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GENOTYPE BY ENVIRONMENT INTERACTION AND YIELD STABILITY ANALYSIS OF QUALITY PROTEIN MAIZE GENOTYPES IN TERAI REGION OF NEPAL

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Abstract

Grain yield stability for the new maize genotypes is an important target in maize breeding programs. The main objective of this study was to identify stable high yielding quality protein maize (QPM) genotypes under various locations and years in terai region of Nepal. Six quality protein maize genotypes along with Poshilo Makai-1 (Standard Check) and Farmer's Variety (Local Check) were tested at three different locations namely Ayodhyapuri-2, Devendrapur, Madi, Chitwan; Rajahar-8, Bartandi, Rajahar, Nawalparasi; Mangalpur-2, Rampur, Chitwan during 2011 and 2012 spring and winter seasons under rainfed condition. The experiment was conducted using Randomized Complete Block Design with two replications in farmer's fields. There was considerable variation among genotypes and environments for grain yield. The analysis of variance showed that mean squares of environments (E) was highly significant and genotypes (G) and genotype x environment interaction (GEI) were non significant. The genotypes S03TLYQ-AB02 and RampurS03FQ02 respectively produced the higher mean grain yield 5422 ± 564 kg/ha and 5274 ± 603 kg/ha across the locations. Joint regression analysis showed that RampurS03FQ02 and S03TLYQ-AB02 with regression coefficient 1.10 and 1.22 respectively are the most stable genotypes over the tested environments. The coefficient of determination (R^2) for genotypes Rampur S03FQ02 and S03TLYQ-AB02 were as high as 0.954, confirming their high predictability to stability. Further confirmation from GGE biplot analysis showed that maize genotype S03TLYQ-AB02 followed by Rampur S03FQ02 were more stable and adaptive genotypes across the tested environments. Thus these genotypes could be recommended to farmers for general cultivation.

Key words: Quality protein maize, GGE biplot, G x E interaction, yield stability

Introduction

Maize is the second most important staple food crop in terms of both area and production after rice in Nepal. It is grown in 0.87 million hectares of land with average yield of 2.5 Mt/ha (MOAC, 2011/12). All the varieties of maize released so far in Nepal are normal type except Poshilo Makai-1. Normal maize has poor nutritional value for monogastric animals such as human and pigs because of reduced content of essential amino acids such as lysine and tryptophan. For humans, lysine is the most limiting amino acid followed by tryptophan in maize protein (Kies *et al.*, 1965). 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. Improving grain yield of QPM genotypes is one of the major objectives of National Maize Research Program in Nepal.

National Maize Research Program, Rampur has one of its mandates for conducting participatory technology verifications in its outreach research sites since 1991. On-farm testing of new technologies increases the probability that the variety will be adopted (Franzel and Coe, 2002). The main objectives of outreach research are to reduce the yield gap between on-station and on-farm of maize. Nepal Agricultural Research Council (NARC) outreach research mainly aims at verifying and validating the technologies developed in the research station for adaptability in farmer's field situation (Upadhyay, 2000).

Maize crop possesses great diversity and can be grown across varied agroecological zones (Ferdu *et al.*, 2002). The improved varieties gave high and stable yields across environments where they were adapted (CIMMYT, 1991). The ability to develop high yielding stable cultivars is a primary focus in most breeding programs and is ultimately of more importance than the

identification of unstable cultivars. Evaluation of genotypes for their stability for yield under different environments is an important task in plant breeding programs. The presence of a high genotype x environment (GE) interaction represents a significant problem of related to phenotypic expression of genetic base and makes it's difficult for decision making in selection. High yield stability usually refers to a genotype ability to perform consistently, whether at high or low yield levels across a wide range of environments. GGE biplot analysis provides a framework for identifying target testing locations and discriminates genotypes that are high yielding and stable. The GGE biplot is constructed by plotting the first two principal components (PC1 and PC2) derived from singular value decomposition of the environment-centered data.

The Information on stability of quality protein maize genotypes under terai environments in Nepal is lacking so the present study was carried out to identify superior stable quality protein maize genotypes for terai region of Nepal.

Materials and method

The table 1 showed the experiments, name of genotypes included, years, seasons and sites. The materials were received from Hill Maize Research

Project (HMRP) of CIMMYT, Nepal. The experiments were designed by researchers and managed by farmers. All the experiments were laid out in a RCB design with two replications. Each trial consisted of farmer's variety to compare the performance of tested varieties. The plot size was 22.5 m². The spaces between row-to-row and plant to plant were 75 and 25 cm. respectively. Two seeds per hill were planted and thinned to a single plant per hill after first weeding. Fertilizers were applied at the rate of 120:60:40 kg/ha N: P₂O₅: K₂O respectively in addition to 15 ton farmyard manure per hectare. Half dose of N and full doses of P and K were applied basally. The remaining half of N was applied as side dressing at knee-high stage. The plots were kept free of weeds manually. Data on grain yield was taken. The plots were harvested individually. Grain yield was adjusted to 80% shelling recovery from the de-husked cob weight /plot. Grain moisture content for each plot was recorded and grain yield was adjusted to 15 % percent moisture basis.

To determine stability and identify superior genotypes across environments, genotype and genotype x environment (GGE) bi-plot analysis was conducted using GGE bi-plot software (Yan and Kang, 2002). Regression analysis was also performed to determine stability and identify superior genotypes across environments on the basis of regression coefficient.

Table 1: List of name of experiments, genotypes, years, seasons and sites.

S.N.	Name of experiment	Genotype	Year	Season	Site
1	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, RampurS03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2011	Winter (September-February)	Ayodhyapuri-2, Devendrapur, Madi, Chitwan
2	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, Rampur S03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2012	Winter (September-February)	Ayodhyapuri-2, Devendrapur, Madi, Chitwan
3	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, Rampur S03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2011	Spring (February-May)	Rajahar-8, Bartandi, Rajahar, Nawalparasi
4	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, Rampur S03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2012	Spring (February-May)	Rajahar-8, Bartandi, Rajahar, Nawalparasi
5	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, RampurS03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2011	Winter (September-February)	Mangalpur-2, Rampur, Chitwan
6	CFFT-QPM set	S03TLYQ-AB01, S03TLYQ-AB02, RampurS03FQ02, S99TLYQ-B, Poshilo Makai-1 and Farmer's Variety	2012	Winter (September-February)	Mangalpur-2, Rampur, Chitwan

Results and Discussion

The mean grain yield of quality protein maize genotypes differed across environments which may be due to differing environmental conditions over time and locations. The locations themselves differ greatly in altitude, temperature and rainfall, a fact that affects performance. The findings of the study showed that on the average across locations and years, the genotype S99TLYQ-B produced the highest grain yield of 5454

kg/ha followed by S03TLYQ-AB02 (5422 kg/ha) and Rampur S03FQ02 (5274 kg/ha) (Table 2).

The pooled analysis of variance for grain yield (Table 3) showed that genotypic variation was highly significant for environments, however the genotype and environment interaction was found non significant. The environment factors contributing differences in mean grain yield across six environments and two years may include soil types, sowing dates, sunshine hours and amount of rainfall during the crop cycle.

Table 2: Mean grain yield (kg/ha) of quality protein maize genotypes evaluated in farmer's field trials at three locations (Madi, Rajahar and Rampur) in 2011 and 2012

S. N	Genotypes	2011				2012				Grand mean
		Madi	Rajahar	Rampur	Mean	Madi	Rajahar	Rampur	Mean	
1	S03TLYQ-AB01	3260	4272	5030	4187	6743	5297	4404	5481	4834
2	S03TLYQ-AB02	3976	4579	6140	4898	7754	6970	3112	5945	5422
3	RampurS03FQ02	4756	4688	5560	5001	7955	5713	2974	5547	5274
4	S99TLYQ-B	5679	4550	5760	5330	7000	5875	3862	5579	5454
5	Poshilo Makai-1	4938	5132	4250	4773	7954	6111	2043	5369	5071
6	Farmer's Variety	4011	3480	5560	4350	5887	6570	2033	4830	4590
	Grand mean	4437	4450	5383	4757	7216	6089	3071	5459	5108
	CV,%	21.9	18.6	7.3		10.3	15.1	9.3		
	LSD _{0.05}	2498.9	2126.8	1003.4		1902.9	4163.9	734.9		
	F-test	ns	ns	*		ns	ns	**		

Table 3: Combined analysis of variance (ANOVA) of grain yield of six quality protein maize genotypes tested across six environments of three locations in 2011 and 2012

Source	df	SS	MSS	F value
Environment	5	126135466	25227093	30.06***
REP (ENV)	6	55345069	9224178	10.99***
Genotypes	5	7085981	1417196	1.69 ns
G x E	25	27251275	1090051	1.3 ns
Error	30	25177859	839262	

Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 'ns' > 0.05

Table 4: Regression parameters of from multi-location trials (n=6) where genotype mean grain yield (kg/ha) was regressed on trial mean yield from 2011 to 2012

Sn	Genotypes	Mean±SEM	Range	CV (%)	R ² (%)	b	SEb	t value
1	S03TLYQ-AB01	4834±364	3091-7147	26.07	64.6	0.650	0.2406	2.70 ns
2	S03TLYQ-AB02	5422±564	2810-8041	36	95.4	1.22	0.1338	9.15***
3	RampurS03FQ02	5274±603	2599-9210	39.59	95.4	1.10	0.1207	9.12***
4	S99TLYQ-B	5454±497	3195-7754	31.59	86.9	0.708	0.1375	5.15**
5	Poshilo Makai-1	5071±659	1810-8324	45.03	84.6	1.25	0.2655	4.69**
6	Farmer's Variety	4590±699	2033-6570	37.29	82.5	1.07	0.2470	4.34*

Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 'ns' > 0.05, SEM:Standard error of mean

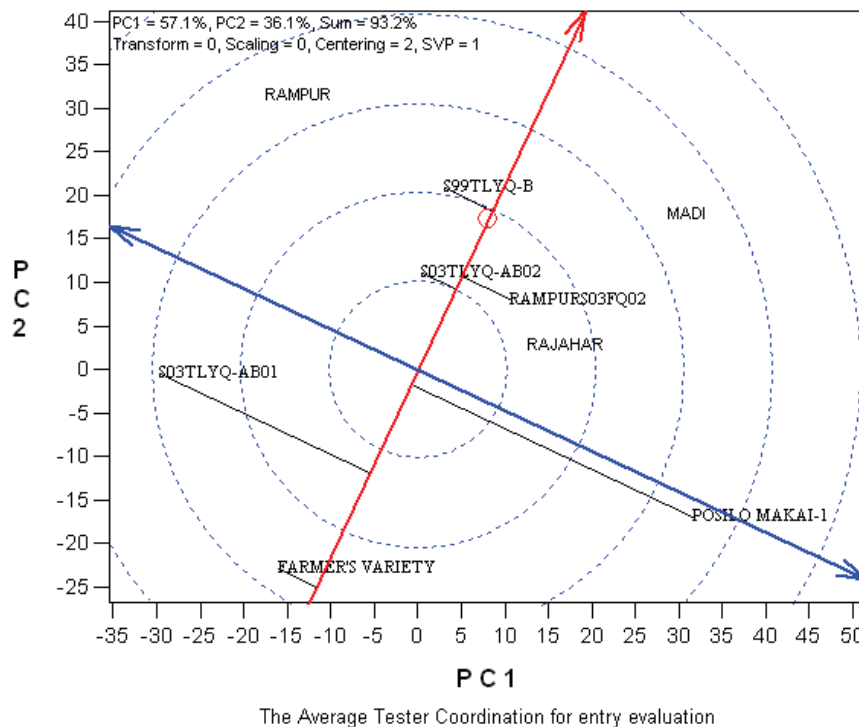


Fig.1: Mean versus stability pattern and ranking of quality protein maize genotypes with reference to ideal maize genotype for grain yield at Madi, Rajahar and Rampur environments (each location had two different environments) during 2011 and 2012

Regression values above 1.0 describe genotypes with higher sensitivity to environmental change (below average stability) and greatly specify adaptability to high yielding environments. A regression coefficient below 1.0 provides a measurement of greater resistance to environmental change (above average stability), and this increases the specificity to adaptability to low yielding environments (Wachira *et al.*, 2002). Thus genotypes S03TLYQ-AB02 and RampurS03FQ02 were found better adapted to high yielding environment and S99TLYQ-B were found better adapted to low yielding environment (Table 4). The genotypes namely S03TLYQ-AB02 ($b=1.22$, $CV=36\%$, $SEM=564$) was found more stable followed by Rampur S03FQ02 ($b=1.10$, $CV=39.59\%$, $SEM=603$), hence their regression coefficient were nearly equal to unity and their grain yield were above the grand mean yield (Table 4).

An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003). In GGE biplot analysis the genotypes more close to concentric circle indicates higher mean yield. An ideal genotype, which is located at the center of the concentric circle is the one that has both high mean yield and high stability. So, here genotype S03TLYQ-AB02 was the most stable followed by RampurS03FQ02 and S99TLYQ-B. A genotype closer to the performance line is considered more stable than the one placed farther. So, here genotype S03TLYQ-

AB02 was most stable followed by RampurS03FQ02 and S99TLYQ-B. This results agreed with the results of NMRP (2010).

Conclusion

Identification of stable superior maize genotypes is the most important task in quality protein maize development program. The analysis of variance showed that mean squares of environments (E) was highly significant where genotype x environment interaction (GEI) were non significant. In joint regression analysis for stability the genotypes namely S03TLYQ-AB02 and Rampur S03FQ02 were found to be stable and good yielder across the locations and years. The result of GGE biplot analysis also confirmed that maize genotype S03TLYQ-AB02 followed by RampurS03FQ02 were the more stable and high yielding genotypes across the tested environments. Thus these genotypes were found promising and could be released and recommended to farmers for general cultivation in terai region of Nepal.

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References

- CIMMYT (1991) High yielding varieties do not necessary yield less under unfavorable conditions. CIMMYT Annual Report 1990. Mexico DF.
- FAO (1992) Maize in human nutrition. *Journal of Nutrition*. FAO, Rome. 1980, 110: 1070-1074.
- Ferdu A, Demissew K and Birhane A (2002) Major insect pests of maize and their management: A Review In: Nigussie M, Tanner D and Twumasi AS(Eds.) Enhancing the contribution of maize to food security in Ethiopia. Proc. 2nd National Maize Workshop, Addis Ababa Ethiopia, 12-16 Nov. 2001.
- Franzel S and Coe R (2002) Participatory on-farm testing: the sustainability of different types of trials for different objectives.. In: Quantitative analysis of data from participatory methods in Plant Breeding (Bellon, M.R and J. Reeves eds.) CIMMYT, Mexico, pp.1-7.
- Kies C, Williams ER and HM Fox (1965) Determination of first-limiting nitrogenous factors in corn protein for nitrogen retention in human adults. *Journal of Nutrition*. 86; 350
- MOAC (2011/12) Agri-business Promotion and Statistics Division (ABPSD). The Ministry of Agriculture and Cooperation, Kathmandu, Nepal.
- NMRP (2010) Annual Report. 2009-10. National Maize Research Program, Rampur, Chitwan, Nepal. Pp.42-45.
- Upadhyay BP (2002) Research-extension interface in outreach .. In: Proceedings of the 5th National Outreach Research Workshop 30-31 May, 2000, Khumaltar, Lalitpur. PP. 13-16.
- Wachira F, Wilson NG, Omolo J and Mamati G (2002) Genotype x environment interactions for tea yields. *Euphytica*, 127: 289-296.
- Yan W and Kang MS (2002) GGE Biplot Analysis: A graphical tool for breeders, geneticists and agronomists. CRC Press, New York, USA. pp.14.
- Yan W and Kang MS (2003) GGE Biplot Analysis: A graphical tool for breeders, geneticists and agronomists. 1st Ed., CRC Press LLC., Boca Roton, Florida, pp: 271.