Original Research Article

Stability Analysis for Grain Yield and Quality Parameters in QPM (*Zea mays* L.) Inbred Line Crosses

Baudh Bharti[1]*, R.B. Dubey, Arun Kumar[2], Amit Dadheech and Rohit Kumar Dhobi[3]

[1]Department of Plant Breeding and Genetics, [3]Department of Horticulture, Maharana Pratap University of Agriculture and Technology, Udaipur-313001, Rajasthan, India
[2]Department of Genetics and Plant Breeding, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India
*Corresponding author

A B S T R A C T

Means quares due to genotypes including both parents and hybrids were significant for all the characters studied. Significant mean squares due to environment (E) plus genotypes x environment (G x E) interaction were also observed for all the characters except shelling percentage and starch content. Mean squares due to environment (linear) were significant for days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent brown husk except anthesis to silking interval, plant height, ear height, ear length, ear girth, number of grain rows per ear, 100- grain weight, grain yield per plant, shelling percentage, havest index, oil content, protein content, starch content, lysine content and tryptophan content indicating that macro For protein content three hybrid viz., L7 x T2, L5 x T3 and L8 x T3 were found stable under different environments whereas, nine hybrids viz., L1 x T1, L5 x T1, L7 x T1, L8 x T1, L14 x T1, L1 x T2, L3 x T2, L12 x T2 and L3 x T3 were found stable under unfavourable environments for protein content. Hybrids stable in favourable environments for protein content. Hybrids L2 x T1, L3 x T1 and L14 x T2 were found stable for tryptophan content under different environment while, four hybrids viz., L11 x T2, L8 x T3, L13 x T3 and L14 x T3 were found stable under unfavourable environments for tryptophan content. Eight hybrids viz., L1 x T1, L8 x T1, L11 x T1, L13 x T1, L4 x T2, L12 x T2, L15 x.

Introduction

Maize (*Zea mays* L.) 2n=20, is the third most important cereal crop after rice and wheat in the world. It is referred to as "Miracle Crop" and "Queen of the Cereals" due to its high productivity potential compared to other Graminae family members. It is believed to have originated in Southern Mexico or Northern Guatemala (Weather wax, 1955). Protein of maize is deficient in two essential amino acids, lysine and tryptophan (Bhatia and Rabson, 1987). In non-QPM, the endosperm contains a high amount of zein which is completely devoid of lysine and tryptophan.

Maize is used as human food, chemicals, medicines, biofuel, ornamental and other uses e. g. variegated and coloured leaf forms as well as those with colourful ears are used (Wikipedia, 2011). The poor nutritional value

of normal maize grain has been well known for a long time (Osborne and Mendel, 1914). Maize has protein content with protein quality limited by deficiencies of two essential amino acids like lysine and tryptophan and has excess of luecine and gsoleucine, leading to a poor growth in children and pellagra in adults (Mertz *et al.,* 1964). Maize protein is characterized by high level of glutamic acid and leucine. Lysine (1.2% of protein) and tryptophan (0.4% of protein) are limiting amino acid in maize. This is due to the fact that major storage protein is a prolamin fraction zein, which forms up to 50 to 60% of the storage protein. Zein consists of a group of hydrophobic proteins, completely devoid of lysine and tryptophan (Inglett, 1970). Hence, genetic manipulation for improved nutritional value, particularly protein quality was considered as a noble goal. This effort was stimulated by the 1963 discovery of mutant maize called as "opaque-2 gene".

The lysine levels in normal and quality protein maize (QPM) average 2.0% and 4.0% of total protein respectively, but range across genetic background from 1.6 to 2.6% in normal maize and 2.7 to 4.5% in their opaque-2 maize converted counter parts (Moro *et al.,* 1996). The lysine content of quality protein maize (QPM) in whole grains range from 0.33 to 0.54 per cent, with the average of 0.38 per cent and 46 per cent higher than normal maize. The tryptophan content is 0.08 per cent, which is 6.6 per cent higher than normal maize (Ortega *et al.,* 1986, Sproule *et al.,* 1988, Osei *et al.,* 1999).

Materials and Methods

The experimental material was generated by making crosses between 15 inbred lines and 3 testers in line x tester mating design. Fifteen parental inbred lines were crossed with three testers during rabi 2013 to generate the experimental hybrids for this study. The

experimental material, thus, consisting of 45 F1s (single crosses), 15 inbred lines, 3 testers and 4 checks (HQPM-1, HQPM-5, Pratap QPM-1 and Vivek QPM-9) were evaluated during kharif and rabi 2014 in the three environments. Three environments were created by two locations and date of sowing viz., E1 (timly sowning, kharif 2014 at Instructional farm Rajasthan college of Agriculture, Udaipur), E2 (timly sowning, kharif 2014 at ARSS, Vallabh Nagar, MPUAT, Udaipur) and E3 (timly sowning, rabi 2014-15 at Instructional farm Rajasthan college of Agriculture, Udaipur). The experimental material was planted under each environment in randomized bock design with three replication in a single row plot of four meter length, maintaining crop geometry of 60 x 25 cm. All the recommended agronomy inputs and practices were applied to the crop during the season, to raise the successful crop. The NPK fertilizer were applied at the rate of 120:60:00 kg/ha. The total amount of phosphatic fertilizer and half of the nitrogenous fertilizer were applied as basal dose and rest of the nitrogenous fertilizer were given in two equal doses, one at knee-high stage and another at flowering stage of the crop. The border rows were also planted to neutralize the border effect. The mean values were used for statistical analysis. Stability analysis was done using the model ofEberhart and Russel (1966).

Results and Discussion

The analysis of variance for phenotypic stability (Table 1) revealed that mean squares due to genotypes including both parents and hybrids were significant for all the characters studied. Significant mean squares due to environment (E) plus genotypes x environment (G x E) interaction were also observed for all the characters except shelling percentage and starch content. Mean squares due to environment (linear) were significant

for days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent brown husk except anthesis to silking interval, plant height, ear height, ear length, ear girth, number of grain rows per ear, 100- grain weight, grain yield per plant, shelling percentage, havest index, oil content, protein content, starch content, lysine content and tryptophan content indicating that macro environmental differences were present under all the three environments studies.

The mean of squares due to genotypes x environment interactions were also significant for all the characters except starch content. Indicating the influence of environmental conditions on the genotypes evaluated.

The significant G x E interaction for various traits were also reported by Sharma and Saikia (2000), Dodiya and Joshi (2003), Singh *et al.,* (2003), Abera *et al.,* (2006), Admassu *et al.,* (2008), Zaidi *et al.,* (2008), Rahman *et al.,* (2010), Arulselvi and Selvi (2010), Beyene *et al.,* (2011), Shiri (2013), Nzuve *et al.,* (2013), Kamutando *et al.,* (2013) and Sserumaga *et al.,* (2016).A perusal of stability parameters for grain yield per plant revealed that out of 67 genotypes 59 genotypes (18 parents, 37 hybrids and 4 checks) exhibited non-significant deviation from regression (S2di) and are as such predictable for this trait. Parental line L6 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean and would remain stable for grain yield per plant in favourable environments. Twenty six hybrids viz., L1 X T1, L4 X T1, L5 X T1, L6 x T1, L8 x T1, L9 x T1, L10 x T1, L12 x T1, L14 x T1, L15 x T1, L2 x T2, L4 x T2, L5 x T2, L6 xT2, L7 x T2, L14 x T2, L3 x T3, L4 x T3, L5 x T3, L6 x T3, L8 x T3, L10 x T3, L11 x T3, L12 x T3, L14 x T3 and L15 x T3 and two checks namely HQPM-1 and Vivek

QPM-9 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean and thereby indicating their stability under favourable environments. Hybrids L2 x T1 and L3 x T1 exhibited non-significant S2di and regression coefficient nearly equal to unity (bi =1) with higher mean values than the population mean, thereby indicating stability under different environments for grain yield per plant. Three other hybrids viz., L9 x T2, L12 x T2 and L15 x T2 and check HQPM-5 exhibited non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) with higher mean values than the population mean, thereby indicating their suitability and stability under unfavourable environments. Out of 67 genotypes, 8 genotypes (2 parents and 6 hybrids) exhibited non-significant deviation from regression (S2di), indicating their predictable behaviour for oil content.

Parental line L12 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean. This line thus showed its superiority and stability under favourable environments. Two hybrids viz., L14 x T3 and L15 x T3 showed non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) with higher mean values than the population mean were as such considered stable and suitable under unfavourable environments for oil content. Hybrid L6 x T3 exhibited non-significant deviation from regression (S2di) and regression coefficient nearly equal to unity (bi =1) with higher mean values than the population mean, thereby indicating stability under different environments. Hybrid L9 x T3 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean

values than the population mean, thereby indicating stability under favourable environments.

Out of 67 genotypes, 65 genotypes showed non-significant deviation from regression (S2di) indicating their predictable behaviour.

Parents L6 and T1 exhibited non- significant S2di and regression coefficient nearly equal to unity (bi =1) with higher mean values than the population mean, thereby indicating stability under different environments for protein content. Two other parents viz., L10 and L13 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean. These parents thus showed its superiority and stability under favourable environments.

The present study showed the improvement of sperm quality during preservation at 5°C Nine

hybrids viz., L1 x T1, L5 x T1, L7 x T1, L8 x T1, L14 x T1, L1 x T2, L3 x T2, L12 x T2 and L3 x T3 exhibited non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) and higher mean values as compared to the population mean, were considered suitable and stable under unfavourable environments. Three hybrids viz., L7 x T2, L5 x T3 and L8 x T3 exhibited non-significant deviation from regression (S2di) and regression coefficient nearly equal to unity (bi =1) with higher mean values as compared to the population mean. These hybrids were found stable in different environments. Eleven other hybrids viz., L4 x T1, L10 x T1, L11 x T1, L6 x T2, L14 x T2, L1 x T3, L9 x T3, L11 x T3, L13 x T3, L14 x T3 and L15 x T3 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean.

Table.1 Analysis of variance Eberhart and Russel (1966) for grain yield and Quality traits in quality protein maize

SN	Characters	Genotype	E+(G x E)	E (L)	G x E (L)	Pool dev.	Pool Err
		[66]	[134]	[1]	[66]	[67]	[396]
1	Grain yield per plant (g)	1275.04**	102.81**	2.19	194.51**	13.99**	9.20
2	Oil content %	0.25**	0.51**	0.00	0.65**	0.39**	0.00
3	Protein content %	2.65**	0.01**	0.00	0.02**	0.00	0.01
4	Starch content %	35.21**	0.01	0.00	0.02	0.00	0.17
5	Lysine content %	0.82**	0.00**	0.00	0.00**	0.00**	0.00
6	Tryptophan content %	0.03**	0.00**	0.00	0.00**	0.00	0.00

*, ** Significant at 5 and 1 per cent respectively.

Table.2 Stability parameters for grain yield and quality traits in quality protein maize

SN	Genotype	Grain Yield Per Plant (g)			Oil content %			Protein content %		
		μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
1	T1	52.89	0.69*	-8.975	3.81	2.42	0.438**	9.46	0.92	0.002
2	T2	60.20	0.53	-3.105	4.12	2.07	0.448**	7.72	1.08	0.009
3	T3	67.48	0.58**	-9.190	4.18	-5.01*	0.004*	7.77	0.63	0.000
4	L1	37.36	0.34	-7.029	4.09	-2.28	0.013**	8.16	1.34	-0.001
5	L2	40.76	0.24	-2.077	4.17	1.47	0.487**	8.67	1.07	-0.005
6	L3	47.82	0.38*	-9.114	3.87	-0.24	0.302**	8.31	1.35	-0.001
7	L4	44.53	0.48	-8.905	3.81	-2.30	0.550**	7.73	1.01	-0.004
8	L5	38.58	0.39	-8.779	3.93	2.56	0.406**	7.54	-0.51	-0.005
9	L6	76.22	1.12	9.600	4.34	4.44	0.284**	8.94	0.96	-0.003
10	L7	31.38	0.22	3.333	3.93	2.79	0.626**	7.95	1.78	0.001
11	L8	43.33	0.31	13.359	4.21	-3.49	1.643**	8.24	1.23	-0.004
12	L9	51.24	0.67**	-9.190	3.72	-3.58	0.150**	8.76	1.26	-0.005
13	L10	36.89	0.25	-1.779	4.30	3.12	0.145**	9.82	1.01	-0.003
14	L11	31.64	0.35**	-9.196	4.25	3.11	0.426**	7.65	0.71	-0.005
15	L12	29.02	0.17	-8.902	4.27	7.53*	0.001	7.75	-0.34	-0.005
16	L13	39.66	0.42*	-9.168	3.74	-2.89	0.700**	9.66	1.48	-0.001
17	L14	46.96	0.44	14.491	4.09	2.69	0.553**	8.61	-0.48	-0.005
18	L15	53.24	0.55	-8.844	4.13	-1.52*	-0.001	7.62	0.96	0.006
19	L1 x T1	84.51	1.35*	-8.993	4.31	2.34	1.664**	9.27	0.89	-0.001
20	L2 x T1	88.42	0.99*	-8.702	4.10	2.44	0.368**	8.65	1.32	-0.005
21	L3 x T1	82.27	0.93	24.003	4.41	4.35	0.472**	8.51	0.87	-0.002
22	L4 x T1	90.63	1.34*	-8.991	4.32	3.28	0.103**	9.27	1.32	-0.004
23	L5 x T1	96.51	1.32	2.798	4.87	-6.30	0.088**	11.54	0.79	-0.005
24	L6 x T1	96.96	1.42*	-8.941	3.91	3.38	0.272**	8.66	0.59	-0.002
25	L7 x T1	72.91	0.68	118.945**	4.23	5.05	0.286**	10.36	-1.86*	-0.005
26	L8 x T1	87.51	1.01	12.104	4.41	-0.77	1.527**	9.61	0.89*	-0.005
27	L9 x T1	77.02	1.19*	-8.574	4.19	6.81	0.732**	8.20	0.29	-0.005
28	L10 x T1	94.64	1.50*	-8.429	4.35	-0.52	0.760**	9.63	1.08	-0.003
29	L11 x T1	86.69	0.47	34.433*	4.14	-4.08*	-0.001	8.94	1.77	0.005
30	L12 x T1	82.78	1.29**	-9.186	3.82	3.97	0.004	8.75	1.05	-0.003
31	L13 x T1	68.44	0.99*	-9.115	4.09	-1.81	0.030**	8.63	0.33	-0.005
32	L14 x T1	99.87	1.77	11.202	4.79	7.77	0.053**	9.19	0.82	-0.005
33	L15 x T1	89.24	1.01	3.964	4.10	-0.91	0.770**	8.75	0.48	-0.001
34	L1 x T2	68.51	0.95*	-9.138	3.74	-1.89	0.354**	12.11	0.69	0.003
35	L2 x T2	94.40	1.30*	-9.022	4.21	0.58	0.032**	8.30	-0.08	-0.002
36	L3 x T2	83.89	0.60	48.232*	3.82	-5.57	1.369**	9.30	0.55	-0.004
37	L4 x T2	89.47	1.03**	-9.175	4.04	0.62	0.474**	8.41	0.50	-0.005
38	L5 x T2	83.93	1.34*	-9.061	4.73	3.02	1.053**	7.12	-0.43	-0.003
39	L6 x T2	94.00	1.92*	-5.877	4.51	-1.27	0.097**	8.87	1.69	-0.002
40	L7 x T2	101.86	1.99*	-8.285	4.61	1.73	1.677**	9.91	0.96	-0.005
41	L8 x T2	89.40	0.58	50.764*	4.13	-0.68	0.259**	8.98	2.04*	-0.005
42	L9 x T2	81.33	0.84*	-8.557	3.86	2.44	0.017**	8.44	0.93	-0.004
43	L10 x T2	65.98	0.47	-8.575	4.65	-0.78	0.349**	8.75	1.44	-0.005
44	L11 x T2	72.82	0.63	-3.234	4.23	-6.11	0.198**	8.44	1.18	-0.003
45	L12 x T2	91.31	0.40	20.219	3.71	-1.70	0.325**	9.73	-1.47	0.000
46	L13 x T2	72.42	0.56	-8.857	4.54	-2.37	0.291**	8.90	0.30	0.034**
47	L14 x T2	91.94	1.98*	-8.279	3.73	-0.20	0.809**	10.16	3.22	-0.005
48	L15 x T2	91.11	0.73**	-9.179	4.75	1.99	0.095**	8.42	0.79	-0.003
49	L1 x T3	67.80	0.45	-7.545	4.16	-3.50	0.762**	9.42	1.49	-0.005
50	L2 x T3	95.33	2.03	26.109*	4.28	2.72	0.161**	8.76	1.49	-0.003
51	L3 x T3	90.27	1.40	-4.215	4.29	9.64	0.060**	9.38	-0.26	-0.003
52	L4 x T3	88.64	1.02	-7.551	4.28	6.09	0.440**	8.96	1.84*	-0.005
53	L5 x T3	88.09	1.70*	-8.540	4.62	1.53	0.013**	9.90	0.96	-0.005
54	L6 x T3	85.20	1.37*	-8.392	4.32	0.90	-0.001	8.69	2.37	0.006
55	L7 x T3	74.10	1.65	63.646**	4.07	-3.50	1.309**	7.74	1.58	-0.005
56	L8 x T3	90.62	1.63	-5.053	4.65	-0.76	0.216**	9.63	0.96	-0.005
57	L9 x T3	69.16	1.37	75.254**	4.58	3.91*	-0.001	8.94	1.99	-0.004

SN	Genotype	Grain Yield Per Plant (g)			Oil content %			Protein content %		
		μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
58	L10 x T3	90.33	1.46	-4.359	4.42	-0.49	0.430**	7.88	2.59	-0.005
59	L11 x T3	92.76	1.67	15.070	4.61	2.91	0.045**	10.12	2.61	0.007
60	L12 x T3	88.99	1.34	4.098	4.24	3.40	0.488**	7.75	1.11	0.001
61	L13 x T3	90.29	1.50	88.479**	4.18	10.70	0.080**	9.71	1.88	0.005
62	L14 x T3	93.61	2.29	0.653	4.38	-0.44	-0.001	10.67	1.04	-0.002
63	L15 x T3	85.22	1.10	2.103	4.24	0.22	-0.000	8.92	1.82	-0.005
64	HQPM-1	88.16	1.10	-5.795	4.46	-1.83	0.109**	9.38	3.51	0.018*
65	HQPM-5	75.16	0.63	-6.853	4.62	1.67	0.005*	7.59	0.58	-0.004
66	Pratap-QPM-1	48.44	0.37	-6.495	4.00	8.54	0.091**	7.77	0.49	-0.005
67	Vivek- QPM-9	94.84	2.21	15.433	4.43	-0.37	0.090**	8.85	0.69	-0.004
	Mean	74.58			4.23			8.87		
	SE (b)	0.21			2.45			0.49		

SN	Genotype	Starch content (%)			Lysine content (%)			Tryptophan content (%)		
		μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
1	T1	61.10	3.06	-0.165	2.26	1.17	-0.000	0.54	0.99	-0.000
2	T2	66.67	2.09*	-0.166	1.75	1.11	-0.000	0.53	0.88	-0.000
3	T3	66.78	3.00	-0.165	1.74	0.90	0.000**	0.56	1.41	0.000
4	L1	57.15	-1.01	-0.131	2.00	1.87	0.001**	0.55	0.38	0.000*
5	L2	62.43	-0.42	-0.157	2.24	1.18	0.000	0.54	1.16	0.000
6	L3	62.26	1.50	-0.153	1.97	0.51	0.000**	0.53	1.38*	-0.000
7	L4	67.19	0.84	-0.143	0.74	0.12	0.000**	0.57	0.91	0.000
8	L5	66.84	1.49	-0.162	0.73	0.65	-0.000	0.56	1.06	-0.000
9	L6	62.84	1.95	-0.158	1.10	1.30*	-0.000	0.98	1.39	-0.000
10	L7	67.49	1.93	-0.156	0.87	1.57	0.000	0.52	1.06	-0.000
11	L8	63.32	1.26	-0.166	1.71	0.45	0.000*	0.99	1.07	0.000*
12	L9	56.55	1.15	-0.166	1.16	1.11	0.000	0.58	0.99	-0.000
13	L10	62.57	1.46	-0.123	1.88	1.69	0.000	0.64	0.26	0.000*
14	L11	67.00	2.31	-0.165	0.57	0.41	0.002**	0.54	1.25	0.000
15	L12	67.37	2.11*	-0.166	0.77	1.31	0.000*	0.56	0.88	-0.000
16	L13	61.25	0.99*	-0.166	0.71	0.65	0.000	0.54	1.45*	-0.000
17	L14	54.44	0.76	-0.165	0.76	1.63	0.000	0.57	0.90	0.000*
18	L15	66.70	1.82*	-0.166	0.72	0.78	0.000	0.56	0.98*	-0.000
19	L1 x T1	56.18	1.61	-0.154	1.20	0.84	0.000	0.60	1.54*	-0.000
20	L2 x T1	57.01	0.59	-0.144	0.98	1.56	0.000	0.60	0.92	0.000
21	L3 x T1	54.34	0.72*	-0.166	0.99	0.78	0.000	0.67	0.91	0.000
22	L4 x T1	61.39	0.67	-0.166	2.05	1.57*	-0.000	0.45	0.81	0.000**
23	L5 x T1	62.78	1.74*	-0.166	1.55	0.98	-0.000	0.68	0.18	0.000*
24	L6 x T1	61.64	0.63	-0.165	0.83	0.65	0.000	0.57	1.53*	-0.000
25	L7 x T1	60.34	0.59	-0.165	2.07	-0.28	0.001**	0.58	1.23	0.000*
26	L8 x T1	61.88	0.27	-0.157	2.00	2.08	0.000*	0.98	1.39	-0.000
27	L9 x T1	62.20	0.59	-0.166	1.69	1.18	0.000	0.57	1.03	-0.000
28	L10 x T1	60.98	1.65	-0.166	0.79	1.31	0.000	0.55	1.54*	-0.000
29	L11 x T1	61.44	0.68	-0.165	0.58	0.84	0.000	0.63	1.48	-0.000
30	L12 x T1	63.75	0.75	-0.166	2.10	0.92	-0.000	0.55	0.89	-0.000
31	L13 x T1	56.57	0.58	-0.166	0.89	1.50	0.000	0.62	1.21	-0.000
32	L14 x T1	61.84	0.94	-0.161	1.61	1.18	-0.000	0.58	1.14*	-0.000
33	L15 x T1	62.08	1.03	-0.166	0.93	0.85	0.000	0.59	1.04	-0.000
34	L1 x T2	63.18	1.24	-0.155	2.38	1.44	0.000	0.54	0.56*	-0.000
35	L2 x T2	63.81	0.62	-0.167	1.49	0.72	0.000	0.61	0.34	0.000*
36	L3 x T2	61.25	0.74	-0.166	1.81	0.91	-0.000	0.57	0.65	-0.000
37	L4 x T2	61.43	0.55	-0.165	1.64	1.18	0.000	0.67	1.08	-0.000
38	L5 x T2	61.02	0.99	-0.165	1.47	1.57	0.000	0.56	0.46	-0.000
39	L6 x T2	58.58	0.81	-0.163	1.09	0.92	0.000	0.57	1.89	0.000
40	L7 x T2	59.61	1.90	-0.140	0.91	0.74	0.001**	0.57	1.15	-0.000
41	L8 x T2	62.27	0.12	-0.160	0.74	0.78	-0.000	0.57	0.87	-0.000
42	L9 x T2	61.02	1.04	-0.167	0.84	1.25	0.000*	0.58	0.94	0.000
43	L10 x T2	56.19	2.29	-0.151	1.25	1.18	-0.000	0.57	1.23	-0.000
44	L11 x T2	61.35	0.62	-0.166	1.55	0.84	-0.000	0.64	0.85	0.000
45	L12 x T2	63.36	0.54	-0.166	1.66	0.71	-0.000	0.63	1.25	0.000

SN	Genotype	Starch content (%)			Lysine content (%)			Tryptophan content (%)		
		μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
46	L13 x T2	61.28	0.65	-0.166	1.01	1.18	0.000	0.57	1.05*	-0.000
47	L14 x T2	59.42	0.67	-0.165	1.66	1.24	0.000	0.65	1.00	0.000
48	L15 x T2	64.38	0.54	-0.166	0.89	0.97	0.000	0.65	1.16	0.000
49	L1 x T3	61.56	0.83	-0.165	0.68	1.51	0.000	0.55	0.92	-0.000
50	L2 x T3	55.46	0.81	-0.164	1.08	0.78	0.000	0.57	1.54*	-0.000
51	L3 x T3	61.63	0.67	-0.166	0.75	0.78	-0.000	0.57	0.82	-0.000
52	L4 x T3	58.28	-0.91	-0.146	1.00	1.24	-0.000	0.59	0.65	-0.000
53	L5 x T3	61.60	0.84	-0.166	1.54	1.05	0.000	0.64	0.73	0.000**
54	L6 x T3	57.13	0.78	-0.166	0.95	0.58	0.000	0.58	1.39	-0.000
55	L7 x T3	66.96	0.63	-0.166	0.75	0.79	0.000	0.53	0.92	-0.000
56	L8 x T3	57.50	0.70	-0.167	1.17	0.78	-0.000	0.62	0.77	0.000
57	L9 x T3	60.86	0.85	-0.163	1.01	1.18	-0.000	0.57	1.03	-0.000
58	L10 x T3	57.36	0.96	-0.165	1.01	0.71	0.000**	0.70	1.47*	-0.000
59	L11 x T3	62.90	0.75	-0.166	1.77	0.58	0.000*	0.57	0.82	-0.000
60	L12 x T3	58.34	0.65*	-0.166	0.67	0.98	-0.000	0.58	0.96*	-0.000
61	L13 x T3	60.37	0.90*	-0.166	1.53	0.08	0.001**	0.61	0.11	0.000
62	L14 x T3	62.18	0.56	-0.164	2.30	0.97	0.000	0.65	0.62	-0.000
63	L15 x T3	61.15	0.97	-0.161	0.97	0.65	-0.000	0.58	1.73	0.000
64	HQPM-1	61.29	0.51*	-0.166	1.94	1.57	0.000	0.57	0.72*	-0.000
65	HQPM-5	66.92	2.12	-0.165	1.86	0.78	-0.000	0.55	0.88	-0.000
66	Pratap-QPM-1	67.13	0.70*	-0.166	1.76	1.18	0.000	0.59	0.73*	-0.000
67	Vivek- QPM-9	56.30	1.04*	-0.166	2.00	0.84	0.000	0.60	0.48	-0.000
	Mean	61.45			1.33			0.60		
	SE (b)	0.40			0.30			0.18		

*, ** Significant at 5 and 1 per cent respectively.

These hybrids thus showed its suitability and stability under favourable environments. Among the checks, Vivek QPM-9 showed non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) with higher mean values as compared to the population mean. It was identified stable and suitable under unfavourable environments. A perusal of data for this character revealed that all 67 genotypes (18 parents, 45 hybrids and 4 checks) showed non-significant deviation from regression (S2di) indicating their predictable behaviour for starch content.

Two parental lines viz., L2 and L4 and fourteen hybrids viz., L6 x T1, L8 x T1, L9 x T1, L12 x T1, L2 x T2, L8 x T2, L12 x T2, L15 x T2, L1 x T3, L3 x T3, L5 x T3, L7 x T3, L11 x T3 and L14 x T3 and check Pratap-QPM-1 exhibited non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) and higher mean values as compared to the population mean, were considered suitable and stable under unfavourable environments for starch content. Nine parental lines viz., L3, L5, L6, L7, L8, L10, L11, L12 and L15 and two testers, namely T2 and T3 and three hybrids viz., L5 x T1, L15 x T1 and L1 x T2 and check HQPM-5 exhibited non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean. These genotypes thus showed its suitability and stability under favourable environments. One hybrid L14 x T1 showed non- significant S2di and regression coefficient nearly equal to unity (bi =1) with higher mean values than the population mean. This hybrid was thus stable and suitable in performance under different environments for starch content. In case of lysine content 53 genotypes (11 parents, 38 hybrids and 4 checks) out of 67 genotypes exhibited non-significant deviation from regression (S2di), indicating their predictable behaviour. Four parents viz., L2, L10, T1 and

T2 showed non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean. These parents were therefore considered suitable and stable in favourable environments. Three hybrids viz., L2 x T2, L11 x T2 and L12 x T2 and two checks HQPM-5 and Vivek QPM-9 exhibited non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) with higher mean values as compared to the population mean, were considered suitable and stable under unfavourable environments. Eight hybrids viz., L4 x T1, L9 x T1, L14 x T1, L1 x T2, L4 x T2, L5 x T2, L14 x T2 and L5 x T3 and two other checks namely HQPM-1 and Pratap QPM-1 exhibited non-significant deviation from regression (S2di) and regression coefficient more than unity (bi >1) with higher mean values than the population mean. These hybrids and checks were therefore considered suitable and stable under favourable environments. Four other hybrids viz., L5 x T1, L12 x T1, L3 x T2 and L14 x T3 exhibited non- significant S2di and regression coefficient nearly equal to unity (bi =1) with higher mean values than the population mean, thereby indicating their suitability and stability under different environments.

Stability parameters for this traits revealed that out of 67 genotypes, 58 genotypes (14 parents, 40 hybrids and 4 checks) exhibited non-significant deviation from regression (S2di), indicating predictable behavior for tryptophan content (Table 2). One parental line L6 and eight hybrids viz., L1 x T1, L8 x T1, L11 x T1, L13 x T1, L4 x T2, L12 x T2, L15 x T2 and L10 x T3 showed non-significant deviation from regression (S2di) and regression coefficient greater than unity (bi >1) with higher mean values than the population mean, thereby indicating their suitability and stability under favourable

environments. Hybrids L2 x T1, L3 x T1 and L14 x T2 exhibited non-significant deviation from regression (S2di) and regression coefficient nearly equal to unity (bi =1) with with higher mean values than the population mean. These hybrids were considered stable under different environments. Four hybrids viz., L11 x T2, L8 x T3, L13 x T3 and L14 x T3 and one check Vivek QPM-9 exhibited non-significant deviation from regression (S2di) and regression coefficient less than unity (bi <1) with higher mean values than the population mean. These hybrids and check were therefore considered suitable and stable in unfavourable environments. Similar findings for identification of genotypes for their stability under varying environmental conditions were also reported by Agrwal *et al.,* (2000), Dodiya and Joshi (2003), Nirala and Jha (2003), Abera *et al.,* (2004), Kumar and Singh (2004), Kaundal and Sharma (2006), Javed *et al.,* (2006), Abdulai *et al.,* (2007), Worku and Zelleke (2008) Singh *et al.,* (2009), Lata *et al.,* (2010), Rahman *et al.,* (2010), Nahar *et al.,* (2010), Arulselvi and Selvi (2010), Brar *et al.,* (2010) Nadagoud *et al.,* (2012), Shiri (2013), Nzuve *et al.,* (2013), Kamutando *et al.,* (2013). Anley *et al.,* (2013), Tiwari *et al.,* (2014) and Bisawas *et al.,* (2014).

References

Abdulai, M.S., Sallah P.Y.K. and Safo, K. O. (2007). Maize grain yield stability analyses in full season lowland maize in Ghana. Int. J. Agric. Biol., 9: 41-45.

Abera, W., Labuschagne, M. T. and Maartnes, H. (2006). Evaluation of maize genotypes using parametric and non-parametric stability estimates. Cereal Res. Commun., 34(2/3): 925-931.

Abera, W., Rensburg, J. B. J-Van., Labuschagne, M. T. and Maartnes, H., (2004). Genotype −environment interactions and yield stability of new

maize in Ethiopia. South African J. Pl. Soil, 21(4): 251-254.

Admassu, S., Nigussie, M. and Zelleke, H. (2008). Genotype- environment interaction and stability analysis for grain yield of maize (*Zea mays* L.) in Ethiopia. Asian Journal of Plant Sciences, 7(2):163-169.

Eberhart, S.A. and Russell, W. A. (1966). Stability parameters for comparing varieties. Crop Sci., 6: 36-40.

Kaundal, R. and Sharma, B. K. (2006). Genotype × environment interaction and stability analysis for yield and other quantitative traits in maize (*Zea mays* L.) under rainfed and high rainfall valley areas of the sub montane. Res. on Crops, 7(1): 171-180.

Kumar, A. and Singh, N. N. (2004). Stability studies of inbred and single crosses in maize. Ann. Agric. Res., 25: 142-148.

Nadagoud, V.K., Jagadeesha, R.C., Wali, M.C., Kachapur, R.M. (2012). Genetic studies on stability among maize inbredlines. Karnataka J. Agric. Sci., 25 (1): 124-126.

Nahar, K., Ahmed, S., Akanda, M. A. L., Mondal, M. A. A. and Islam, A. A. (2010). Genotype-environment interaction for cob yield and maturity in baby corn (*Zea mays* L.). Bangladesh J. Agril. Res., 35 (3): 489-496.

Nirala, R. B. P. and Jha, P. B. (2003). Phenotypic stability for fodder traits in maize (*Zea mays* L.). Range Management and Agroforestry, 24(1): 9-13.

Nzuve, F., Githiri, S., Mukunya, D. M. and Gethi, J. (2013). Analysis of genotype x environment interaction for grain yield in maize hybrids. Journal of Agricultural Science, 5(11): 75-85.

Singh, S. B., Sharma, M. M. and Singh, A. K. (2009). Stability analysis for grain yield and yield-contributing traits in maize (*Zea mays*) single cross hybrids under mid hills. Indian Journal of Agricultural Sciences, 79 (11):890-896

Tiwari, R., Sharma, A. K. and Kumar, B. (2014). Genotype-environment inter-action for yield and its attributes in maize (*Zea mays* L.). Plant Archives, 14 (2): 841-845.