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Variability for Seedling Vigour in Two Maize (*Zea mays* L.) Populations. II: Correlations and Response to Selection

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Abstract: Estimated gains from selection and interrelationships among seedling traits in two maize populations (UAF Population-1 and UAF Population-2) were evaluated using data from S_1 families. In UAF Population-1, shoot fresh weight showed significant and positive genetic correlations with shoot fresh length and root fresh weight. Similar relationship was also observed between root fresh weight and root dry weight. Whereas shoot dry weight showed perfect positive genetic correlation ($r_g=1.04$) with emergence rate index. In UAF Population-2, shoot fresh weight had positive and significant genetic correlations with shoot fresh length and root fresh weight. Whereas shoot dry weight showed perfect positive genetic correlations with shoot fresh length ($r_g=1.03$) and shoot fresh weight ($r_g=1.01$). The estimates of response to selection had greater magnitudes for shoot fresh weight in both populations (24.28 and 27.69%, respectively), which indicated that S_1 family selection would be effective for improving seedling vigour. Thus, shoot fresh weight appeared to be the most appropriate indicator of seedling vigour.

Key words: Variability, seedling vigour, genetic correlation, phenotypic correlation, response to selection.

INTRODUCTION

Random-mating populations of maize (*Zea mays* L.) with improved seedling vigour may be graduated directly to the farmer's field and may also yield superior inbreds for a simultaneous hybrid programme^[1]. Mehdi and Ahsan^[2] developed a synthetic maize population by improving seedling vigour that had the potential to produce maximum green fodder. Knowledge concerning the interrelationships among various seedling traits in source population is one of the primary requisites to plan any effective selection or breeding programme for the improvement of seedling vigour in maize. Correlation is a measure of the extent of relationship between two or more variables. Genetic correlation expresses the extent to which the two traits are genetically associated. Information on such an association permits the feasibility of indirect selection for various parameters. Such relationships provide useful information to the plant breeder in identifying characters that have little or no importance in the selection programmes. Positive and linear inter-relationships were noted among some seedling traits in maize^[3-8] and Sorghum^[9,10]. These seedling studies have been associated with field performance and yield as mentioned by DeHaan *et al.*^[11] and some clover breeders^[12,13].

Estimates of response to selection or genetic gain are useful for predicting the genetic improvement of a population in a selection programme. The response of a

population to selection must depend on the amount, distribution and system of genetic variability in the population^[14]. The expected genetic advance is a gain or a change produced by selection and is of main interest to a plant breeder since it changes the population mean. An expected improvement in a particular trait in the preceding generation can best be judged through relative expected genetic advance at some appropriate selection intensity. Significant estimates of genetic gains for seedling vigour have been observed by Ahmad^[7] and Aleem^[8] in maize seedlings. DeHaan *et al.*^[11] determined changes in plant biomass due to selection by measuring seedling fresh weights. It provided a rapid approach to measuring response to selection. Keeping these facts in view, it was considered imperative to evaluate the potential of S_1 progenies of maize populations at seedling stage. The objectives of present study were (i) to estimate the correlation coefficients both at genetic and phenotypic levels for various seedling traits among S_1 families of maize populations, (ii) to estimate genetic gains to determine the response of various seedling traits to S_1 family selection and (iii) to select a seedling trait as the best indicator of seedling vigour.

MATERIALS AND METHODS

The plant genotypes, experimental procedures, design, layout and statistical calculations employed in our study have been described in previous study^[15].

In brief, S₁ families of two maize populations, viz., UAF Population-1 and UAF Population-2 were used. From each population, three hundred S₁ families were developed after selfing the S₀ plants at random and evaluated for various seedling traits in wire house in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad on January 24, 2002.

The genetic components of covariance were calculated as outlined by Robinson *et al.*^[16]. Genetic correlation coefficients were estimated by using the formula given by Kown and Torrie^[17]. Similarly, phenotypic correlation coefficients were also calculated. Standard errors of genetic correlation coefficients were computed by using the equation given by Reeve^[18] and Robertson^[19]. However, the significance of phenotypic correlation coefficients was tested by using T-test^[20]. Estimates of genetic correlation coefficients were considered significant if their absolute value exceeded twice of their respective standard errors. Response to selection (ΔG) for each trait was calculated following Falconer^[21], Empig *et al.*^[22] and Sprague and Eberhart^[23]. Response to selection was also calculated in relative terms by dividing the magnitudes with respective mean values.

RESULTS AND DISCUSSION

The estimates of genotypic correlation coefficients tended to be larger than the corresponding estimates of phenotypic correlation coefficients for most of the trait pairs in both maize populations (Table 1 and 2). This tendency resulted from the fact that the estimated genotypic variances were smaller than the corresponding estimated phenotypic variances. The estimates of correlation coefficients at both genetic and phenotypic level were, in general, larger in magnitude in UAF

Population-2 as compared to UAF Population-1, which suggested that improvement in various plant traits through indirect selection is more feasible in UAF Population-2 as compared to UAF Population-1.

Shoot fresh weight paired with shoot fresh length and root fresh weight root fresh weight paired with root dry weight; and shoot dry weight paired with emergence rate index showed significant positive genetic correlations in UAF Population-1 (Table 1). These results support the observations of other researchers^[4]. Similarly, shoot fresh weight when paired with shoot fresh length, root fresh weight and shoot dry weight and shoot dry weight when paired with shoot fresh length and root fresh weight showed significant positive genetic correlations in UAF Population-2 (Table 2). The remaining trait pairs showed non-significant genetic correlations, however, the values were mostly positive. The results indicated that the information drawn from significant positive estimates of genetic correlation compared with negative correlations might be fruitful to favour selection of desired traits. This confirms the findings of Simmonds and Smartt^[24].

Shoot dry weight showed positive and perfect genetic correlation with emergence rate index in UAF Population-1; and with shoot fresh length and shoot fresh weight in UAF Population-2. These relationships provide an indication that for the improvement of seedling vigour measured on traits like shoot fresh length, shoot fresh weight and emergence rate index in maize populations, dry weight of shoots is of considerable importance and should receive due importance in selection. It is evident from Table 2 that in UAF Population-2, the three shoot traits, namely, shoot fresh length, shoot fresh weight and shoot dry weight have significant positive correlations among them at both genetic and phenotypic levels, which indicated that these seedling traits were strongly associated with each other. Thus, improvement in either of these will simultaneously improve the other.

Table 1: Estimates of genetic (top figures) and phenotypic (bottom figures) correlation coefficients for various seedling traits among S₁ families of UAF population-1

Traits	Root fresh length (cm)	Shoot fresh weight (mg)	Root fresh weight (mg)	Shoot dry weight (mg)	Root dry weight (mg)	Emergence percentage	Emergence index	Emergence rate index
Shoot fresh length (cm)	0.1438	0.8732 ⁺	0.6269	0.6325	0.4484	-0.0826	0.4490	0.5708
	0.2413**	0.7155**	0.4520**	0.4169**	0.2751**	-0.0119	0.3043**	0.1737**
Root fresh length (cm)		0.2005	0.0945	0.3596	0.0941	0.2556	-0.0396	-0.3025
		0.2271**	0.1912**	0.2247**	0.1140	0.1194*	0.0443	-0.0481
Shoot fresh weight (mg)			0.8357 ⁺	0.6985	0.6687	-0.0705	0.5677	0.5936
			0.6423**	0.4884**	0.4372**	-0.0352	0.3394**	0.1835**
Root fresh weight (mg)				0.4931	0.8112 ⁺	0.0644	0.4573	0.3393
				0.3033**	0.6186**	0.0162	0.2928**	0.1302*
Shoot dry weight (mg)					0.7047	-0.2572	0.6284	1.0366 ⁺
					0.3155**	-0.0823	0.2767**	0.2096**
Root dry weight (mg)						-0.1040	0.6192	0.5350
						-0.0635	0.3062**	0.1839**
Emergence percentage							0.1151	-0.6987
							0.0610	-0.5420**
Emergence index								0.6266
								0.2686**

+ = The estimate of genetic correlation coefficient differs significantly from zero as its absolute magnitude exceeded twice its respective standard error
 *, ** = Significant at 0.05 and 0.01 probability levels, respectively

Table 2: Estimates of genetic (top figures) and phenotypic (bottom figures) correlation coefficients for various seedling traits among S₁ families of UAF Population-2

Traits	Root fresh length (cm)	Shoot fresh weight (mg)	Root fresh weight (mg)	Shoot dry weight (mg)	Root dry weight (mg)	Emergence percentage	Emergence index	Emergence rate index
Shoot fresh length (cm)	0.3306	0.9444 ⁺	0.7192	1.0281 ⁺	0.5749	0.0205	0.5422	0.3623
	0.1880 ^{**}	0.7958 ^{**}	0.4696 ^{**}	0.5554 ^{**}	0.3306 ^{**}	0.0306	0.3552 ^{**}	0.2070 ^{**}
Root fresh length (cm)		0.4530	0.6268	0.2564	0.3302	-0.0179	0.2087	0.1596
		0.3050 ^{**}	0.4755 ^{**}	0.1591 ^{**}	0.2824 ^{**}	-0.0017	0.1509 ^{**}	0.1177
Shoot fresh weight (mg)			0.7820 ⁺	1.0080 ⁺	0.6565	0.0238	0.5302	0.3573
			0.5697 ^{**}	0.6143 ^{**}	0.4115 ^{**}	0.0202	0.3358 ^{**}	0.2149 ^{**}
Root fresh weight (mg)				0.8493 ⁺	0.7082	-0.0401	0.5273	0.3949
				0.2033 ^{**}	0.6133 ^{**}	0.0105	0.3410 ^{**}	0.2408 ^{**}
Shoot dry weight (mg)					0.7678	0.1578	0.7125	0.4802
					0.3061 ^{**}	0.1021	0.2755 ^{**}	0.1247
Root dry weight (mg)						-0.1320	0.3650	0.3715
						-0.0574	0.2323 ^{**}	0.2149 ^{**}
Emergence percentage							0.1195	-0.5489
							0.0633	-0.6321 ^{**}
Emergence index								0.7452
								0.6110 ^{**}

+ = The estimate of genetic correlation coefficient differs significantly from zero as its absolute magnitude exceeded twice its respective standard error
 *, ** = Significant at 0.05 and 0.01 probability levels, respectively

Furthermore, both shoot fresh weight and root fresh weight had positive correlations with their corresponding dry weights in both populations. Similar associations between fresh and dry weights were also reported by many other researchers^[3-6]. This further indicated that the shoot traits in the present study are better indices of screening for seedling vigour.

Positive genotypic correlations with greater magnitudes among various seedling traits suggested that seedlings with heavy green foliage (shoot fresh weight) had longer shoots (fresh shoot length), well developed root system (root fresh weight) and more dry weight of shoots in both populations. Additionally, seedlings which emerged later had more dry weight of shoots in UAF Population-1. Thus, seedling vigour may be characterized by longer shoots with more fresh and dry weights. The results, therefore, finally suggested that shoot fresh weight might be considered as an indicator of seedling vigour.

Negative values for the estimates of genetic correlation were noted for emergence percentage paired with shoot fresh length, shoot fresh weight, shoot dry weight, root dry weight and emergence rate index; and for root fresh length paired with emergence index and emergence rate index in UAF Population-1. It can, therefore, be concluded that more the emergence percentage less will be the seedling vigour and vice versa. Similarly, emergence percentage paired with root fresh length, root fresh weight, root dry weight and emergence rate index showed negative values for genetic correlations in UAF Population-2. Moreover, lowest values for the estimates of genetic correlation coefficients were noted for emergence percentage when paired with all other seedling traits in both maize populations. From these

results, it can be concluded that selection for high seedling vigour measured on traits like shoot fresh length, root fresh length, shoot fresh weight, root fresh weight, shoot dry weight and root dry weight can not be based on high percentage and speed of emergence. In contrast, Li^[25] suggested that emergence percentage and emergence index could be considered as an indicator of seedling vigour.

Estimates of positive and significant ($p \leq 0.05$) phenotypic correlation were noted for emergence percentage paired with root fresh length and emergence rate index paired with root fresh weight in UAF Population-1. Estimates of phenotypic correlation coefficients were negative and highly significant between emergence percentage and emergence rate index in both populations. Significant phenotypic correlations indicated that seedlings which emerged earlier had more emergence percentage whereas ones emerging later possessed more seedling vigour in both maize populations. Moreover, phenotypic selection for seedling vigour in this particular environment may be based on shoot and root traits in both populations.

In general, the estimates of genetic advance and relative expected genetic advance were, mostly, higher in magnitude in UAF Population-2 than in UAF Population-1 (Table 3). It gives a clear indication that UAF Population-2 has more scope for improvement of seedling vigour traits through S₁ family selection as compared to UAF Population-1.

It is evident from Table 3 that in UAF Population-1, the estimates of response to selection for traits like shoot fresh weight, root fresh weight, root dry weight and shoot dry weight were considerably higher than other traits at

Table 3: Estimates of genetic advance and relative expected genetic advance for various seedling traits among S₁ families of two maize populations

Traits	UAF Population-1		UAF Population-2	
	ΔG	REAG (%)	ΔG	REAG (%)
Shoot fresh length (cm)	3.1397	15.25	3.4676	18.43
Root fresh length (cm)	1.4619	10.77	1.5057	11.56
Shoot fresh weight (mg)	163.2830	24.28	168.6774	27.69
Root fresh weight (mg)	125.2967	17.62	148.1093	18.86
Shoot dry weight (mg)	10.1103	27.24	4.5333	13.88
Root dry weight (mg)	18.7955	19.75	20.7231	20.84
Emergence percentage	6.5273	6.85	2.6797	2.77
Emergence index	2.7860	6.23	3.6908	8.26
Emergence rate index	0.0360	7.50	0.0360	7.66

ΔG=Genetic advance, REAG=Relative expected genetic advance

15% selection intensity. Likewise, in UAF Population-2, the same traits showed high estimates of expected genetic advance at 15% selection intensity. But, the relative expected genetic advance at the same selection intensity was found higher for shoot fresh weight, root fresh weight, root dry weight and shoot fresh length and low for shoot dry weight, root fresh length and emergence rate index. The highest values of expected genetic advance for shoot fresh weight in both populations revealed that selection for this trait is effective. However, the estimates of relative expected genetic advance were found to be minimal for emergence index in UAF Population-1 and emergence percentage in UAF Population-2 (6.23 and 2.77%, respectively).

A further perusal of Table 3 indicated greatest estimate of relative expected genetic advance for shoot fresh weight in UAF Population-2 (27.69%), whereas in UAF Population-1 it ranked second (24.28%) after shoot dry weight (27.24%). It may be concluded here that maximum progress can be achieved by making selection for shoot fresh weight. These results agree with the findings of many other researchers^[5,7,8,11].

Present results suggested that through S₁ family selection the seedling vigour of UAF Population-1 may be improved by an associated change in the means of shoot fresh weight from 672.38 to 835.66 mg, root fresh weight from 711.05 to 836.35 mg, shoot dry weight from 37.12 to 47.23 mg and a gain of 18.80 mg in root dry weight. Similarly, the seedling vigour of UAF Population-2 may be improved by an associated change in the means of shoot fresh weight from 610.12 to 778.80 mg, root fresh weight from 785.18 to 933.29 mg, root dry weight from 99.42 to 120.14 mg and a gain of 4.53 mg in shoot dry weight.

Shoot fresh weight was considered as precise indicator of seedling vigour in both populations and it might be used as selection criterion for picking up the best families with vigorous seedlings in both populations to improve (grain or fodder) yield.

Significant improvement in seedling vigour could be more efficiently made in UAF Population-2 as evident from strong positive and significant associations among all shoot traits.

Progress from either direct or indirect S₁ selection could be efficiently made in UAF Population-2 as compared to UAF Population-1.

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