

## GENETIC VARIANCES AND HERITABILITY OF SUNFLOWER TRAITS ASSOCIATED WITH DROUGHT TOLERANCE

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### SUMMARY

The objective was to determine the additive and dominance genetic variances and the broad- and narrow sense heritabilities of eleven traits in sunflower hybrids obtained from drought tolerant inbred lines. There were 32 hybrids that were evaluated in irrigation, drought and rainfed conditions. The N.C Design II was used for environments, male and female factors. Additive variance was more important than the dominance variance for the traits affecting the reproductive period, stem dry weight, total dry weight, and head weight. Dominance variance was more important for the days to beginning of flowering, days to end of flowering, days to physiological maturity, reproductive index, plant height, leaf dry weight and achene yield. All traits reached the limit of selection in consequence to their very low genetic variance, and the level of endogamy of the lines was adequate to test them in hybrid combinations. The very low narrow sense heritability values observed in all traits reflected the low proportion of total genetic variance and the varied environmental conditions. The traits with lowest heritabilities were those related to the reproductive ability, while the traits with higher heritabilities were those associated with biomass production and distribution. The usefulness of the line-hybrid correlations to select lines *per se* depended of the amount of the additive variance, the control of environment and the distribution of genetic variances among the female and male lines.

**Key words:** drought tolerance, genetic variances, heritability, morphophysiological and phenological traits, sunflower

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## INTRODUCTION

The drought manifested in the rainfed agricultural region of Durango during the sunflower (*Helianthus annuus* L.) reproductive cycle significantly reduces the achene yield (Gómez and Martínez, 1987). There are many characteristics associated with yield improvement, e.g., plant vigor, head size, seed weight, and the physiological factors affecting the efficiency of photosynthesis. It is the objective of each breeder to combine as many traits as possible in order to provide the highest yield and quality. Without information on inheritance, a breeder will not be able to understand the control of a trait or how to proceed in transferring that trait to adapted lines (Miller, 1992).

Using genetic designs or mating designs among individuals in a population, it is possible to estimate the genetic and environment components of variance, beginning with phenotypic variance, to estimate the heritability in the narrow and broad sense and to make predictions for selection response (Márquez, 1985). The North Carolina Design II (Comstock and Robinson, 1948; Comstock and Robinson, 1952) has been utilized in alogamous plants to obtain the genetic parameters mentioned before. This design can be used in open-pollinated populations or endogamic lines extracted from an open pollinated variety (Gardner and Lonnquist, 1966; Becker, 1967).

To select for an increases sunflower productivity in the rainfed region of Durango, the following traits should be taken in consideration: a) phenological traits: effective reproductive period and reproductive index; and b) morphophysiological traits at physiological maturity: dry weight of stems, leaves, head, total biomass and achene yield (Gómez *et al.*, 1990; Gómez *et al.*, 1991; Gómez and Elizondo, 1992).

The objective of this research was to determine the additive and dominance genetic variances, and the broad- and narrow sense heritabilities of phenological and morphophysiological traits related to drought tolerance in sunflower hybrids obtained from inbred lines selected previously on the basis of their yield potential under drought conditions.

## MATERIALS AND METHODS

This research was conducted at the Experiment Fields of INIFAP "Valle del Guadiana" and "Madero" in Durango, México. The first one is located at 24° 01' 00" northern latitude and 104° 44' 00" western longitude at 1889 m.a.s.l. The soil is a fine-texture castagnozem luvic, with gravel physical phase. The climate classification according to Koeppen is: BS<sub>1</sub> K(W)(e); dry, temperate, with summer rain season. The mean annual precipitation is 471 mm. The second field is located at 24° 24' 00" northern latitude and 104° 18' 00" western longitude at 1932 m.a.s.l. The climate is the same as the one mentioned before and the mean annual precipitation

is 350 mm. The genetic material were eight restorer lines (R) that were used as male parents (R1, R2, R3, R4, R5, R6, R7, and R8), and four male sterile lines (CMS) that were used as female parents (H5, CM5, GM1, CH1). All lines were in the  $S_6$  generation of selfing, with an estimated endogamic coefficient of  $F = 0.98$ . The inbred lines were derived from Argentario, an open-pollinated variety selected at the University of Pisa, Italy.

In 1991, each male line was crossed with all female lines and 32  $F_1$  progenies were produced. In 1992, these materials were evaluated in two environments, irrigation and drought, at the Experiment Field "Valle del Guadiana", and in 1993 they were evaluated in the rainfed environment at the Experiment Field "Madero". The experiment under irrigation had optimal soil water content during the entire crop cycle - one irrigation was applied before seeding and the plots received 583 mm of rain well distributed during the crop cycle. The experiment under drought had optimal soil water content only during the vegetative phase. Before the beginning of flowering the soil was covered with a plastic mulch to avoid rain and induce drought during the reproductive phase. The experiment under rainfed conditions received 390 mm of precipitation distributed during the entire crop cycle.

In each one of the three environments, each  $F_1$  progeny was seeded in a single row 5 m long and 0.81 m wide. These plots were arranged in a completely randomized block experimental design with two replications. The following traits were measured: a) phenological: days to beginning of flowering (DBF), days to end of flowering (DEF), days to physiological maturity (DFM), effective reproductive period (ERP) and reproductive index (RI); b) morphophysiological: plant height (PH), leaves dry matter weight (LDW), stems dry matter weight (SDW), total dry matter weight (TDW), head weight (HW) and achene yield (AY).

The statistical analysis of data was made utilizing a trifactorial analysis of variance for randomized complete blocks. The first factor was the environment, the second factor the male lines and the third factor the female lines. The ANOVA statistical model of Gardner and Lonnquist (1966) adjusted for the North Carolina Design II by Comstock and Robinson (1948 and 1952) was utilized. The RI data were adjusted by means of the arc-sin transformation procedure. The variance among male and female lines was calculated by  $2FV_G$ , where  $F$  is the coefficient of endogamy and  $V_G$  is the variance taken from the ANOVA for the male and female sources; the variance inside lines was calculated as  $(1-F)V_G$  (Falconer, 1970).

## RESULTS AND DISCUSSION

### Analysis of variance

The analysis of variance for the phenological traits (Table 1) showed significant differences for all sources of variation, except for the effect of male lines (M) on the trait ERP and the effect of the interaction environments-male lines (ExM) on the traits ERP and RI.

Table 1: Mean squares from the phenological traits: DBF=days to beginning of flowering, DEF=days to end of flowering, DFM=days to physiological maturity, ERP=effective reproductive period, RI=reproductive index

Source	DF	DBF	DEF	DFM	ERP	RI
Environment (E)	2	769.7 **	1992.4 **	3676.7 **	1326.8 **	43.8 **
Males (M)	7	52.2 **	30.4 **	31.0 **	5.2	2.8 *
Females (F)	3	11.4 *	16.4 **	31.1 **	26.9 **	5.1 *
E x M	14	17.3 **	15.3 **	24.6 **	5.4	1.7
E x F	6	9.2 *	26.4 **	70.3 **	61.8 **	5.0 *
M x F	21	37.3 **	30.0 **	53.4 **	10.7 *	2.4 *
E x M x F	42	18.1 **	19.8 **	38.2 **	15.2 **	2.0 *
Error	93	3.8	2.4	4.9	5.9	1.34
C.V.%		2.9	1.8	1.98	5.4	2.9

\*  $p \leq 0.05$ , and \*\*  $p \leq 0.01$

The effects of the environments (E) and the environment-genotype interactions (ExM, ExF and ExMxF) were important in the expression of all phenological traits, reflecting the consequences of the three levels of available soil water. The results of the analysis of variance for the morphophysiological traits are shown in Table 2.

Table 2: Mean squares from the morphophysiological traits: PH=plant height, LDW=leaves dry matter weight, SDW=stems dry matter weight, TDW=total dry matter weight, HW=head weight, AY=achene yield

Source	DF	PH	LDW	SDW	TDW	HW	AY
Environment (E)	2	10602 **	21199	648904 **	628235 *	18730	13977 **
Males (M)	7	348	4702	11905 *	32604	23379	1660
Females (F)	3	1567 **	19040 **	37514 **	203798 **	17895	808
E x M	14	466 *	3310	18251 **	69734	25064 *	5310 **
E x F	6	865 **	6041	19376 **	153315 **	24635	1700
M x F	21	516 **	7334 **	14252 **	87988 *	16775	2961 **
E x M x F	42	397 *	4145	19952 **	95360 **	18863	2776 **
Error	93	227	3571	5427	47510	12244	1327
C.V.%		10.2	27.4	20.7	22.1	26.5	18.6

\*  $p \leq 0.05$ , and \*\*  $p \leq 0.01$

The effects of the environments (E) and the interactions with the environment (ExM, ExF, ExMxF) were significant for PH, SDW, TDW and AY, except the interactions ExM for the trait TDW and ExF for AY. There were no significant differences for the effect of the environments and their interactions on LDW and HW, except for the interaction ExM and the trait HW. The low effect of the environments on LDW and HW means perhaps that these traits manifested stability, even in the contrasting soil moisture environments. These data confirm that these traits are important in the drought adaptation process, as reported by Gómez *et al.* (1991) and Gómez and Elizondo (1992). Among the male lines (M), the only trait that showed variability was SDW; among the female lines (F), variability was observed in PH, LDW, SDW and TDW. However, the crosses between the lines (MxF) showed significant differences for all traits except HW. These differences could be understood as the effect of

heterosis since the progenies had different values than the progenitors. This relationship could be observed more clearly for achene yield where no significant differences existed among male or female lines, but such differences did occur among their hybrids.

### Genetic variances

Table 3 shows that the additive variance was more important than the dominance variance for the traits ERP, SDW, TDW and HW, while the dominance variance was more important for the traits DBF, DEF, DFM, RI, PH, LDW and AY. Similarly to these results, many authors have reported that the genetic control for reproductive period (from DBF to DFM), and achene yield was predominantly based on the dominance effects of allelic interactions, while the effects of additive and non-additive gene action were equally important for plant height (Lay and Khan, 1985; Cecconi and Baldini, 1991; El-Hamid, 1992; Ortegón *et al.*, 1992; Ortegón and Escobedo, 1996; and Sindagi *et al.*, 1996). According to the results obtained in this study and those obtained by the authors cited above, it appears that there existed a decreasing effect of the additive genes, continuing from the first reproductive phenological phase to the last one. At the same time there was an increase in the effect of the dominance genes during the same period. Additive genetic control was probably better in ensuring the plants' adaptation and development at the beginning of the process of flowering in the contrasting conditions of soil water availability. During physiological maturity, the effect of dominance genes became more important in ensuring the process of achene filling.

Table 3: Additive variance ( $\sigma^2A$ ), dominance variance ( $\sigma^2D$ ), dominance degree ( $\sqrt{\sigma^2D/\sigma^2A}$ ), broad sense heritability ( $H^2$ ) and narrow sense heritability ( $h^2$ ) of sunflower phenological and morphophysiological traits

Trait	$\sigma^2A$	$\sigma^2D$	$\sqrt{\sigma^2D/\sigma^2A}$	$H^2$	$h^2$
Days to beginning of flowering (DBF)	0.65	3.20	2.22	42.7	7.2
Days to end of flowering (DEF)	0.20	1.70	2.92	18.9	2.0
Days to physiological maturity (DFM)	0.00	2.50	$\infty$	13.9	0.00
Effective reproductive period (ERP)	0.18	0.00	0.00	3.0	3.0
Reproductive index (RI)	0.03	0.08	1.63	25.4	7.6
Plant height (PH)	12.10	19.90	1.28	32.6	12.3
Leaves dry weight (LDW)	204.40	531.40	1.61	80.6	22.4
Stem dry weight (SDW)	496.60	0.00	0.00	10.9	10.9
Total dry weight (TDW)	1205.30	0.00	0.00	10.3	10.3
Head weight (HW)	16.83	0.00	0.00	1.1	1.1
Achene yield (AY)	0.00	30.78	$\infty$	9.6	0.00

$\infty$  = infinite, because the additive variance is 0 and the entire genetic variance is non-additive

It can be observed in Table 3 that the phenological traits DBF, DEF, and RI and the morphophysiological traits PH and LDW exhibited a grade of dominance greater than 1. DFM and AY exhibited the  $\infty$  value which in this case is also equivalent to a grade of dominance greater than 1, indicating the presence of overdominance. All these traits would be able to utilize the heterotic effects of their genotypes. All traits

showed very low genetic variance, this condition could be increased during the processes of selection and inbreeding of the parental lines, fixing the responsible alleles of the studied traits and consequently losing genetic variance. If there is no genetic variance it means that the limit of selection has been reached and there will not be any further response to selection on traits depending mainly on additive genetic variance.

Endogamy leads to genetic differentiation among lines and to genetic uniformity inside them. This consequence can be seen easily in traits depending on low non-additive genetic variance and a high proportion of additive genetic variance (Falconer, 1970). This behavior could be seen in the results shown in Table 4, where all variance values among lines were increased and all variance values inside lines were decreased in the traits ERP, SDW, TDW and HW, in which the entire genetic variance was additive. This genetic differentiation was more evident among the female lines, and perhaps another generation of selfing ( $S_7$ ) will be needed to observe significant differences among the male lines for the traits ERP, TDW and HW and among the female lines for the trait HW.

Table 4: Variance values for the traits in which the entire genetic variance is additive at two levels of endogamy, when the coefficient  $F=0$  in the open-pollinated population ( $S_0$ ) and when  $F=0.98$  in the  $S_6$  generation of inbreeding, ERP=effective reproductive period, SDW=stems dry matter weight, TDW=total dry matter weight, HW=head weight

Trait	Males				Females			
	Among lines		Inside lines		Among lines		Inside lines	
	F=0	F=0.98	F=0	F=0.98	F=0	F=0.98	F=0	F=0.98
ERP	2.65	5.20	2.60*	0.05	13.72	26.90**	13.45*	0.27
SDW	6073.98	11905.0*	5952.5*	121.48	19139.79	37514.0**	18754.0*	382.80
TDW	16634.70	32604.0	16302.0*	332.69	103978.57	203798.0**	101899.0*	2079.57
HW	11928.06	23379.0	11689.5*	238.56	9130.10	17895.0	8947.50*	182.60

\*  $p \leq 0.05$ , and \*\*  $p \leq 0.01$

Another consequence of endogamy is an increment of the genetic variance among crosses of lines. Genetic variance among crosses is the component among crosses ( $M \times F$ ) estimated by the ANOVA (Falconer, 1970). Significant differences among crosses, for all studied traits except for HW, can be seen in Tables 1 and 2. This variation among crosses is a good indicator that the level of endogamy reached is adequate to test the lines in hybrid combinations.

### Heritability

The heritability values in the broad sense were higher than those in the narrow sense for the traits DBF, DEF, DFM, RI, PH, LDW, and AY. The heritability values in the broad sense were equal to those in the narrow sense for the traits ERP, SDW, TDW, and HW (Table 3). In general, the heritability values estimated in this study, in the broad and narrow sense, were lower than the values reported in literature. In our case, the value for days to beginning of flowering was 7.2%, while some of the reported values are: 90% in the broad sense (Fick, 1978); 52.1 to 72.1% in the broad and 38.1 to 61.4% in the narrow sense (El-Hamid, 1992); 91 to 95% in the

narrow sense (Alza, 1995); 66.7% in the broad sense (Ortegón and Escobedo, 1996). The heritability in the narrow sense for the trait DFM was 0.0%. Days to physiological maturity is often closely correlated with days to flowering, although genetic differences in the time required from flowering to maturity exist (Fick, 1978; Cecconi and Baldini, 1991). In means that RI is an independent trait in respect to days to flowering and days to maturity. The heritability value observed in the narrow sense for RI was 7.6%.

The heritability for plant height was 12.3% in the narrow and 32.6% in the broad sense. Fick (1978) reported heritability estimates from some authors, ranging from 49 to 90% in the broad sense and from 20 to 37% in the narrow sense; from 41.7 to 72.5% in the broad and from 21.7 to 45.4% in the narrow sense (El-Hamid, 1992); from 57 to 88% in the narrow sense (Alza, 1995); from 48.6 to 74.2% in the narrow sense (Gonçalves and Branco de Miranda, 1996); 86.8% in the broad sense (Ortegón and Escobedo, 1996). For total dry matter weight, the heritability of 10.3% in the narrow sense has been reported, while Alza (1995) found values from 55 to 79% in the narrow sense.

The heritability for seed yield was relatively low compared with the other traits, the heritability in the narrow sense estimated in this study with 0.0% (Table 3). The same value was reported by Lay and Khan (1985). Other values reported for seed yield were: from 18 to 69% in the broad sense (Fick, 1978); 19% in the narrow sense (Cecconi and Baldini, 1991); from 49.9 to 57.3 in the broad sense and from 28.2 to 39.9% in the narrow sense (El-Hamid, 1992); from 7.0 to 86.0% in the narrow sense (Alza, 1995); from 40.0 to 65.4% in the narrow sense (Gonçalves and Branco de Miranda, 1996); and 17.5% in the broad sense (Ortegón and Escobedo, 1996). The heritability value in the narrow sense was 2.0% for DEF, 0.0% for DFM, 3.0% for ERP, 7.6% for RI, 22.4% for LDW, 10.9% for SDW and 1.1% for HW. There were no literature data for the heritability values for these last 7 traits.

It can be said that the very low heritability values in narrow sense observed in all traits were a reflection of the low proportion of total genetic variance that was attributable to the mean gene frequencies effects. This condition could be increased during the processes of selection and inbreeding of the parental lines, fixing the responsible alleles of the studied traits and consequently losing genetic variance. The absence of genetic variance means that the limit of selection has been reached and there will not be any further response to selection for the traits DBF, DEF, ERP, RI and HW which depend mainly of the additive genetic variance. But, heritability of a trait does not depend only on genetic factors, it also depends on the environmental circumstances to which an individual is subjected (Falconer, 1970). In our case, the environmental variance depended on the cultural and management conditions, mainly the effects of year, drought, rainfed and irrigation treatments. These varied environmental conditions which occurred during the experiment produced the very low heritability estimates. Otherwise, higher estimates could be expected under more homogeneous environmental conditions.

### Line-hybrid correlations

Heritability has also a predictive role, that expresses the confidence of the phenotypic value as an indicator of the reproductive value (Falconer, 1970). But the strict dependence of heritability on the management and environment conditions is an indication that the heritability estimates for a particular trait must be taken with caution. Consequently the comparison of heritability values for a particular trait obtained by different authors is of doubtful utility (Vega, 1988). With the intention to clarify this discrepancy, we have estimated the correlation coefficient ( $r$ ) as a complementary parameter, to measure the association of phenotypic values between the lines and their  $F_1$  progenies. The practical scope of this estimation has been the evaluation and selection of parental lines *per se* to obtain superior hybrids. However, contrasting results have also been reported.

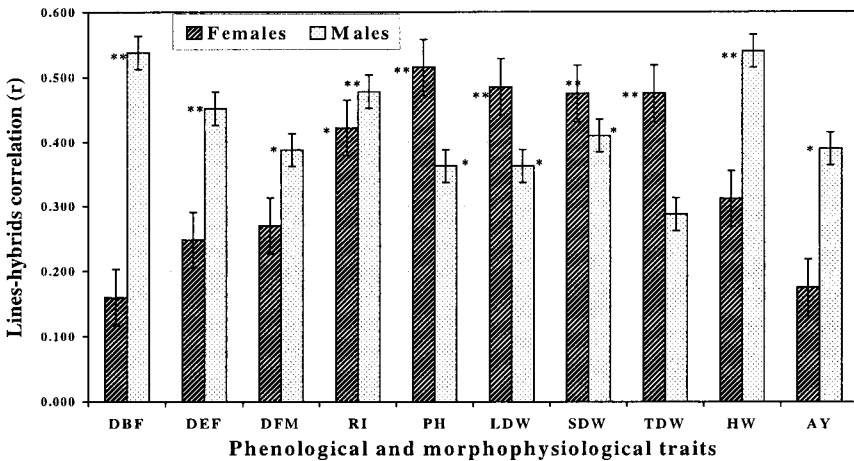


Figure 1: Correlation values of traits between female and male sunflower inbred lines and their respective hybrids; the significance levels are: \*  $p \leq 0.05$  and \*\*  $p \leq 0.01$ ,  $n=32$ . Days to beginning of flowering (DBF), days to end of flowering (DEF), reproductive index (RI), plant height (PH), leaves dry weight (LDW), stem dry weight (STW), total dry weight (TDW), head weight (HW) and achene yield (AY)

Figure 1 shows the correlation coefficients between the female and male lines on one side and their hybrids on the other. It can be seen that the correlations for phenological traits were significant only in the male lines, in descending order from DBF, DEF to DFM. In the like manner Ortegon *et al.* (1992) reported that days to flowering in the male lines expressed a greater influence on the flowering of the respective hybrids, but the females showed a greater association with the hybrids at physiological maturity. This is contrary to the results obtained in this work. The RI trait that measures the relative duration of vegetative and reproductive phenological phases showed a significant correlation for both females and males.

The males showed significant correlations for the traits HW and AY (Figure 1); contrarily, Škorić (1982) found that  $F_1$  hybrids showed greater correlations for grain yield with the female than with the male lines. Petakov (1992) observed that both females and males had a proportional dependence in seed productivity with



their hybrid combinations. Other researchers reported low correlations between the yield of lines and hybrids (Kováčik and Škaloud, 1990) and others did not find any correlation among the behavior of the lines *per se* and their hybrid combinations (Miller *et al.*, 1982; Ortegón *et al.*, 1992). Both females and males, but mainly the former, were significantly correlated with their hybrids in the morphophysiological traits PH, LDW and SDW. The trait in which only the females had significant correlations with their hybrids was TDW.

Correlations among lines and their hybrids depend not only on the genetic composition of the individuals and the environmental conditions in which they grow, but also on the sex of the lines (CMS or R). It was found in this study (data not shown) that a significant correlation ( $r = 0.742^{**}$ ) existed between the heritability of traits (x) and the line-hybrid (y) correlation only among the female lines. A non-significant and negative correlation ( $r = -0.389$ ) was found only for the male lines. It means that among the female lines low heritability values were related with low line-hybrid correlation values and high heritability values were related with high correlation values. On the contrary, among the males, low heritability values were correlated with high line-hybrid correlation values and high heritability values were correlated with low line-hybrid correlations. In other words it means that among the female lines the main component of genetic variance was additive and among the male lines it was the dominance variance, coinciding with the data in Table 3. To understand the relationship observed between the heritability and the line-hybrid correlation, one must remember that heritability is the square root of the correlation between reproductive and phenotypic values or  $h = r_{AP}$  (Falconer, 1970). It means that heritability will be related with the line-hybrid correlation in proportion to the quantity of additive variance component of the trait. The females contributed mainly to traits connected with the production and accumulation of photosynthates (PH, LDW, SDW and TDW). The males contributed mainly to traits related to the reproductive processes: duration of the phenological reproductive phases (DBF, DEF, DFM, RI), accumulation of photosynthates in the inflorescence (HW) and translocation of photosynthates to the achenes (AY).

## CONCLUSIONS

The effect of moisture level was more evident on the expression of phenological than morphophysiological traits and it also influenced greatly the expression of traits determined mainly by additive genetic variance. The same trait can have a predominant dominance variance effect in females and a predominant dominance variance effect in male lines. There is still some genetic variability for the traits PH, LDW, SDW and TDW among female lines, which could be used for selection, to increase the means of these traits in synthetic varieties developed from these lines. The average level of manifested heterosis is one that can be obtained by crossing individuals coming from the same population. So, highest levels of heterosis may be expected in crosses made between lines differing in genic frequencies.

Familial selection is recommended for increase of the mean values of the traits PH, LDW, SDW, and TDW. The overdominance effect may be used for obtaining

new hybrids with improved traits of DBF, DEF, DFM, RI, PH, LDW and AY. Endogamy and exogamy (hybridization) can be utilized to improve these traits. The level of endogamy reached is sufficient to test the lines in hybrid combinations. The heritability values in the broad- and narrow sense were very low, indicating that there was no variability and the lines practically reached the limit of selection for the traits DBF, DEF, DFM, ERP, RI, HW and AY, which had fixed gene frequencies. In general, the traits with lowest heritabilities were those more strictly connected with the reproductive ability, while traits with higher heritabilities were those connected with biomass production and distribution. Now it can be said that the usefulness of the line-hybrid correlation for selecting lines by their behavior *per se*, depends of the amount of the additive variance component of the trait in the studied lines, the effect of the environment and the distribution of genetic variances between the female and the male lines.

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## VARIANTES GENÉTICAS Y HEREDABILIDAD DE LAS CARACTERÍSTICAS RELACIONADAS CON LA TOLERANCIA DE SEQUÍA EN EL GIRASOL

### RESUMEN

El objetivo ha sido de determinar la variancia genética aditiva y dominante y, en el sentido más amplio y más estricto, la heredabilidad de once características de los híbridos de girasol obtenidos de las líneas inbred resistentes a la sequía. Fueron utilizados 32 híbridos que eran evaluados en las condiciones de irrigación, sequía y precipitados naturales. El método N.C. Design II era utilizado para la determinación de relaciones entre los factores mascu-

linos y femeninos. La variancia aditiva era más importante que esa dominante en las características que determinan la duración del periodo reproductivo, la masa seca de tronco y la masa de cabeza. La variancia dominante era más importante para el número de días hasta el empiezo de florecimiento, el número de días hasta la madurez fisiológica, el índice reproductivo, la altura de planta, la masa seca de hojas y el rendimiento de grano. Todas las características llegaron a la posibilidad límite de selección como consecuencia de la variancia genética muy baja, y el nivel de endogamia era suficiente para investigar las líneas en las combinaciones híbridas. Los valores muy bajos de la heredabilidad en el sentido más estricto observados a todas las características son reflejos de la pequeña relación de la variancia genética completa con las condiciones diferentes del ambiente. Los más pequeños valores de heredabilidad fueron constatados para las características ligadas con la capacidad reproductiva, y los más grandes valores de heredabilidad eran ligados con la producción y la distribución de biomasa. La utilidad de correlaciones línea-híbrido en la selección *per se* de líneas depende de la grandeza de la variancia aditiva, de la influencia del ambiente y de la distribución de la variancia genética de líneas femeninas y masculinas.

## **VARIANCE GENETIQUE ET TRANSMISSIBILITE DES CARACTERISTIQUES LIEES A LA TOLERANCE A LA SECHERESSE CHEZ LE TOURNESOL**

### **RÉSUMÉ**

Le but de la recherche était de déterminer la variance génétique additive et dominante et la transmissibilité au sens le plus large et le plus étroit pour onze caractéristiques d'hybrides de tournesol obtenus de lignes inbred résistantes à la sécheresse. Les trente-deux hybrides utilisés ont été évalués dans des conditions d'irrigation, de sécheresse et de précipitations naturelles. La méthode N.C. Design II a été utilisée pour déterminer les relations entre les facteurs de l'environnement et entre les facteurs des lignes mâles et femelles. La variance additive s'est montrée plus importante que la variance dominante pour les caractéristiques qui déterminent la longueur de la période de reproduction, le poids de la tige séchée, le poids total de la plante séchée et le poids de la tête. La variance dominante, elle, pour le nombre de jours avant le début de la floraison, le nombre de jours avant la fin de la floraison, le nombre de jours avant la maturité physiologique, l'index de reproduction, la hauteur de la plante, le poids des feuilles séchées et le rendement en achènes. En conséquence d'un très bas niveau de variances génétiques, toutes les caractéristiques ont atteint la possibilité limite de sélection et le niveau d'endogamie a été suffisant pour qu'on examine les lignes dans des combinaisons hybrides. De très basses valeurs de transmissibilité au sens étroit observées dans toutes les caractéristiques sont l'expression de la faible proportion de variance génétique totale et des diverses conditions de l'environnement. Les valeurs les plus basses de transmissibilité ont été trouvées dans les caractéristiques reliées à l'aptitude à la reproduction alors que les plus hautes étaient reliées à la production et à la distribution de la biomasse. L'utilité de la corrélation des lignes-hybrides dans la sélection *per se* des lignes dépend du niveau de la variance additive, de l'influence de l'environnement et de la distribution des variances génétiques entre les lignes mâles et les lignes femelles.