CORRELATION AND CAUSATION AMONG SUNFLOWER TRAITS (1)

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SUMMARY

Usually, plant traits integrate structures of components with complex correlations and causal effects. The purpose of this research was to estimate associations and causations among different traits in sunflower. Twenty- one morphological, phenological and agronomic traits were evaluated in 37 populations and three environments at Pergamino, Argentina. Grain and oil yield were strongly correlated with morphological traits, grain number, and grain weight. Correlations between grain yield and oil content were not significant (P<0.95). The relationship among different groups of traits was studied by a hierarchical cause-effect path analysis. Grain number, grain weight, and grain volume were important to determine grain yield. Morphological traits and total grain number were strongly associated with filled grain number. Grain yield was more important than oil content to determinate oil yield.

INTRODUCTION

Asociations among traits are very useful in selecting a desirable type of plant. Selection for ultimate agronomic traits is not alwais succesfull because the more distant the final expression of a trait is, the less efficient the selection for it is. A trait like yield, for example, is the ultimate expression of a structure with several partially interdependent components.

The objective of this research was to estimate associations and causations among morphological, phenological and agronomical traits on a broad sample of sunflower (Helianthus annuus L.) populations.

MATERIAL Y METHODS

Plant material.in this study included 37 open populations (23 foreign and 14 domestic) from the sunflower germplasm collection of INTA-Manfredi, Argentina.

The experimental design was a randomized complete block with four replicates. Each plot was composed of three rows, 5.10 m long and 0,30 m apart. Evaluations were performed only on the central row. The study, including thee separated experiments, was conducted at the Experimental Station of Pergamino, INTA during the 1985/1986 and 1986/1987 growing seasons.

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Twenty-one morphological, phenological, and agronomic traits were evaluated, according to the following detail: a)**Morphological:** leaf width (LW), plant height (PH), stem diameter (SD), and head diameter (HD); b)**Phenological** (or cycle): emergence to begining of blooming (EB), begining to end of blooming (BE), begining of blooming to maturity (BM), end of blooming to maturity (EM), and emergence to maturity (EM); c)**Agronomical:** total *grain number* (TG), filled *grain number* (FG), grain weight (GW), grain lenght (GL), grain width (GA), grain thickness (GT), grain volume (GV), grain oil content (GO), oleic acid content (OC), linoleic acid content (LC), grain yield (GY), and oil yield (OY).

The expectations for the analysis of variance and covariance for the combined model are given in Table 1.

Table 1-EXPECTATIONS FOR THE ANALYSIS OF VARIANCE AND COVARIANCE

Source of Variation	D F	E M S	E P M
Environment	e-1 = 2		
Rep/Env	e(r-1)= 9		
Genotype	g-1 = 36	$\sigma^2E+r\sigma^2GE+re\sigma^2G$	$\sigma E_{xy}+r\sigma GE_{xy}+re\sigma G_{xy}$
G x E	(g-1)(e-1)= 72	$\sigma^2E+r\sigma^2GE$	$\sigma E_{xy}+r\sigma GE_{xy}$
Error	e(r-1)(g-1)=324	σ^2E	σE_{xy}
Total	erg-1 =443		

where: a=number of environments; r=number of replications in each environment; g=number of genotypes per replication in each environment; σ^2E=Experimental error component of variance; σ^2GE=Genotype-environment interaction component of variance; σ^2G=Genotypic component of variance; σE_{xy}=Error component of covariance; σGE_{xy}=Interaction genotype-environment component of covariance; σG_{xy}=Genotypic component of covariance.

Phenotypic (r_P) and genotypic (r_G) correlations among all the traits were calculated according to Hanson et al. (1956):

$$r_P = \frac{\sigma P_{xy}}{\sqrt{\sigma^2 P_x \cdot \sigma^2 P_y}} \qquad r_G = \frac{\sigma G_{xy}}{\sqrt{\sigma^2 G_x \cdot \sigma^2 G_y}}$$

where:σP_{xy} = Phenotypic component of covariance for **x** and **y** traits; σG_{xy} = Genotypic component of covariance for **x** and **y** traits; $\sigma^2 P_x$ and $\sigma^2 P_y$ = Phenotypic component of variance for **x** and **y** traits; $\sigma^2 G_x$ and $\sigma^2 G_y$ = Genotypic component of variance for **x** and **y** traits.

Path coefficient analysis based on phenotypic correlations were calculated using Li (1956) and Ottaviano and Camussi (1981) procedures. Several systems with different levels of complexity were utilized to analyze direct effects of components on ultimate traits.

RESULTS

Genotypic and phenotypic correlations among the 21 traits are shown in Table 2.

Phenological traits were positively and higly correlated among themselves (specially EB with EM), and with TG and FG. There was also a positive correlation between phenological and morphological traits.

Morphological traits showed a positive correlation among themselves, and GW, FG and TG. GW was positively associated with TG, FG, GL, GA, GT, GV, and LC.

GO exhibited a negative correlation with EM, EB, TG, and FG, but a positive correlation with GW, GL, GA, GT, GV, OC, and OY. FM was the only phenological trait positively associated with GO. Correlations between GO and GY were not significant.

There was a strong and positive correlation of GY and OY with morphological traits, and with TG, FG, and GW. OY also showed a positive association with GY and GO.

Nine cause-effect analysis systems are shown in Table 3. In system 1, OY was identified as the final complex trait while all the remaining traits appear to be just components of it. EB, BM, EM, GO, and GY had the greatest direct effects on OY.

System 2 was constructed using 17 component traits (BM, EM, and GV were eliminated from the analysis) and considering again OY as the final complex trait. Under these conditions, EB, FM, TG, GL, GA, GT, GO, and GY showed the highest direct effects on OY. In both system 1 and system 2, the coefficient of determination (R^2) was very high ($R^2=0.98$ and $R^2=0.99$, respectively).

In system 3, only eight components traits were considered (GY, FG, GW, GO, GV, GL, GA, and GT) and three hierarchical levels among them were included into the analysis. In the first level, GY had the greatest direct effect on OY, which was identified as the final complex trait. The coefficient of determination for the first level was $R^2=0.97$. In the second level, FG, GW, and GV accounted for most of the variation in GY ($R^2=0.86$). FG was the most important component of this level ($P=0.79$). In the third level, GT, GA, and GL accounted for the variation in GV ($R^2=0.97$).

TG and morphological traits were very important to explain the variability in FG -which was the motgst important component of GY in system 3, second level- ($R^2=0.84$) in system 8. On the contrary, TG and morphological traits had little effect on GW and GO ($R^2=0.57$ and $R^2=0.42$ respectively), according to the analysis of systems 7 and 9. HD was the only morphological trait that exhibited a positive direct effect with all the components of GY in systems 4 to 9.

Table 2-PHENOTYPIC AND GENOTYPIC CORRELATIONS AMONG 21 TRAITS IN 37 SUNFLOWER POPULATIONS AND 3 ENVIRONMETS.

(*) TRAIT		BE	BM	FM	EM	LW	PH	SD	HD	TG	FG	GW	GL	GA	GT	GV	GO	OC	LC	GY	OY
		(**)																			
EB	P	0.37	0.27	0.07	0.95	0.45	0.75	0.76	0.29	0.49	0.38	0.03	-0.40	-0.18	-0.36	-0.36	-0.41	-0.51	0.52	0.35	0.16
	G	0.58	0.47	0.20	0.98	0.52	0.77	0.82	0.34	0.53	0.39	0.68	-0.42	-0.16	-0.40	-0.39	-0.42	-0.71	0.73	0.39	0.18
SE	P		0.56	0.03	0.49	0.55	0.65	0.63	0.47	0.73	0.61	0.19	0.08	-0.41	-0.46	-0.33	-0.16	-0.24	0.24	0.56	0.46
	G		0.93	0.59	0.70	0.83	0.94	0.92	0.76	1.27	1.22	0.44	0.10	-0.56	-0.71	-0.49	-0.18	-0.30	0.31	1.18	1.05
SM	P			0.81	0.55	0.59	0.51	0.60	0.47	0.51	0.57	0.22	0.02	-0.23	-0.21	-0.19	0.12	-0.01	0.04	0.55	0.51
	G			0.85	0.62	0.80	0.83	0.89	0.73	0.97	1.22	0.28	0.06	-0.42	-0.48	-0.41	0.08	-0.11	0.15	1.14	1.08
FM	P				0.32	0.32	0.16	0.28	0.25	0.11	0.26	0.13	-0.34	-0.01	0.06	0.00	0.21	0.16	-0.12	0.27	0.30
	G				0.35	0.55	0.48	0.62	0.50	0.33	0.93	-0.01	-0.02	-0.12	-0.48	-0.21	0.42	0.17	-0.09	0.80	0.85
EM	P					0.58	0.81	0.85	0.40	0.58	0.51	0.09	-0.34	-0.23	-0.38	-0.37	-0.32	-0.45	0.46	0.48	0.30
	G					0.62	0.85	0.91	0.45	0.67	0.60	0.12	-0.36	-0.23	-0.45	-0.43	-0.36	-0.65	0.68	0.58	0.38
LW	P						0.82	0.84	0.87	0.71	0.69	0.59	0.08	0.22	0.07	0.14	0.03	-0.19	0.19	0.81	0.77
	G						0.92	0.87	0.95	0.74	0.93	0.68	0.10	0.24	0.01	0.12	-0.01	-0.29	0.27	0.99	0.96
PH	P							0.95	0.74	0.76	0.73	0.41	-0.06	0.01	-0.22	-0.10	-0.26	-0.36	0.35	0.78	0.62
	G							1.00	0.85	0.82	0.86	0.50	-0.07	0.01	-0.26	-0.12	-0.28	-0.44	0.44	0.91	0.74
SD	P								0.72	0.71	0.70	0.37	-0.12	-0.02	-0.24	-0.15	-0.24	-0.37	0.37	0.74	0.59
	G								0.75	0.81	0.84	0.43	-0.15	-0.04	-0.34	-0.22	-0.27	-0.53	0.51	0.87	0.71
HD	P									0.66	0.77	0.62	0.17	0.33	0.10	0.23	-0.02	-0.10	-0.10	0.89	0.84
	G									0.79	0.98	0.71	0.16	0.33	-0.01	0.17	-0.02	-0.23	0.20	1.07	1.01
TG	P										0.86	0.19	-0.14	-0.29	-0.48	-0.36	-0.37	-0.18	0.17	0.77	0.57
	G										1.06	0.16	-0.16	-0.34	-0.63	-0.45	-0.41	-0.28	0.27	0.86	0.64
FG	P											0.23	-0.05	-0.18	-0.40	-0.25	-0.29	-0.04	-0.05	0.90	0.73
	G											0.48	-0.02	-0.14	-0.44	-0.25	-0.29	-0.21	0.21	0.98	0.79
GW	P												0.67	0.73	0.61	0.76	0.39	0.15	-0.16	0.60	0.71
	G												0.76	0.70	0.56	0.76	0.41	0.23	-0.26	0.73	0.84
GL	P													0.39	0.44	0.68	0.62	0.28	-0.29	0.23	0.46
	G													0.36	0.47	0.70	0.66	0.41	-0.42	0.27	0.55
GA	P														0.88	0.91	0.26	0.23	-0.24	0.16	0.27
	G														0.91	0.92	0.25	0.29	-0.32	0.19	0.29
GT	P															0.93	0.48	0.33	-0.33	-0.08	0.13
	G															0.94	0.55	0.39	-0.40	-0.15	0.09
GV	P																0.50	0.33	-0.34	0.11	0.31
	G																0.56	0.40	-0.42	0.11	0.35
GO	P																	0.23	-0.21	-0.07	0.32
	G																	0.32	-0.30	-0.07	0.36
OC	P																		-0.99	0.03	0.13
	G																		-0.01	-0.03	0.09
LC	P																			-0.02	-0.11
	G																			0 01	-0.10
GY	P																				0.91
	G																				0.91

(*) See text for the meaning of the abbreviations.

(**) Significance levels are: r ≥ ± 0.12, P ≥ 0.99; ± 0.12 ≥ r ≥ ± 0.11, P ≥ 0.95; ± 0.10 ≥ r, P non significant.

Table 3-DIRECT EFFECTS (P) AND COEFFICIENTS OF DETERMINATION (R^2) FOR NINE CAUSE-EFFECT PATH ANALYSIS SISTEMS AMONG 21 TRAITS IN 37 SUNFLOWER POPULATIONS AND 3 ENVIRONMENTS.

(*) TRAIT	P										
	(1) OY	(2) OY	GV	(3) GY	OY	(4) GL	(5) GA	(6) GT	(7) GW	(8) FG	(9) GO
EB	1.50	-0.12									
BE	-0.03	-0.05									
BM	0.51										
FM	-0.02	-0.33									
EM	-1.76										
LW	-0.06	-0,05				0.40	0.57	1.01	0.73	-0.41	1.08
PH	0.00	0.09				0.66	0.77	0.67	0.73	-0.11	-0.04
SD	0.11	0.01				-1.05	-0.99	-1.18	-0.83	0.24	-0.59
HD	0.03	-0.03				0.35	0.63	0.26	0.41	0.59	-0.09
TG	0.08	-0.19				-0.41	-0.99	-1.05	-0.56	0.68	-0.62
FG	-0.03	-0.01		0.79	0.73						
GW	0.13	0.01		0.44	0.41						
GL	0.00	0.42	0.32	-0.01	-0.01						
GA	0.05	0.23	0.39	-0.01	-0.01						
GT	-0.03	0.19	0.43	-0.01	-0.01						
GV	0.07			-0.02	-0.02						
GO	0.45	0.62			0.38						
OC	0.00	0.25									
LC	-0.01	0.28									
GY	0.95	1.40			0.93						
R^2	0.98	0.99	0.97	0.86	0.97	0.23	0.66	0.74	0.57	0.84	0.42

(*) See text for the meaning of the abbreviations.

There was a coincidence between the values of direct effects and the values of genotypic and phenotypic correlation coefficients when the association between OY and important component traits (like GY, GO, and FG) was considered. Nevertheless, values of correlation coefficients were higher than the values of direct effects for unimportant traits (like GL, GA, GT, and GV).

DISCUSSIONS AND CONCLUSIONS

The lack of association between GO and GY, and the strong correlation between GO and OY have important implications in sunflower breeding.

GY was more important than GO in determining OY.

The most important component of GY was FG, wich in turn was strongly associated with TG, HD, SD, PH, and LW. From the latter, HD -due to its effects on GY components- and LW -due to its incidence on GO- were the most important components.

Path coefficient analysis proved to be of more practical value in plant breeding than correlation coefficients. Since correlation analysis tend to simplify relationships among traits, to base a beeding program on just correlation estimations may be somewhat risky. The use of path analysis appears to be an interesting and safer alternative in sunflower breeding.

ACKNOWLEDGEMENTS
We are grateful to Dr. Daniel Basigalup for contributing in translation of the paper into English.

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