

Variability, correlation and path coefficient analysis in Maize (*Zea mays* L.) genotypes in Baitadi, Nepal

Pratima Pahadi¹ and Manoj Sapkota^{2*}

¹Gokuleshowar Agriculture and Animal Science, Tribhuvan University, Baitadi, Nepal Postal code: 10202, Nepal; ²Institute of Agriculture and Animal Science, Tribhuvan University, Chitwan, Nepal Postal code: 44209, Nepal.

***Corresponding Author:** manoj34sapkota@gmail.com

Abstract

Six maize genotypes were evaluated in three replicated randomized block from July-October, 2015 to assess the association among yield components, correlation and variability. Days to tasseling (DTT), days to silking (DTS), days to pollen shed anthesis (DTPSA), ear height (EH), ear length (EL), ear circumference (EC), silk length (SL), plant height (PH), number of kernels row per ear (NKRPE) and number of kernels per row (NKPR) and grain yield per plant (GYPP) were recorded. The genotypes significantly differed in all traits except EH and GYPP. EH (0.222), SL (0.189), PH (0.304), EC (0.419), NKRPE (0.310) and NKPR (0.399) had positive correlation with grain yield per plant. Similarly, DTT (-0.185), DTS (-0.324) and EL (-0.150) had negative correlation with GYPP. Path coefficient analysis showed that NKRPE (0.752) had highest positive and direct contribution on GYPP followed by DTT (0.385), PH (0.351), NKPR (0.298), SL (0.071) and EL (0.044). DTS (-1.384) had highest direct negative effect on GYPP followed by EH (-0.393) and EC (-0.136). The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all characters; difference of which was high in SL and EH indicating these traits are affected by environment as well. NKRPE, NKPR, DTT, DTS, PH, SL and EL had highest positive direct contribution on grain yield, which are the pre-requisites for attaining improvement in yield of maize genotypes.

Keywords: Correlation, maize, *Zea mays*, path coefficient, variability.

Introduction

Maize is one of the most important food crops in the world. Superior position of maize is due to its very wide and variety utilization (Bekric and Radosavljevic, 2008).

Maize is an integral crop of hill farming system and can be grown both under and irrigated conditions. It is the second most important crop of Nepal in terms of areas and forms the most important staple cereal

of the Hills. After paddy, maize is the second important cereal crop of Nepal in terms of area, production and productivity (MoAD, 2014). At present, maize grown area in Nepal is 9, 28, 761 ha with a total production of 22, 83, 222 metric tons and productivity of 2458 kg/ha (MoAD, 2014).

Path coefficient analysis has been widely used in crop breeding to determine the nature of relationship between grain yield and its contributing components, and to identify those components with significant effect on yield for potential use as selection criteria (Puriet *al.*, 1982; Kang *et al.*, 1983; Milligan *et al.*, 1990; Williams *et al.*, 1990; Board *et al.*, 1997; Samonte *et al.*, 1998). Path analysis should direct and indirect effect of cause variables on effect variables. In this method, the correlation coefficient between two traits is separated into the components which measure the direct and indirect effects (Farshadfar, 2004). Generally this method provides more information among variables than do correlation coefficients. Since this analysis provides the direct effect of specific yield components on yield, and indirect effect via other yield components. (Garcia del Moral *et al.*, 2003; Arshad *et al.*, 2006). The study of correlation and direct and indirect effects of yield components provides the basis for successful breeding plan (Choudhry *et al.*, 1968).

The purpose of this study therefore, was to estimate correlation between yield attributing traits as well as the direct and indirect effects of these traits on yield. The information so derived could be exploited in devising further breeding strategies and select procedures to develop new varieties of maize capable of high productivity.

Materials and Methods

Research site

The field experiment was conducted at the research field of Gokuleshowar Agriculture and Animal Science College (GAASC) in the academic year of 2015 from July 24, 2015 to October 29, 2015. It is located at an elevation of 700 meters above mean sea level. The experimental material was collected from National Maize Research Program (NMRP), Rampur and agrovet of Chitwan. In total, six maize genotypes (Table 1) were included in the study. Out of which, 5 were advanced maize genotypes from NMRC, Rampur, Chitwan and one check variety (NANO) from Baitadi. The experiment was laid out in randomized block design with three replications. There were six treatments within a replication and twenty seeds of same genotypes within a treatment. There were total of 18 plots and the plot size was $2.25 \text{ m} \times 1.25 \text{ m} = 2.8125 \text{ m}^2$ each. The row spacing of each treatment for maize sowing was 75 cm and there were four rows per plot. The spacing between two plot was 50 cm and inter spacing between two replications was 1 m.

Ten plants were selected randomly for each observation in each treatment without tagging. Data were collected for different quantitative agronomic characters as per the genotypes. Days to tasseling, days to silking, days to pollen shed anthesis, ear height, silk length, plant height, ear length, ear circumference, number of kernel row per ear, number of kernel per row and grain yield per plant were recorded.

On the basis of individual plant observations, the population mean for each character was computed. The analysis of variance for different characters was carried out by using the mean data for each

location separately in order to partition the variability due to different sources. The method given by Andreas et al. (2007) was followed. The genotypic and phenotypic coefficient of variation was computed according to and expressed as percentage.

$$\text{Genotypic coefficient of variation (GCV)} = \left(\frac{\sigma_g}{\bar{X}}\right) \times 100$$

$$\text{Genotypic coefficient of variation (PCV)} = \left(\frac{\sigma_p}{\bar{X}}\right) \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

\bar{X} = General mean of the trait

In the above case, PCV and GCV values were categorized as low, moderate and high indicated by Sivasubramanjan and Menon (1973) as follows:

0 – 10 % = Low

10 – 20 % = Moderate

>20 % = High

The broad sense heritability estimated as the ratio of genotypic variance (V_g) to the phenotypic variance (V_p) and expressed in percentage (Hanson et al., 1956).

$$\text{Broad sense heritability } (h_{bs}^2) = \left(\frac{V_g}{V_p}\right)$$

The heritability percentage categorized as low, moderate and high as followed by (Robinson et al., 1949) as follows:

0 – 0.30: Low

0.30 – 0.60: Moderate

> 0.60: High

The extent of genetic advance to be expected by selecting about five percent of the genotypes was calculated by using the following formula given by Robinson et al., (1949).

$$GA = i \cdot \sigma_p \cdot h_{bs}^2$$

Where,

i = Efficacy of selection which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h_{bs}^2 = Broad sense heritability

GA as per cent of mean (GAM) =

$$\left(\frac{GA}{\bar{X}}\right) \times 100$$

GA = Genetic advance

\bar{X} = General mean of the trait

The GA as percent of mean was categorized as low, moderate and high as suggested by Johnson et al. (1955).

0 - 10 %: Low

10 -20 %: Moderate

> 20 %: High

Results and Discussion

Mean performance

Significant variation was found among the studied genotypes for days to tasseling, days to silking, days to pollen shed anthesis, silk length, plant height, ear length, number of kernel rows per ear and number of kernels per row. The mean value of all the studied traits are presented in Table 2.

Estimates of genetic parameters

The estimated genetic parameters PCV, GCV, h^2 and GAM for different traits are presented in Table 3.

The considerable differences in heritability were observed for different characters. Among the traits number of kernel row/ear (0.886), days to pollen shed anthesis (0.809), days to silking (0.789), ear length (0.784), ear circumference (0.773) and number of kernel/row (0.681) had high heritability. Days to tasseling (0.587), silk length (0.575) and plant height (0.456) had moderate heritability whereas low

heritability was exhibited by Ear height (0.277) and grain yield per plant (0.005).

Genetic advance as percentage of mean was observed to be high for silking length (27.34%) and moderate was found to be for number of kernel row per ear (18.99%) followed by number of kernel per row (16.19%), ear circumference (11.72%) and ear length (11.08%). Low genetic advance as percentage of mean was observed for days to anthesis (8.21%), days to silking (6.68%), days to tasseling (6.75%), plant height (5.80%), ear height (4.01%) and grain yield per plant (0.240%).

Considerable differences were found in PCV values for different traits. Of the measured traits, silk length and grain yield per plant had higher PCV as compared to other traits and the PCV values for silk length, grain yield per plant, number of kernel row per ear, number of kernel per row were 23.07, 20.77, 10.40 and 11.53, respectively. The traits having lower PCV were days to tasseling (5.58), days to silking (4.11), days to pollen shed anthesis (4.92), ear height (7.00), plant height (6.16) and ear length (6.85), ear circumference (7.36).

Similar to PCV, considerable differences were found in GCV values for different traits. Grain yield per plant (20.77) only had high GCV and moderate GCV was found to be of silking length (17.50).

Remaining all the traits had low GCV as days to tasseling (4.28), days to silking (3.65), days to pollen shed anthesis (4.43), ear height (3.69), plant height (4.16), ear length (6.07), ear circumference (6.47), number of kernel row/ear (9.79) and number of kernel/row (9.52).

Correlation coefficient analysis

Pearson's correlation coefficients between different studied traits are presented in table 4.

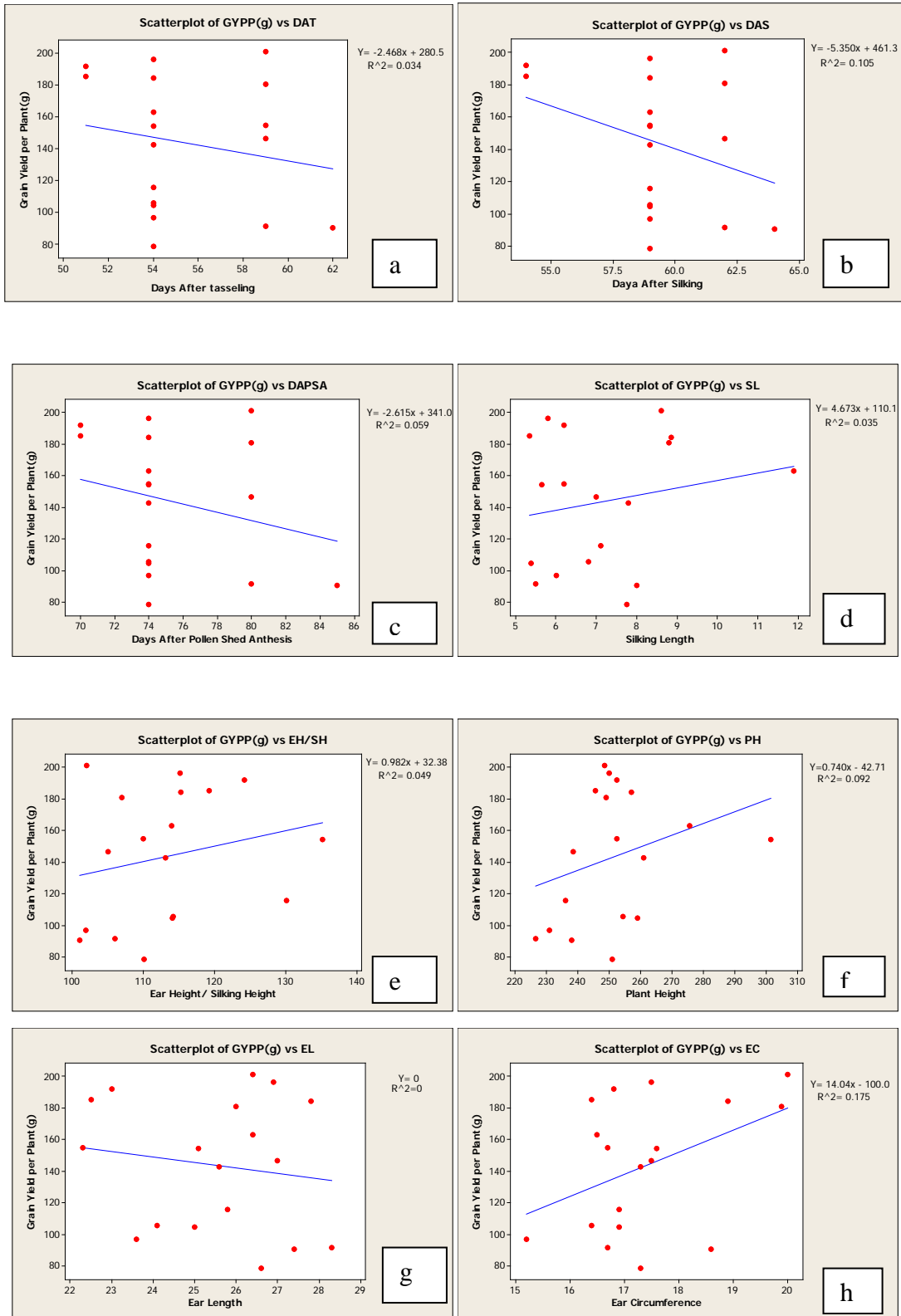
Positive significant correlation was observed among DTT with DTS, EC and NKRE, whereas it was found significantly negatively correlated with EH. DTS was observed to be positively and significantly correlated with EL and NKRE, whereas negative significant correlation was seen with EH. EH had positive and significant correlation with PH. SL had positive and significant correlation with NKR. EL had positive and significant correlation with EC, NKRE and NKR. EC was also positively and significantly correlated with NKRE and NKR. NKRE was found to be positively and significantly correlated with NKR. The GYPP was not found to be correlated in significant way with any of the traits studied.

The linear correlation between different eleven grain yield attributing traits and grain yield per plant are represented in the scatter plots (Figure 1a-1k). The scatter plots give a vague idea about the presence or absence of correlation and nature (positive or negative correlation). The R^2 value indicates the coefficient of determination.

Path analysis

Path coefficient analysis using grain yield per plant as dependent variable and days to tasseling, days to silking, ear height, silk length, plant height, ear length, ear circumference, number of kernel row per ear, and number of kernel/row as independent variables is presented in Table 5. The highest (0.30-0.99) positive direct effect on grain were exhibited by number of

Figure 1. Scatter plots of 11 traits of maize genotypes with grain yield per plant.



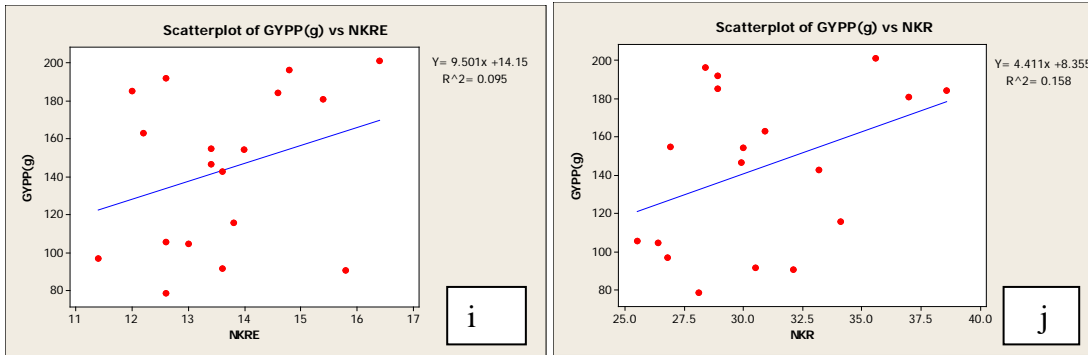


Table 1. List of the genotypes under study.

Genotype Entry	Cross Name	Origin
1	Khumal Rato	Agriculture Botany Division National Agricultural Research Council
2	Rampur Yellow	National Maize Research Program, Rampur
3	Khumal Yellow	Agriculture Botany Division National Agricultural Research Council
4	CP808	Foreign Germplasm
5	Local (NANO)	Baitadi
6	Rajkumar	Foreign Germplasm

Table 2. Mean Performance of the Six Genotypes with their CV and Significance test value.

Genotype	DTT	DTS	DTPSA	EH/SH	SL	PH	EL	EC	NKRE	NKR	GYPP(g)
Khumal Rato	55.67b	59.00b	74.00bc	119.81	5.74c	271.00a	25.00b	17.06bc	13.46b	27.76c	137.82
Rampur Yellow	52.00b	55.66c	71.33c	115.16	5.85bc	243.00bc	25.00b	16.13c	12.00c	28.20c	158.08
Khumal Yellow	55.67b	60.00b	76.00b	117.10	6.13bc	237.50c	25.00a	17.03bc	14.06b	31.00bc	134.46
CP808	60.00a	62.67a	81.66a	103.40	8.46a	245.16bc	25.00a	19.50a	15.86a	34.90a	157.45
Local (NANO)	54.00b	59.00b	74.00bc	112.78	8.81a	260.33ab	25.00a	16.73bc	12.46c	28.16c	115.74
Rajkumar	55.67b	60.00b	76.00b	111.13	7.88ab	252.16abc	25.00a	17.90b	13.86b	33.9ab	157.93
Mean	55.5	59.38	75.5	113.23	7.14	251.52	25.54	17.39	13.62	30.65	143.58
CV	3.58%	1.88%	2.14%	5.95%	15.03%	4.54%	3.18%	3.50%	3.51%	6.50%	20.72%
F	*	***	***	-	*	*	***	***	***	**	-

Means followed by the same letter (s) within a column are non-significantly different from each other according to Duncan's Multiple Range. DTT = Days to tasseling, DTS = Days to silking, DTPSA= Days to pollen shed anthesis, EH = Ear height, SL = Silk length, PH = Plant height, EL = Ear length, EC = Ear circumference, NKRE = Number of kernel row per ear, NKR = Number of kernel per row, GYPP (g) = Grain yield per plant.

Table 3. Estimation of genetic parameters for quantitative and yield attributes traits of maize.

	PCV	GCV	h ²	GAM
Days to tasseling	5.58	4.28	0.587	6.75
Days to silking	4.11	3.65	0.789	6.68
Days to pollen shed anthesis	4.92	4.43	0.809	8.21
Ear height	7.00	3.69	0.277	4.01
Silk length	23.07	17.50	0.575	27.34
Plant height	6.16	4.16	0.456	5.80

Ear length	6.85	6.07	0.784	11.08
Ear circumference	7.36	6.47	0.773	11.72
Number of kernel row/ear	10.40	9.79	0.886	18.99
Number of kernel/row	11.53	9.52	0.681	16.19
Grain yield per plant	20.77	20.77	0.005	0.240
PCV= Phenotypic coefficient of variation; h ² = Broad sense heritability; GCV= Genetic coefficient of variation; GAM= Genetic advance as percentage of mean.				

Table 4. Correlation Coefficients of ten traits for Grain Yield per Plant in advanced maize genotypes.

	DTT	DTS	EH	SL	PH	EL	EC	NKRE	NKR	GYPP (g)
DTT	1									
DTS	0.890**	1								
EH	-0.653**	-0.603**	1							
SL	0.188	0.303	-0.23	1						
PH	-0.337	-0.236	0.577*	0.201	1					
EL	0.447	0.693**	-0.288	0.403	-0.129	1				
EC	0.507*	0.516*	-0.217	0.41	0.09	0.499*	1			
NKRE	0.634**	0.636**	-0.211	0.234	-0.017	0.542*	0.900**	1		
NKR	0.276	0.346	-0.042	0.557*	-0.007	0.529*	0.771**	0.667**	1	
GYPP (g)	-0.185	-0.324	0.222	0.189	0.304	-0.15	0.419	0.31	0.399	1

DTT= Days to tasseling, DTS= Days to silking, DTPSA= Days to pollen shed anthesis, EH= Ear height, SL= Silk length, PH= Plant height, EL= Ear length, EC = Ear circumference, NKRE= Number of kernel row per ear, NKR= Number of kernel per row, GYPP (g) = Grain yield per plant.

Table 5. Path Analysis Matrix of direct and indirect effects of ten traits on grain yield per plant of advanced maize genotypes.

	DTT	DTS	EH/SH	SL	PH	EL	EC	NKRE	NKR
Via DTT	0.385468	0.343068	-0.2518	0.072398	-0.12998	0.172326	0.195546	0.244355	0.106273
Via DTS	-1.23173	-1.38396	0.834672	-0.41958	0.327266	-0.95973	-0.71462	-0.87994	-0.47924
Via EH	0.256402	0.236729	-0.39252	0.090227	-0.22631	0.11322	0.085114	0.082629	0.01631
Via SL	0.013376	0.021591	-0.01637	0.071216	0.01434	0.028727	0.029202	0.01669	0.039685
Via PH	-0.11823	-0.08291	0.202151	0.070602	0.350617	-0.04539	0.031443	-0.00579	-0.00243
Via EL	0.01968	0.030527	-0.0127	0.017757	-0.0057	0.044021	0.021966	0.02386	0.023298
Via EC	-0.06911	-0.07034	0.029539	-0.05586	-0.01222	-0.06798	-0.13623	-0.12267	-0.10501
Via NKRE	0.476558	0.477981	-0.15825	0.176179	-0.01242	0.407468	0.676958	0.751768	0.501675
Via NKR	0.08215	0.103183	-0.01238	0.166042	-0.00207	0.157703	0.229695	0.198844	0.297971
Total	-0.18543	-0.32414	0.222344	0.188981	0.303532	-0.14963	0.419078	0.309746	0.398524

The numbers on the bold face are positive direct effects where as values in the off diagonal or columns show indirect effects on grain yield per plant. DTT= Days to tasseling, DTS= Days to silking, DTPSA= Days to pollen shed anthesis, EH= Ear height, SL= Silk length, PH= Plant height, EL= Ear length, EC= Ear circumference, NKRE= Number of kernel row per ear, NKR= Number of kernel per row. High= 0.30-0.99, moderate= 0.20-0.29, low= 0.10-0.19.

kernel row per ear (0.751768) followed by days to tasseling (0.385468) and plant height (0.350617). Parimala et al., (2011) and Kumar *et al.* (2011) also found direct effect on plant height and number of kernel row per ear.

Simple correlation coefficients revealed that the association of grain yield per plant with ear height, silk length, plant height, ear circumference, number of kernel row per ear and number of kernel per row had positive relationship. Whereas, grain yield per plant had negative relation with days to tasseling, days to silking and ear length.

Besides, path analysis explains positive and direct effect of number of kernel row per ear followed by days to tasseling, plant height, number of kernel per row, silking length and ear length. This indicates these traits must be considered during selection to improve the grain yield of maize genotypes. Whereas, ear circumference, ear height and days to silking exhibited negative direct effect on the grain yield. Thus, for increasing the grain yield through selection for these traits, the indirect positive yield attributing traits must be considered simultaneously in selection breeding.

From the study of genetic parameters, it was found that number of kernel row per ear, ear length, ear circumference, number of kernel per row had high heritability with high genetic advance as percentage of mean indicating that these traits are effective for selection. Moderate heritability with high genetic advance as percentage of mean was observed for, silk length indicating that this trait was prominent variable for selection for higher grain yield based on these traits.

As revealed from Simple correlation coefficient association of grain yield per plant with ear height, silking length, ear circumference, number of kernel row per ear and number of kernel per row had positive relationship. From the path coefficient number of kernel row per ear and number of kernel per row were the most yield determinative traits. From the genetic parameters number of kernel row per ear, number of kernel per row and ear circumference had high heritability with high genetic advance as percentage of mean which means that these traits are highly heritable. Thus, indirect selection of yield determinative secondary traits such as number of kernel row per ear, number of kernels per row and ear circumference for improvement of yield will be impressive and effective.

Acknowledgement

Authors are thankful to Associate Professor Ganga Ram Kohar, Institute of Agriculture and Animal Science and Assistant Professor Raju Kharel, Agriculture and Forestry University for their guidance, support and comments that greatly improved the manuscript. The authors would also like to show their sincere gratitude to Dr. Dhruva Bahadur Thapa, Wheat Breeder, Nepal Agriculture Research Centre for sharing his pearls of wisdom during the course of this research. The authors are thankful to Mukti Poudel and Saraswati Kadel for their regular insights and are also immensely grateful to Kabita, Smriti and Sadikshya and other colleagues for their comments and support.

References

- Andreas, B., Krajewski, P., Kristensen, K. and Pilarczyk, G. (2007). Trial setup and statistical analysis. Suvar Handbook.
- Arshad, M. (1985). Correlation and path coefficient analysis of grain yield with some morphological characters in wheat. M.Sc. Thesis, Deptt. Pl. Br. Genet., Univ. Agric., Faisalabad–Pakistan
- Bekrić, V. and Radosavljević, M. (2008). Savremeni pristup i upotreba kuruza. PTEP 12:93-96.
- Board, J.E., Kang, M.S. and Harville, B.G., (1997). Path analyses identify indirect selection criteria for yield of late-planted soybean. *Crop. Sci.* 37: 879-884
- Chaudhary, L.B. and Prasad, B. (1968). Genetic variation and heritability of quantitative characters in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Science.* 38: 820-825.
- Farshadfar, E. (2004). Multivariate principles and procedures of statistics. Taghbostan Pub. Kermanshah, Iran. Pp.734.
- Garcia, Del Moral, L.F., Rharrabti, Y., Villegas, D. and Royo, C.(2003). Evaluation of Grain Yield and Its Components in Durum Wheat under Mediterranean Conditions. An Ontogenic Approach. *Agron. J.* 95: 266–274.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal.* 48(6): 268-272.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy journal.* 47(7): 314-318.
- Kang, M.S., Macus, S.Z. and Gary, F.K. (1983). Path coefficient analysis of grain yield and harvest grain moisture in maize. *Tropical Agric. (Trinidad).* 60:253-256.
- Kang, M. and Gorman, D. (1989). Genotype x Environment Interaction in Maize. *Agronomy Journal.* 81: 662-664.
- Kumar, V., Singh, P.K. and Gupta, A., (2011). Studies of genetic diversity in quality protein maize (*Zea mays* L.) inbreds. *Current Advances in Agricultural Sciences.* 3 (2): 96-99.
- Milligan, S.B., Gravois, K.A., Bischoff, K.P. and Martin F.A. (1990). Crop effects on genetic relationships among sugarcane traits. *Crop Sci.* 30: 927-931.
- MoAD (2014). Statistical Information on Nepalese Agriculture 2013/14. Singa Durbar, Kathmandu Nepal: Ministry of Agriculture and Development, Agri-Business Promotion and Statistics Division.
- Parimala, K., Raghu, B. and Reddy, A.V. (2011). Correlation and path analysis for yield and quality traits in maize (*Zea mays* L.). *Plant Arch.* 11 (2): 1045-1047.
- Puri, Y.P., Qualset, C.O. and Williams, W.A. (1982). Evaluation of yield components as selection criteria in barley breeding. *Crop Sci.* 22: 927-931.
- Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal.* Pp. 353.

Samonte, O.P.B., Wilson, L.T. and McClung, A.M. (1998). Path analyses of yield and yield related traits of fifteen diverse rice genotypes. *Crop Sci.* 38:1130-1136.

Sivasubramanjan, S., Menon, M.(1973). Heterosis and inbreeding depression in rice. *Advances in Agronomy.* 47: 85-140.

Williams, W.A., Jones, M.B. and Demment, M.W. (1990). A concise table for path analysis statistics. *Agron. J.* 82: 1022–1024