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Genotype x Environment Interaction and Stability Analysis for Yield and Quality Traits in QPM (*Zea mays* L.)

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A B S T R A C T

Maize is one of the most important grain crops in South Asia and is produced throughout the country under diverse environments. The grain of quality protein maize (QPM) varieties contain nearly twice as much lysine and tryptophan, amino acids that are essential for humans and monogastric animals. Evaluation of maize hybrids under different environments would be useful for identifying hybrids that combine stability with high yield potential for diverse environments. This study was conducted to evaluate 30 maize hybrids and 06 parents including two checks (Shaktiman-3 & Shaktiman-4) to study the stability parameters for grain yield per plant and quality parameters under varied environmental conditions. Among the different environments studied environment-5 (Rabi seasons) recorded the highest and positive environment index for the trait grain yield per plant. Hence, this trait appeared to be the most favourable for environment-5. The environment-2(Kharif seasons) was favourable for the expression of lysine and tryptophan content in kernel protein since it had positive and high environmental index. Hence, these traits appeared to be the most favourable for environment-2. The hybrid CML161 x CML171 responded favourably under all environment, whereas the hybrid CML167 x CML171 suitable for rich environment (Rabi season) and the hybrid 167x161 suitable for poor environment (Kharif season) for higher grain yield per plant. The hybrid CML 161 x CML 171 and VL 1037 x VL1056 stable for all the six environments and it is adaptable to wider environments for yield and quality parameters. Therefore, these aforesaid maize hybrids are the promising genotypes in future for evolution of location specific superior maize hybrids for different maize growing situations.

Introduction

Maize (*Zea mays* L.) is the world's most widely grown cereals and is the staple food in many developing countries (Morris *et al*., 1999). It is a miracle crop in view of its widespread use as food and nonfood items. Maize is also the third most important crop in the world, after wheat and rice, in terms of

growing area, production and grain yield (Shiri *et al.*, 2010).

The area, production and productivity of maize in India was 9.25 million ha, 23.70 million tones and 25.60 q/ha respectively (Annonymous, 2014) whereas in Bihar it was cultivated over 0.70 million ha with a production of 2.40 million tones having average productivity of 34.16 q/ha. (Annonymous, 2015-16). Maize is a good source of carbohydrates, fats, protein, important vitamins and minerals, providing food (25%), animal feed (12%), and poultry feed (49%), starch (12%), brewery (1%) and seeds (1%). Apart from normal maize, it has many other types viz., quality protein maize, sweet corn, baby corn, popcorn, waxy corn, high oil corn etc. It accounts for 15 to 56% of the daily total calories of people in many of the developing countries.

Maize is a potential source of protein for human food, cattle and poultry feed. However, it is deficient in several amino acids essential for monogastric animals in which lysine is the most limiting amino acid (Bhan *et al.*, 2003). Main reasons for the poor quality of normal maize is the relatively high concentrations of prolamines or zeins storage proteins (50-60%) which are deficient in lysine and tryptophan causing maize to be nutritionally inferior in protein quality as compared with rice, wheat and other major cereals. The other storage proteins in the maize endosperm are albumins (3%), globulins (3%) and glutelins (30-45%) that have a relatively higher lysine content of 5-6%, 5-8% and 4-5%, respectively (Wilson,1991). The discovery of mutant alleles, *opaque-2* (o2*o2*) (Mertz *et al.*, 1964) by Purdue University researchers were found to alter the amino acid profile and the composition of maize endosperm protein and result in two fold increase in the levels of lysine and tryptophan compared to what is encountered in normal maize genotypes. Yet, it expresses negative pleiotropic effects on the grain quality such as lower density, susceptibility to pests and diseases and a floury appearance (Vasal, 2001). The International Maize and Wheat Research Center (CIMMYT) has developed quality protein maize (QPM) that improves kernel quality characteristics over *opaque-2* (o2*o2*) soft genotypes, by introducing modifier genes and selecting for a hard, vitreous endosperm in *opaque-2* (o2*o2*) germplasm (Vasal, 2001).

After the discovery of the nutritional benefits of the opaque-2 (op2) mutation, it has been incorporated into many breeding programs worldwide, with a major emphasis on conversion of normal endosperm populations and inbred lines to opaque-2 (op2) versions through a modified back crossing cum recurrent selection method.

The studies indicated that the QPM protein contains, in general, 55% more tryptophan, 30% more lysine and 38% less leucine than that of normal maize (Prasanna *et al*., 2001). The biological value of QPM protein is about 80% that of milk, which is about 90% and that of normal maize is only about 45% (FAO, 1992). QPM also provides better quality feed and fodder to poultry, cattle, swine, and fishmeal industries. Bressani (1991) stated that people eating QPM had significantly higher nitrogen retention than those who ate normal maize, indicating that QPM protein is more "bioavailable". Besides the increased biological value, QPM has additional nutritional advantages, such as higher concentrations of niacin (vitamin B_3) and improved absorption of potassium (Graham *et al.*, 1980) and carotene (De Bosque *et al.*, 1988). Substituting normal maize with high lysine maize on an equal weight basis can maintain proper amino acid balance (Wilson, 1991). The adoption of QPM can contribute immensely to alleviation of malnutrition in maize based economies in developing countries. The nutritional quality

of the protein in QPM grain approaches that of protein derived from cow's milk.

In India in the 1970, three opaque-2 composites were developed and commercially released such as Shakti, Ratan and Protina. In 1997 Shakti-1 (OPV) was developed with modified endosperm and nutritionally superior opaque-2 composites. Later on in India several QPM hybrids were developed for different agroclimatic conditions like HQPM 4, HQPM 1, HQPM 5, HQPM 7, Vivek QPM 9, Shaktiman 1, Shaktiman 2, Shaktiman 3 and Shaktiman 4 (Dass *et al.*, 2009a).

The ideal maize genotype could produce high yield regardless of environmental conditions. In reality, genotypes not performed equally well in all environments but some trend to be closer than others. Genotypes response to changing environments can be measured statistically by genotype x environment interaction. Stable genotypes would have a small genotypes x environment interaction, while those with large interaction could be called unstable. A reliable method of estimation of stability was proposed using regression analysis by Eberhart and Russell (1966). Further, its genotype x environmental interaction and stability of across environments help in identifying suitable QPM parents and its hybrid that are widely or specifically adapted to environments.

Keeping in view of aforesaid information, the present investigation is undertaken to explore the genetic potentiality of QPM inbred lines in view of the development of single cross QPM hybrids, with objectives to identifying productive, nutritionally superior and stable single cross hybrids.

Materials and Methods

The experimental material consist of six inbreed line with 2 checks (Shaktiman-3 and Shaktiman-4) as mentioned in table-1. The parent were evaluated and crossed during rabi 2016-17 in crossed in full diallel fashion [Griffing, 1956(b), method 1 model 1] to derived the single cross hybrid at Maize Section, BAC Sabour. The hybrid were evaluated for stability at three different locations such as sabour, purnea and mokama during kharif 2017 and rabi 2017-18 in randomized complete block design (RCBD) with three replications, 06 parents along with checks .The plots selected were uniform in topography, fertile and well drained soil. The experiment was laid out, with a row length of 4 m, with inter and intra row spacing of 75cm and 20cm respectively. Each genotype was sown with 2 rows. Five plants from each replication were randomly selected and tagged for recording observations in each genotype.

Data were recorded on different morphological and Quality parameters viz., Morphological data, namely, grain yield/plant were recorded on 5 randomly taken competitive plants from middle row of plot. Data for protein content in kernel, tryptophan content in kernel protein and lysine content in kernel protein were taken from the sample of bulk seeds. The stability of yield performance for each genotype was calculated by regressing the mean yield of individual genotypes on environmental index, similarly calculating the deviations from regressing the mean yield of individual genotypes on environmental index as suggested by Eberhart and Russell model (1966). Regression coefficient (bi) was considered as an indication of the response of the genotype to varying environment while the environment and genotype × environment interactions were partitioned into three components viz., environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes).

Results and Discussion

Analysis of variance for stability showed significant mean squares for genotypes and environments (linear), indicating that the genetic variation was present and the environments were distinct from one another (Table 2). Variance due to environment plus interaction of genotype and environment and pooled deviation (nonlinear) were significant for grain yield per plant indicating presence of variation in the mean performance of all genotypes over environments i.e., differential behaviour of the genotypes under different environments except lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel. These findings are in consistent with Deshpande and Dalvi (2006), Panwar *et al.,* (2008), Ramya and Senthilkumar (2008) and Krishnappa *et al.*, (2009). The pooled analysis of variance revealed that genotype x environment (linear) interactions were highly significant for a character i.e., grain yield per plant implying differential response of genotypes under six locations for the character, Similar reports were earlier made by Panwar *et al.,* (2008) and Ramya and Senthilkumar (2008).The genotype x environment (linear) interactions for the remaining 3 characters i.e., lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel were non-significant. Therefore, further analysis of stability was not carried out for these 3 characters.

The environmental indices computed for 4 characters are presented in the (Table 3) Environmental index directly reflects the environment by negative and positive values. Among the 6 environments, Environment-5 (Rabi seasons) recorded the highest and positive environmental index for the trait like grain yield per plant. Therefore, this environment appeared to be the most favourable for particular conditions. None of the traits had positive indices in Environment-5. The Environment-2(Kharif seasons) was favourable for the expression of high lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel, since it had positive and high environmental index. Hence, these traits appeared to be the most favourable for environment-2 conditions. Negative values of environmental index indicated the unfavourable nature of that particular condition.

In this study, the mean performance coupled with the regression coefficient (bi) and variance of deviation from regression (δ2di) of each genotype represented its stability (Table 4a and 4b). With these conditions, the parents and hybrids were classified and evaluated for their adaptability and stability in respect of yield and other component characters studied.

Eberhart and Russell (1966) described an ideal variety as one which should have high mean value over a wide range of environments, a regression coefficient around unity and non-significant deviation from regression coefficient. Genotypes based on their stability for different traits under the study were categorized in (Table 5). The ability to develop high yielding and stable cultivars is an ultimate goal in most breeding programs. The consistent performance of a genotype, both with high or low yield across different environments is referred as yield stability (Epinat-Le Signor *et al*., 2001). An ideal maize hybrid should have a high mean yield combined with a low degree of fluctuation under different environments (Annicchiarico, 2002).

Table.1 Details of QPM genotypes studied

SN.	Inbred line	Pedigree	Colour	Source
1	CML161	CML161	Yellow	CIMMYT, HYD. (India)
2	CML167	CML167	Yellow	CIMMYT, HYD. (India)
3	CML171	CML171	Yellow	CIMMYT, HYD. (India)
4	CML193	CML193	Yellow	CIMMYT, HYD. (India)
5	VL1037	CL 02450Q-B-B*6	Yellow	CIMMYT, HYD. (India)
6	VL1056	CML 451Q-B*7-#	Yellow	CIMMYT, HYD. (India)
7	Check-1	Shaktiman-3	Yellow	RAU, PUSA, Samastipur (Bihar)
8	Check-2	Shaktiman-4	Yellow	RAU, PUSA, Samastipur (Bihar)

Table.2 Analysis of variance of Stability for different traits in QPM

Source of Variations	df	Mean Square			
		Grain yield per plant	Lysine % in kernel protein	Tryptophan % in kernel protein	Protein % in kernel
Genotype	37	5868.24**	0.41**	0.02**	0.28**
Environment + Genotype x Environment	190	669.86**	0.02	0.01	0.00
Environment (Lin.)	1	101057.15**	0.16**	0.01**	0.03**
Genotype x Environment.(Lin.)	37	374.68**	0.02	0.01	0.01
Pooled Deviation	152	81.27**	0.02**	0.01	0.01
Pooled Error	444	32.71	0.01	0.01	0.01

*, ** Significant at 5 % & 1 % level of probability, respectively

Table.3 Environmental indices for different characters in QPM

Parameters	Kharif			Rabi		
	Sabour	Mokama	Purnea	Sabour	Mokama	Purnea
	(E_1)	(E_2)	(E_3)	(E_4)	(E_5)	(E_6)
Grain yield/plant	-25.837	-14.935	-21.526	18.178	22.982	21.138
Lysine % in kernel protein	-0.023	0.031	-0.038	0.017	-0.015	0.028
Tryptophan % in kernel protein	-0.006	0.004	-0.010	0.006	-0.003	0.009
Protein % in kernel	-0.007	0.010	0.001	0.010	-0.025	0.011

Note: E: Environment

Table.4a Estimates of stability parameters for different traits in QPM

SN	Entry	Protein % in kernel			Lysine % in kernel protein		
		X_i	b_i	S^2d_i	X_i	b_i	S^2d_i
1	CML161xCML167	9.883	2.693	0.0015	3.582	1.207	0.1252***
2	CML161xCML171	9.724	1.555	-0.0011	3.244	-0.417**	-0.0010
3	CML161xCML193	9.667	0.523	0.0023	3.183	1.223	0.0237***
4	CML161xVL1037	9.492	3.626	-0.0020	3.250	0.257	-0.0008
5	CML161xVL1056	9.183	0.977	-0.0019	3.461	3.757	0.1421***
6	CML167xCML161	9.379	-1.296	0.0111**	3.111	1.059	0.0002
7	CML167xCML171	9.622	1.130	-0.0020	3.133	0.547	0.0063***
8	CML167xCML193	9.579	0.944	-0.0025	3.156	-0.929	0.0144***
9	CML167xVL1037	9.267	1.446	0.0002	3.267	-0.716*	-0.0001
10	CML167xVL1056	9.811	3.063	-0.0029	3.678	-0.259	0.0063***
11	CML171xCML161	9.994	0.549	-0.0025	3.457	8.241	0.0367***
12	CML171xCML167	9.761	-0.027	-0.0035	3.628	4.196	0.0543***
13	CML171xCML193	9.739	0.353	-0.0035	3.977	-0.503*	-0.0005
14	CML171xVL1037	9.239	5.454	0.0008	3.106	1.078	0.0011
15	CML171xVL1056	9.317	-1.647	-0.0018	3.417	0.772	0.0058***
16	CML193xCML161	9.417	1.056	-0.0003	3.278	1.481	0.0080***
17	CML193xCML167	9.433	-1.021	-0.0022	3.233	-0.090	-0.0001
18	CML193xCML171	9.582	0.689	-0.0015	3.139	1.634	0.0134***
19	CML193xVL1037	9.294	6.206	0.0102**	3.144	1.020	0.0136***
20	CML193xVL1056	9.933	0.579	-0.0033	3.328	-2.974	0.0191***
21	VL1037xCML161	9.194	3.176	0.0068*	3.106	1.692	0.0038**
22	VL1037xCML167	9.571	2.354	-0.0007	3.767	1.226	0.0444***
23	VL1037xCML171	9.684	-1.556	0.0022	3.272	-0.472	0.0016
24	VL1037xCML193	9.525	-0.735	0.0191***	3.933	2.552	0.0258***
25	VL1037x VL1056	9.692	-2.322	0.0004	4.067	-0.379	0.0003
26	VL1056xCML161	9.552	-1.764**	-0.0036	3.200	2.176	0.0021*
27	VL1056xCML167	9.536	0.500	-0.0024	3.272	0.676	0.0063***
28	VL1056xCML171	9.723	-3.324	-0.0012	3.244	0.552	0.0000
29	VL1056xCML193	9.818	-2.415*	-0.0032	3.256	1.475	0.0013
30	VL1056x VL1037	9.961	1.125	0.0006	3.350	3.063	0.0265***
31	CML161	9.787	1.571	-0.0029	3.391	-0.097	0.0349***
32	CML167	9.681	3.329	-0.0005	3.322	-0.763	0.0141***
33	CML171	9.647	1.141	-0.0012	3.350	-0.609	0.0122***
34	CML193	9.598	1.684	-0.0022	3.294	-0.439	0.0166***
35	VL1037	9.680	3.579	-0.0005	3.277	6.544	0.0882***
36	VL1056	9.782	4.173	-0.0015	3.449	-4.507	0.0857***
37	Shaktimsn-3(check)	9.88	-0.06	-0.00	3.68	3.35	0.00
38	Shaktiman-4(check)	9.87	0.69	-0.00	3.89	1.37	0.00
	General mean	9.61			3.39		
	SEm (±)	0.02			0.06		
	$SE(b_i)$	1.94			2.34		

*, ** Significant at 5 % & 1 % level of probability, respectively

Table.4b Estimates of stability parameters for different traits in QPM

S.N	Entry	Tryptophan % in kernel protein			Grain yield/plant		
		X_i	b_i	S^2d_i	X_i	b_i	S^2d_i
1	CML161xCML167	0.894	1.889	0.0085***	164.876	0.155*	59.264*
2	CML161xCML171	0.803	-0.217**	0.0000	146.839	1.154	-12.413
3	CML161xCML193	0.787	2.942	0.0013***	140.525	1.308	5.323
4	CML161xVL1037	0.803	0.513	0.0000	143.486	1.139	28.738
5	CML161xVL1056	0.867	3.547	0.0075***	138.506	1.301	22.758
6	CML167xCML161	0.764	0.933	0.0001*	166.463	0.333*	43.684
7	CML167xCML171	0.777	0.756	0.0004***	137.479	1.349**	-20.757
8	CML167xCML193	0.787	-0.247	0.0011***	137.842	1.098	7.658
9	CML167xVL1037	0.817	0.210	0.0001*	159.683	0.701	272.389**
10	CML167xVL1056	0.912	-0.810	0.0009***	152.578	0.252	396.064**
11	CML171xCML161	0.858	8.916*	0.0019***	136.518	0.980	6.405
12	CML171xCML167	0.901	4.560	0.0035***	144.096	1.049	61.352*
13	CML171xCML193	0.996	0.006	0.0000	124.630	0.959	1.086
14	CML171xVL1037	0.767	1.028	0.0000	136.915	1.320*	-8.718
15	CML171xVL1056	0.850	0.719	0.0007***	134.938	1.354*	-4.800
16	CML193xCML161	0.813	0.837	0.0004***	143.045	1.170	41.879
17	CML193xCML167	0.813	0.093	0.0001*	133.916	1.304*	-2.595
18	CML193xCML171	0.779	1.618	0.0006***	135.542	1.299	63.304*
19	CML193xVL1037	0.781	0.402	0.0006***	134.927	1.251	91.249**
20	CML193xVL1056	0.833	-1.831	0.0012***	124.905	1.602*	20.330
21	VL1037xCML161	0.769	1.776	0.0001*	131.609	1.110	28.669
22	VL1037xCML167	0.934	2.226	0.0029***	137.380	1.221	11.963
23	VL1037xCML171	0.811	0.017	0.0001	144.008	1.492	63.329*
24	VL1037xCML193	0.983	2.183	0.0017***	138.327	1.186	28.007
25	VL1037x VL1056	1.033	0.119**	-0.0001	134.690	1.054	33.253
26	VL1056xCML161	0.795	1.038	0.0004***	123.683	1.291*	-15.705
27	VL1056xCML167	0.814	0.961	0.0003***	156.361	0.446	345.587**
28	VL1056xCML171	0.809	0.278	0.0000	114.611	1.414	264.690**
29	VL1056xCML193	0.808	0.803	0.0000	127.028	1.423**	-28.246
30	VL1056x VL1037	0.833	2.502	0.0013***	130.841	0.804	6.484
31	CML161	0.849	-2.150	0.0021***	60.606	0.591*	1.532
32	CML167	0.827	-1.115	0.0015***	62.715	0.987	-10.104
33	CML171	0.829	-0.283	0.0007***	67.262	0.846	-16.091
34	CML193	0.821	-0.875	0.0014***	64.534	0.742**	-28.288
35	VL1037	0.813	3.837	0.0088***	62.108	0.614*	-9.536
36	VL1056	0.863	-4.618	0.0058***	68.006	0.787	-0.590
37	Shaktimsn-3(check)	0.92	3.12	0.00**	135.3	0.53**	-12.65
38	Shaktiman-4(check)	0.98	2.30	0.00**	139.7	0.33**	82.60**
	General mean	0.84			129.1		
	SEm (±)	**0.01**			**4.0**		
	SE(b_i)	2.37			0.2		

*, ** Significant at 5 % & 1 % level of probability, respectively

Table.5 Stable genotypes for different traits in Maize

Parameters	Hybrids for all environments	Hybrids for favourable environments (Rabi)	Hybrids for unfavourable environments (Kharif)
Protein %in kernel	CML171 x CML161 VL1056 x VL1037 CML193 x VL1056 CML161 x CML167 CML167 x VL1056	VL1056 x CML193	-
Lysine % in kernel protein	VL1037 x VL1056	-	CML171 xCML193
Tryptophan % in kernel protein	CML171 x CML193	-	VL1037 x VL1056
Grain yield/plant	CML161 x CML171 CML161 x VL1037 CML193 x CML161 CML161 x CML193 VL1037 x CML193	CML167 x CML171 CML171 x VL1037 CML171xVL1056 CML193 x CML167	CML167x CML161

From stability analysis studied, it can be inferred that the hybrid. For grain yield per plant showed high mean than the general mean (129.1), regression coefficient more than unity and non-significant deviation from regression were observed in the hybrids CML 167 x CML 171, CML 171 x VL 1037, CML 171 x VL1056 and CML 193 x CML 167 indicating that these hybrids responded to favourable conditions and can produce higher yields when provided with suitable environments. Similar reports were earlier reported by Kalla *et al.,* (2001). The hybrid CML 167 x CML 161 (129.1) showed high mean than the general mean, regression coefficient less than 1 and non-significant deviation from regression was specifically adapted to poor environments and suitable for kharif seasons. These findings are consistent with Rahman *et al.,* (2010), Dushyantha Kumar *et al.,* (2010), Sreedhar *et al.,* (2011). The hybrid CML 161 x CML 171, CML 161 x VL 1037, CML 193 x CML 161, CML 161 x CML 193 and VL1037 x CML 193 appeared with high mean than the general mean, regression coefficient around unity and non-significant deviation from regression are considered to be stable for wider conditions. Similar findings were reported by Gouri Shankar *et al.,* (2008).

Maize protein is highly characterized by high levels of glutamic acid, leucine and low levels of lysine and tryptophan. The QPM endosperm proteins showed significantly higher percentage of lysine and tryptophan. For protein content, high mean than the general mean (9.61), regression coefficient

more than unity and non-significant deviation from regression as reported by Kozubenko *et al.,* (1990) were observed in the hybrids VL 1056 x CML 193. None of the hybrid showed high mean than the general mean, regression coefficient less than unity, non-significant deviation from regression. The hybrids CML 171x CML 161, VL1056 x VL 1037, CML 193 x VL 1056, CML 161 x CML 167 and CML 167 x VL 1056 showed with high mean than the general mean(9.61), regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

For lysine content, none of the hybrid showed high mean than the general mean (3.39), regression coefficient more than unity and non-significant deviation from regression. The hybrid CML 171 x CML 193 (3.39) showed high mean than the general mean, regression coefficient less than 1 and non-significant deviation from regression was specifically adapted to poor environments and suitable for kharif seasons. The hybrids VL1037 x VL 1056 (3.39) showed high mean than the general mean, regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

None of the hybrid showed high mean for tryptophan content than the general mean (0.84), regression coefficient more than unity and non-significant deviation from regression. The hybrid VL 1037 x VL 1057 showed high mean than the general mean (0.84), regression coefficient less than 1 and non-significant deviation from regression was specifically adapted to poor environments and suitable for kharif seasons. The hybrids CML 171 x CML 191 showed high mean than the general mean (0.84), regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

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