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Genetic Variability, Heritability and Genetic Advance of Yield Attributing Traits in Winter Maize

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Abstract

The major objectives of the study were to evaluate genotypic yield performances of eleven maize genotypes and estimate variance components and heritability of yield and yield-related traits. The eleven open pollinated maize varieties were evaluated using randomized complete block design with three replications. The experiment was carried at National Maize Research Program, Rampur, Chitwan, Nepal out in winter season of 2013. The findings showed that the high genetic advance was estimated for yield per plant (80.15%), number of kernels per row (38.29%), plant height (26.20%) ear length (23.89%) indicating that these parameter were under the control of additive gene. Number of kernels rows per ear, plant height could be the important selection criteria in improving open pollinated maize varieties for high grain yield.

Key words: Maize; heritability; grain yield

Introduction

Maize-an important cereal crop, cultivated throughout the world, is of significant importance for countries like Nepal, where rapid increase in population have already out stripped the available food supplies. Maize has a high yield potential than any other cereals and popularly known as the 'queen of cereals' (Singh, 1998). The suitability of maize to diverse environments is unmatched by any crop as the expansion of maize to new areas and environment still continues, as it has a range of plasticity. It is grown from latitude 58N to 40S, from sea level to higher than 3000 m altitude and in areas receiving yearly rainfall of 250 to 5000 mm (Downsell *et al.*, 1996). Maize (*Zea mays* L.) is an important cereal crop belongs to the tribe Maydeae, of the grass family, poaceae. The plant is native to South America. *Zea mays* is the only species in the genus *Zea* with chromosome number $2n=20$. Since the beginning of its domestication, grain yields have increased continuously and steadily. Maize cultivation has changed along with the revolution in genetics and breeding.

Heritability of a metric character is one of its important properties, and this expresses the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives (Falconer, 1960). Heritability estimates allow breeders to develop more efficient selection strategies (population structure and size, selection differential) and to predict Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about genetic advance coupled with heritability is most useful. Character exhibiting high heritability may not necessarily give high genetic advance Johanson *et al.* (1955) showed

high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The most important functions of heritability in the genetic study of metric characters are its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. Only the phenotypic values of individuals can be directly measured, but it is the breeding value that determines their influence on the next generation. If a breeder therefore chooses parents according to their phenotypic values, his success in changing the characteristics of the population can be predicted only from the knowledge of the degree of correspondence between the phenotypic values and breeding values.

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

0-30%:	Low
30-60%:	Moderate
>60%:	High

If heritability of traits is very high (>0.8), selection for such a traits should be fairly easy. This is because there would be close correspondence between the genotype and phenotype (Singh, 1993). In case of lower heritability estimates (<0.3), selection may be considerably difficult or virtually impractical due to the masking effect of environment on genotypic effects (Singh, 1993). Heritability estimates allow breeders to develop more efficient selection strategies (population structure and size, selection differential) and to predict gain from selection (Allard. 1999). While it is useful to have an estimate of the total genetic effect on a particular trait, such as broad-sense heritability, narrow-sense

heritability provides a better estimate of the breeding value (Allard, 1999). High value of heritability have been reported by Chen *et al.* (1996) for grain yield per plant. High heritability estimates for maize grain yield have been reported by (Kashiani *et al.*, 2010). High heritability to days to silking, plant height and number of grains ear⁻¹ was showed by (Najeeb *et al.*, 2009).

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955). The extent of genetic advance to be expected by selecting five percent of the superior progeny was calculated by formula presented by Robinson *et al.* (1949):

$$\text{Genetic advance} = i \cdot \delta p \cdot h^2$$

Where,

i = selection intensity at 5 %, which is 2.06

δp = phenotypic standard deviation

h^2 = heritability in broad sense

The genetic advance was classified as low, moderate and high as following by Johnson *et al.* (1955)

0-10%: low

10-20%: moderate

>20%: high

Lush (1940) defined heritability in both broad sense and narrow sense. In broad sense, heritability refers to the functioning of the whole genotype as a unit and is used in contrast with the environmental effects. In the narrow sense, heritability largely includes only the average effect of genes transmitted additively from parent to off spring.

Since most of the economic characters (grain yield) are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, the study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection. The reliability of a parameter to be selected for breeding programme among other factors is dependent on the magnitude of its coefficient of variations (CV) especially the GCV. However, the differences between genotypic and phenotypic coefficient of variability indicate the environmental influence. While a lower value of CV generally depicts low variability among the tested sample; a high proportion GCV to the PCV is desirable in breeding works.

Surveys of genetic variability with the help of suitable parameters such as GCV, heritability estimates, and GA are absolutely necessary to start an efficient breeding program

(Atta *et al.*, 2008). Heritability value alone may not provide clear predictability of the breeding value. Heritability in conjugation with genetic advance over mean (GAM) is more effective and reliable in predicting the resultant effect of selection (Patil *et al.*, 1996; Ramanjinappa *et al.*, 2011). GA is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 2003).

The major ultimate goal of agricultural research is to develop high yielding, internal & external input responsive and biotic stress resistant/ abiotic stress tolerant new cultivar. There are several traditional methods to develop such ideal variety. The primary method is selection of well performing genotypes. Therefore, most of research experimented to select high yielding genotypes primarily based on yield performance.

Materials and Methods

The experiment material consist of 11 genotypes including a standard check. The Inbred lines was provided by NMRP, Rampur. Standard agronomic practices were used to provide adequate nutrition and kept the plots disease free. Each plot consisted of a row 5 m long with an inter and intra row plant spacing of 0.75 × 0.25 m, resulting in a population density of 53,000 plants ha⁻¹. Area of individual plots in each replication was 15 m².

A field experiment was conducted at National Maize Research Program (NMRP Rampur) during 2013 from last week of September to first week of February. The Area is located at 27° 37' N latitude and 84° 25' E longitude with an elevation of 228 masl.

The soil type is sandy loam and climatically humid sub-tropical with average annual rainfall of 2000 mm (mainly during mid to late summer). The meteorological data (Figure 1) were obtained from meteorological station, National Maize Research Program, (NMRP), Rampur.

The experiment was laid out in RCBD design with three replications. The genotypes were allocated randomly to the 11 Plots of each replication. The plot size was 5.0 m × 3m with inter and intra row spacing of 75 and 25 cm, respectively. Each genotype was sown with four rows. The recommended package of practices were followed in full to raise good crop.

This degree of correspondence is measured by the heritability which is defined in broad sense as the ratio of genetic variance to phenotypic $h^2 = [V_g/V_p]$.

Broad sense heritability (H^2_b) = V_g/V_p ,

Where, V_g = genetic variance and V_p = phenotypic variance.

Results and Discussion

Considerable difference in phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) value for different traits were observed (Table 1). Among studied quantitative trait high PCV and GCV valued were found for yield per plant, high value of PCV was found for ear height while its GCV value is moderate. Moderated value of PCV and GCV were estimated for number of kernel rows per ear followed by hundred kernel weight, plant height, ear length. Moderate and low values of PCV and GCV were found for number of kernel per row respectively. Both values were low for days to 50% tasseling, days to 50% silking, SPAD chlorophyll, ear girth

Table 1: Estimation of genetic parameters (GCV, PCV, Heritability and GA)

Traits	GCV	PCV	Hbs%	GA
DTT	7.985738	8.876397	80.93879	14.79996
DTS	7.521984	7.897359	90.71959	14.75877
SPAD	7.36347	9.893052	55.39933	11.29021
PH	13.66519	14.68031	86.64843	26.20374
EH	19.92129	23.69925	70.65873	34.49591
EG	3.759496	6.745789	31.05945	4.316122
NKRE	18.80276	19.01669	97.76268	38.29793
NKR	9.685897	14.64939	43.71603	13.19251
EL	12.32804	13.10492	88.49511	23.89025
HKW	12.61537	17.84065	50.00096	18.37623
YPP	40.86857	42.92514	90.64739	80.15568

DTT= Days to 50% tasseling, DTS= Days to 50% silking, PH= Plant height, EH= Ear height, SPAD= SPAD chlorophyll, EG= Ear girth, NKRE=Number of kernel rows per ear, NKR= Number of row ear⁻¹, EL= Ear length HKW=Hundred kernels weight weight, and YPP (kg/ha) = Yield per hectare. GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, Hbs% = heritability, GA=Genetic advance

High genetic advance having value more than 20% were estimated for yield per plant, Number of kernel rows per plant, ear length, ear height, plant height. Genetic advance between 10 to 20% were observed for days to 50% tasseling, days to 50% silking, SPAD chlorophyll, Hundred kernel weight, Number of kernel per row while low lower value were estimated for ear height (Table 3).

Difference between GCV and PCV range from 0.21 to 5.22 for all trait studied. This showed that environmental effect were minimum in this parameter. Higher broad heritability revealed that larger portion of variation is heritable to offspring. Genetic advance showed that these parameter were under the control of additive gene.

GCV was highest in case grain yield per plant followed by ear height, number of kernel rows per ear and plant height. Heritability for this trait showing more than 70% indicating high heritable variation among phenotypes. Genetic advance for these trait was also higher and more than 25% showing control of additive gene for this trait. Similar

finding were also reported by Alvi *et al.* (2003), Annapurna *et al.* (1998) and You *et al.* (1998) for ear height, plant height and grain yield per plant.

The ear height, number of kernels rows per ear influence grain yield per plant directly and pre dominantly followed by plant height. Selection of genotype with more number of kernels per row having maximum ear and plant height is a pre requisite for improving grain yield.

Conclusion

By evaluating genetic parameter, number of kernel rows per ear, plant height, ear height and ear length were found to have high heritability, high genetic advance and high genotypic coefficient of variation indicate to play efficient role for high grain yield through indirect selection based on these traits. Hundreds kernels weight was also superior variable for indirect selection as they exhibited moderate high value for all genetic parameter. days to 50% tasseling, days to 50% silking and ear girth has high heritability but low genetic coefficient of variation value were also effective selection criteria for improving grain yield in maize genotype.

References

- Allard RW (1960) Principles of plant breeding. 1st Edn., John Wiley and Sons Inc., New York, pp. 213-218.
- Alvi MB, Rafique M, Tariq MS, Hussain A, Mahmood T and Sarwar M (2003) Character association and path coefficients analysis of grain yield and yield components maize (*Zea mays* L.). *Pak. J. Biol. Sci.*, **6**(2): 136-138
- Annapurna D, Khan HA and Mohammad S (1998) Genotypic-phenotypic correlations and path coefficient analysis between seed yield and other associated characters in tall genotypes of maize. *Crop Res. Hisar*. **16**: 205-9.
- Atta BM, Haq MA, Shah TM (2008). Variation and inter relationships of quantitative traits in chickpea (*Cicer arietinum* L.). *Pak J Bot* **40**: 637-647
- Chen L, Cui SP and Sun YB (1996) Analysis of the gene effect on ear characters in maize. *Acta Agr. Boreali Sinica* **11**: 28-32.
- Hamdi A, El-Ghareib AA, Shafey SA, Ibrahim MAM (2003). Genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil. *Egypt J Agr Res* **81**: 125-137.
- Kashiani P, Saleh G, Abdullah SN and Abdullah NAP (2008) Performance, eritability correlation studies on nine advance sweet corn inbred lines. *Proceeding of the 10th Symposium of Malaysian Society of Applied Biology*, Nov. 6-8, 2008, Malaysia, pp 48- 49.
- Najeed S, Rather S, Parray GA, Sheikh FA and Razvi SM (2009) Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under high altitude temperate ecology of Kashmir. *Maize Genetics Cooperation Newsletter*. **83**: 1-8.

Patil YB, Madalageri BB, Biradar BD, Hoshmani RM (1996) Variability studies in okra (*Abelmoschus esculentus* L. Moench.). *Karnataka J Agr Sci* **9**: 289–293.

Ramanjinappa V, Arunkumar KH, Hugar A, Shashibhaskar MS (2011) Genetic variability in okra (*Abelmoschus esculentus* L. Moench.). *Plant Arch* **11**: 435–437.

Singh SN, Singh JN and Singh HG (1993) Genetic variability and inter relationship in maize. *Narendra Deva J. Agric. Res.*, **6**: 233-237

You J, Dong JP, YZ GU, LL Ma and Zhao S (1998) Target characteristics to develop for improved seed production in maize hybrids, *J. Henan Agric. Sci.* **10**:3-4.