Evaluation of performance and genetic parameters in quality protein maize genotypes

Aradhana Regmi^{1*}, Dikshya Niraula¹, Upasana Shrestha¹, Suraj Shrestha² and Bishnu Prasad Kandel³

¹Institute of Agriculture and Animal Science (IAAS), Prithu Technical Campus (PTC), Lamahi, Dang, Nepal

²Agriculture and Forestry University, Rampur, Chitwan, Nepal

³Institute of Agriculture and Animal Science (IAAS), Lamjung Campus, Lamjung, Nepal

*Corresponding author email:_aradhanaregmi1999@gmail.com

*ORCID: https://orcid.org/0000-0003-1429-1403

Received: September 11, 2022; Revised: October 24, 2022;

Accepted: November 15, 2022; Available online: December 25, 2022

© Copyright: Regmi et al. (2022).

This work is licensed under a <u>Creative Commons Attribution-NonCommercial 4.0</u> International License.

ABSTRACT

Quality protein maize (QPM) contains opaque-2 mutant genes that increases lysine and tryptophan level which are not normally found in maize. The objective of this study was to evaluate the performance of QPM genotype based on their yield, yield attributing and other relevant characteristics. A varietal trial on QPM was conducted in the research field of Lamahi municipality-3, Dang, Nepal from February to June 2021. This experiment was performed in Randomized Complete Block Design with three replications. Thirteen genotypes of QPM and one standard check (Poshilo Makai-2) were evaluated. Each genotype was assigned an area of $3m \times 3m$ with a net plot area of $452.5m^2$ per block. Analysis of variance revealed significant data for the most of the genotypes. Four genotypes Rampur-S13FQ-02 Rampur-SO3FQ-02, Rampur-S13FQ010 and Rampur-S13FQ-08 were found superior with a yield of 4.32*t*/ha, 3.97 *t*/ha, 3.89 *t*/ha, 3.63 *t*/ha respectively in comparison to the standard check Poshilo makai-2 (2.66 *t*/ha). Significant and positive correlation were observed for the ear length, ear diameter, number of kernels per ear, number of kernel row per ear, ear weight whereas negative for ear aspect with grain yield was observed. Ear weight without husk had the highest contribution to grain yield. For all observed traits, the coefficient of phenotypic variation (PCV) was found to be higher than that of genotypic coefficient of variation (GCV). The highest GCV, PCV, genetic advance and heritability were observed in ear aspect, thousand grain weight, ear height, plant height respectively. As a result, breeding programs can be further improved by selecting these traits.

Keywords: Quality protein maize; Heritability; Correlation, path analysis; Genetic variability.

Correct citation: Regmi, A., Niraula, D, Shrestha, U, Shrestha, S, & Kandel, B.P. (2022). Evaluation of performance and genetic parameters in quality protein maize genotypes. *Journal of Agriculture and NaturalResources*, *5*(1), 52-62. DOI: https://doi.org/10.3126/janr.v5i1.50514

INTRODUCTION

Maize (*Zea mays L.*), which is native to Mexico belongs to the Poaceae family. Among cereals, maize ranks third after wheat and rice in the world and is an important food and feed crop (Tesfaye & Sime, 2021). In Nepal, it ranks in second position (Sapkota & Joshi, 2021). The production and productivity of maize crop has increased by 3.22 % and 3.0 %, respectively in the year 2020/21 (MoF Economic Survey, 2020/21). It plays a significant role in human, animal

nutrition as well as agro-based industries. However, children, pregnant and lactating women, and elderly persons having normal maize have suffered from malnutrition. The animals fed with normal maize had shown the lack of appetite, delayed growth, defective skeletal development, and abnormal behavior not only this but also the addition of synthetic lysine and tryptophan in fishes has increased the cost of production. Even though effort for improvement in maize production has been done, the results are not satisfactory (K.C. *et al.*, 2016). Therefore, the discovery of Quality protein maize (QPM) is crucial as it contains higher amounts of lysine (Holding *et al.*, 2011) and 47% higher tryptophan content with an increase in albumin, glutelin, and globulins than the normal maize (Choudhary & Chaudhary, 2020). The introgression of *opaque 2* genes with the desired modifiers has led to the development of QPM containing twice the amount of lysine and tryptophan as compared to normal endosperm of maize (Babu *et al.*, 2005).

Selection is the most pivotal program either to select or cull the plants. Maize provides a basis for selection as it contains wide morphological, physiological and biochemical traits and consists of immense genetic variability and adaptability (Pajic, 2007). Various other parameters are done for selection in a plant breeding program for further enhancement of crops and these parameters are: Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for yield attributing traits (Tiwari *et al.*, 2019). The other basic tool that interrelates the different independent parameters is correlation coefficient (Sravan *et al.*, 2012). Similarly, the direct effects from the indirect effects of the traits can be separated by the path coefficient analysis (Baye *et al.*, 2020). A comparative study of various traits, especially those associated with the yield, is useful for the plant breeder to select breeding materials through secondary traits to initiate an efficient and successful breeding program. (Ghimire *et al.*, 2015). The major objective of this study is to evaluate the production performance of different varieties of maize. This study helped us to determine the high yielding varieties as well as the agro-morphological, phenological and yield component traits of QPM maize genotype.

MATERIALS AND METHODS

Site selection for research material

The experiment was conducted at the research plot of IAAS, Prithu Technical College, Lamahi Municipality, Dang district during June to September, 2019. The experiment site was located at 27°51'15.7"N Latitude and 82°32'21.6"E Longitudes at the elevation of 257 masl. Climate of the experimental site was nearly tropical and well irrigated.

Selection of genotype used

Fourteen genotypes were used in the trial: Poshilo makai 2, Rampur SO3FQ -02, Rampur S13FQ-08, Rampur S13FQ-06, S99TLYQ-H5B, Rampur-S13FQ-02, RPOPYQ-12, SO3TLYQ-AB-01, SO1SIYQ, RPOPYQ-06, RPOPYQ-10, Rampur S13FQ010, RPOPYQ-4 and RPOPYQ-8 whereas Poshilo Makai 2 was used as a standard check.

Experimental design and cultural practices

The experiment was conducted in Lamahi, Dang during June to September 2019. Experimental field was laid out in RCBD with three replications. Fourteen genotypes were allotted randomly on each replication. The total area of the research field was 452.5 m² with an individual plot size

of $9m^2$ ($3m\times3m$) and spacing of 75 cm \times 25 cm (RR \times PP) retaining 48 plants in a plot. The distance between each plot was maintained at 0.25 m and distance between each replication maintained at 0.5 m. Two seeds/hill were sown in the spacing of 75 cm row to row and 25 cm plant to plant. Well decomposed farm yard manure @ 6 t/ha was mixed into soil a week before sowing and fertilizer was applied @120:60:40 kg NPK/ha, through Urea, DAP and MOP. Half dose of N and full dose of P and K were applied as basal dose during field preparation and remaining half dose of N was top dressed in two splits 45 and 90 days after sowing respectively. Other agronomic practices were performed as per the requirement.

Data collection and observation

Observations were taken on randomly selected 5 plants from each experimental plot for the traits: Plant height (PH), ear height (EH), no. of leaves (NOL), no. of cob (NC), Ear length (EL), Ear weight (EW), Ear diameter (ED), No. of kernels rows per ear (NKRPE) and no. of kernels per row (NKPR), Grain yield (GY) kg/plot and whole plot basis for traits: Days to silking (SD), Days to anthesis (AD), Thousand grain weight (TGW), ear aspect (EA) (UPOV, 2009). Grain yield was calculated using formula adopted by Carangal *et al.* (1971) and Shrestha *et al.* (2018) by adjusting the grain moisture at 12% and converting to the grain yield per hectare basis.

Statistical analysis

The experimental data were processed using MS-Excel and analyzed by using RStudio software. Analysis of variance of the characters was done as per standard statistical procedure for randomized complete block design as given by Panse & Sukhatme (1978) and Gomez & Gomez (1984). Least significant difference (LSD $p \le 0.05$) test was used for mean comparison to identify the significant components of the treatment means (Jan *et al.*, 2009; Sharma *et al.*, 2016; Gomez & Gomez, 1984). Phenotypic and genotypic coefficient of variation was calculated as suggested by Falconer (1981). Heritability (broad sense) (Johnson *et al.*, 1955), genetic advance (Burton, 1952) and genetic advance as a percent of mean (Johnson *et al.*, 1955) were also estimated. For character association, phenotypic correlation coefficients were estimated according to Miller *et al.* (1958) and path coefficients according to Dewey & Lu (1959).

RESULTS AND DISCUSSION

Phenological traits

Longest days to anthesis was shown by RPOPYQ-06 whereas the shortest days to anthesis was shown by Poshilo makai-2 and RPOPYQ-08. Longer the anthesis days, longer would be the vegetative period. This results in a late reproductive period which affects grain yield. Similar findings were also observed by Kumar *et al.* (2016). Longest days to silking was shown by RPOPYQ-06 whereas shortest days to silking was shown by Poshilo Makai-2 and RAMPUR S13FQ-08. Significant differences for 50% silking was also supported by Kumar *et al.* (2016). The earliest silking might be due to the higher temperature at the early vegetative phase which reduced the no. of days to silking under the normal plantation (Kandel & Shrestha., 2020). Non-significant results for (Anthesis-Silking Interval) ASI means there was synchronous flowering. This result was also found similar with the finding of Kandel *et al.* (2020).

Growth traits

Maximum plant height was observed in Rampur-S13FQ-08 whereas the lowest plant height was observed by Poshilo Makai-2. Poshilo Makai -2 showed the lowest plant height; this might be due to the genetic potential of these strains to overcome drought (Kandel & Shrestha, 2020). The lower plant height results in lower transpiration rate that eventually reduces the drought stress Rampur-S13FQ-08 showed the maximum number of leaves while RPOPYQ-04 showed the minimum number of leaves. The highest ear height was observed in the Rampur-S13FQ-08 whereas the lowest ear height was observed in Poshilo Makai-2.

Yield and yield related traits

Rampur-SO3FQ-02 and Rampur-S13FQ-08 showed the highest ear length whereas lowest ear length was shown by SO3TLYQAB-01. Highest ear length might be due to the suitable environmental condition which utilized the optimum solar radiation, and had more assimilation rate with maximum conversion of starches (Derby *et al.*, 2004). The maximum no. of kernels per ear was found in RPOPYQ-04 whereas lowest was shown by SO3TLYQAB-01. RPOPYQ-08 showed the highest number of kernel rows per ear whereas the lowest number of kernel rows per ear was observed in Poshilo Makai-2.

Genotypes	AD	SD	EW	ED	NOL	TGW	GY	NKRPE
Poshilo Makai 2	76 ^f	77 ^f	0.85	4.3	12 ^{cd}	0.286	2.66 ^{de}	34 ^{ab}
Rampur- SO3FQ-02	81 ^{de}	82 ^{de}	1.12	4.8	14 ^{ab}	0.283	3.97ab	38 ^{ab}
Rampur- S13FQ-08	78 ^{ef}	79 ^{ef}	1.04	4.7	15 ^a	0.280	3.63 ^{abc}	34 ^{ab}
Rampur- S13FQ-06	82 cd	84 ^{cd}	0.92	4.4	14 ^{ab}	0.270	2.95 ^{cd}	35 ^{ab}
S99TLYQ-H5B	86 ^{abc}	88 ^{abc}	0.96	4.7	13 ^{bcd}	0.880	3.47 ^{bcd}	36 ^{ab}
Rampur- S13FQ-02	84 ^{bcd}	86 ^b	1.13	4.8	14 ^b	0.280	4.32 ^a	36 ^{ab}
RPOP YQ- 12	80 ^{de}	82 ^{de}	0.94	4.5	13 ^{bc}	0.260	3.05 ^{cde}	34 ^b
SO3TLYQ AB-01	82 cd	84 ^{cd}	0.75	4.4	13 ^{bc}	0.250	2.28 ^e	29 ^c
SO1SIYQ	86 ^{abc}	87 ^{abc}	0.93	4.4	13 ^{bc}	0.230	2.74 ^{de}	37 ^{ab}
RPOPYQ-06	88 ^a	90 ^a	0.82	4.3	12 ^d	0.290	2.86^{cde}	37 ^{ab}
RPOPYQ-10	87 ^{ab}	88 ^{ab}	0.87	4.32	12 ^d	0.240	3.01 ^{cde}	36 ^{ab}
Rampur S13FQO10	85 ^{abc}	87 ^{abc}	0.98	4.9	13 bcd	0.260	3.89 ^{ab}	35 ^{ab}
RPOPYQ-04	86 ^{abc}	87 ^{abc}	0.85	4.4	11 ^d	0.240	3.15 ^{bcd}	39 ^a
RPOPYQ-08	76 ^f	78 ^{ef}	1.026	4.7	14 ^b	0.265	3.46 ^{bcd}	34 ^b
F-test	***	***	NS	NS	***	NS	*	*
LSD (0.05)	3.80	4.31	0.28	0.47	1.47	0.45	0.95	4.50
CV%	2.75	3.05	18.23	6.14	6.81	0.312	17.71	7.60

Table 1: Mean Performances of QPM genotypes f	for various	traits	evaluated	at	Lamahi,
Dang during growing season of Feb – Jun 2021.					

AD: Days to anthesis, SD: Days to silking, EW: ear weight (g), ED: ear diameter (cm), NOL: number of leaves, TGW: Thousand grain weight (g), NKRPE: No. of kernels rows per ear, GY: Grain yield (t/ha).

NS: Not significant, *Significant at 0.05 level of significance, *** Significant at 0.001 level of significance. CV: Coefficent of variation, LSD: Least Significant Difference. Means followed by the same letters in the same column are not significantly different at the 0.05 level of probability.

The maximum no. of kernel row per ear might be due to the ability of stress tolerance capacity of the genotype. The highest cob weight was shown by Rampur-S13FQ-02 whereas lowest was shown by RPOPYQ-06. Highest grain yield was observed in Rampur-S13FQ-02 and the lowest grain yield was observed in SO3TLYQAB-01. Similar findings were reported by Mafouasson*et al.* (2018). Grain yield is the result of several yield attributing factors. Optimum utilization of solar light, higher assimilates production and its conversion to starches resulted in higher grains number and weight that resulted in more grain yield (Derby *et al.*, 2004). The highest grain yield of Rampur-S13FQ-02 might be due to its highest ear length, ear height, cob weight, and shortest silking period.

Genetic Variability

Phenotypic variance was higher than the genotypic variances for all the traits (Table 2). Low PCV and GCV was observed for days to 50% anthesis and days to 50% silking with the value of 5.57/4.48 and 5.34/ 4.51 respectively. Similarly, PCV and GCV for plant height was 5.49/ 5.24, no. of leaves was 9.84/7.27, ear length was 7.80/5.46, ear diameter was 7.01/3.53, no. of kernel row per ear was 8.25/5.4, no. of kernel per row 9.22/4.92. Moderate PCV and GCV was observed for the trait ear height 10.55/10.07. The PCV observed for the ear weight was moderate (19.40) whereas the GCV for cob weight was low (4.48). Maximum PCV and moderate GCV was found in ear aspect 50.02/24.22, thousand grain weight 89.33/15.7, and grain yield had 21.74/11.97.

Heritability and Genetic Advance

In our findings we observed low, moderate and high estimates of heritability for different examined traits. High heritability estimates were found for plant height and ear height (0.91) followed by tassel branch (0.83) tassel length (0.79) days to 50% anthesis (0.75), and days to 50% silking (0.71). Moderate heritability was found in no. of leaves (0.54) followed by ear length (0.49), no. of kernel row per ear (0.42), and grain yield (0.30). Low heritability was observed in no. of kernel per ear (0.28), ear diameter (0.25), ear aspect (0.23), cob weight (0.05), thousand grain weight (0.03). Traits with high heritability revealed that variations were transmitted to progeny and indicated potential for developing high yielding variety through selection of desirable genotypes. High heritability for these characters indicates the scope of genetic improvement of these characters through selection, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values (Wedwessen & Zeleke, 2020).

Similarly, GAM ranges from 0.90 for no. of cobs to 39.07 for tassel branch. Highest GAM for tassel branch was followed by tassel length (32.02), ear aspect (24.14). Low estimation for GAM for cob weight (2.13) followed by ear diameter (3.65), no. of kernel per ear (5.41), thousand grain weight (5.67), no. of kernel row per ear (7.29), ear length (7.8), days to 50 % silking days (7.8), and days to 50 % anthesis (8.02). This means the traits having low GAM are governed by non-additive gene action so direct selection not recommended because most of variations are influenced by environments. Tassel branch (0.83; 39.07) and tassel length (0.79; 32.02) and shows high heritability and high GAM.

Both higher heritability and genetic advance in conjugation indicates the trait is controlled by additive gene action, whereas high heritability but poor genetic advance is attributed to non-additive gene action (Krishna *et al.*, 2009).

genotypes evaluated at Lamani, Dang during growing season of Feb – Jun 2021										
Traits	GCV	PCV	H2	GA	GAM	_				
AD	4.48	5.17	0.75	6.63	8.02					
SD	4.51	5.34	0.71	6.64	7.8					
ASI	0.56	36.42	0.03	0.05	2.92					
PH	5.24	5.49	0.91	20.3	10.32					
EH	10.07	10.55	0.91	17.41	19.8					
EL	5.46	7.8	0.49	1.51	7.8					
ED	3.52	7.01	0.25	0.16	3.65					
NKRPE	5.4	8.25	0.42	1.09	7.29					
NKPR	4.92	9.22	0.28	1.92	5.41					
EW	4.48	19.4	0.05	0.02	2.13					
EA	24.22	50.08	0.23	0.61	24.14					
TGW	15.7	89.33	0.03	0.01	5.67					
GY	11.97	21.74	0.3	0.43	13.58					

Table 2:	Estimation of PCV, GCV,	Heritability,	Genetic Gain	and GAM f	or QPM
genotypes	s evaluated at Lamahi, Dar	ng during gro	wing season of	f Feb – Jun	2021

GCV= Genotypic Coefficient of variance, PCV= Phenotypic Coefficient of Variance, H²b =Broad sense heritability, GA= Genetic advance, GAM= Genetic Advance Mean

AD: Days to anthesis, SD: Days to silking, ASI: Anthesis silking interval, PH: plant height, EH: Ear height, EL: ear length (cm), ED: ear diameter (cm), NKPRE: number of kernel rows/ear, NKPR: number of kernel/row, EW: ear weight (g), EA: Ear aspect, TGW: Thousand grain weight (g), GY: Grain yield (t/ha).

Phenotypic correlation Coefficient:

The result showed that grain yield was found to be positive and significantly correlated with cob weight, ear diameter ear length, no. of kernel per ear, and no. of kernel row per ear. Similar results were found by Boćanski *et al.* (2009) for no. of kernel per ear and ear length; Kandel *et al.*(2018) for ear diameter and no. of kernel row per ear; and Chukwudi *et al.* (2018) for ear weight. The negative correlation with grain yield was found for the trait days to 50% anthesis, days to 50% silking and no. of cobs (r=0.019) whereas negative and significant correlation was observed for the trait ear aspect.

Olakojo *et al.* (2021) also found similar results between grain yield and ear aspect. The highest positive significant phenotypic correlation existed between days to 50% anthesis and days to 50% silking whereas highest negative significant phenotypic correlation existed between ear aspect and ear weight.

The significant positive correlation between the characters implies that these characters can be simultaneously improved by selection in a breeding program due to the strong association between them (Olawamide *et al.*, 2020). Hence, the characters: cob weight, ear diameter, ear length, no. of kernel per ear, and no. of kernel row per ear are very crucial during consideration for indirect selection to improve grain yield.

Traits	AD	SD	PH	EH	NOL	EL	ED	NKRPE	NKPE	EW	EA	TGW	GY
AD	1												
SD	0.99^{**}	1											
PH	0.14	0.13	1										
EH	0.81	0.62	0.75**	1									
NOL	-0.29	-0.28	0.34	0.37	1								
EL	-0.11	-0.11	0.20	0.28	0.03	1							
ED	-0.12	-0.11	0.22	0.24	0.34*	0.31*	1						
NKRPE	-0.05	-0.02	0.33	0.27	0.22	0.25	0.42**	1					
NKPR	0.23	0.19	-0.07	0.06	-0.23	0.61**	0.12	0.15	1				
EW	-0.25	-0.26	0.18	0.22	0.26	0.45**	0.61**	0.47**	0.42**	1			
EA	0.19	0.23	-0.29	-0.37	-0.28	-0.21	-0.32*	-0.03	-0.19	-0.38*	1		
TGW	0.18	0.18	0.08	0.07	0.13	-0.06	-0.03	0.11	0.07	-0.03	-0.07	1	
GY	-0.24	-0.24	0.21	0.26	0.19	0.50**	0.60**	0.39**	0.42**	0.93**	-0.34*	0.001	1

AD: Days to anthesis, SD: Days to silking, PH: plant height (cm), EH: Ear height (cm), NOL: number of leaves, EL: ear length (cm), ED: ear diameter(cm), NKPRE: number of kernel rows /ear, NKPR: number of kernel /row, EW: ear weight (g), EA: Ear aspect, TGW: Thousand grain weight (g), GY: Grain yield (t/ha).

Path analysis:

Correlation coefficients were partitioned into direct and indirect effects through path analysis.

Table	4:	Path	coefficient	analysis	showing	the	direct	and	indirect	effect	of	different
	ch	aracte	r on grain y	ield of m								

	AD	SD	PH	EH	NOL	EA	EL	ED	NKRP	NKPR	EW	TGW
									E			
AD	-0.137	0.101	-0.0011	-	0.050	-	-	-0.0066	-0.013	0.0005	-0.20	0.0030
				0.0031		0.00051	0.0088					
SD	-0.136	0.102	-	-	0.048	-	-	-0.0066	-0.011	0.0010	-0.19	0.0026
			0.00083	0.0039		0.00061	0.0072					
PH	-0.017	0.0095	-0.012	0.081	0.025	0.00018	-0.012	0.0054	-0.058	0.0032	0.18	0.0031
EH	0.0048	-	0.009	0.107	0.026	0.00044	-0.017	0.0058	-0.048	-	0.22	-0.0026
		0.0045								0.0024		
NOL	0.040	-0.028	-0.0041	0.0401	0.0724	0.00072	-0.001	0.0083	-0.039	0.0094	0.264	-0.0022
EA	-0.027	0.024	0.00063	-	0.047	-0.0025	-	-0.017	-	0.0146	-	0.0016
				0.0151			0.0139		0.00955		0.425	
EL	0.015	-0.009	-0.0024	0.0306	0.0022	0.00044	-0.062	0.00751	-0.045	-0.025	0.450	-0.0037
ED	0.019	-0.014	-0.0027	0.0259	0.0249	0.00097	-0.019	0.0242	-0.074	-	0.60	-0.0049
										0.0050		
NKR	0.030	-0.020	-0.0039	0.0298	0.016	0.00042	-0.016	0.0102	-0.176	-	0.462	-
PE										0.0064		0.00016
NKP	0.0012	-	0 00094	0.0064	-	0.00071	-	0.00296	-0.027		0416	-
R		0.0019	0.000071	0.0001	0.0167		0.0381	0.00270	0.027	0.0410	0.110	0.00078
EW	0.031	-0.022	-0.0022	0.0242	0.010/	0.00126	-0.028	0.01/18/	-0.083		0.08	-0.0054
			-0.0022	0.0242	0.0174		-0.028	0.01404	-0.005	-	0.70	
TGW	_	0.019	0.0019	_	0.0279	_	-0.021	-0.016	_	0.0173	-0.34	0.014
10 W	-	0.019	0.0019	-	0.0279	-	-0.021	-0.010	-	0.0050	-0.54	0.014
	0.0298			0.0105		0.00050			0.00008			

AD: Days to anthesis, SD: Days to silking, PH: plant height (cm), EH: Ear height (cm), NOL: number of leaves, EL: ear length (cm), ED: ear diameter (cm), NKPRE: number of kernel rows/ear, NKPR: number of kernel /row, EW: ear weight (g), EA: ear aspect, TGW: Thousand grain weight (g), GY: Grain yield (t/ha).

The highest value for direct and positive effect on grain yield was found on ear weight and the lowest value for direct and positive effect on grain yield was found on ear diameter. Similar results were found by Eleweanya *et al.* (2005). Cob weight had positive indirect effects on grain yield through ear diameter, number of kernel rows per ear, ear length, No. of kernel per row, number of leaves, ear height, plant height, number of cobs.

CONCLUSION

The GCV value estimates were less than its corresponding PCV value for all the traits examined, which means a significant role of environment in the expression of these traits. High heritability estimates were found for traits plant height, ear height, anthesis days, silking days. Highest genetic advance mean was followed by ear aspect, thousand grain weight, ear height, plant height respectively. The dominance of additive gene effects controlling a trait usually resulted in both higher heritability and genetic advance whereas those governed by non-additive gene actions could give high heritability with low genetic advance. Grain yield was found to be positively correlated with the plant height, ear height, no. of leaves, ear length, ear diameter, no. of kernel row per ear, no. of kernel per ear, cob weight and thousand grain weights. In general, the results obtained in this study indicated the existence of genetic variability in the maize genotypes studied and this could be exploited in the future maize breeding program.

References

- Babu, R., Nair, S.K., Kumar, A., Venkatesh, S., Sekhar, J.C., Singh, N.N., Srinivasan, G., & Gupta, H.S. (2005).Two-generation marker-aided backcrossing for rapid conversion of normal maize lines to quality protein maize (QPM). *Theoretical and Applied Genetics*, 111(5), 888-897. DOI: 10.1007/s00122-005-0011-6.
- Baye, A., Berihun, B., Bantayehu, M., & Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food and Agriculture*, 6(1), 1752603. DOI: 10.1080/23311932.2020.1752603
- Bhusal, T., Lal, G.M., Marker, S., & Synrem, G.J. (2017). Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plants and Soil Research*, 19(1), 59-65.
- Boćanski, J., Srećkov, Z., & Nastasić, A. (2009). Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). *Genetika*, 41(2), 145-154. DOI: https://doi.org/10.2298/GENSR0902145B
- Burton, G.W. (1952). Quantitative inheritance in grasses. Pro VI Int Grassl Cong, 1952, 277-283.
- Carangal, V.R., Ali, S.M., Koble, A.F., Rinke, E.H., & Sentz, J.C. (1971). Comparison of S1 with testcross evaluation for recurrent selection in Maize 1. *Crop Science*, *11*(5), 658-661. DOI: https://doi.org/10.2135/cropsci1971.0011183X001100050016x
- Choudhary, P., & Chaudhary, D.P. (2020). Comparison of Protein Composition of Normal and Quality Protein Maize. *Int. J. Curr. Microbiol. App. Sci*, 9(12), 3297-3302. DOI: 10.20546/ijcmas.2020.912.392
- Chowdhary, A.K., & Chaudhari, L.B. (2002). Genetic studies in some crosses of maize (Zea mays L.). Journal of research-Birsa agricultural university, 14(1), 87-90.

- Chukwudi, U.P., Efusie, A.A., & Muojiama, S.O. (2018). Field evaluation of yield and yield component traits of breeding lines of maize over two seasons in derived Savannah agro-ecology. *Notulae Scientia Biologicae*, *10*(4), 567-574.
- Derby, N.E., Casey, F.X., Knighton, R. E., & Steele, D.D. (2004). Midseason nitrogen fertility management for corn based on weather and yield prediction. *Agronomy journal*, 96(2), 494-501.
- Dewey, D.R., & amp; Lu, K. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. Agronomy journal, 51(9), 515-518. DOI: https://doi.org/10.2134/agronj1959.00021962005100090002x
- Eleweanya, N.P., Uguru, M.I., Ene-Obong, E.E., & Okocha, P.I. (2005). Correlation and pthat coefficient analysis of grain yield related chatacters in maize (*Zea mays* L.) under umudikecondtitions of south eastern Nigeria. *Agro-Science*, 4(1). DOI: 10.4314/as.v4i1.1517
- Falconer, D.S., & Mackay, T.F.C. (1996). Introduction to quantitative genetics. Longman Group, Essex, UK. *Introduction to quantitative genetics. 4th ed. Longman Group, Essex, UK*.
- Ghimire, B., & Timsina, D. (2015). Analysis of yield and yield attributing traits of maize genotypes in Chitwan, Nepal. *World Journal of Agricultural Research*, *3*(5), 153-162. DOI:10.12691/wjar-3-5-2
- Gibbon, B.C., & Larkins, B.A. (2005). Molecular genetic approaches to developing quality protein maize. *Trends in Genetics*, 21(4), 227-233. DOI: 10.1016/j.tig.2005.02.009.
- Gomez, K.A., & Gomez, A.A. (1984). Statistical procedures for agricultural research. John wiley& sons.
- Govind, K. C., Karki, T.B., Shrestha, J., & Achhami, B.B. (2015). Status and prospects of maize research in Nepal. *Journal of maize research and development*, *1*(1), 1-9. DOI: 10.3126/jmrd.v1i1.14239.
- Holding, D.R., Hunter, B.G., Klingler, J.P., Wu, S., Guo, X., Gibbon, B.C., & Larkins, B.A. (2011). Characterization of opaque2 modifier QTLs and candidate genes in recombinant inbred lines derived from the K0326Y quality protein maize inbred. *Theoretical and applied genetics*, 122(4), 783-794. DOI: 10.1007/s00122-010-1486-3.
- Jaliya, M.M., Othman, M.K., Sani, B.M., Babaji, B.A., Sani, Y.A., & Zongoma, A.M. (2015). Nitrogen and sulfur absorption by quality protein maize (QPM) maize as affected by interaction between nitrogen and sulfur fertilizers at Samaru, Zaria, Nigeria. *African Journal of Agricultural Research*, 10(28), 2687-2694. DOI: 10.5897/AJAR2015.9499
- Jan, M.T., Shah, P., Hollington, P.A., Khan, M.J., & Sohail, Q. (2009). Agriculture research: design and analysis, a monograph. *NWFP Agric. Univ. Pesh. Pak*, *1*, 232.
- Johnson, H.W., Robinson, H.F., & Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, 47(7), 314-318.
- Kandel, B.P., & Shrestha, K. (2020). Performance evaluation of maize hybrids in inner-plains of Nepal. *Heliyon*, 6(12), e05542. https://doi.org/10.1016/j.heliyon.2020.e05542
- Kandel, B.P., Poudel, A., Sharma, S., & Subedi, M. (2017). Variability studied in yield attributing traits of early maize genotypes in western hill of Nepal. *Nepalese Journal of Agricultural Sciences*, 15, 13-18.
- Kandel, B.P., Sharma, B.K., Sharma, S., & Shrestha, J. (2018). Genetic variability, heritability and genetic advance estimate in maize (*Zea mays*) genotypes in Nepal. *Agricultura*, 107(3-4), 29-35.

- Kandel, M., Ghimire, S.K., Ojha, B.R., & Shrestha, J. (2018). Correlation and path coefficient analysis for grain yield and its attributing traits of maize inbred lines (*Zea mays L.*) under heat stress condition. *International Journal of Agriculture Environment and Food Sciences*, 2(4), 124-130. https://doi.org/10.31015/jaefs.18021
- Kumar, B., Guleria, S.K., Khanorkar, S.M., Dubey, R.B., Patel, J., Kumar, V., Parihar, C.M., Jat, S.L., Singh, V., Yatish, K.R., & Das, A. (2016). Selection indices to identify maize (*Zea mays L.*) hybrids adapted under drought-stress and drought-free conditions in a tropical climate. *Crop and Pasture Science*, 67(10), 1087-1095. https://doi.org/10.1071/CP16141
- Mafouasson, H.N.A., Gracen, V., Yeboah, M.A., Ntsomboh-Ntsefong, G., Tandzi, L.N., & Mutengwa, C.S. (2018). Genotype-by-environment interaction and yield stability of maize single cross hybrids developed from tropical inbred lines. *Agronomy*, 8(5), 62. https://doi.org/10.3390/agronomy8050062
- Miller, P.A., Williams Jr, J.C., Robinson, H.F., & Comstock, R.E. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection 1. Agronomy journal, 50(3), 126-131. DOI: https://doi.org/10.2134/agronj1958.00021962005000030004x
- MoF- Economic Survey. 2020/21. Economic survey fiscal year 2020/21 (2077/78). Government of Nepal, Ministry of Finance, Singhadurbar, Kathmandu, Nepal. Retrived on 9 December 2021.
- Mohana Krishna, D., Reddy, D.M., Reddy, K.H.P., & Sudhakar, P. (2009). Character association and interrelationship of yield and quality attributes in rice (*Oryza sativa* L.). *The Andhra Agric. J*, *56*(3), 298-301.
- Olakojo, O.O., Bankole, F., & Ogunniyan, D. (2021). Correlation, regression and cluster analyses on yield attributes and popping characteristics of popcorn (*Zea mays* L. everta) in derived savanna and rainforest agro-ecologies of Nigeria. *Acta agriculturaeSlovenica*, 117(3),1-11. DOI: http://dx.doi.org/10.14720/aas.2021.117.3.1625
- Olawamide, D.O., & Fayeun, L.S. (2020). Correlation and path coefficient analysis for yield and yield components in late maturing provitamin a synthetic maize (*Zea mays* L.) breeding lines. *J Exp Agric Int*, 42, 64-72.
- Pajić, Z. (2007). Breeding of maize types with specific traits at the Maize Research Institute, Zemun polje. *Genetika*, 39(2), 169-180. DOI: 10.2298/GENSR0702169P
- Panse, V.G., & amp; Sukhatme, P.V. (1954). Statistical methods for agricultural workers. Statistical methods for agricultural workers.
- Sapkota, M., & Joshi, N. P. (2021). Factors Associated with the Technical Efficiency of Maize Seed Production in the Mid-Hills of Nepal: Empirical Analysis. *International Journal of Agronomy*, 2021. https://doi.org/10.1155/2021/5542024
- Sharma, H.P., Dhakal, K.H., Kharel, R., & Shrestha, J. (2016). Estimation of heterosis in yield and yield attributing traits in single cross hybrids of maize. *Journal of Maize Research and Development*, 2(1), 123-132.
- Shrestha, J., Yadav, D.N., Amgain, L.P., & Sharma, J.P. (2018). Effects of nitrogen and plant density on maize (*Zea mays* L.) phenology and grain yield. *Current agriculture research Journal*, 6(2), 175-182.
- Singh, D., Kumar, A., Kumar, R., Kushwaha, N., Mohanty, T. A., & Kumari, P. (2020). Genetic variability analysis of QPM (*Zea mays L.*) inbreds using morphological characters. *International Journal Current Microbiology Applied Science*, 9(2), 328-338. DOI: 10.20546/ijcmas.2020.902.042

- Sravan, T., Rangare, N.R., Suresh, B.G., & Kumar, S.R. (2012). Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *Journal of Rice Research*, 5(1), 2.
- Tesfaye, S., & Sime, B. (2021). Heterosis of Highland Maize (*Zea mays* L.) Hybrids for Grain Yield and Yield Related Components. DOI: 10.36349/easjbg.2021.v03i02.003
- Tiwari, D.N., Tripathi, S.R., Tripathi, M.P., Khatri, N., & Bastola, B.R. (2019). Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Advances in Agriculture, 2019. https://doi.org/10.1155/2019/5975901
- UPOV (2009). Guidelines for the conduct of tests for distinctness, uniformity and stability; maize. TG/2/7. UPOV, Geneva, Switzerland.
- Wedwessen, T., & Zeleke, H. (2020). Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *International Journal of Novel Research in Life Sciences*, 7(2), 10-16.