROSA(250)//KAUZ//3/SASIA/4/	-do-
9	CMT 125	MINO/898.97	-do-
10	CMT 1202	SHA7/VEE \neq 5/5/VEE \neq 8//JUP/BJY/3/F3.71/TRM/4/	-do-
11	CMT 1147	LERKE/5/KAUZ/3/MYNA/VUL//BUC/FLK/4/MILAN/6/	-do-
12	CMT 1004	D6301/HN7//ERA/3/BUC/6/WRM/4/FN/3*TH//K58/	-do-
13	CMT 1191	03FDBW30.1110/SUNSTATE//TACUPETO	-do-
14	CMT 1193	WAXWING*2/TUKURU	-do-
15	CMT 1148	TACUPETOF2001*2/BRAMBLING	-do-
16	CMT 1014	COOK/VEE//DOVE/SERI/3/GEN/4/PASTOR/5/MILAN/	-do-
17	CMT 1142	PBW343/PASTOR//OTUS/TOBA97	-do-
18	CMT 1088	PBW 343/TONI//TROST/3/SOVA	-do-
19	CMT 1003	EJIC//ATTLA/2*PASTOR/4/VEE/PJN//2*TUI/3/	-do-
20	CMT 1176	CHEN/AEGILOPS SQUAROSA(TAUS)//BCN/3/BAV92/	-do-
21	CMT 1194	NG8201/KAUZ/4/SHA7//PRL//VEE \neq 6/3/FASAN/5/	-do-
22	CMT 1187	SHA7//PRL/VEE \neq 6/3/FASAN/4/HAAS8446/2*FASAN/	-do-
Check	SKW-355	-	SKUAST-K
Check	SW-1	-	-do-

CMT 198, CMT 1137, CMT 1007, CMT 1006, CMT 125, CMT 1202, CMT 1004, CMT 1003, CMT 1176, CMT 1194 and CMT 1187 matured earlier and these genotypes had mean values lesser than the population mean and thus, were well adapted to all the environments. Genotypes showing average stability were CMT 1138, CMT 1148, CMT 1142 and CMT 1176 for no. of spikelet spike⁻¹ and mean range from 15.2- 21.0 with population mean of 17.8. Genotypes CMT 1004 and CMT 1142 were found average and stable for spike length.

The genotypes showing average stability were CMT 198, CMT 1137, CMT 1191, CMT 1193, CMT 1148, CMT 1088 and CMT 1003 for no. of grains spike⁻¹ and the mean value were ranges from 48.11 (CMT 1003) to 37.10 (CMT 1138). Genotypes CMT 162, CMT 1173, CMT 1202, CMT 1176 and CMT 1194 were found stable and average responsive with high to moderate mean performance than the population mean for 1000 seed weight. Its mean value ranged from 32.00 (CMT 1191) to 40.00 (CMT 125). CMT 198, CMT 125, CMT 1142, CMT 1148 and CMT 1187 were found stable and average responsive for grain yield plot⁻¹. Its mean value ranged from 1024.2 (CMT 1007) to 1583.6 (CMT 125) with the mean grain yield of 1306.5g plot⁻¹. Genotypes showing

average stability were CMT 198 and CMT 1187 for harvest index. CMT 1004, CMT 1191 and CMT 1176 were found stable and average responsive for protein content. Its mean value ranged from 10.3 (CMT 1194) to 14.6 (CMT 1191) with population mean 12.4.

Genotype showing below average stability (b_i significant and greater than 1) and specifically adapted to favorable environments were CMT 1137, CMT 1138, CMT 1027, CMT 125, CMT 1191, CMT 1014 and CMT 1088 for no. of productive tillers plant⁻¹; CMT 1137, CMT 1173, CMT 1147, CMT 1004, CMT 1191, CMT 1193, CMT 1003, CMT 1176, CMT 1194 and CMT 1187 for days to 50% heading; CMT 1006, CMT 1191 and CMT 1148 for days to 50% maturity; CMT 1137, CMT 1007, CMT 1006, CMT 1202, CMT 1147, CMT 1191 and CMT 1088 for no. of spikelets spike⁻¹; CMT 1137, CMT 1173, CMT 125 and CMT 1088 for spike length; CMT 1006, CMT 1007, CMT 1027 and CMT 1003 for no. of grains spike⁻¹; CMT 198, CMT 1138, CMT 1191, CMT 1142 and CMT 1003 for 1000 grain weight; CMT 1007, CMT 1138, CMT 1027, CMT 1173 for grain yield plot⁻¹; CMT 1173, CMT 1027, CMT 1137, CMT 125 and CMT 1003 for harvest index; CMT 1173, CMT 1202, CMT 1014, CMT 1003 and CMT 1187 for protein content.

Table 2 : Analysis of variance for stability of yield, yield components and quality traits in wheat (*Triticum aestivum* L.) genotypes across random environment in Kashmir valley.

Source of variation	d. f.	Mean squares				
		Plant height	No. of effective tillers meter ⁻¹	Days to 50% heading	Days to 50% maturity	Spikelets spike ⁻¹
Genotypes	23	1355.64**	116.18**	68.89**	54.899**	11.22**
Environment + (genotype × environment)	72	1072.76*	17.87	9.47	0.312	0.53
Environments	3	852.93*	36.50*	15.40*	1.266*	0.96*
Genotype x environments	69	1082.32*	17.06*	19.21*	3.279**	0.54
Environments (linear)	1	2558.80*	109.50*	46.20*	3.799**	1.08
Genotype × environment (linear)	23	2287.82**	25.21*	11.27	0.139	0.64
Pooled deviation	48	459.58	12.45*	7.84*	0.323	0.47
Pooled error	184	1099.20	2.05	3.56	0.623	0.41

*Significant at p = 0.05, **Significant at p = 0.01

Table 2 contd...

Table 2 contd...

Source of variation	d. f.	Mean squares					
		Spike length (cm)	Grains spike ⁻¹	1000 grain weight (gm)	Grain yield plot ⁻¹ (gm)	Harvest index (%)	Protein (%)
Genotypes	23	12.229**	40.71**	33.34**	103217.40**	330.20**	7.633**
Environment + (genotype × environment)	72	6.130*	0.48	3.92	14817.04	20.53	0.371
Environments	3	31.756**	0.23	18.79*	39639.61*	15.85*	0.357
Genotype x environments	69	7.016*	0.99*	7.28*	23737.7*	20.73	0.372
Environments (linear)	1	95.268**	0.69	56.37**	118918.83*	47.56	1.073
Genotype × environment (linear)	23	6.979*	0.55	3.11	20229.86*	9.21	0.301
Pooled deviation	48	3.866**	0.44	3.22**	10054.61	25.39	0.390*
Pooled error	184	0.793	0.63	1.14	7092.72	32.41	0.086

*Significant at p = 0.05, **Significant at p = 0.01

Table 3 : Stability parameters for yield, yield components and quality traits in wheat (*Triticum aestivum* L.) genotypes across random environment in Kashmir valley.

Genotypes	Plant height (cm)			No. of effective tillers meter ⁻¹			Days to 50% heading (in days)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
CMT 1162	100.4	1.391	-1078.0387	151.4	1.027	-0.1907	174.3	1.212	-2.6755
CMT 198	106.1	0.646	-1081.1353	151.8	0.999	-1.3022	175.3	1.223	-3.0703
CMT 1137	100.9	-0.870*	-952.0450	158.2	2.305*	3.6818*	181.1	2.009*	0.5042*
CMT 1007	96.8	0.441	-1053.5827	141.7	1.394	1.9644	183.2	0.037	-2.7884
CMT 1006	106.8	0.211	-1027.3858	148.1	1.038	4.6611*	184.2	0.578	-7.8910
CMT 1138	104.3	0.231	-932.5374	153.3	3.095*	5.5623*	181.0	1.621	-0.0732
CMT 1027	101.5	-0.605*	-821.9471	154.1	4.471*	3.9524*	187.6	1.871*	-3.1723
CMT 1173	106.9	-0.207*	-1028.0828	151.5	1.348	-1.8785	180.9	2.058*	-1.4011

Table 3 continued...

Table 3 continued...

CMT 125	111.3	0.898	-959.0592	145.9	2.475*	-1.0811	177.8	1.506	-5.4605
CMT 1202	103.2	0.300	-1064.6876	144.9	0.200	0.9179	177.7	0.050	1.1550
CMT 1147	103.0	0.939	-783.1504	157.9	1.818	-5.8021	185.3	2.510*	-0.0905
CMT 1004	107.8	0.662	-1035.9189	144.4	0.430	-1.0792	176.2	1.790*	-2.0166
CMT 1191	102.8	0.004*	-1060.4591	156.1	3.926*	5.1875 *	182.3	2.508*	-1.1991
CMT 1193	107.5	0.746	-1037.1869	151.2	1.491	-1.5066	187.5	1.954*	0.0939
CMT 1148	105.3	1.195	-773.6216	155.8	1.592	-1.1585	178.1	0.755	-2.7197
CMT 1014	108.3	0.135*	-1099.6901	148.8	1.834	-0.4606	183.9	0.418	-2.5245
CMT 1142	103.2	0.373	-1068.6538	143.8	1.627	-0.5837	188.5	0.619	-3.2672
CMT 1088	98.8	0.051*	-1064.9183	145.3	3.379*	-2.0699	187.8	0.251	-1.7503
CMT 1003	106.6	0.061*	-1096.7681	151.7	1.854	-1.9053	177.3	2.221*	0.6715
CMT 1176	105.2	0.043	-1030.7667	154.7	1.870	-1.0322	182.8	2.966*	4.9660*
CMT 1194	100.9	0.301	-1089.5242	156.9	1.870	-3.7164	179.32.	747*	-2.1983
CMT 1187	100.7	-0.187	-1079.4835	151.1	4.654*	-1.8237	177.7	1.119	-3.0904
SKW-355#	122.0	0.006	-1099.6129	159.5	3.710	-4.3178	182.1	1.024	-3.1861
SW-1#	117.2	-0.631	-1097.0939	157.7	0.256	-2.8612	179.5	1.194	0.6186
Mean	109.1	-	-	151.0	-	-	181.3	-	-
SE(m)	12.4	-	-	2.0	-	-	1.6	-	-
SE(b)	-	2.1	-	-	1.7	-	-	2.0	-

Check varieties, * Significant at p=0.05; ** Significant at p=0.01

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Table 3 continued...

Genotypes	Days to 50% maturity (in days)			Grain filling period (in days)			No. of spikelets spike ⁻¹		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
CMT 1162	221.8	1.352	-0.5001	46.7	0.096	-187.7718	17.0	1.099	-0.2866
CMT 198	220.8	1.141	-0.4514	49.5	1.11	-1167.53	19.4	0.792	-0.0513
CMT 1137	232.6	0.431	-0.5923	43.3	0.097	-188.3718	17.5	1.968	-0.4308
CMT 1007	234.2	0.980	-0.4174	46.3	-0.183*	-180.1040	19.5	4.141*	-0.1891
CMT 1006	234.3	1.462	-0.0107	46.4	-0.134*	-188.9163	18.9	2.786*	-0.3239
CMT 1138	239.7	0.848	-0.3428	44.7	-0.234*	-184.6377	19.7	1.125	-0.1890
CMT 1027	239.4	-0.548*	-0.4902	46.7	1.017	-185.6226	18.8	1.585	-0.1911
CMT 1173	238.8	0.855	0.6979*	49.0	0.143*	-184.1800	20.1	1.789	-0.3178
CMT 125	226.3	1.162	-0.4623	46.3	0.322	-179.4884	17.0	1.815	-0.2227
CMT 1202	220.2	-0.687*	-0.3788	46.3	0.557	-180.4579	17.3	5.214*	-0.2498
CMT 1147	235.3	1.023	-0.3688	49.2	0.513	-184.8587	20.0	2.863*	-0.2642
CMT 1004	226.4	0.446	-0.4822	47.3	-0.128*	-187.9317	17.1	1.719	-0.1499
CMT 1191	236.9	1.455	-0.3006	43.7	0.237*	-186.8812	16.5	3.527*	-0.1937
CMT 1193	239.1	1.323	-0.2717	46.9	0.528	-179.449	15.2	1.712	-0.2145
CMT 1148	235.9	3.648*	-0.4087	47.4	-0.661*	-186.8456	18.1	1.534	2.3125*
CMT 1014	239.5	1.038	-0.0934	50.1	0.193*	-182.0005	18.9	1.866	-0.3381
CMT 1142	244.5	0.716	-0.4932	47.2	0.285*	-186.8456	21.0	1.099	0.4912
CMT 1088	243.6	0.285	-0.4729	47.7	1.570	-124.6860	15.5	1.994	-0.2242

Table 3 continued...

Table 3 continued...

CMT 1003	227.1	1.177	-0.2428	44.3	1.991	-156.1794	15.7	1.866	-0.3381
CMT 1176	223.3	1.045	-0.2196	41.2	0.730	-186.5345	19.0	1.227	-0.0017
CMT 1194	230.7	-0.673*	-0.3217	44.4	0.467	-185.1188	19.1	1.856	-0.3349
CMT 1187	225.1	1.469	-0.1929	45.8	0.204	-156.5130	19.7	1.406	1.0293
SKW-355 [#]	237.3	0.965	0.0848	47.5	0.723	-172.2355	15.0	1.840	0.2891
SW-1 [#]	230.3	1.579	-0.3722	45.5	0.640	-162.8323	16.8	2.639	0.6204
Mean	235.7	-	-	47.9	-	-	17.8	-	-
SE(m)	0.3			4.7	-	-	0.39	-	-
SE(b)	-	1.4	-	-	1.422	-	-	3.2330	-

Check varieties, *Significant at p = 0.05, **Significant at p = 0.01

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Table 3 continued...

Genotypes	Spike length (cm)			Grains spike ⁻¹			1000-grain weight (g)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
CMT 1162	18.1	1.604	-1.5886	45.1	1.900	-0.1298	36.3	1.114	-0.5217
CMT 198	17.5	1.399	-1.2292	46.8	1.308	-0.4305	36.0	2.613*	-1.1036
CMT 1137	19.4	2.962*	-0.6288	44.0	1.164	-0.5993	37.5	1.657	-0.7366
CMT 1007	17.1	0.355	-0.5364	43.2	5.612*	-0.3804	36.2	0.759	-0.0181
CMT 1006	15.8	0.950	-0.7948	47.0	3.502*	-0.4758	37.0	0.861	0.0648
CMT 1138	15.8	1.881	-0.2707	37.1	1.512	-0.0582	38.3	2.065*	-0.8543
CMT 1027	18.7	0.515	0.5061	47.2	3.965*	-0.6278	32.1	0.033	0.1241
CMT 1173	19.8	2.268*	-0.7134	42.0	0.159	0.1466	39.7	1.092	-0.2995
CMT 125	19.1	3.472*	-0.1150	43.6	1.662	-0.4924	40.0	0.243	-1.5883
CMT 1202	16.0	0.146	0.6163	38.9	1.418	0.1271	39.5	1.215	-0.9947
CMT 1147	16.5	0.816	-0.3996	40.8	1.104	-0.4931	38.8	0.635	5.3212 *
CMT 1004	19.2	1.077	-0.5590	41.0	1.299	0.1006	37.8	0.995	-0.3796
CMT 1191	17.0	1.289	-0.1720	43.4	1.154	-0.4974	32.0	2.630*	-0.9366
CMT 1193	16.5	1.846	-0.1858	43.5	1.194	0.2929	35.6	0.513	-1.4350
CMT 1148	18.5	0.955	-0.0947	43.9	1.055	-0.6893	32.9	0.737	-1.0386
CMT 1014	19.2	0.403	-0.5099	39.9	0.408	-0.4084	32.6	1.997	-0.3544
CMT 1142	18.4	1.235	-0.1880	40.4	0.701	-0.3439	38.7	2.838*	-1.2932
CMT 1088	17.3	2.895*	1.9099 *	47.1	1.104	-0.6043	38.0	0.797	1.5698*
CMT 1003	19.5	0.516	-0.1708	48.1	1.900	0.2036	39.0	2.969*	-0.3775
CMT 1176	18.1	0.962	-0.6020	39.5	0.398	-0.1331	36.6	1.143	-0.8463
CMT 1194	18.0	0.399	-1.8523	39.5	1.348	0.6640	38.6	1.483	1.5006*
CMT 1187	18.0	0.940	-0.6099	47.2	0.806	-0.1515	32.5	0.734	-0.4840
SKW-355 [#]	13.1	0.499	-0.2671	44.8	4.060	-0.3019	39.5	0.513	2.498*
SW-1 [#]	13.7	0.141	-0.5565	39.5	1.353	-0.6704	35.5	0.647	1.253
Mean	17.5	-	-	42.9	-	-	35.9	-	-
SE(m)	1.13	-	-	0.38	-	-	1.03	-	-
SE(b)	-	0.9870	-	-	3.9121	-	-	1.1717	-

Check varieties, * Significant at p=0.05; ** Significant at p=0.01

contd...

Table 3 contd...

Genotypes	Grain yield plot ¹ (g)			Harvest index (%)			Protein (%)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
CMT 1162	1036.3	1.569	-2288.7806	35.8	1.106	-25.8290	12.6	1.199	-0.0846
CMT 198	1389.8	1.031	-6478.8131	36.7	1.372	-22.5933	11.8	0.052	0.0688
CMT 1137	1307.4	0.689	-25375.615	40.9	4.354*	-11.2517	10.9	0.863	0.0217
CMT 1007	1024.2	2.365*	-1614.6611	34.9	0.310	-17.7627	11.3	0.099	-0.0709
CMT 1006	1180.4	0.165	-6971.6838	40.0	0.404	-27.8369	10.5	0.990	0.0213
CMT 1138	1122.7	5.764*	-5376.2720	38.2	0.446	-56.7438	12.3	1.163	0.0271
CMT 1027	1251.3	5.048*	-648.7266	32.5	3.465*	-22.0269	14.3	1.529	0.0228
CMT 1173	1116.4	2.868*	-2430.8021	24.5	2.415*	-17.5461	14.1	2.375*	0.0726
CMT 125	1583.6	1.130	-159.2361	33.8	2.202*	-29.5353	13.7	0.194	0.0245
CMT 1202	1280.1	0.874	-846.2749	30.4	0.830	-28.6351	12.7	4.128*	0.0178
CMT 1147	1192.9	1.315	-1852.5750	22.9	0.436	-19.9354	13.1	0.057	0.0799
CMT 1004	1083.9	1.480	-655.2451	30.7	1.570	-26.3463	13.6	1.333	0.0520
CMT 1191	1237.3	0.415	80.2922*	31.5	1.104	-14.7379	14.6	1.341	-0.0421
CMT 1193	1530.3	0.464	-1418.2361	33.1	0.444	-23.4013	13.8	1.749	0.0835
CMT 1148	1515.0	1.429	-1110.7676	40.1	0.041	-23.9984	14.1	0.554	0.0201
CMT 1014	1065.1	0.599	-1312.9363	23.4	0.133	-27.4334	12.2	4.267*	0.0368
CMT 1142	1432.0	1.132	-2916.7003	32.8	1.654	-30.8252	10.8	0.085	0.1149
CMT 1088	1355.4	0.836	-422.2781	39.3	0.489	-21.074	11.3	0.137	0.0379
CMT 1003	1350.5	1.641	-6452.3297	39.4	4.536*	-22.0182	11.5	2.179*	0.0848
CMT 1176	1450.5	0.743	-5946.5055	37.0	0.696	-22.2625	13.1	1.452	0.0649
CMT 1194	1133.8	0.047	1.8413*	33.4	1.447	-30.1042	10.3	1.578	0.1584
CMT 1187	1412.8	1.401	-2163.5292	38.5	1.287	-31.5533	10.8	2.781*	-0.0529
SKW-355 [#]	1513.2	0.473	-185.7425	36.2	0.456	-17.4772	13.2	3.810	-0.0674
SW-1 [#]	1390.9	1.317	-3448.5881	32.0	0.856	-27.4620	12.4	1.094	0.2045
Mean	1306.5	-	-	35.8	-	-	12.4	-	-
SE(m)	57.9	-	-	2.9	-	-	0.3	-	-
SE(b)	-	1.4	-	-	3.579	-	-	2.956	-

Check varieties, *Significant at $p = 0.05$, **Significant at $p = 0.01$

The genotypes showing above average stability (bi significant and less than 1) were CMT 1137, CMT 1027, CMT 1173, CMT 1191, CMT 1014, CMT 1088, CMT 1003 for plant height; CMT 1202, CMT 1004 for no. of productive tillers plant⁻¹; CMT 1007, CMT 1006, CMT 1202, CMT 1148, CMT 1014, CMT 1142 and CMT 1088 for days to 50% heading; CMT 1137, CMT 1027, CMT 1202, CMT 1088 and CMT 1194 for days to 50% maturity; CMT 198 for no. of spikelets spike⁻¹; CMT 1007, CMT 1027, CMT 1202, CMT 1014, CMT 1003, CMT 1194 for spike length; CMT 1142, CMT 1187 for no. of grains spike⁻¹; CMT 1027, CMT 1191 for 1000 grain weight; CMT 1137, CMT 1006, CMT 1014 and CMT 1194 for grain yield plot⁻¹; CMT 1148 and CMT 1014 for harvest

index; CMT 197, CMT 1147 and CMT 1088 for protein content. The varieties showing above average in stability for various traits would do better under low management conditions.

In the present investigation, the genotypes CMT 1162, CMT 198, CMT 1006, CMT 125, CMT 1193 were average in stability across all the environments for various yield and yield related traits. Similar findings have also been reported by Adjabi *et al.* (2014) and Salim *et al.* (2015). Further the compensating mechanism of component characters in imparting homeostasis being important, these genotypes would be useful in future breeding programmes as in a homeostatic genotype, the component characters may shift in a compensatory

manner in changing environment to give consistent performance of the economic characters.

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