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Research Article

Genetic variability, heritability and genetic advance for growth, yield and yield related traits in maize genotypes

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Abstract

Evaluation of the genetic variability, heritability and genetic advance of traits is an essential task in any plant improvement program. Twenty maize genotypes were replicated twice in a randomized complete block design on a research plot of Prithu Technical College, Deukhuri Dang of Nepal from June 2017 to September 2017 to determine genetic variability, heritability, and genetic advance for different agronomic traits. Analysis of variance showed significant differences in the traits tassel length, ear height, days to fifty percent tasseling, days to fifty percent silking, kernels' rows ear^{-1}, kernels row^{-1} and grain yield. The highest GCV (31.53%) and PCV (39.20%) were recorded on grain yield. Grain yield and ear height recorded high heritability along with high genetic advance as a percent of mean (GAM). Tassel length and kernels row^{-1} showed high heritability integrated with moderate GAM and moderate heritability integrated with moderate GAM respectively. Further, grain yield showed a significant and positive correlation with plant height, tassel length, ear height, cob length, cob diameter, kernels' rows ear^{-1}, and kernels row^{-1}. Thus the selection of ear height, tassel length and kernels row^{-1} is suggested as they performed better in terms of both heritability and GAM than other traits and they also recorded a significant and positive correlation with yield.

Introduction

Maize (*Zea mays* L.) is a cereal crop of the Poaceae family. In the world, maize is the third major cereal food crop after wheat and rice (Bhiusal et al., 2017). In Nepal, maize is grown almost all around the country and second major cereal crop after rice. In Nepal, maize was cultivated on 956,447 hectares of land during the duration of 2017/18 with the production of 2,713,635 metric tonnes (Statistical Information on Nepalese Agriculture., 2020). In Dang, during the period of 2018/19 maize was grown on 25,691 hectares of land with a production of 62,095 metric tonnes (Statistical Information on Nepalese Agriculture., 2020).

In the breeding program, selection is one of the major steps. For agronomic characters, genetic variability is an essential part of breeding

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programs through which the gene pool of crops can be broadened (Ahmad et al., 2011). The selection is effective in the presence of genetic variability between the individuals in a population (Vashistha et al., 2013). The initial step for any crop advancement plan and acquiring suitable selection techniques is the critical investigation of genetic variability existing in the germplasm of a crop and its analysis (Sravanti et al., 2017). The parameters like the genotypic coefficient of variation and phenotypic coefficients of variation help to find out the amount of variability present in given characteristics (Sesay et al., 2016). Heritability and genetic advance of the individual trait are the major factors determining the efficiency by which the genotypic variability can be utilized through selection (Bilgin et al., 2010). The estimation of heritability and genetic advance enables to find out the gain under selection. Heritability gives knowledge about how much a certain morphogenetic feature can be transferred to future generations (Bello et al., 2012). Plant breeders can determine the route of the selection method to be followed under a given circumstance with the help of heritability. Estimation of both heritability and genetic advance is better to determine the gain under selection as compared to an estimation of heritability only(Johnson et al ., 1955). Both heritability and genetic advance would be more applicable and helpful to formulate selection procedures (Jaiswal et al., 2019). Genetic advance express the degree of the gain secured in a character under certain selection pressure. Thus, the research was performed to determine genetic variability, heritability and genetic advance for different agronomic traits of maize at Dang district of Nepal**.**

Materials and methods

Site of study

The research was performed on a research plot of Prithu Technical College, Lamahi municipality of Dang district, Nepal from June 2017 to September 2017. Geographically, it is situated at 27.9904 °N latitude, 82.3018 °E longitudes and an elevation of 275 meters above sea level (Pandit et al., 2020). Lamahi is in the sub-tropical climatic zone of Nepal and has sub-humid weather conditions (Bartaula et al., 2019). The climatic condition of the research area during the research period is demonstrated in Figure 1.

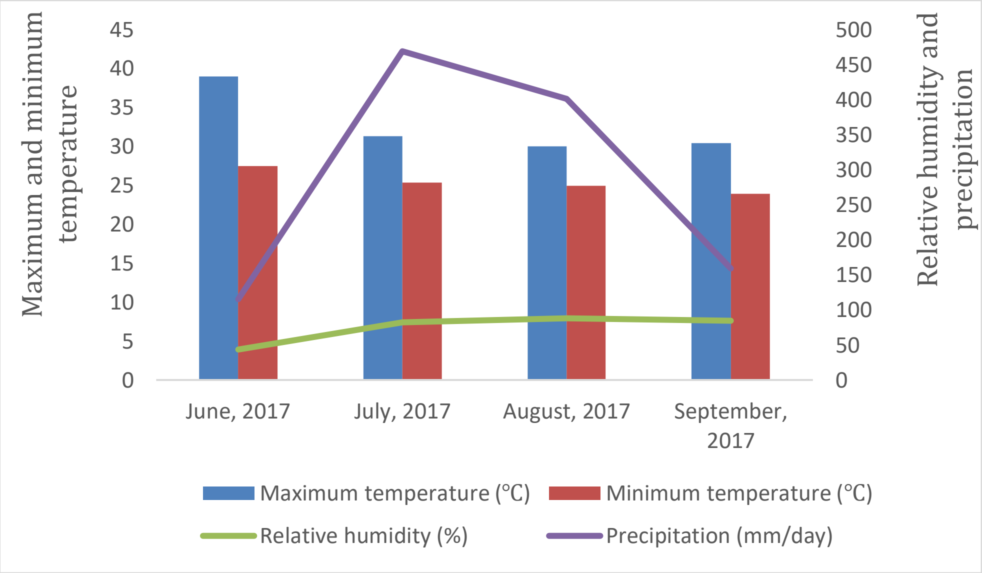

Figure 1. Climatic data of the research site during the research period

Experimental details

The research was carried out on Randomized Complete Block Design (RCBD) with twenty treatments which were replicated twice. Seeds of twenty maize genotypes were gathered from National Maize Research

Program (NMRP), Rampur, Chitwan (Table 1). The research field was prepared by plowing with a tractor two weeks before sowing. Thereafter, by using spades, followed by leveling, the soil was made fine. During field preparation, the stubbles of the former crop, weeds were taken out manually. Well-decomposed farmyard manure (6 ton ha^{-1}) was mixed into the soil one week before sowing. The rate of nitrogen (N), phosphorus (P) and potassium (K) was 120 kg ha^{-1}, 60 kg ha^{-1} and 40 kg ha^{-1} respectively in which urea, single super phosphate (SSP) and muriate of potash (MOP) were the source of N, P and K respectively. Half amount of nitrogen and an entire amount of phosphorus and potassium were given as basal dose during final plowing and the remaining half quantity of nitrogen was top-dressed 45 days after sowing. The area of each plot was 6 m^2 (5 m ×1.2 m). Seeds were sown at the rate of 2 seeds/hill on June 14, 2017 by maintaining the space of 75cm × 25 cm (row× plant). Thinning of plants was done at 30 days of sowing in all the treatments and one plant/hill was maintained. The first manual weeding was done at 35 and 75 days of sowing. Since the crop was raised under rainfed conditions, irrigation was not done during the growing period. The crop was harvested manually on September 20, 2017, when the plant turned yellow and ear husk turned into a brown color.

Table 1. List of genotypes used for the research

Treatment	Genotypes	Source
T1	S97TLYG4AYB	NMRP, Rampur
T2	BLSBRS07F12	NMRP, Rampur
T3	Rampur#2	NMRP, Rampur
T4	Rampur-42	NMRP, Rampur
T5	Rampur-10	NMRP, Rampur
T6	ACROSS-9331RE	NMRP, Rampur
T7	S99 TLYQ-B	NMRP, Rampur
T8	COTAXCA-0024	NMRP, Rampur
T9	11-b-xb-11	NMRP, Rampur
T10	ACROSS-0031	NMRP, Rampur
T11	RampurS03F06	NMRP, Rampur
T12	RampurS03F08	NMRP, Rampur
T13	R-PoP-3	NMRP, Rampur
T14	Rampur-40	NMRP, Rampur
T15	Rampur-3	NMRP, Rampur
T16	S99 TLWQ HG-AB	NMRP, Rampur
T17	TLBRS07F16	NMRP, Rampur
T18	Rampur-2	NMRP, Rampur
T19	Rampur composite	NMRP, Rampur
T20	Rampur#43	NMRP, Rampur

Data Collection

Five plants per plot were chosen randomly and were tagged in each plot to collect data. Then, data of different traits were recorded from those selected plants. The plant height, tassel length, ear height, cob length, cob diameter, kernels' rows ear^{-1}, kernels row^{-1}, days for fifty percent tasseling, days for fifty percent silking, anthesis silking interval, thousand kernels weight and grain yield were taken. The thousand kernels weight and grain yield were taken by adjusting seed moisture at 15 %. Grain yield (kg ha^{-1}) at fifteen percent moisture was computed with the formula adopted by (Carangal et al., 1971).

$$\text{Grain yield (kg ha}^{-1}\text{)} = \frac{\text{F.W}\times(100-\text{HMP})\times\text{S}\times10000}{(100-\text{DMP})\times\text{NPA}}$$

Where,
F.W. = Fresh weight of ear in kg per plot at harvest
HMP = Grain moisture percentage at harvest
DMP = Desired moisture percentage, i.e. 15%
NPA = Net harvest plot area in m^2
S = Shelling coefficient, i.e. 0.8

Statistical analysis

Analysis of variance and correlation between traits were determined with Genstat 18th edition. The treatment means were compared by the least significant difference (LSD) at a 5% level of probability (Gomez & Gomez, 1984).

The phenotypic, as well as genotypic variance, was computed with the procedure suggested by Fehr (1987). The estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance and genetic advance as a percent of mean (GAM) and categorization of GAM was done as per the procedure suggested by Johnson et al. (1955). GCV and PCV were categorized according to the suggestion provided by Sivasubramanjan and Menon (1973). Broad sense heritability was computed by the formula reported by Allard (1960). Heritability in the broad sense is categorized as described by Robinson et al. (1949).

Results and discussion

Analysis of variance

ANOVA showed significant differences in the traits tassel length, ear height, days to fifty percent tasseling, days to fifty percent silking, kernels' rows ear^{-1}, kernels row^{-1} and grain yield (Table 2). Ishaq et al. (2015), Jaiswal et al. (2019) obtained a significant result in tassel length. Rajesh et al. (2013), Neupane et al. (2020) obtained significant results in ear height, kernels' rows ear^{-1}, kernels row^{-1}, days to fifty percent tasseling, days to fifty percent silking and grain yield. Whereas, no significant differences were recorded in the traits plant height, cob length, cob diameter, anthesis silking interval and thousand kernel weight (Table 2). This might be due to the low genetic variability of these traits or due to environmental factors. Shengu et al. (2016), Aci et al. (2018) obtained similar results on anthesis silking interval. Markovic et al. (2011), Bartaula et al. (2019) obtained non-significant results on cob length.

Table 2. Mean squares from ANOVA of different observed traits

Traits	Mean Square	
	Between genotypes df=19	Error df=19
Plant height (cm)	501.63	270.26
Tassel length (cm)	16.43**	5.14
Ear height (cm)	381.63**	73.68
Cob length (cm)	2.47	3.22
Cob diameter (cm)	0.19	0.11
Kernels' row ear^{-1}	1.80**	0.65
Kernels row^{-1}	17.38**	7.17
Days to tasseling (fifty percent)	15.05**	2.42
Days to silking (fifty percent)	17.42**	3.82
Anthesis silking interval (days)	2.42	1.98
Thousand kernels weight (gm)	1039.34	927.76
Grain yield (kg ha^{-1})	1628750.79*	575216.64

df= degree of freedom, * Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

In all the traits the GCV value was recorded less than their corresponding PCV value (Table 3). It means the environment shows an important impact on the expression of traits (Reddy et al., 2013). High GCV (31.53%) and PCV (39.20%) were recorded on grain yield and moderate GCV (11.85%) and PCV (13.19%) were recorded on ear height. High to moderate GCV and PCV indicates the presence of sufficient variabilities in these traits that provides an opportunity for genetic advancement by the selection of these traits (Vashistha et al., 2013). Bartaula et al. (2019) obtained similar results on yield and ear height. Ghimire and Timsina (2015) also obtained high GCV and PCV for yield. Neupane et al. (2020) obtained similar results on ear height

Plant height, kernels' rows ear^{-1}, cob diameter, days to fifty percent tasseling, days to fifty percent silking showed low GCV and PCV (Table 3). Neupane et al. (2020) recorded similar results on plant height, kernels' rows ear^{-1}, days to fifty percent tasseling, days to fifty percent silking. Vashistha et al. (2013), Jaiswal et al. (2019) recorded similar results on plant height, days to fifty percent tasseling, days to fifty percent silking. Kumar et al. (2014) obtained low GCV and PCV on kernels' rows ear^{-1}, days to fifty percent tasseling and days to fifty percent silking. Low GCV and moderate PCV were found on cob length, kernels row^{-1} and thousand kernels weight (Table 3). Bartaula et al. (2019) recorded a similar result on cob length. Beyene et al. (2005) recorded a similar result on thousand seed weight. Ghimire and Timsina (2015) obtained low GCV and moderate PCV on kernels row^{-1}.

Heritability and genetic advance as a percent of mean (GAM)

High heritability was recorded on days to fifty percent tasseling (83.91%), ear height (80.69%), days to fifty percent silking (78.06%), tassel length (68.73%), grain yield (64.68%) and kernels' rows ear^{-1} (64.19%). High heritability means less effect of the environment on the expression of these traits (Neupane et al., 2020). Raut et al. (2017), Neupane et al. (2020) obtained high heritability on days to fifty percent tasseling, ear height, days to fifty percent silking and grain yield. Taye (2014) obtained high heritability on ear height, days to fifty percent tasseling and days to fifty percent silking. Rajesh et al. (2013), Kumar et al. (2014) obtained high heritability on kernels' rows ear^{-1}. Jaiswal et al. (2019) obtained high heritability on tassel length.

Kernels row^{-1} (58.74%), plant height (46.12%) and cob diameter (42.29%) recorded moderate heritability. It might be because of the environmental impact on the phenotypic nature of traits (Neupane et al., 2020). Abe and Adelegan (2019) obtained moderate heritability for plant height. Jaiswal et al. (2019) obtained medium heritability for cob diameter. Ghimire and Timsina (2015), Shengu (2017) obtained moderate heritability on kernels row^{-1}.

Low heritability was recorded on cob length (18.75%), anthesis silking interval (18.26%) and thousand kernels weight (10.74%). The low heritability of these traits means the expression of these traits is more affected by the environment (Islam et al., 2015). Abe and Adelegan (2019) obtained low heritability on anthesis silking interval. Beyene et al. (2005) obtained low heritability on thousand kernels weight.

Similarly, GAM ranged from 3.20 to 52.24 (Table 3). Grain yield (52.24) and ear height (21.93) showed high estimates of GAM. Raut et al. (2017) obtained high GAM on grain yield. Bhiusal et al. (2017) obtained high GAM on ear height. Ghimire and Timsina (2015), Kandel et al. (2018), Bartaula et al. (2019) obtained high GAM on ear height and grain yield.

Kernels row^{-1} (15.73) and tassel length (11.79) showed a moderate estimate of GAM. Ghimire and Timsina (2015) observed moderate GAM on kernels row^{-1}.

Other traits plant height (7.57), cob length (3.89), cob diameter (7.04), kernels' rows ear^{-1} (9.42), days to fifty percent tasseling (9.20), days to fifty percent silking (8.39), ASI (8.28) and thousand kernels weight (3.20) showed low estimates of GAM. Ghimire and Timsina (2015) obtained low GAM on kernels' rows ear^{-1}. Shengu (2017) obtained low GAM on plant height and thousand kernel weight. Meena et al. (2016), Raut et al. (2017) obtained low GAM on days to fifty percent tasseling and days to fifty percent silking. Abe and Adelegan (2019) obtained low GAM on plant height, cob length, cob diameter and ASI.

High heritability combined with high GAM was reported on grain yield and ear height (Table 3). High heritability integrated with high GAM means there is the control of additive gene action and a larger opportunity for choosing these traits. Meena et al. (2016) obtained similar results on grain yield and ear height.

High heritability integrated with low GAM was observed on the kernels' rows ear^{-1}, days to fifty percent tasseling and days to fifty percent silking (Table 3). High heritability combined with low GAM indicates the control of the non-additive gene action and gives the low opportunity to improve traits by selection. Raut et al. (2017), Neupane et al. (2020) obtained high heritability integrated with low GAM on days to fifty percent tasseling and days to fifty percent silking.

Moderate heritability integrated with low GAM was observed on plant height and cob diameter (Table 3). Sesay et al. (2016), Abe and Adelegan (2019) obtained moderate heritability coupled with low GAM on plant height. It means there is the control of the non-additive gene actions for those traits and provides limited opportunity to improve traits by selection.

Cob length, anthesis silking interval and thousand kernel weight recorded low heritability combined with low GAM (Table 3) which means there is control of the non-additive gene actions and provides limited opportunity to improve traits by selection. Abe and Adelegan (2019) obtained low heritability coupled with low GAM on anthesis silking interval.

Kernels row^{-1} recorded moderate heritability integrated with moderate GAM (Table 3). It means there is the existence of intermediate additive as well as non-additive gene actions and phenotypic performance of these traits can be obtained by selecting carefully. Ghimire and Timsina (2015) obtained moderate heritability coupled with moderate GAM on kernels row^{-1}.

Tassel length recorded high heritability combined with moderate GAM (Table 3) which means the careful selection on tassel length may also lead towards improvement in this trait.

Table 3. Mean, variability, heritability, and genetic advance for observed traits

Traits	Mean	SE	MSG	MSE	σg^2	σ_p^2	GCV (%)	PCV (%)	h^2_{bs} (%)	GA (%)	GAM
PH	198.82	3.10	501.63	270.26	115.69	250.82	5.41	7.97	46.12	15.05	7.57
TL	34.42	0.52	16.43	5.14	5.65	8.22	6.90	8.33	68.73	4.06	11.79
EH	104.71	2.37	381.63	73.68	153.98	190.82	11.85	13.19	80.69	22.96	21.93
CL	13.99	0.26	2.47	3.22	0.37	1.98	4.36	10.06	18.75	0.54	3.89
CD	3.82	0.06	0.19	0.11	0.04	0.10	5.25	8.08	42.29	0.27	7.04
KRE^{-1}	13.33	0.17	1.80	0.65	0.58	0.90	5.71	7.13	64.19	1.26	9.42
KR^{-1}	22.68	0.55	17.38	7.17	5.11	8.69	9.96	13.00	58.74	3.57	15.73
DT (fifty percent)	51.55	0.46	15.05	2.42	6.31	7.52	4.87	5.32	83.91	4.74	9.20
DS (fifty percent)	56.55	0.52	17.42	3.82	6.80	8.71	4.61	5.22	78.06	4.75	8.39
ASI	5.00	0.25	2.42	1.98	0.22	1.21	9.40	22.00	18.26	0.41	8.28
TGW	157.75	4.94	1039.34	927.76	55.79	519.67	4.73	14.45	10.74	5.04	3.20
GY	2301.91	178.60	1628750.79	575216.64	526767.07	814375.39	31.53	39.20	64.68	1202.47	52.24

SE= Standard error, MSG=Mean square of genotypes, MSE = Error mean square (Mean square of environment), σ_g^2 = Genotypic variance, σ_p^2 = Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of Variation,, h^2_{bs} =Broad sense heritability, GA= Genetic advance, GAM= Genetic advance as a percent of mean, PH=Plant height, , TL= Tassel length,

EH= Ear height, CL= Cob length, CD= Cob diameter, KRE^{-1}= Kernels' rows ear^{-1}, KR^{-1}= Kernels row^{-1}, DT (fifty percent) = Days to fifty percent tasseling, DS (fifty percent) = Days to fifty percent silking, ASI= Anthesis silking interval, TKW= Thousand kernels weight, GY= Grain yield.

Correlation between traits

Grain yield showed a significant and positive correlation with plant height (r=0.42), tassel length (r=0.66), ear height (r=0.47), cob length (r=0.49), cob diameter (r=0.45), kernels' rows ear^{-1} (r=0.50) and kernels row^{-1} (r=0.63). Selvaraj and Nagarajan (2011) obtained positive significant relation of plant height and ear height with yield. Similarly, Kharel et al. (2017) obtained positive significant relation of plant height, ear height and kernels row^{-1} with yield. Bhiusal et al. (2017) obtained positive significant relation of cob length with yield.

Thousand kernel weight exhibited non-significant but positive relation with grain yield (Table 4). Raut et al. (2017) obtained a similar result between thousand kernel weight and yield.

Days to fifty percent tasseling, days to fifty percent silking and ASI showed a negative correlation with grain yield (Table 4) suggesting that the increase in value of these traits will decrease the yield of the maize. Therefore, these traits may not be selected simultaneously. Bhiusal et al. (2017) also recorded similar results in days to fifty percent tasseling and days to fifty percent silking with yield. Bartaula et al. (2019), Neupane et al. (2020) obtained similar results on ASI and yield.

Table 4. Phenotypic correlation coefficient among different observed traits of maize

	PH	TL	EH	CL	CD	KRE^{-1}	KR^{-1}	DT (fifty percent	DS (fifty percent)	ASI	TGW	GY
PH	1											
TL	0.33*	1										
EH	0.63**	0.291	1									
CL	0.46**	0.39*	0.42**	1								
CD	0.36*	0.33*	0.255	0.39*	1							
KRE^{-1}	0.261	0.34*	0.32*	0.37*	0.53**	1						
KR^{-1}	0.45**	0.38*	0.57**	0.69**	0.38*	0.379*	1					
DT (fifty percent)	-0.09	-0.45**	-0.15	-0.38*	-0.33*	-0.49**	-0.45**	1				
DS (fifty percent)	-0.11	-0.510**	-0.14	-0.41**	-0.31	-0.49**	-0.52**	0.87**	1			
ASI	-0.08	-0.21	-0.02	-0.15	-0.01	-0.12	-0.25	-0.03	0.45**	1		
TKW	0.093	0.02	-0.07	0.43**	0.076	-0.02	0.22	-0.16	-0.223	-0.166	1	
GY	0.42**	0.66**	0.47**	0.49**	0.45**	0.50**	0.63**	-0.58**	-0.69**	-0.35*	0.162	1

PH=Plant height, TL= Tassel length, EH= Ear height, CL= Cob length, CD= Cob diameter, KRE^{-1}= Kernels' rows ear^{-1}, KR^{-1}= Kernels row^{-1}, DT (fifty percent) = Days to fifty percent tasseling, DS (fifty percent) = Days to fifty percent silking, ASI= Anthesis silking interval, TKW= Thousand kernels weight, GY= Grain yield, * Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$.

Conclusion

The best trait was ear height as it recorded high heritability integrated with high GAM and a positive and significant correlation with grain yield. Tassel length also performed well as it recorded high heritability coupled with moderate GAM and also a positive and significant correlation with grain yield. Kernels row^{-1} also performed well as it recorded moderate heritability coupled with moderate GAM and also a positive and significant correlation with grain yield. Thus, selection of ear height, tassel length and kernels row^{-1} is suggested to enhance the yield potential of maize in the study area.

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Author's declaration and contribution

The authors declare that there is no conflict of interest for the publication of this paper. RR planed the research, gathered data, analyzed data and wrote this paper. PK gathered data, wrote and edited this manuscript. PC helped in data gathering. RD supervised the research. All authors read the final manuscript and approved the final version.

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