Genetic variability estimates of hybrid maize genotypes in inner terai of Nepal

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ABSTRACT

To access the genetic variability present on hybrid maize genotypes, a research was carried out at Farmers field of Rapti municipality-7 Chitwan, Nepal during the winter season of 2018. Ten hybrid maize genotypes were replicate thrice in a randomized complete block design. Analysis of variance showed that all the studied traits were significantly different except the number of kernel row per ear, Anthesis-silking interval (ASI), ear aspect, days to physiological maturity and thousand kernel weight which showed the existence of enough genetic potential present for crop improvement Program. Plant height, ear height, number of kernel row, ear aspect, ear length, thousand kernel weight, and grain yield showed moderate to the high genotypic coefficient of variation, phenotypic coefficient of variation along with high heritability with moderate to high genetic advance as a percentage of the mean. Selection can be performed on those traits showing the high genotypic and phenotypic coefficient of variation, heritability with high genetic advance as a percentage of the mean for yield improvements program. Cluster analysis showed that the hybrid genotypes showed considerable genetic diversity among themselves by occupying three different clusters.

INTRODUCTION

Maize is one of the most important cereal crop in the world. In case of Nepalese condition it is most important staple crop of mid hill and high hill. In Nepal maize rank second position after rice in terms of area and production (MOAD 2017/18 and Thapa et al. 2019). At present, the maize cultivate area in Nepal is 9, 51, 158 ha with a total production of 25, 55, 847 metric tons and productivity of 2.69 ton ha⁻¹ (MOAD 2017/18). It accounts 25.02% in total for cereal production, 6.54% in AGDP (Pandey and Basnet 2018). It is a primary food crop for farmers of hilly area and in terai region it is source of animal feed for different feed industries (KC et al. 2015). In hilly area of Nepal, above 86% maize production has been used for human consumption and 80% for poultry and animal feed in terai

(Gurung et al. 2011). Productivity of maize in Nepal is low compared to other developed nations (France and the United states both 9.5 ton ha⁻¹, Canada (8.5 ton ha⁻¹), Argentina (7.5 ton ha⁻¹) due to numerous factors that directly affect the maize productivity. Development of high yield potential maize varieties for normal planting season is one of the coping strategies for food deficiency whereas yield gap can be lower by cultivation of improved varieties.

Genetic variability is key to crop improvement (Welsh 1981). In maize improvement program the breeding objective is to obtain genetic progress in yield component traits along with maintaining high amount of variability (Hallauer 1972). Effective selection is carried out only when there is presence of sufficient genetic variability in a population. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for stating a judicious breeding program (Hemavathy et al. 2008; Mohamed et al. 2012). Estimate heritability suggest plant breeder for effective selection; population structure and size, selection differential by using information of estimated heritability. Heritability alone has no reliable for remark of genetic progress from individual genotype selection. Hence

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knowledge about heritability along with genetic gain is very useful (Johnson et al. 1955). This study was performed to investigate genetic variability of ten hybrid maize genotype.

MATERIALS AND METHODS

Research site

The experiment was carried out at the farmer's field of Rapti municipality, 07, Chitwan. The research site is lies 235 meters above mean sea level (masl) having south facing slopes at 27 40' N and 84 19' E coordinates (Sharma et al. 2018). Geographically, the research site falls in the inner terai region of Province no.3 of Nepal.

Experimental details

The research was carried out in Randomized Complete Block Design (RCBD) consisting ten hybrid maize genotypes with three replications. Each hybrid maize genotypes received the plots of 9 m² area with the net plot area of 90 m² per replication. Seed sowing was performed at the rate of two seeds per hill with the crop geometry of 75*25 cm² (RR * PP). Each genotype will be sown in four rows of 3m length. Details of genotype used in research was shown in table 1.

Data Taken

All data were taken from sample row from five randomly selected plant except days to 50 % anthesis, days to 50 % silking and days to physiological maturity. Ear aspect was scored based on scale (1 to 5) proposed by UPOV (2009). All collected data were entered in MS excel and analysis of data carried by statistical tools like R studio and R package.

Calculation

Phenotypic and genotypic coefficient of variation was calculated by method suggested by Lush (1940) and Chaudhary and Prasad (1968).

GCV and PCV was categorized as Sivasubramanjan & Menon categorized as follows:

Value categories

0-10 % Low
10-20 % Medium
>20 % High

Broad sense heritability was calculated by formula given by Falconer (1996). Robinson et al. (1949) categorized heritability percentage category as low, moderate and high as follows:

0 – 30% : Low
30 – 60% : Medium
> 60% : High

Genetic advance under selection at 5 % selection intensity was computed by the formula proposed by Johnson et al. (1955). Genetic advances as percent of mean (GAM) was calculated by using the formula suggested by Falconer (1996) as $GAM = GA/100$. Johnson et al. (1955) categorized GAM as low, moderate and high as follow:

Value Category
0-10% Low
10-20% Medium
>20 % High

RESULTS

Analysis of variance (ANOVA)

The analysis of variance suggest that there was significant differences for all the studies traits except for ASI, ear aspect, days to physiological maturity, number of kernel row per ear, number of kernel per row and thousand kernel weight (Table 2). ANOVA table indicate that there was existence of sufficient genetic variability among the genotypes. Similar results were reported by Saikia and Sharma (2000) for different maize characters i.e. plant height, ear height and grain yield per plant. Kumar et al. (2015) and Kandel et al. (2019) also reported significant variability for various traits in maize genotypes. Analysis of variance for important traits in hybrid maize genotypes presented in table 2.

Genotypic coefficient of variation (GCV) and

Table1. Genotypes used in Research

Entry no.	Name of genotypes	Other details
1	Rampur Hybrid-2	Released Nepalese hybrid cultivar
2	Rampur Hybrid-4	Released Nepalese hybrid cultivar
3	Rampur Hybrid-6	Released Nepalese hybrid cultivar
4	RML-86/RML-96	Pipeline
5	RML-95/RML-96	Pipeline
6	Bisco 940 New	Hybrids from multinational companies
7	Ganga Kaveri	Hybrids from multinational companies
8	Rajkumar	Hybrids from multinational companies
9	Shrestha	Hybrids from multinational companies
10	P3393	Hybrids from multinational companies

Table 2. Analysis of variance for important traits in hybrid maize genotypes

Source of variation	Genotype	Replication	Error
Character	Df 9	2	18
Days to 50% anthesis	31.87 ***	0.03	1.14
Days to 50% silking	32.39***	0.31	1.36
ASI	0.18	0.23	0.60
Days to physiological maturity	2.904	0.83	7.31
Plant height	603.6***	105.5	92.4
Ear height	223.31*	18.07	70.85
Ear length	4.64**	1.00*	1.04
Ear diameter	0.12*	0.05	0.04
Ear weight	0.89***	0.27	0.13
Number of kernel per row	9.02	7.60	3.75
Number of kernel row per ear	1.92	0.05	1.36
Thousand kernel weight	2127.8	302.5	931.6
Ear aspect	0.36	0.06	3.178
Grain yield	2241480***	1032922.	309492

Significant codes: **** 0.001 *** 0.01 ** 0.05 * . 0.1, df= Degree of freedom

phenotypic coefficient of variation (PCV)

Moderate to high genotypic and phenotypic coefficient was recorded for 1000-kernel weight, ear height, plant height, ear length, ear weight, ear aspect and grain yield ton ha⁻¹. Taye (2014) and Kandel et al. (2018) also reported moderate to high genotypic and phenotypic coefficient of variation were recorded plant height, ear height, cob length, thousand grain weight and grain yield. The phenotypic coefficients of variations were higher than the genotypic coefficient variations for all traits studied in maize (Yusuf 2010; Kandel et al. 2018). The smaller the different between GCV and PCV value for the traits, those traits are less influenced by environment effect.

Heritability (Board sense heritability)

Highest heritability was recorded for anthesis days (0.96) followed by silking days (0.95), Grain yield kg ha⁻¹(0.87), plant height (0.86), ear weight (0.85), ear length (0.80), ear height (0.73), number of kernel per row (0.67) and thousand kernel weight (0.66) whereas moderate heritability was recorded for trait like number of kernel row per ear (0.51), ear aspect (0.55) as presented in table 3. Maturity days showed low heritability. Taye (2014) reported that high heritability estimate for ear height, plant height, 50% silking days, days to 50 % anthesis, number of kernel row per ear. Kandel et al. (2017) also reported that grain yield, plant height ear height, days to tasseling, days to silking, ear weight and ear length, which is accordance to our findings. Environmental effect is

low for the traits having high values of heritability in broad sense.

Genetic Gain (GA) & Genetic Advance as percentage of mean (GAM)

Ear height, plant height, thousand kernel weight and grain yield kg ha⁻¹ showed high estimated heritability with high genetic advance. Similiar result of high heritability couple with high genetic advance were recorded for ear height and plant height by Dar et al. (2014). Maturity days showed low heritability with low genetic gain. All other remaining traits showed moderate to high heritability with moderate to low genetic gain.

High GAM were recorded for ear aspect (64.21) followed by grain yield (29.75), ear weight (26.28), ear height (25.14), ear length (22.70) and plant height (22.14). Moderate GAM were observed from thousand grain weight (17.89) followed by number of kernel per row (17.00), number of kernel row per ear (13.19), ear diameter (12.09) days to 50% anthesis (10.52) and 50 % silking days (10.38). Low GAM were recorded for days to physiological maturity (0.20).

Cluster analysis

Cluster analysis of hybrid maize genotypes under this study showed that the hybrid genotypes showed considerable genetic diversity among themselves by occupying three different clusters (Table 4). These hybrid maize genotypes were grouped based on mainly agro-morphological traits such as tasseling and silking days, ASI, plant height and ear height, ear length, ear diameter, ear weight, ear aspect, number of kernel per row, number of

Table 3. Genotypic coefficient of variance (GCV), Phenotypic coefficient of variance (PCV), heritability (H), Genetic advance (GA) and Genetic advance as percentage of mean (GAM) of hybrid maize genotypes

Traits	GCV	PCV	H	GA	GAM
AD	5.202666	5.296002	0.965063	11.35616	10.52861
SD	5.145455	5.253871	0.959155	11.40135	10.38091
PH	11.77933	12.6939	0.861094	45.75032	22.51714
EH	14.20801	16.5375	0.73812	25.00992	25.14571
EL	12.29409	13.71078	0.804022	3.826461	22.70897
ED	7.036019	8.429525	0.696703	0.558934	12.09813
NKPR	10.04714	12.23141	0.674733	4.719491	17.00105
NKRPE	8.891778	12.34412	0.518868	1.797055	13.19424
EA	41.8709	56.24239	0.554239	2.183267	64.21374
EW	14.04732	15.15228	0.85947	1.754502	26.82725
GY	15.45662	16.5374	0.873564	2815.467	29.75973
MD	0.408747	1.674215	0.059605	0.34234	0.205572
TGW	10.68406	13.14026	0.661097	71.40178	17.89518

AD=Anthesis days, SD= Silking days, PH=Plant height, EH= Ear height, EL=Ear length, ED= Ear diameter, NKPR= Number of kernel per row, NKRPE= Number of kernel row per ear, EA= Ear aspect, EW= Ear diameter, GY= Grain yield, MD= Maturity days and TGW=Thousand grain weight

kernel row per ear, thousand kernel weight and grain yield.

Ten hybrid maize genotypes were grouped into 3 clusters based on various agro-morphological traits (Table 4). Cluster analysis showed that cluster I was comprised of 8 genotypes, cluster II of 1 and cluster III of 1 hybrid maize genotype (Figure 1). Genotype fall into clusters II had early anthesis and silking days, delay maturity, higher ear weight and highest thousand kernel weight and high yield potential (Bisco 940 New). The cluster III was characterized with delay anthesis and silking days, highest ear and plant height, ear length, number of kernel per row along with highest ear aspect. The genotype fall into cluster I had highest number of kernel row per ear with lowest ASI, ear weight

thousand kernel weight and low yielding potential.

Bisco 940 New has height yield potential and showed in figure 2. Bisco 940 New fall in cluster 2 having early anthesis and silking days, delay maturity, higher ear weight and highest thousand kernel weight might be the reason for high yield potentials from rest of tested genotypes.

DISCUSSION

The analysis of variance showed that majority of studied traits were highly significant ($P < 0.01$), which indicates the presence of sufficient genetic variability and potential for selection and improvement on the characters. In systematic breeding program genetic variability for a given trait is a basic prerequisite (Engida et al. 2007). The

Table 4. Agro-morphological traits of ten hybrid maize genotypes within and among three clusters

Variable	Cluster 1	Cluster 2	Cluster 3
50 % anthesis days	107.46	106.2	109.0
50 % silking days	109.26	108.7	111.3
Maturity days	166.03	169.3	167.3
ASI	1.80	2.7	2.3
Plant height	204.13	189.3	211.3
Ear height	100.63	87.1	105.0
Ear length	16.74	16.4	17.2
Ear diameter	4.61	4.7	4.7
Ear weight	6.30	7.9	7.3
Ear aspect	2.73	2.3	3.1
Number of kernel per row	27.05	29.1	31.9
Number of kernel row per ear	13.79	12.0	13.1
Thousand kernel weight	389.87	457.9	430.6
Grain yield	91112.13	11832.6	10549.9

amount of genotypic and phenotypic variability that exists in a species is essential in developing better varieties and initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exist in a

Figure 1. Clustering of hybrid maize genotypes based on agro-morphological traits. (RH-2= Rampur Hybrid-2 , RH-6= Rampur Hybrid-6 and RH-4 = Rampur Hybrid-4)

given population (Burto and Devane 1953). In our study difference between GCV and PCV was less its means character is less influenced by environmental variation. PCV was found to be higher than GCV for all studied traits. Heritability studied showed all traits except maturity days showed moderate to high genetic heritability. If the predicated heritability is about 80 % or more, selection for such character could be fairly easy (Singh 1990). This is because there would be a close correspondence between genotype and phenotype due to relatively smaller influence of environment on the phenotype. However, for a character with low heritability, less than 40%, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on the phenotypic effect.

Because of genetic diversity among important traits of hybrid maize might be the major causes of variability in performance among genotypes. Shrestha and Kunwar (2014) from two years observation recorded that there was significant variation in eighteen maize hybrids for flowering and grain yield. Tripathi et al. (2016) from two year data reported that three was significant variation among yield potential of tested genotypes among different location. Climatic and soil variability, genetic potentials among the genotypes and G*E interaction might be reason for causing the variable performance of hybrid maize genotypes. In our findings significant variation was found among the yield potential of tested genotypes. Cluster analysis also showed considerable genetic diversity among tested genotypes and fall under three distinct cluster based on agro-morphological and yield traits. Bisco 940 high yielding genotype fall under second cluster having early anthesis and silking with late maturity,

its means there is longer reproductive period so produced high yield.

CONCLUSIONS

Figure 2. Yield potentials of tested ten hybrid maize genotypes

Hence in conclusion high value of genotypic and phenotypic coefficient of variation were observed for plant height, ear height, ear length, ear weight, number of kernels per row and ear aspect suggesting existence of sufficient variability and can be utilize in efficient selection for genetic improvement program. From above research high to moderate heritability with moderate genetic gain recorded for, grain yield, plant height and ear height, thousand kernel weight. Characters having moderate to high GCV, PCV, H and GAM should be selected for further yield improvement program.

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CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

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