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, 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.

Keywords: Genetic potential, heritability, Genetic gain, GCV, PCV

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
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 350 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 takened 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 | Category |
|-------|----------|
| 0-10 % | Low |
| 10-20 % | Medium |
| >20 % | High |

Broad sense heritability was calculated by formula given by Falconer (1996). Robinson et al. (1949) catgrorized heritability percentage categ 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.

| 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 |
Moderate to high genotypic and phenotypic coefficient of variation 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 similar findings was reported by earlier on 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 per row per ear (0.51),ear aspect (0.55) as presented in table no 3. Maturity days showed low heritability. Taye (2014) reported that high heritability estimate for ear height, plant height, 50% anthesis, 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. Similier 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 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 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 '***' 0.001 '**' 0.01 '*' 0.05 ' ' 0., Df= degree of freedom
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 anthes 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 anthes 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
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 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 there 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

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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