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Genetic Coefficient of Variation, Relative Expected Genetic Advance and Inter-relationships in Maize (*Zea mays* L.) For Green Fodder Purposes at Seedling Stage

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Abstract: Five hundred S_1 families were evaluated in the greenhouse for seedling traits in C_1 recurrent selection cycle. Higher values of GCV% were found for fresh shoot and dry root weight (28.85 and 41.95 respectively). Moderate broad-sense heritability (h^2_{BS}) estimates were found for fresh shoot weight, dry root weight and fresh shoot length (42.45, 48.94 and 55.0 respectively). Fresh shoot weight was phenotypically, highly significantly and positively correlated with other indicated traits. High values of coefficients of variation, positive highly significant inter-relationships, moderate broad-sense heritability (h^2_{BS}) estimates and relative expected genetic advance (REAg %) was also found greater for fresh shoot weight and dry root weight. It is generally concluded from the results that fresh shoot weight can be used as selection criteria while comparing S_1 families at seedling stage in maize as it is easy to determine as compared to dry root weight.

Key words: Maize, fodder, genetic and phenotypic correlations, heritability, genetic coefficients of variation, response to selection

Introduction

Maize (*Zea mays* L.) is an important kharif fodder crop, adaptable to varying range of climatic and soil conditions. Its staggered planting from February to September helps cope with the fodder scarcity problems faced in May-June and October-November (Nazir, 1994). Its nutritious fodder is relished by all kinds of livestock especially milch animals. Maize is also widely grown for sale as green fodder around cities. Significant variation exists for nutritional quality traits of the stover and whole-plant forage in maize (Wolf *et al.*, 1993). Differences in the rate of dry matter accumulation in different parts of the plant are related to changes in morphological structure. However, peak yield of green herbage occurs at the beginning of milky ripeness (Kirilov and Naidenov, 1990).

The production of maize fodder crop per acre is very low in Pakistan as compared to many other countries of the world. This is because, very little attention has been paid in the past to the improvement of maize as fodder crop. An adequate and regular supply of nutritious fodder is needed in Pakistan for livestock production in order to meet the requirements of milk, meat, butter and other products for human population. Therefore, this experiment was conducted to select superior families to be inter-crossed to develop high green fodder yielding population.

Materials and Methods

The experiment was conducted in a greenhouse in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad on January 7, 1999. Five hundred S_0 maize families were raised in 5 blocks and each block was assigned with 100 S_0 families. The experiment was conducted in a modified randomized complete block design with two replications. Ten seeds per family were sown in iron trays filled with river sand by keeping row-to-row and plant-to-plant distances of 5 and 3.5 cm, respectively. Water was applied to the seedlings regularly and was not a limiting factor for growth. Temperature was not fully controlled in the greenhouse and no supplementary lighting was used. The experiment was harvested after two weeks of planting and data were recorded for fresh shoot length (cm), fresh root length (cm), fresh shoot weight (g) and fresh root weight (g).

Fresh samples were left for drying in the oven. When they were completely dried, data were recorded for dry shoot weight (g) and dry root weight (g). Data were analyzed for the analysis of variance technique (Steel and Torrie, 1980). The data collected for each seedling trait was also analysed to estimate components of genetic, phenotypic and environmental variances (Johnson *et al.*, 1951). Thereafter phenotypic (r_p) and genetic (r_g) correlation coefficients (Kwon and Torrie, 1964) and estimates of broad sense heritability were also obtained to determine the superior progenies by using 20% selection intensity. Mean and coefficients of variation (CV%) were also calculated for each seedling trait. Response to selection (Ag) was also calculated as:

Response to selection $(\Delta g) = i \cdot h^2 \cdot \sigma_p$
(where $i = 1.40$)

Relative expected genetic advance (REAg %) = $(\Delta g) \times 100 / \text{Mean}$

Results and Discussion

Pooled means and genetic coefficients of variation (GCV %) for seedling traits among five hundred S_1 families are given in Table 1. The GCV (%) magnitudes were found lower for fresh shoot and root length per plant (16.25 and 9.11%, respectively). They were also low values of GCV found for dry shoot weight and fresh root weight (19.92 and 20.45% respectively). However the values of GCV (%) for fresh shoot and dry root weight per plant were found to be higher (28.85 and 41.95 respectively). However, it suggested from the results that fresh shoot weight and dry root weight may be a useful selection criteria, while selecting for high green fodder yielding S_1 families. Mehdi and Ahsan (1999) found low values for dry shoot weight (CV = 17.85%), dry root weight (CV 19.92%), fresh shoot length (CV = 17.51%) and fresh root length (CV = 19.01%) in S_1 maize families. On the other hand they found high values of coefficient of variation (CV%) for fresh shoot and root weight (29.91 and 36.06 respectively) and also suggested fresh shoot weight, a useful selection criteria as it is easy to determine as compared to dry root weight.

The phenotypic correlation coefficients (r_p) were highly significant and positive and ranging between (0.352** - 0.842**) among all indicated traits (Table 2). The fresh shoot weight had positive and highly significant phenotypic

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correlation (0.842**) with fresh root weight. The magnitudes

Table 1: Mean, genetic coefficients of variation (GCV %) of some indicated seedling-traits among 500 maize families

Trait	Mean	σ^2_g	σ^2_e	GCV %
Fresh shoot weight (g)	0.3844	0.0123	0.0166	28.85
Fresh root weight (g)	0.6543	0.0179	0.0536	20.45
Dry shoot weight (g)	0.0502	0.0001	0.0004	19.92
Dry root weight (g)	0.0892	0.0014	0.0014	41.95
Fresh shoot length (cm)	11.665	3.5955	2.9422	16.25
Fresh root length (cm)	12.653	1.3296	8.2199	9.11

Where: σ^2_g = component of genetic variance. σ^2_e = components of environmental variance

Table 2: Phenotypic (rp) and genetic correlation coefficients (r_G , in parenthesis) among some indicated seedling traits of S1 maize families

Trait	Fresh	Dry	Dry	Fresh	Fresh
Fresh root length	0.557** (0.664)	0.408** (0.977)	0.455** (0.865)	0.412** (0.953)	0.415** (0.702)
Fresh shoot length		0.372** (0.453)	0.557** (0.791)	0.620** (0.763)	0.807** (0.857)
Dry root weight			0.596** (0.969)	0.760 (0.868)	0.573** (0.854)
Dry shoot weight				0.627** (0.921)	0.713** (0.762)
Fresh root weight					0.8424** (0.909)

** = Significant at 0.01% probability level

Table 3: Broad-sense heritability (h^2 %) estimates and relative expected genetic advance (REAg %) for some indicated seedling traits among S1 maize families

Trait	h^2 %	Δg	REAg (%)
Fresh shoot weight (g)	42.45	0.1010	26.27
Fresh root weight (g)	25.08	0.0939	14.34
Dry shoot weight (g)	25.49	0.0081	16.07
Dry root weight (g)	48.94	0.0365	40.94
Fresh shoot length (cm)	55.00	1.9688	16.88
Fresh root length (cm)	13.92	0.6022	4.74

of genetic correlation coefficients (r_G) among all traits (Table 2) were found positive and ranging between (0.453-0.977). Mehdi and Ahsan (1999) reported in maize at seedling, that fresh shoot weight was positively and significantly correlated with fresh shoot length, fresh root length, fresh root weight, dry shoot weight and dry root weight. There was also positive and significant linear correlation for dry shoot weight with fresh root length and dry root weight. Fresh root weight was positively and significantly correlated with dry shoot weight, dry root weight, fresh shoot and root length. Fresh shoot length was also positively and significantly correlated with fresh root length. But fresh shoot length was negatively and significantly correlated with dry root weight. Mehdi and Ahsan (2000) reported highly significant and positive linear correlation coefficients among fresh shoot weight, fresh root weight, dry shoot weight, dry root weight, fresh shoot length and fresh root length.

Moderate broad-sense heritability ($h^2_{(BS)}$) estimates (Table 3) were found for fresh shoot weight, fresh shoot length and dry root weight ($h^2_{(BS)}$ % = 42.45, 48.94 and 55.0 respectively). But lower $h^2_{(BS)}$ % values were found for fresh root weight (25.08), dry shoot weight (25.49) and fresh root length (13.92). Mehdi and Ahsan (2000) reported moderate broad-sense heritability estimates for fresh shoot weight, dry root weight, fresh shoot length and fresh root length (53.91, 50.26, 62.50 and 48.74% respectively). The magnitudes of

relative expected genetic advance (REAg %) for fresh shoot weight and dry root weight were found high (26.27 and 40.94 respectively). However, low values for fresh root weight (REAg % = 14.34), dry shoot weight (REAg % = 16.07), fresh shoot length (REAg % = 16.88) and fresh root length (REAg % = 4.74).

The genetic coefficient of variability, phenotypic and genetic inter-relationships, heritability estimates and relative expected genetic advance (REAg %) suggesting that fresh shoot weight may be used as selection criteria, while selecting for superior families. Similarly, Mehdi and Ahsan (1999) suggested fresh shoot weight as good indicator, while selecting families for high green fodder yield. Dhillon (1991) reported two new methods of selection, alternative recurrent selection of S_1 and half-sib families. The new methods have greater expected genetic gains/year than mass, S_1 , modified S_1 , full-sib, modified full-sib, half-sib, modified ear-to-row and alternative modified S_1 -half sib selections. But, Li (1993) reported that emergence percentage has been extensively used as an indicator for seedling vigour. Similarly, Fakorede and Ayoola (1980) used emergence percentage, emergence index and dry matter accumulation growth rate and relative growth rate as an indicator for seedling vigour during the first 30 days of growth.

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