

Original Research Article

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Assessment of Genetic Variability and Trait Association in Maize (*Zea mays* L.) Genotypes for Growth and Yield under Alfisols of SAT Region

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Understanding the magnitude and pattern of genetic variability is important for developing superior genotypes with maximum yield potential. A field experiment of twelve maize genotypes was evaluated for growth, yield and yield attributing components during *kharif* and summer seasons of 2017 and 2018. The magnitude of genetic variability, heritability, genetic advance as a percent of mean, phenotypic and genotypic correlation of growth, yield and yield components was assessed. Pooled analysis of variation revealed that, among the maize genotypes, the differences for growth, biomass and yield traits were highly significant ($p < 0.01$), indicating the presence of considerable genetic variability. The range of PCV for all traits was higher (12.14-47.59%) as compared to the corresponding GCV (12.09-47.47%), revealing that there was an environmental impact on the performance of the genotypes. The grain yield was highly and positively correlated with total biomass, vegetative biomass, cob weight, kernel number and 100 kernel weight, therefore direct selection of these traits might bring an improvement in grain yield. However, higher estimate of GCV (%), H^2 (%) and GAM were recorded with total biomass (43.4, 99.7, and 89.4%), vegetative biomass (47.4, 99.5, 97.5%), cob weight (41.9, 99.6, 86.1%), and grain yield (38.3, 98.9, 78.6%) respectively. Therefore, maize genotypes with these high heritable traits associated with high estimate of GCV and GAM can serve as base population to develop superior maize cultivars.

Introduction

Maize (*Zea mays* L.) is the third most important cereal crop in the world after wheat and rice in terms of production. This crop is cultivated in 125 developing countries in a 100 million hectares due to its wide adaptability features (FAOSTAT, 2010). In 2018 India has attained 26 Mt of maize production and by 2022 it is projected that the

requirement as feed will be 30 Mt and another 15 Mt for food, seed and industrial use (FICCI's 'India Maize Summit' 2018). Although having the maximum productivity and production in the world as compared to other cereal crops, the demand for maize is assumed to be increased further by 2050 (Rosegrant *et al.*, 2009). Maize has huge diversity as it is cultivated across the world. Utilization of this diversity requires the assessment of variability

present in the base germplasm population. The diverse population will help in breeding programs for improving the tolerance to biotic, abiotic stresses as well as yield of the crop. Improvement of maize crop is determined by the magnitude of genetic variability coupled with heritability present in the population (Hussain *et al.*, 2011; Ullah *et al.*, 2012). Heritability estimates helps breeders to utilize as genetic resources effectively to select desired traits and to reach maximum genetic advantage with little time and resources (Falconer and Mackay, 1996; Smalley *et al.*, 2004).

Maize is an important cereal crop of the tropics and semi-arid tropics (SAT) and improvement of cereal production is a crucial requirement under changing climatic conditions (Cairns *et al.*, 2012). The importance of screening for variability before starting any breeding program was suggested and justified by many researchers (Lu *et al.*, 1994, Zhang *et al.*, 1995). Along with this, estimating association of traits to the yield is beneficial as it helps in selection of high yielding genotype based on highly correlated traits. A correlation study can also provide constant and helpful information about the type, scope, and direction of selection (Zeeshan *et al.*, 2013). The coefficient of correlations supports in determining the level of relationship between two separate traits as well as the level at which these traits are equally variable (Nagabhushan *et al.*, 2011). Grain yield can be increased by understanding the correlation relationship among yield and yield components and the type of association between them (Kalla *et al.*, 2001). Most of the studies suggested that phenotypic selection according to desirable traits with higher heritability with higher genetic advance as a percent of mean is effective for the success of breeding to develop superior maize genotypes. Therefore, searching for additional genetic variability and utilizing maximum genetic variability in the existing germplasm for selection will facilitate development of high yielding maize genotypes. A detailed analysis of genetic variability present in the genotypes of a crop and its estimation is essential for initiating any crop development program as well as assuming

appropriate selection techniques (Sravanti *et al.*, 2017). The main objective of the present study was to quantify the genetic variability, heritability, genetic advance as a percent of mean, phenotypic and genotypic correlation among the maize genotypes for growth, biomass, yield and yield contributing traits.

Materials and Methods

Out of twelve maize genotypes selected - three genotypes M-16 (R1HKI-46), M-22 (R1HKI-L-287), M-24 (R1LM6) were obtained from ICAR-IIMR, New Delhi; one genotype M-59 (NSJ-221) from ICAR-NBPGR, Hyderabad; five genotypes DTL-3, DTL-4, DTL-4-1, DTL-9 and DTL-11 from ICAR-CRIDA; and three popular maize genotypes DHM-117, Varun and Harsha from Maize Research Center, PJTSAU, Hyderabad. This study was carried out in the experimental site located at Hayathnagar Research Farm (HRF), ICAR- Central Research Institute for Dryland Agriculture (CRIDA), Hyderabad, Telangana, India during kharif and summer seasons of 2017 & 2018. Area is geographically situated at 17°19' 52.549" to 17° 21' 42.986" N latitude and 78° 35' 03.295" to 78° 36' 46.990" E longitudes. The soils (alfisols) are moderately deep, moderately acidic to near neutral in reaction, slightly alkaline, rich in iron oxides coatings on soil surfaces is reflected in their brown or red colour, which indicates that these soils are fairly well weathered and much of the deep profiles developed. A field experiment was laid down in a Randomized Complete Block Design (RCBD) with three replications. Each experimental plot was 6m² having 75x30 cm spacing. The recommended dose of fertilizers were applied @ 60 kg N ha⁻¹ and 60 kg P ha⁻¹, 30 kg K ha⁻¹ as basal dose; second dose of 30 kg N ha⁻¹ at knee-high stage and third dose of 30 kg N ha⁻¹ and 30 kg potassium ha⁻¹ was side dressed at tasselling stage. The crop was maintained pest and disease free by adopting recommended plant protection measures and irrigated as and when required to maintain adequate soil moisture. The weather data was taken from meteorological station near the experimental plots during *kharif* and

summer season, 2017 and 2018 (Table.1). The average temperature during crop growth period was more than 30.0°C and with a minimum of more than 20.0°C and maximum of 33.5°C in both years of *kharif* 2017 and 2018 respectively. During the crop growth period crop received 606 mm rainfall in 35 rainy days in 2017 *kharif*, while 331.2 mm rainfall in 22 rainy days in 2018 *kharif*. During the summer season of 2017 and 2018 the crop experienced the average temperature was more than 35.0°C with a minimum of around 28.0°C and maximum of more than 40.0°C. The crop received 25 mm rainfall in 4 rainy days in 2017 and 167.4 mm rainfall in 6 rainy days in 2018.

All the plant parameters were recorded on three plants randomly selected and representative of each experimental plot. The data on phenological parameters such as days to 50% tasselling, anthesis, silking, Anthesis silking interval (ASI) were recorded during both *kharif* and summer seasons of 2017 and 2018. At maturity, each genotype was uprooted carefully from each plot and data on morphological parameters such as plant height (cm), number of leaves, tassel length (cm), root length (cm), root volume (ml) and yield parameters such as cob weight (g), cob diameter (mm), cob length (cm), number of kernel rows per cob, kernel number, grain yield (g/pl) and 100 kernel weight (g) were recorded. Total biomass (g/pl), vegetative biomass (g/pl) and HI (%) were calculated from the recorded data sets. The data collected were subjected to standard methods of analysis of variance (Panse and Sukhatme, 1985). The phenotypic and genotypic coefficients of variability (GCV & PCV) (Singh and Chaudhary, 1985), broad sense heritability (H^2) (Johnson *et al.*, 1955), genetic advance as percent of mean (GAM) (Burton, 1952), phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955) were analysed. The experimental data were processed by using Excel 2010 and analysis of variance was computed according to the methods proposed by Gomez and Gomez (1984) using SAS 9.3 software. Selected genotypes were measured to be significant at ($p < 0.01$) and ($p < 0.05$) level of significance. Least significant difference test (LSD)

was used for evaluation of mean to identify the significant components of the treatment means (Sharma *et al.*, 2016).

Results and Discussion

Estimation of variability of traits in the population is prerequisite to initiate the varietal development programme. The pooled analysis of variance for morpho - phenological, biomass, yield and its related traits of twelve maize genotypes was presented in Table 2 and Table 3. The pooled ANOVA revealed that most of the traits in the selected maize genotypes significant differences recorded between genotypes (G), years (Y), seasons (S), and their combinations. For all the 19 traits highly significant ($p < 0.01$) differences were present in genotypes. Similarly, five traits namely plant height, total biomass, cob diameter, kernel number and grain yield showed highly significant ($p < 0.01$) variation between genotypes, years, seasons, and their combinations of Y x S, Y x G, S x G and Y x S x G, indicating the presence of considerable genetic variability, hence there is sufficient scope for improvement of these traits through selection. Similar findings of significant variability for various traits in the maize genotypes was also reported by many researchers (Kumar *et al.*, 2015; Kandel *et al.*, 2018). The estimates of mean, range, genotypic variance (σ^2_g), phenotypic variance (σ^2_p), environmental variance (σ^2_e), genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense heritability (H^2) and genetic advance (GA) of all twelve maize genotypes were calculated for growth, phenology, biomass, yield and yield attributes (Table 4). The results showed that total biomass ranged from 211.6 to 495.2 g/pl with a mean of 315.5 g/pl, vegetative biomass ranged from 98.0 to 225.9 g/pl with a mean of 136.8 g/pl, cob weight ranged from 113.6 to 269.2 g/pl with a mean of 178.6 g/pl, grain yield ranged from 58.0 to 127.9 g/pl with a mean of 98.9 g/pl and HI ranged from 24.7 to 37.2 % with a mean of 30.73%. However higher range of phenotypic coefficient of variation (PCV) (12.14 - 47.59%) as compared to the corresponding genotypic coefficient of variation

(GCV) (12.09-47.47%) was recorded for all traits suggesting that there was an environmental impact on the performance of these maize genotypes. Sivasubramanian and Menon (1973), categorized PCV and GCV of the traits assessed in their study into low (below 10%), moderate (10 - 20%) and high (above 20%). In the present study estimates of higher PCV and GCV were recorded with vegetative biomass (47.47, 47.59%), total biomass (43.46, 43.51%), root volume (42.76, 43.38), cob weight (41.92, 42.01%), grain yield (38.37, 38.58%) and ASI (35.89, 40.03%) indicating high variability for these traits among the genotypes, hence there is an ample scope for direct selection to improve these traits. Similar results were reported by Bhusal *et al.*, (2017) and Sharma *et al.*, (2018) in maize crop for higher variability in grain yield and ASI.

Medium variability was recorded with root length (17.28, 19.07%), plant height (15.91, 16.23%), leaf number (15.71, 17.67%), cob length (15.02, 16.75%) and cob dia (12.17, 13.33%) of selected maize genotypes, indicating increased genetic variability of these traits in base population is required for improvement. The remaining eight traits with lower variability need not to be considered in maize improvement programs. The presence of a significant genetic diversity is specified by GCV, but the amount of heritable variation can only be considered by using heritability estimates as well as genetic gain (Rao and Rao, 2015).

The broad sense heritability was highest for total biomass (99.7%) and cob weight (99.6%) followed by vegetative biomass (99.5%), kernel numbers

(99.6%), days to 50% anthesis (99.1%), days to 50% silking (99.1%), grain yield (98.9%) and HI (97.0%), while lower heritability was with number of kernel rows per cob (58.0%) (Table 4). The traits with high heritability provide scope for genetic improvement through selection, as these traits are less impacted by environment and there could be better correspondence between phenotypic and breeding values.

Similar findings of higher heritability for maize grain yield was also reported by Ghimire and Timsina (2015) and Jyothi Lakshmi *et al.*, (2020). Johanson *et al.*, (1955) and Udeh & Ogbu (2011) suggested that, relatively higher heritability associated with higher estimate of GCV and GAM need to be considered to ensure effective selection for improvement, as only high broad sense heritability doesn't always provide high prediction of genetic gain. Genetic advance as a percent of mean was the highest for total biomass (89.4%), vegetative biomass (97.5%), cob weight (86.1%), grain yield (78.6%) and revealed that high heritability of these traits are coupled with high GAM. Panse (1957) reported that high heritability associated with high genetic advance specifies the additive gene effects while high heritability associated with low genetic advance specifies the non-additive gene effects for control of the particular trait. Among the traits studied, total biomass, cob weight, vegetative biomass and grain yield are important traits to be considered for direct selection and improvement of maize yield as they recorded high heritability and high GAM.

Table.1 Weather parameters during experimental period

Seasons	Temperature (°C)			Relative humidity (%)		
	Min.	Max.	Average	Min.	Max.	Average
Kharif- 2017	21.6	33.5	30.1	67	100	87.9
Summer- 2017	28.6	41.5	36.4	17	97	70.0
Kharif- 2018	24.0	33.5	30.8	69	98	84.8
Summer- 2018	28.5	41.0	35.9	25	97	73.7

Table.2 Pooled analysis of variance for morpho - phenological traits of twelve maize genotypes across the seasons

Source	DF	PH	L.No	TL	RL	RV	DT	DA	DS	ASI
Year	1	3084.88**	28.44**	1	13.75	106.77	23.36**	18.77**	11.67**	0.84
Season	1	5568.89**	2.77	21.77	103.87**	3.36	87.11**	191.36**	79.50**	24.17**
Rep (Year * Season)	8	21.56	0.604	2.68	2.29	21.87	0.604	0.833	0.729	0.229
Genotype	11	2794.61**	10.04**	46.09**	29.86**	1630.36**	131.15**	124.10**	134.46**	3.24**
Year * Season	1	6366.71**	18.77**	0.027	39.37**	850.69**	0.694	0.00	0.562	0.562
Year * Genotype	11	201.98**	1.76	9.75	5.00*	151.29**	2.90**	3.12**	3.11**	0.082
Season * Genotype	11	336.94**	1.76	6.83	5.78**	226.66**	1.86*	2.25**	1.30*	2.50**
Year*Season*Genotype	11	148.84**	2.73	16.23	6.04**	221.08**	0.603	0.621	0.729	0.107
Error	88	37.89	0.816	5.24	1.42	15.74	0.513	0.34	0.373	0.244

* Significant at (p < 0.05) and **Significant (p < 0.01) level of significance; df= degrees of freedom. PH= plant height; L.No= number of leaves; TL=Tassel length, RL=root length, RV=root volume; DT= days to 50% tasseling; DA= days to 50% anthesis; DS= days to 50% silking ; ASI=anthesis silking interval.

Table.3 Pooled analysis of variance for biomass, yield and its related traits of twelve maize genotypes across the seasons

Source	DF	TBM	VBM	Cob wt.	Cob dia	CL	NKR	KN	GY	100 Kwt.	HI
Year	1	1679.42**	576.16**	4223.05**	138.68**	18.06	0.062	10327.9**	391.84**	1.12	6.14
Season	1	39596.68**	2.88	38923.34**	1776.482**	0.00	4.34	207516**	26003.7**	453.2**	989.8**
Rep (Year * Season)	8	39.6	17.5	17.57	6.36	1.49	2.55	40.89	6.35	1.35	1.96
Genotype	11	56442.57**	12686.1**	16846.35**	71.89**	20.14**	9.86**	47651.7**	4128.9**	111.52**	204.82**
Year * Season	1	22259.39**	18955.7**	132.63	225.70**	1.44	0.006	12145.5**	328.4**	13.63	100.06**
Year * Genotype	11	1112.30**	390.51**	561.45**	32.17**	7.52**	2.56	1534.5**	106.1**	12.12**	11.68**
Season * Genotype	11	5892.69**	279.66**	5283.60**	142.58**	7.01**	1.74	27490.8**	1534.1**	36.28**	46.67**
Year*Season*Genotype	11	1261.83**	349.49**	816.03**	15.81*	5.27*	3.41	885.1**	395.2**	5.41	22.37**
Error	88	44.26	21.78	23.09	4.48	1.52	1.88	55	14.94	2.75	2.06

* Significant at (p < 0.05) and **Significant (p < 0.01) level of significance; df= degrees of freedom; TBM= total biomass; VBM= vegetative biomass; Cob wt.= cob weight; Cob dia=Cob diameter; CL=cob length, NR= no.of rows per cob; KN= kernel number; GY= grain yield; 100 Kwt.= 100 kernel weight; HI= harvest index

Table.4 Mean, genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability (H^2) and genetic advance as a percent of mean (GAM) of twelve maize genotypes during *Kharif* and Summer seasons of 2017 and 2018

Parameters	Mean	Min.	Max.	σ^2_g	σ^2_p	σ^2_e	GCV(%)	PCV(%)	H^2 (%)	GAM(%)	SE	LSD	CV
PH	190.59	176.17	235.00	918.91	956.80	37.89	15.91	16.23	96.04	32.11	1.78	4.99	3.23
L.No	11.17	10.33	13.58	3.07	3.89	0.82	15.71	17.67	79.03	28.76	0.26	0.73	8.09
TL	32.71	30.25	35.50	13.62	18.86	5.24	11.28	13.28	72.21	19.75	0.66	1.85	6.99
RL	17.31	14.78	21.12	9.48	10.90	1.42	17.78	19.07	86.97	34.17	0.34	0.97	6.88
RV	54.25	37.08	76.67	538.21	553.95	15.74	42.76	43.38	97.16	86.83	1.15	3.21	7.31
TBM	315.51	211.63	495.23	18799.44	18843.70	44.26	43.46	43.51	99.77	89.42	1.92	5.39	2.10
VBM	136.87	98.00	225.98	4221.44	4243.22	21.78	47.47	47.59	99.49	97.54	1.35	3.70	3.41
Cob wt.	178.64	113.63	269.25	5607.75	5630.84	23.09	41.92	42.01	99.59	86.18	1.39	3.89	2.69
Cob dia	38.95	35.11	42.72	22.47	26.95	4.48	12.17	13.33	83.38	22.89	0.61	1.71	5.43
CL	16.59	14.97	19.15	6.21	7.73	1.52	15.02	16.75	80.33	27.73	0.36	1.00	7.43
NKR	14.52	12.75	16.00	2.66	4.54	1.88	11.23	14.67	58.59	17.71	0.40	1.11	9.44
KN	407.66	284.08	505.00	15865.57	15920.57	55.00	30.90	30.95	99.65	63.54	2.14	6.01	1.81
GY	96.51	58.09	127.98	1371.32	1386.26	14.94	38.37	38.58	98.92	78.61	1.12	3.13	4.00
100 Kwt.	24.84	19.66	29.06	36.26	39.01	2.75	24.24	25.14	92.95	48.13	0.48	1.34	6.68
HI	30.73	24.71	37.22	67.59	69.65	2.06	26.75	27.16	97.04	54.29	0.41	1.10	4.67
DT	49.92	44.58	55.75	43.55	44.06	0.51	13.22	13.30	98.80	27.07	0.21	0.58	1.43
DA	52.51	47.25	58.25	41.25	41.59	0.34	12.23	12.28	99.18	25.09	0.17	0.47	1.11
DS	55.30	50.67	60.83	44.70	45.07	0.37	12.09	12.14	99.17	24.80	0.18	0.50	1.10
ASI	2.78	2.08	3.83	1.00	1.24	0.24	35.89	40.03	80.36	66.27	0.14	0.40	17.74

PH= plant height (cm); L.No= number of leaves; TL=Tassel length (cm), RL=root length (cm), RV=root volume (ml); TBM= total biomass (g/pl); VBM= vegetative biomass (g/pl); Cob wt.= cob weight (g/pl); Cob dia=Cob diameter (mm); CL=cob length (cm), NKR= no. of kernel rows per cob; KN= kernel number; GY= grain yield (g/pl); 100 Kwt.= 100 kernel weight (g); HI= harvest index (%) ; DT= days to 50% tasseling; DA= days to 50% anthesis; DS= days to 50% silking ; ASI=anthesis silking interval; σ^2_g = genotypic variance; σ^2_p = phenotypic variance; σ^2_e = environmental variance; GCV= genotypic coefficient of variance; PCV= phenotypic coefficient of variance; H^2 = heritability broad sense; GAM= genetic advance as a percent of mean; SE=standard error; LSD= least significant difference; CV= coefficient of variation.

Table. 5 Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients among different growth, biomass, yield and yield attributing traits of twelve maize genotypes across the seasons.

Traits	PH	RL	RV	TBM	VBM	Cob wt.	CL	KN	GY	100 Kwt.	HI	DA	DS	ASI
PH	1.000	0.682**	0.563	0.846**	0.797**	0.954**	0.622*	0.639*	0.727**	0.661*	-0.369	0.388	0.415	0.646*
RL	-0.508	1.000	0.656*	0.884**	0.826**	1.000**	1.000**	0.561	0.645*	0.508	-0.524	-0.006	0.033	0.624*
RV	-0.080	0.102	1.000	0.855**	0.823**	0.940**	1.000**	0.879**	0.848**	0.505	-0.268	0.790**	0.763**	0.082
TBM	-0.117	0.200	0.526	1.000	1.000**	1.000**	0.688*	0.535	0.819**	0.622*	-0.483	0.502	0.573	1.000**
VBM	-0.210	0.163	0.622*	0.928**	1.000	1.000**	0.871**	0.779**	0.899**	0.597*	-0.455	0.510	0.553	0.869**
Cob wt.	-0.044	0.209	0.419	0.968**	0.804**	1.000	0.547	0.308	0.779**	0.680*	-0.539	0.520	0.624*	1.000**
CL	-0.206	0.481	0.751**	0.423	0.474	0.354	1.000	0.449	0.427	0.225	-0.470	0.557	0.587*	0.685**
KN	-0.018	-0.045	0.444	0.481	0.487	0.438	0.378	1.000	0.862**	0.734**	0.398	0.350	0.333	0.029
GY	0.001	0.034	0.331	0.717**	0.559	0.765**	0.337	0.810**	1.000	0.958**	0.117	0.348	0.391	0.794**
100Kwt	0.385	-0.073	0.212	0.635*	0.413	0.734**	0.245	0.625*	0.881**	1.000	0.306	0.351	0.368	0.461
HI	0.083	-0.166	-0.078	-0.031	-0.185	0.076	0.027	0.633*	0.672*	0.569	1.000	-0.332	-0.402	-1.000
DA	0.077	-0.429	0.660*	0.388	0.422	0.333	0.357	0.177	0.164	0.200	-0.151	1.000	0.998**	0.556
DS	0.058	-0.434	0.624*	0.377	0.425	0.314	0.303	0.067	0.086	0.133	-0.253	0.988**	1.000	0.606*
ASI	-0.118	-0.080	-0.164	-0.026	0.062	-0.083	-0.315	-	-0.495	-0.417	-	0.030	0.183	1.000

* Significant at (p < 0.05) and **Significant (p < 0.01) level of significance; PH= plant height; RL=root length, RV=root volume; TBM= total biomass; VBM= vegetative biomass; Cob wt.= cob weight; CL=Cob length; KN= kernel number; GY= grain yield; 100 Kwt. = 100 kernel weight; HI= harvest index; DA= days to 50% anthesis; DS= days to 50% silking; ASI = anthesis silking interval.

Estimates of genotypic and phenotypic correlation of grain yield and other related traits are presented in Table 5. Magnitude of genotypic correlations were high as compared to corresponding phenotypic correlations for all the traits studied indicating that there is a strong inherent genetic association between these traits and decreased phenotypic correlations were due to significant interaction of environment. The genotypic and phenotypic correlation of grain yield with yield attributing traits was significant and positive. Grain yield showed significantly and positively genotypic correlation with plant height ($r_g=0.727$), root length ($r_g=0.645$), root volume ($r_g=0.848$), ASI ($r_g=0.794$), total biomass ($r_g=0.819$), vegetative biomass ($r_g=0.899$), cob weight ($r_g=0.779$), kernel number ($r_g=0.862$), 100 kernel weight ($r_g=0.958$). Similarly grain yield showed significant and positive phenotypic correlation with total biomass ($r_p=0.717$), cob weight ($r_p=0.765$), kernel number ($r_p=0.810$), 100 kernel weight ($r_p=0.881$) and HI ($r_p=0.672$). High magnitude of genotypic correlations indicated that there was a strong inherent genetic association between these different traits.

The present correlation studies revealed that significant and positive association among yield and yield attributing traits is useful in direct selection for an improvement of maize grain yield. Similar results were also reported in maize by Sreckov *et al.*, (2010), Chinnadurai and Nagarajan (2011) and Kharel *et al.*, (2017).

The current study showed that differences in all the growth and yield traits are highly significant, Hence the presence of genetic variability can be exploited for improvement of maize crop. As all traits of selected maize genotypes recorded higher phenotypic than genotypic correlation coefficient, revealing environmental impact on the performance of the genotypes. Total biomass, vegetative biomass, cob weight, kernel number and 100 kernel weight were positively and highly correlated with grain yield. Hence, selection of these traits might bring an improvement in grain yield. The total biomass, vegetative biomass, cob weight and grain yield can

be utilized in varietal development program due to their higher heritable characteristics associated with higher estimate of GCV, PCV and GAM.

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