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Variability for Seedling Vigour in Two Maize (*Zea mays* L.) Populations I: Means, Variance Components and Heritabilities

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Abstract: The objective of this study was to evaluate genetic variability and heritability for various seedling traits among S_1 families of both maize populations. Three hundred S_1 families of two maize populations, viz., UAF Population-1 and UAF Population-2 were evaluated for various seedling vigour traits in two replicates. Highly significant mean squares for almost all the seedling traits indicated the presence of sufficient amount of variability for these traits. Genotypic coefficients of variation were comparatively higher for shoot dry weight, shoot fresh weight and root dry weight in both populations. The estimates of genetic variance were found significant for almost all the seedling traits except for emergence rate index which indicated the presence of exploitable genetic variability. The estimates of broad sense heritability were significant for all the seedling traits except for emergence rate index in UAF Population-1. The most heritable traits were shoot fresh length ($h^2 = 0.63$ and 0.68) and shoot fresh weight ($h^2 = 0.59$ and 0.63) in both populations which suggested that improvement in seedling vigour is possible by using S_1 family selection.

Key words: Variability, S_1 family selection, seedling vigour, coefficients of variation, genetic variance, phenotypic variance, heritability

INTRODUCTION

Breeders of our country are continuously seeking to increase grain and fodder yields of maize crop and to improve the quality of the crop, which mainly depends upon crop stand in the field. Since the final stand of a crop depends primarily on the vigour of its young seedlings, the information on the nature and extent of variation for some seedling traits and interrelationships among them would help to evaluate and select superior genotypes of maize to be used in field experiments. A plant breeder can improve seedling vigour by exploiting genetic variability available either within cultivars or breeding lines, or between different cultivars or lines.

Selection for seedling vigour under field conditions is a slow process because many micro-environmental conditions such as variability in depth of planting, soil compaction and depression in the soil surface (where water accumulates) can mask genetic effects on seedling vigour. Hence, readily measurable traits and effective screening procedures under laboratory conditions are needed. Several maize selection experiments for intra-population improvement by using the S_1 or S_2 family methods have been reported in literature^[1-8]. Previous studies^[9-13] suggest that genetic progress from S_1 selection can be made effectively in improving or

developing the genotypes having vigorous seedlings. In another study, significant selection for high seedling vigour in maize was found responsible for increasing germination time^[14]. Keeping these facts in view, the present experiment was planned to investigate the amount and nature of genetic variability present in various seedling traits among S_1 families of two maize populations. The objectives of this study were (I) to determine the extent and nature of genetic variability for various seedling traits among S_1 families of two maize populations; and (ii) to estimate components of variance and broad sense heritability for all the traits.

MATERIALS AND METHODS

The experiment was conducted in wire house in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad on January 24, 2002. The layout was a modified Randomized Complete Block Design with two replicates. A replicate-in-block design was used. The experimental material comprised of following two maize populations, viz., UAF Population-1 and UAF Population-2 which were developed in the Department for green fodder purposes in Fodder Research Project DF Pakistan Science Foundation, Islamabad (Project No. PSF/Res/P-AU/Agr (192)^[10].

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Three hundred S_1 families of each maize population were developed after selfing the S_0 plants at random from the base populations. The seed of these S_1 families were sown in iron trays filled with an equal amount of fresh sun dried river sand. Three hundred S_1 families of each maize population were assigned into six blocks where each block contained 50 families. Each experimental unit consisted of 10 plants of each S_1 family with plant to plant and row to row distances of 5.0 cm and 3.5 cm, respectively. One seed was sown per hill at uniform depth of 3.0 cm. Uniform amount of water was applied to the seedlings on regular intervals and it was not a limiting factor. Seedlings were uprooted and evaluated twenty days after planting as suggested by International Seed Testing Association^[15]. Recording of data regarding various seedling traits was started from the appearance of first emerging seed. The data on three emergence traits like emergence percentage (E%), emergence index (EI) and emergence rate index (ERI) were recorded till twenty days after planting (DAP). Total number of seedlings that emerged 20 DAP out of total number of seeds sown in each genotype was expressed as emergence percentage (E%)^[16]. Emergence index (EI), an estimate of relative rate of emergence for S_1 families was calculated from daily emergence counts made for each genotype up to 20 DAP^[16-18]. Emergence rate index for each S_1 family was calculated as the ratio of emergence index to emergence percentage (ERI = EI / E%). The plants from each S_1 family were carefully up-rooted, washed free of sand and divided at cotyledonary node into their respective root and shoot portions. Data on seedling traits namely shoot fresh length (cm), root fresh length (cm), shoot fresh weight (mg) and root fresh weight (mg) were recorded on per seedling basis. Fresh samples were left for drying in the oven. After complete drying, data for two other traits, viz., shoot dry weight (mg) and root dry weight (mg) were also recorded.

The analyses of variance and covariance for all plant traits and pairs of traits were carried out for S_1 families of UAF Population-1 and UAF Population-2 following standard statistical techniques^[19] by using appropriate soft wares. The genetic component of variance and covariance were calculated as outlined by Robinson *et al.*^[20]. Phenotypic variances were calculated by dividing S_1 family mean squares with number of replicates. The genetic and phenotypic variances were calculated separately for both populations. Phenotypic and genotypic coefficients of variation (PCV% and GCV%) were calculated using the formula given by Lothrop^[21] *et al.* Estimates of genetic variance and broad-sense heritability along with their standard errors (S.E of h^2) on S_1 family mean basis were estimated by using the procedures outlined by Lothrop *et al.*^[21]. Estimates of broad-sense heritability were considered

significant if their absolute value exceeded twice of their respective standard errors.

RESULTS AND DISCUSSION

The results of the analyses of variance revealed useful information regarding the equality of treatment means. Mean squares of all the seedling traits among S_1 families of UAF Population-1 and UAF Population-2 exhibited highly significant ($p \leq 0.01$) differences for almost all of the traits. In general, UAF Population-1 showed more variation as compared to UAF Population-2. Table 1 indicated that mean values of majority of the traits were higher in UAF Population-1 as compared to UAF Population-2 except the values of root fresh weight, root dry weight and emergence percentage. However, the pattern of increase or decrease in the mean values of various traits was similar in both the populations. The range values were mostly greater in UAF Population-1 as compared to UAF Population-2 (Table 1). Higher range values for UAF Population-1 indicated the presence of more variation in this population for these traits. The presence of variability for shoot fresh weight points to a hopeful situation for improving seedling vigour. The range values also indicated that S_1 families of maize differ greatly for the speed of emergence. Theoretically, seedlings which emerged earlier would have the advantage over the seedlings emerging later because fast emerging seedlings will have increased photosynthetic activity and a more developed root system capable of absorbing more water and nutrients. All these factors will add to the vigour of seedling by enhancing its growth. In general, the estimates of coefficients of variation were found greater in UAF Population-2 as compared to UAF Population-1 for almost all the traits except root fresh weight, emergence percentage and emergence rate index. In UAF Population-1, the largest values of coefficient of variation were observed for shoot dry weight (49.73%) and emergence rate index (45.41%) followed by root dry weight (24.41%) and shoot fresh weight (23.72%). Similarly, in UAF Population-2, the largest values of coefficient of variation were observed for shoot dry weight (54.17%) followed by root dry weight (27.49%) and shoot fresh weight (24.05%). These results are in agreement with the findings of other workers^[10,11]. Whereas these estimates were lower for shoot fresh length (13.39%), root fresh length (14.90%), emergence percentage (8.75%) and emergence index (9.39%) in UAF Population-1 and for shoot fresh length (14.07%), root fresh length (17.36%), emergence percentage (7.45%), emergence index (10.07%) and emergence rate index (12.84%) in UAF Population-2. Smaller estimates of coefficient of variation for emergence percentage (8.75 and 7.45%) and emergence index (9.39 and 10.07%) were almost consistent in both populations. In

Table 1: Mean, range and coefficient of variation for various seedling traits among S₁ families of two maize populations

Traits	UAF Population-1			UAF Population-2		
	Mean	Range	CV (%)	Mean	Range	CV (%)
Shoot fresh length (cm)	20.59	6.3-34.8	13.39	18.81	9.1-38.8	14.07
Root fresh length (cm)	13.58	3.8-22.5	14.90	13.03	5.0-32.1	17.36
Shoot fresh weight (mg)	672.38	92.0-1481.1	23.72	610.12	208.8-1503.3	24.05
Root fresh weight (mg)	711.05	160.0-2010.0	23.24	785.18	267.8-1866.7	22.46
Shoot dry weight (mg)	37.12	0.9-124.0	49.73	32.65	1.0-196.7	54.17
Root dry weight (mg)	95.17	4.0-252.0	24.41	99.42	20.0-213.0	27.49
Emergence percentage	95.23	10.0-100.0	8.75	96.60	40.0-100.0	7.45
Emergence index	44.71	29.5-63.0	9.39	44.67	26.1-61.8	10.07
Emergence rate index	0.48	0.3-4.5	45.41	0.47	0.3-1.1	12.84

CV (%) = Coefficient of Variation

Table 2: Estimates of genetic and phenotypic coefficients of variation for various seedling traits among S₁ families of two maize populations

Traits	UAF Population-1		UAF Population-2	
	GCV (%)	PCV (%)	GCV (%)	PCV (%)
Shoot fresh length (cm)	12.36	15.57	14.41	17.51
Root fresh length (cm)	10.04	14.55	11.09	16.54
Shoot fresh weight (mg)	20.28	26.32	22.35	28.09
Root fresh weight (mg)	16.17	23.06	16.73	23.07
Shoot dry weight (mg)	28.09	45.00	19.61	43.03
Root dry weight (mg)	17.73	24.75	19.12	27.27
Emergence percentage	6.22	8.78	3.34	6.23
Emergence index	5.99	8.94	7.39	10.26
Emergence rate index	12.93	34.61	7.65	11.87

GCV (%) = Genotypic Coefficient of Variation, PCV (%) = Phenotypic Coefficient of Variation

general, the estimates of both genetic and phenotypic coefficients of variation in UAF Population-1 were found smaller as compared to UAF Population-2 for almost all the traits except for shoot dry weight, emergence percentage and emergence rate index (Table 2). It is evident from the table that the estimates of genotypic coefficients of variation were found to be comparatively lower than their corresponding phenotypic coefficients of variation for all the traits studied in both populations. These greater phenotypic coefficients of variation for all the seedling traits reflect a favourable genotype-environment interaction.

In general, the estimates of phenotypic variance exceeded their respective genotypic variance estimates for all the traits evaluated in both populations (Table 3 and 4). Likewise, the estimates of genetic variance were greater than the estimates of environmental variances for traits like shoot fresh length, shoot fresh weight, root dry weight and emergence percentage in UAF Population-1 and for shoot fresh length, shoot fresh weight, root fresh weight and emergence index in UAF Population-2. These results indicate that these traits were less affected by environment and exhibited sufficient amount of genetic variability. The remaining traits showed smaller estimates of genetic variance than their respective environmental variance in both populations. Therefore, these traits were much sensitive to the environmental effects. The estimates of phenotypic variances were larger than their respective genetic variances as well as environmental

variances in both populations. The estimates of genetic variance were significant for all the seedling traits studied as their absolute magnitude exceeded twice their respective standard error in both populations except emergence rate index in UAF Population-1 which showed non-significant estimate of genetic variance. This statistic revealed that significant genetic variability existed among S₁ families of both populations. Significant genotypic variation for most of the seedling vigour traits has also been noted in a recombinant inbred (RI) sorghum (*Sorghum bicolor* L. Moench) population^[22] and in S₁ testcross progeny of maize^[9]. The genetic variance estimates were comparatively larger for most of the traits in UAF Population-2 than UAF Population-1 except for shoot dry weight, emergence percentage and emergence rate index. The estimates of environmental variance were found greater in UAF Population-1 as compared to UAF Population-2 except for root fresh length, root fresh weight, root dry weight and emergence index. The higher genetic variance in UAF Population-2 indicated the presence of greater genetic variability in it as compared to UAF Population-1.

Estimates of broad sense heritability of all traits were significant as their absolute values exceeded twice their respective standard errors in both the populations except emergence rate index in UAF Population-1 (Table 3 and 4). Significant estimates of broad sense heritability for seedling traits like emergence percentage, shoot fresh length, root fresh length, shoot fresh weight, root fresh

Table 3: Estimates of components of variance and broad sense heritability for various seedling traits among S₁ families of UAF Population-1

Traits	$\sigma^2_g \pm SE(\sigma^2_g)$	σ^2_e	σ^2_p	$h^2 \pm SE(h^2)$
Shoot fresh length (cm)	6.4763 [±] ±0.9004	3.7985	10.2748	0.6303 [±] ±0.0876
Root fresh length (cm)	1.8590 [±] ±0.3624	2.0459	3.9048	0.4761 [±] ±0.0928
Shoot fresh weight (mg)	18594.6151 [±] ±2778.6640	12723.4135	31318.0286	0.5937 [±] ±0.0887
Root fresh weight (mg)	13218.2829 [±] ±2478.1380	13658.2144	26876.4973	0.4918 [±] ±0.0922
Shoot dry weight (mg)	108.6877 [±] ±26.8781	170.3934	279.0811	0.3894 [±] ±0.0963
Root dry weight (mg)	284.8395 [±] ±50.6965	269.7772	554.6167	0.5136 [±] ±0.0914
Emergence percentage	35.1020 [±] ±6.4118	34.7381	69.8401	0.5026 [±] ±0.0918
Emergence index	7.1658 [±] ±1.4997	8.8102	15.9759	0.4485 [±] ±0.0939
Emergence rate index	0.0039 [±] ±0.0030	0.0238	0.0276	0.1395 [±] ±0.1084

± = Standard error value,

* = The estimate of genetic variance / broad-sense heritability differs significantly from zero as its absolute magnitude exceeded twice its respective standard error

Table 4: Estimates of components of variance and broad sense heritability for various seedling traits among S₁ families of UAF Population-2

Traits	$\sigma^2_g \pm SE(\sigma^2_g)$	σ^2_e	σ^2_p	$h^2 \pm SE(h^2)$
Shoot fresh length (cm)	7.3511 [±] ±0.9374	3.5019	10.8530	0.6773 [±] ±0.0864
Root fresh length (cm)	2.0887 [±] ±0.4360	2.5583	4.6400	0.4495 [±] ±0.0938
Shoot fresh weight (mg)	18601.5066 [±] ±2571.2170	10767.1686	29368.6749	0.6334 [±] ±0.0875
Root fresh weight (mg)	17264.3247 [±] ±2984.6290	15547.9613	32812.2860	0.5262 [±] ±0.0910
Shoot dry weight (mg)	40.9832 [±] ±20.3990	156.3856	197.3688	0.2076 [±] ±0.1034
Root dry weight (mg)	361.5235 [±] ±67.7650	373.4402	734.9637	0.4919 [±] ±0.0922
Emergence percentage	10.3837 [±] ±03.6618	25.8776	36.2612	0.2864 [±] ±0.1010
Emergence index	10.8873 [±] ±01.9174	10.1262	21.0135	0.5181 [±] ±0.0912
Emergence rate index	0.0013 [±] ±0.0003	0.0018	0.0031	0.4153 [±] ±0.0952

± = Standard error value,

* = The estimate of genetic variance / broad-sense heritability differs significantly from zero as its absolute magnitude exceeded twice its respective standard error

weight and shoot dry weight have been reported in the literature^[11,12]. In contrast, emergence rate index showed non-significant heritability estimate in UAF Population-1. These results were supported by the findings of some other plant breeders working on maize seedlings^[23,24] who also observed non-significant broad sense heritability estimate for this particular trait. Table 3 and 4 indicated that broad sense heritability estimates were, in general, larger for most of the traits in UAF Population-2 as compared to UAF Population-1 except for root fresh length, shoot dry weight, root dry weight and emergence percentage which showed smaller estimated values. However, smallest estimates of both genetic and environmental variance for emergence rate index in UAF Population-1 resulted in smallest estimate of broad sense heritability. This suggested that emergence rate index was not a reliable indicator of seedling vigour

It is evident from these tables that the estimates of heritability ranged from 0.14 (emergence rate index) to 0.63 (shoot fresh length) in UAF Population-1 and from 0.21 (shoot dry weight) to 0.68 (shoot fresh length) in UAF Population-2. Shoot fresh weight ranked second highest in both the populations. Similar trends have also been reported by other maize breeders^[11]. However, shoot fresh length was the most heritable trait with the values of 0.63 and 0.68 in UAF Population-1 and UAF Population-2, respectively thus supporting the results of some other researchers^[11,12] what they observed in maize seedling studies. However, in a study root dry weight was found as the most heritable trait^[13].

It is well evident from the magnitudes of mean, range and coefficients of variation that both maize populations seemed to possess sufficient exploitable genetic variability that may be useful for selecting young seedlings having greater vigour.

Greater genetic variability in UAF Population-2 as compared to UAF Population-1 indicated the scope of this population for making progress from selection in further breeding work.

It can also be concluded that most of the traits in UAF Population-2 were better heritable as compared to UAF Population-1. This implies that the proportion of total variation due to average effects of genes for these traits was of a reasonable magnitude; hence this would play a vital role in a selection scheme. Moreover, it is also evident from the moderately high heritability estimates of all these traits that these could be further improved through simple selection procedures.

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