

## VARIABILITY FOR AGRONOMIC TRAITS IN SUNFLOWER RANDOM-MATING POPULATIONS: CORRELATIONS, ESTIMATED GAINS FROM SELECTION, AND CORRELATED RESPONSES TO SELECTION

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### SUMMARY

Estimated gains from selection and interrelationship among agronomic characters were evaluated in the random-mating sunflower populations Local Open and UAF using data from two seasons (spring and fall).

Among 66 combinations of 12 traits included; number of leaves per plant with days to anthesis and head diameter; plant height with seed yield per plant; days to flowering with days to anthesis, days to maturity and head diameter; days to anthesis with days to maturity, head diameter and seed yield per plant; and days to maturity with seed yield per plant showed significant, positive correlations in both sunflower populations during spring.

Most often, genetic correlations were slightly higher than their respective phenotypic correlations in UAF sunflower population during spring and fall. But the trend was almost reverse in Local Open during both seasons.

Estimates of percentage gain per generation for selection at 20% intensity indicated that this selection would be effective for improving seed and oil yield. The estimated gain for achene yield was 31.33 and 24.38% per generation (Local Open and UAF) when S<sub>1</sub> testing was conducted in spring season.

Correlated responses to S<sub>1</sub> selection for yield and the components of yield indicated that indirect selection for achene yield and oil yield would be effective. Direct selection for yield was estimated to result in favorable increases in all yield components.

**Key words:** sunflower, random matting population, agronomic traits, selection and breeding, statistical analysis

### INTRODUCTION

Random-mating sunflower populations of sunflower (*Helianthus annuus* L.) are expected to be useful for the development of new inbred lines (Eberhart, 1967;

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Ross, 1980). These lines may serve as parental stocks for the production of hybrid sunflower and further enhancement of breeding populations. Populations breeding for specific traits may be improved by using different recurrent selection methods.

Predicted gains from recurrent selection in a population may be determined by using estimates of means, variance components, and heritabilities. Formulae for estimating the predictions have been proposed by Empig *et al.* (1972) and Sprague and Eberhart (1977). Rational choices among selection methods are possible when predicted gains are expressed as percentage gain per generation or gain per year.

Knowledge concerning phenotypic and genetic correlations among agronomic traits is important because it permits estimation of the feasibility of indirect selection for seed and oil yield and of correlated responses to selection. Correlations among sunflower traits have been determined (Russel, 1953; Morozov and Beshjatova, 1967; Burns, 1970; Ivanov and Stoyanova, 1980; Rostova *et al.*, 1984; Sheriff *et al.*, 1984; Tyagi, 1985; Burns, 1970; Kovari and Weinbremer, 1988; Pasda and Diepenbrock, 1990; Singh and Labana, 1990; Ahmad *et al.*, 1991; Visic, 1991; Krizmanic *et al.*, 1992; Chaudhary and Anand, 1993; Punia and Gill, 1994; Boujghagh, 1994; Gangappa and Virupakshappa, 1994; Mirza *et al.*, 1994; Buttar and Uppal, 1998; Razi and Assand, 1999). Usually the components of yield were highly correlated with achene and oil yield.

Tall and late maturing genotypes/families have tended to be highest in yield. But the correlations between these traits have been low enough not to preclude improvement for achene and oil yield without large increases in plant height and maturity.

The objective of research with the sunflower populations i.e., Local Open and UAF were to (i) determine correlations among agronomic traits (ii) estimate gains from  $S_1$  families to selection, and (iii) estimate correlated responses among traits to selection.

## MATERIALS AND METHODS

The plant materials, experimental design, procedures, and data analysis methods employed in our experiments have been described (Syed *et al.*, 2003). In brief, we used  $S_1$  families in two experiments/seasons. Both experiments were conducted at Faisalabad (Pakistan), Postgraduate Experimental Research Station of University of Agriculture, Faisalabad during 1997 and 1999.

Several statistics, beyond these presented in the preceding report (Syed *et al.*, 2003), are presented in this paper. Phenotypic correlations among traits were calculated by using mean products and estimates of genetic variance obtained from the combined analysis of variance for each experiment.

The following formulae were used for the estimation of variances and covariances:

$$\sigma^2g = (MS_2 - MS_1)/r$$

$$\sigma^2p = MS_2/r$$

$$\sigma g = (MP_2 - MP_1)/r$$

$$\sigma p = MP_2/r$$

where,

$\sigma^2g$  = the estimates of family genetic variance;

$\sigma^2p$  = the estimates of family phenotypic variance;

$\sigma g$  = the estimates of family genetic covariance between i and j traits;

$\sigma p$  = the estimates of family phenotypic covariance between i and j traits;

$MS_2$  and  $MS_1$  = the estimates of family mean square and error mean square, respectively

$MP_2$  and  $MP_1$  = The estimates of family mean cross product and environmental mean cross product for i and j traits, respectively.

$r$  = the number of replicates.

Estimates of broad sense heritability on  $S_1$  family mean basis were calculated for each trait in both the populations with the formula:

$$h^2_{(BS)} = \sigma^2g / \sigma^2p$$

Where,  $\sigma^2g$  and  $\sigma^2p$  are the estimates of genetic and phenotypic variances, respectively.

Standard error (SE) of broad sense heritability on a plot mean basis were calculated by using the procedure described by Lothrop *et al.* (1985b) as under:

$$SE_{(h^2)} = SE(\sigma^2g) / \sigma^2p$$

Where,  $SE_{(h^2)}$  = the standard error of the broad sense heritability,

$SE(\sigma^2g)$  = the standard error of the family genetic variance, and

$\sigma^2p$  = the family phenotypic variance.

Standard error of genetic variance ( $SE \sigma^2g$ ) was calculated by using the formula presented by Lothrop *et al.* (1985):

$$SE(h^2) = SE(r^2g) / \sigma^2p$$

$$SE(\sigma^2g) = [2/C^2 \{ \sum MS_i^2 / (df_i + 2) \}]^{1/2}$$

Where,  $C$  = the coefficient of the components in the expected mean squares,

$MS_i$  = the mean square for the  $i^{th}$  trait and

$df_i$  = the degree of freedom for the  $i^{th}$  trait.

The estimates of genetic correlation coefficient were computed for all pairs of traits in each sunflower population with data from both the seasons separately. The formula used was:

$$rg = \sigma g_{xy} / (\sigma^2g_x \times \sigma^2g_y)^{1/2}$$

Where,  $\sigma^2g_x$  = the family genetic variance for trait x;

$\sigma^2g_y$  = the family genetic variance for trait y, and

$\sigma g_{xy}$  = the family co-genetic variance between traits x and y.

Phenotypic correlation coefficients were also calculated in a similar way using the phenotypic covariance and variances estimates. The significance of phenotypic correlation coefficients was tested by using "t"-test:

$$t = \frac{r}{\sqrt{\frac{n-2}{n-1} \frac{1-r^2}{n-1}}}$$

Where, r=correlation coefficient

n=Total number of observation/error df

This "t" value was tested against the table value of "t" with (n-2) degrees of freedom. If the observed value is more than the tabulated one, the correlation coefficient is said to be significant (Fisher and Yates, 1938).

The estimates of standard error of genetic correlation coefficients were computed after Reeve (1955) and Robertson (1959) given as under:

$$SE(r_g) = 1 - (r_g)^2 / \sqrt{2 \{ (\sqrt{h^2_x} / h^2_x \sqrt{h^2_y} / h^2_y) \}^{1/2}}$$

Where SE(r<sub>g</sub>)=the standard error of genetic correlation;

r<sub>g</sub>=the genetic correlation coefficient;

h<sup>2</sup><sub>x</sub>, h<sup>2</sup><sub>y</sub>=the broad sense heritability estimates of trait x and trait y, respectively.

The estimates of broad sense heritability and genetic correlation coefficients were considered significant if their absolute value exceeded twice of their respective standard errors.

Predicted responses or Genetic gains for selections (Δg) were calculated after Falconer (1989):

$$\Delta g = k \sigma_p h^2$$

Where:

K is the standardized selection differential (20% selection intensity k=1.40).

σ<sub>P</sub>=the phenotypic standard deviation.

h<sup>2</sup>=the broad sense heritability in fraction.

Correlated response to selection was calculated by using the formula presented by Falconer (1989):

$$CR_y(x) = Kx h_x r_{gxy} \sigma_{gy}$$

where:

CR<sub>y</sub>(x)=the expected correlated response in trait Y when selection is for trait X.

Kx=the standardized selection differential applied in selection for trait X.

h<sub>x</sub>=the square root of the heritability of trait X.

r<sub>gxy</sub>=the genetic correlation between trait X and Y, and

σ<sub>gy</sub>=the genetic standard deviation for trait Y.

## RESULTS

### Correlations

In our study, among 66 combinations of 12 traits included; number of leaves per plant with days to anthesis and head diameter; plant height with seed yield per plant; days to flowering with days to anthesis, days to maturity and head diameter; days to anthesis with days to maturity, head diameter and seed yield per plant; and days to maturity with seed yield per plant showed significant, positive, genetic correlations in both sunflower populations during spring (Tables 1 and 2).

Similarly, number of leaves per plant with days to flowering, days to anthesis, days to maturity, head diameter and seed yield per plant; Plant height with days to anthesis, days to maturity and seed yield per plant; days to flowering with days to anthesis, days to maturity, seed yield per plant and oil content; days to anthesis with days to maturity and seed yield per plant; days to maturity with head diameter; and seed yield per plant with oil content have shown significant, positive correlations in both sunflower populations during the fall season.

However, significant positive genetic interrelationships were found between head diameter with achene weight; number of leaves with days to flowering, days to maturity and seed yield per plant; plant height with days to maturity; and days to maturity with head diameter in Local Open during spring.

Whereas, number of achenes per head with oil yield; seed yield per acre with oil content and oil yield per acre; plant height with head diameter; days to flowering with achene weight; and days to anthesis with head diameter and achene weight were also found positive and significant during the fall.

Likewise, days to flowering with plant height and seed yield per plant have exhibited significant, positive, genetic interrelationships during spring in the sunflower population UAF.

Whereas, during the fall, genetic associations between head diameter with oil content; Number of leaves per plant with oil content; Plant height with days to flowering, oil content and oil yield per acre; and days to flowering with head diameter and days to anthesis with oil content were found significant and positive during the fall season.

Negative and weak genetic associations were noticed in the sunflower population Local Open (fall) among number of leaves per plant with plant height, but non-significant and coefficients of -0.086.

### Genetic gains

When 20, S<sub>1</sub> families from the sunflower population Local Open with the highest values of traits were selected, the progenies were predicted to have highest average *i.e.*, 31.60% higher for seed yield per plant followed by 31.33% for seed yield per acre than the progenies of unselected families during spring. The lowest predicted average increase was for days to maturity (1.84%).

Table 1.: Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of sunflower population Local Open in spring (top figure) and fall (bottom figure)

TRAITS	LPP	PLHT	DF	DA	DM	HDDIA	ACWT	ACPERHD	SDYLD/PLT	SDYLD/ACR	OILC	OILYLD
LPP		0.097 NS	0.630*	0.651*	0.934*	0.322*	0.250 NS	0.250 NS	0.309*	0.0161 NS		
		-0.086 NS	0.665*	0.928*	0.354*	0.597*	0.250 NS	0.250 NS	0.010 NS	1.977 NS	0.026 NS	
PLHT	0.105 NS		0.120 NS	0.100 NS	0.211 NS	0.040*	0.087 NS	0.054 NS	0.376*	0.08 NS		
	0.770**		0.213 NS	0.260*	0.661*	0.127*	0.087 NS	0.054 NS	0.818*	10.380 NS	4.608 NS	0.080 NS
DF	0.688**	0.129 NS		0.146*	0.548*	0.314*	0.371 NS	0.018 NS				
	0.271**	0.230**		0.421*	0.262*	1.037 NS	0.430*	0.016 NS	0.280*	0.013 NS	0.983*	0.0215 NS
DA	0.680**	0.110 NS	0.245**		0.891*	0.226*	0.274*	0.013 NS				
	2.527 NS	0.330**	0.436**		0.350*	0.805 NS	0.356*	0.019 NS	0.370*	0.017 NS	1.230 NS	0.026 NS
DM	0.579**	0.135 NS	0.434**	0.539**		0.455*	0.513*	0.014 NS				
	1.330 NS	0.606**	0.331**	0.494**		0.285*	0.119 NS	0.050 NS	0.093*	0.039 NS	3.538 NS	0.067 NS
HDDIA	0.417**	0.062**	0.410**	0.560**	0.329**		0.061 NS	0.005 NS				
	0.233**	0.135 NS	0.644**	0.611 NS	0.300**		0.74*	0.006 NS	0.080 NS	0.006 NS	0.125 NS	0.091 NS
ACWT	0.105 NS	0.089 NS	0.028 NS	0.278**	0.140*	0.416**		0.006 NS	0.110 NS	0.004 NS	0.446 NS	0.008 NS
ACPERHD	0.062 NS	0.059 NS	0.017 NS	0.020 NS	0.046 NS	0.007 NS	0.006 NS		0.003 NS	0.030 NS	65.040 NS	1.064*
SDYLD/PLT	0.281**	0.460**	0.326**	0.248 **	0.285**	0.094**			0.0167 NS			
	1.060 NS	0.830**	0.240**	0.360 **	0.536**	0.090 NS	0.090 NS	0.011 NS	-0.0009 NS	3.803*	0.060 NS	
SDYLD/ACR	0.010 NS	0.055 NS	0.011 NS	0.008 NS	0.015 NS	0.004 NS			0.015 NS		82.353 NS	1.250 NS
	0.042 NS	16.060 NS	0.010 NS	0.016 NS	0.031**	0.005 NS	0.004 NS	0.457**	0.006 NS			
OILC	4.116 NS	4.575 NS	1.050 NS	2.481 NS	1.922 NS	0.969*	0.872*	63.340 NS	4.316 NS	92.940 NS		0.018 NS
OILYLD	0.036 NS	0.039 NS	0.009 NS	0.014 NS	0.0269 NS	0.008 NS	0.003 NS	0.530*	0.035 NS	0.753 NS	0.008 NS	

\*, \*\* Significant at 0.05 and 0.01 probability levels, respectively.

NS Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error

LPP number of leaves per plant;

PLHT plant height (cm),

DF days to flowering,

DM days to maturity

HDDIA head diameter (cm),

ACPERHD number of achenes per head,

ACWT 100-achene weight (g),

SDYLD/PLT seed yield per plant (g)

SDYLD/ACR seed yield per acre (kg/acre), OILC oil content (%),

OILYLD oil yield per acre (kg/acre),

Table 2: Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients of sunflower population UAF in spring (top figure) and fall (bottom figure)

TRAITS	LPP	PLHT	DF	DA	DM	HDDIA	ACPERHD	SDYLD/PLT	SDYLD/ACR	OILC	OILYLD
LPP		0.180 NS	0.240 NS	1.1240*	2.220*	0.940*		0.050 NS	0.003 NS		
		0.170 NS	0.942*	0.600*	0.449*	1.220*	0.036 NS	0.350*	0.010 NS	0.920*	0.040 NS
PLHT	0.660**		0.230*	0.130*	0.240 NS	0.065 NS		0.376*	0.040 NS		
			0.235*	0.360*	0.402*	0.130 NS	0.130 NS	1.140*	0.050 NS	3.553*	0.148*
DF	2.500 NS	0.220*		0.210*	0.390*	0.230*		0.360*	0.010 NS		
		1.020 NS	0.261**	0.370*	0.350*	0.774*	0.030 NS	0.320*	0.010 NS	0.865*	0.039 NS
DA	0.238**	0.140*	0.360**		0.430*	0.693*		0.200*	0.010 NS		
		0.500**	0.460**	0.422**	0.580*	2.000 NS	0.040 NS	0.460*	0.020 NS	1.443*	0.061 NS
DM	0.410**	0.240*	0.620**	0.490**		0.240 NS		0.280*	0.014 NS		
		0.458**	0.470**	0.820**		0.369*	0.070 NS	0.650*	0.030 NS	1.571*	0.077 NS
HDDIA	0.170*	0.070 NS	0.300**	0.685**	0.296**			0.060 NS	0.002 NS		
		1.300 NS	0.120 NS	2.650 NS	0.338**		0.010 NS	0.111 NS	0.005 NS	0.698*	0.013 NS
ACPERHD	0.020 NS	0.100 NS	0.020 NS	0.050 NS	0.050 NS	0.010 NS		0.020	0.200 NS	23.116 NS	0.101 NS
SDYLD/PLT	1.000 NS	4.260 NS	0.330**	0.220**	0.310**	0.08 NS	0.020 NS		0.0007		
		0.130**	1.100 NS	0.330**	0.591**	0.137 NS			0.012	2.443	0.002
SDYLD/ACR	0.040 NS	0.050 NS	0.010 NS	0.010 NS	0.010 NS	0.003 NS	0.197**	0.003 NS	0.012		
		0.014 NS	0.050 NS	0.010 NS	0.030 NS	0.005 NS		0.010 NS		52.483	0.11
OILC	1.033 NS	4.075 NS	1.083 NS	1.984 NS	2.0173 NS	0.741 **	36.378 NS	3.102 NS	68.160 NS		0.042
OILYLD	0.037 NS	0.134 NS	0.040 NS	0.073 NS	0.078 NS	0.015 NS	0.408*	0.024 NS	0.216*	0.035 NS	

\*, \*\* Significant at 0.05 and 0.01 probability levels, respectively.

NS Correlation coefficients differ significantly from zero as its absolute magnitude exceeded twice its standard error

LPP number of leaves per plant;

PLHT plant height (cm);

ACPERHD number of achenes per head,

DF days to flowering,

ACWT 100-achene weight (g),

SDYLD/PLT seed yield per plant (g)

DM days to maturity

OILYLD oil yield per acre (kg/acre),

Similarly, the maximum predicted gain was found for number of leaves per plant (50.08%) followed by number of achenes per head (37.03) and the minimum gain was observed for days to flowering, which was only 1.95% during the fall. Mentioned that population is already uniform for maturity and no further gain is desirable as early leads to low yield.

The highest gain was calculated in UAF, was also for seed yield per plant (26.06%) followed by seed yield per acre (24.38%). Days to anthesis responded minimum on single trait selection giving 2.24% increase on 20% selection intensity during spring.

The predicted gain in UAF sunflower population for the fall was estimated for oil yield followed by seed yield per plant and the best for days to flowering with 30.04%, 29.96% and 3.43%, respectively genetic gains (Table 3).

### **Correlated response**

When selection and evaluation for seed and oil yield per acre was carried out in UAF sunflower population favorable correlated responses for seed yield per acre (130.47%) and oil yield (73.02%), were predicted. All correlated responses, however, were appreciably more than responses attained from direct selection for each trait. Likewise, selection for each yield component was expected to result in improvement for seed yield but the greatest improvement was 31.331% of the expected gain from direct selection for seed yield (Table 4). Our results indicated that improvement in seed yield per plant (the fall season) would be accompanied by unfavorable decreases in seed yield per acre.

## **DISCUSSION**

### **Correlations**

In our case, both genotypic and phenotypic interrelationships among traits under study were high. If both characters have low heritabilities, then the phenotypic correlations are determined by their environmental correlation because they have high heritabilities, than the genetic correlation are more important. Correlations between characters are ubiquitous, particularly between fitness characters and their component traits. The majority of commercially important correlations, e.g. those between the seed number, size and oil content, are generally undesirable and therefore impede selection. Genetic correlations are rarely absolute and there is normally sufficient independent variation between traits to permit joint improvement in both (Kearsey and Pooni, 1996).

The genetic cause of correlation is pleiotropy, though linkage is a cause of transient correlation, particularly in population like ours, derived from crosses between divergent strains whatever their cause, there is normally some possibility of partially breaking the correlation. Pleiotropy is simply the property of a gene whereby it



Table 3: Estimated gains (%) of S<sub>1</sub> families from sunflower populations Local Open and UAF for single-trait selection, using selection intensity of 20%, grown during spring and fall

SEASON	TRAIT									
	LPP	PLHT	DF	DA	DM	HDDIA	ACWT	ACPERHD	SDYLD/PLT	SDYLD/ACR
SUNFLOWER POPULATION LOCAL OPEN										
Spring	12.062	2.622	5.404	3.497	1.845	8.915			31.602	31.331
Fall	50.080	8.113	1.950	2.686	6.079	14.246	10.308	37.028	29.499	28.407
SUNFLOWER POPULATION UAF										
Spring	9.617	8.043	5.256	2.241	3.350	11.011			26.059	24.376
Fall	9.022	8.995	3.433	3.831	3.841	11.954		15.649	29.960	28.176
LPP number of leaves per plant, PLHT plant height (cm), DF days to flowering, HDDIA head diameter (cm), ACPERHD number of achenes per head, ACWT 100-achene weight (g), SDYLD/ACR seed yield per acre (kg/acre), OILC oil content (%), OILYLD oil yield per acre (kg/acre), DM days to maturity, SDYLD/PLT seed yield per plant (g)										

Table 4: Correlated responses in other traits when S<sub>1</sub> family selection is for indicated traits determined from progeny of populations Local Open and UAF, using selection intensity of 20%, grown during spring and fall<sup>+</sup>

SEASON	TRAITS									
	LPP	PLHT	DF	DA	DM	HDDIA	ACWT	ACPERHD	SDYLD/PLT	SDYLD/ACR
SUNFLOWER POPULATION LOCAL OPEN										
Spring	SDYLD/ACR	34.3020	168.350	21.824	27.699	17.888	8.983		30.581	
Fall		56.1248		11.665	18.820	39.785	8.766	5.375	40.034	-1.069
OILYLD										
Fall		89.653	65.865	11.578	17.684	62.451	17.055		43.794	914.097
SUNFLOWER POPULATION UAF										
Spring	SDYLD/ACR	0.975	67.168	19.213	17.055	24.638	3.568		1.185	
Fall		12.384	64.991	11.953	20.521	36.836	6.831		14.294	
OILYLD										
Fall		18.803	73.020	17.695	23.758	35.888	6.742		0.904	48.967

+ Responses are expressed as percentages of the expected gains from S<sub>1</sub> family selection for a given trait.

LPP number of leaves per plant, PLHT plant height (cm), DF days to flowering, DM days to maturity  
HDDIA head diameter (cm), ACPERHD number of achenes per head, ACWT 100-achene weight (g), SDYLD/PLT seed yield per plant (g)  
SDYLD/ACR seed yield per acre (kg/acre), OILC oil content (%), OILYLD oil yield per acre (kg/acre),

affects two or more characters, so that if the gene is segregating it causes simultaneous variation in its affected characters. Pleiotropy is a common property of major genes (Mather and Jinks, 1977; Falconer, 1989; Toms *et al.*, 1994; and Kearsey and Pooni, 1996).

However, estimates of genetic correlations are usually subject to rather large sampling errors and are therefore seldom very precise. Furthermore, genetic correlations are strongly influenced by gene frequencies (Bohren *et al.*, 1966), therefore, they may differ markedly in different populations.

High, significant and positive interrelationship among studied traits in both the populations, during the most favorable environment of spring indicates that larger number of leaves per plant, delays anthesis and maturity but resulted into increased head diameter and more seed yield per plant. Moreover, the spring season is fit for plant growth in Pakistan favorable environment.

The same was the trend in phenotypic coefficients among traits in both populations in spring, which resulted into high oil content.

In the fall, similar trend of genotypic and phenotypic associations was apparent as pointed in spring, which indicated that more number of leaves per plant increased plant height, delayed flowering, anthesis and maturity but resulted in larger head diameter, seed yield, oil content and yield (seed and oil).

#### **Genetic gain**

This response was due to superior families, carrying better inheritance and not because of environmental effects alone. However, the response achieved is always lower than the one predicted by standard methods, and the optimum selection intensity may be much lower than predicted unless population size is small (Hospital and Chevalet, 1993).

Family selection method was estimated to be best for improving seed yield and oil yield. Though, family method require costly yield trial. In addition, it is inferred that it is difficult to control plant height and maturity trait when selecting for seed and oil yield. However, the use of more than one site and up to four replications in a year would increase the expected genetic advance (Cespedes Torres *et al.*, 1984). The evaluation of five plants per plot in two replications and four environments appears to be a reasonable allocation of resources in order to optimize the selection response (Degener *et al.*, 1998).

#### **Correlated response**

It was proposed that strong stabilizing selection cannot act on an indefinitely large number of independent traits. This makes it likely that heritable variation in any one trait is maintained as a side effect of polymorphisms which have nothing to do with selection which is often observed is likely to be caused by correlations with a limited number of directly selected traits (Burton, 1993). The correlated response

to selection CR(Y) like response to selection in general, however, will depend on the additive genetic effects only (Kearsey and Pooni, 1996).

It is suggested that improvement in two characters (seed yield and oil yield) may be practiced simultaneously.

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### **VARIABILIDAD DE LAS CARACTERÍSTICAS AGRONÓMICAS EN DOS POBLACIONES DE GIRASOL CRUZADAS AL AZAR; CORRELACIONES, BENEFICIO DE SELECCIÓN EVALUADO Y LAS RELACIONES CORELATIVAS EN LA SELECCIÓN**

#### **RESUMEN**

El beneficio de selección evaluado y las relaciones mutuas entre las características agronómicas, fueron evaluados en las poblaciones de girasol Local Open y UAF cruzadas al azar, sobre la base de los datos de dos campanas (primavera y otoño).

De las 66 combinaciones de 12 características, las correlaciones positivas significantes fueron obtenidas en ambas poblaciones a lo largo de la primavera, para las siguientes relaciones: el número de hojas por planta con el número de días hasta la antesis y diámetro del capítulo, la altura de la planta con el rendimiento de semilla por planta, el número de días hasta la floración con el número de días hasta la antesis, el número de días hasta la madurez y el diámetro del capítulo, el número de días hasta la antesis con el número de días hasta la madurez, el diámetro del capítulo y el rendimiento de semilla por planta, y el número de días hasta la madurez con el rendimiento de semilla por planta.

Las correlaciones genéticas más a menudo eran un poco más altas de las correspondientes correlaciones fenotípicas en la población UAF a lo largo de la primavera y del otoño. Esa tendencia era casi al revés en la población Local Open en ambas campanas.

La evaluación del porcentaje del beneficio de selección por generación de 20%, ha demostrado que tal selección sería eficaz para el mejoramiento del rendimiento de semilla y de aceite. El beneficio evaluado para el rendimiento de grano era 31,33 y 24,38% por generación respectivamente (Local Open y UAF) cuando la generación  $S_1$  fue sometida a la prueba en primavera.

Las relaciones de correlación en la selección  $S_1$  al rendimiento y los componentes de rendimiento, han indicado que la selección indirecta para el rendimiento de grano y de aceite, pudiera ser eficaz. Fue evaluado que la selección directa llevaría hasta unos incrementos deseables en todos los componentes del rendimiento.

**VARIABILITÉ DES CARACTÉRISTIQUES AGRONOMIQUES  
DE POPULATIONS DE TOURNESOLS CROISÉES AU  
HASARD; CORRÉLATIONS, PRÉVISION DES GAINS DUS  
AU CROISEMENT ET RÉACTIONS CORRÉLATIONNELLES  
DANS LA SÉLECTION**

RÉSUMÉ

Les données obtenues au cours de deux saisons (printemps et automne) ont servi à évaluer les gains prévus par le croisement et les rapports entre les caractéristiques agronomiques dans une population de tournesols Local Open croisés au hasard.

Parmi 66 combinaisons de 12 caractéristiques, des corrélations significativement importantes ont été obtenues dans les deux populations au cours du printemps dans le rapport suivant : le nombre de feuilles par plante avec le nombre de jours avant l'anthèse et le diamètre de la tête; la hauteur de la plante avec le rendement de graines par plante, le nombre de jours avant la floraison avec le nombre de jours avant l'anthèse, le nombre de jours avant la maturation et le diamètre de la tête, le nombre de jours avant l'anthèse avec le nombre de jours avant la maturation, le diamètre de la tête et le rendement de graines par plante et enfin le nombre de jours avant la maturation avec le rendement de graines par plante.

Le plus souvent, les corrélations génétiques étaient légèrement plus élevées que les corrélations des phénotypes correspondants dans la population de tournesol UAF pendant le printemps et l'automne. Mais la tendance était presque inverse dans la population Local Open pour les deux saisons.

Le pourcentage de 20% de gain estimé par génération a démontré qu'une telle sélection serait efficace pour ce qui concerne l'amélioration du rendement de graines et d'huile. Le gain estimé pour le rendement d'achènes a été de 31, 331 et 24,376% par génération (Local Open et UAF) quand la génération S<sub>1</sub> était analysée au printemps.

Les rapports de corrélation dans la sélection S<sub>1</sub> pour le rendement et les composants de rendement indiquent qu'une sélection indirecte pour le rendement d'achènes et d'huile serait efficace. On estime qu'une sélection directe pour le rendement résulte en augmentation favorable dans tous les composants de rendement.

