DIALLEL ANALYSIS IN SUNFLOWER (HELIANTHUS ANNUUS L.), GENETIC AND PHENOTYPIC CORRELATIONS FOR SOME AGRONOMICAL AND PHYSIOLOGICAL CHARACTERS.

Franco Cecconi. *Pisa University, Dipartimento di Biologia delle Piante Agrarie sez. Genetica.Via Matteotti 1/b 56124 – Pisa Italy. Fax +39-050-576750 ; e-mail: fcecconi@agr.unipi.it*

Monica Gaetani. *Pisa Univerity, Dipartimento di Agronomia e Gestione dell'Agroecosistema, Via S. Michele degli Scalzi, 2 56124 – Pisa Italy. Fax +39-050-540633*

Raul Srebernich, Nestor Luciani. *Agromania S.A., Estado de Israel 190 – 3100 Parana (E.R) Argentina.Fax +54-3434-350264*

Summary

A complete set of diallel crosses among 11 inbred lines of sunflower was used to study the genetic control of the following characters: duration of phenological phases, dry matter production for each phases, leaf area per plant, oil content, seed yield and harvest index.

Statistical analysis of data were performed according to the model of Hayman (1954a, 1954b).

The results indicate that genetic variability is important for all the analysed characters. As far as the genetic control is concerned, it becomes more complex approaching the end of the ontogenetic cycle when the unfixable component of variation becomes the major part of genetic variability. This is the case of seed yield, dry matter production during the phase of grain filling, oil content and harvest index.

The high genetic correlation of oil content and seed yield with physiological traits such as leaf area development and dry matter production, indicates that these characters are important limiting factors by which the efficiency of plant assimilation may be evaluated. Considering the high heritability of these characters especially during the first phases of plant development, their use in early screening may be useful when a large amount of hybrid combinations are included in selection programs.

Key Words: Sunflower, Diallel analysis, Seed Production, Plant Development.

Introduction

Development of improved inbred lines for hybrid production is the most important objective of sunflower breeding programs. Seed yield and oil content are the primary target traits of genetic improvement. Many authors found the variability for yield production to be dependent on both additive and non-additive gene actions (Fick, 1978; Cecconi et al., 1987; Miller, 1980). Dominiquez Gimenez et al. (1987) found that genotype-environment interactions were an important component of variance for seed yield and oil content.

Several simple plant traits, as leaf area per plant, total dry matter and harvest index have been found to be correlated with seed yield (Skoric, 1974; Chervet and Vear, 1990), but few information is available on the genetic control of these characters at the different stage of plant development.

The present study was carried out to gain information on the genetic control of some physiological traits related to plant development and to analyse the phenotypic and the genetic correlation with seed yield and oil content.

Materials and Methods

11 inbred lines of sunflower coming from a joint selection program between the Agromania S.A. and the Plant Biology Department of Pisa University were used. Crosses were made by hand emasculation. On April 1999, parents and hybrid combinations including reciprocals were sown at the experimental station of Pisa University in three randomised blocks. The experimental unit was a plot of four rows five meters long , the distance between rows was 0,5 meters and the plant interval 0,3 meters resulting a plant density of about seven plants per square meter.

According to Schneiter and Miller (1981), phenological phases were defined as follows:

V-R1: days from the emergence to the visible head.

R1-R5: days from the visible head to the beginning of flowering.

R5-R9: days from flowering to physiological maturity of seeds

For each phase the following characters were analysed:

1) Dry matter production per plant calculated as a difference between data collected at the end and data collected at the beginning of each phase.(for identification purpose in tables are reported D.M1, D.M2, D.M3, which identify dry matter production in the first, second and third phase).

2) Leaf area per plant determined by Haiashi Denko electronics planimeter.(in tables L.A1 and L.A2 identify leaf area developed at the end of the first and the second phase).

Seed oil content was determined by the New Port NMR Analyser.

Statistical analysis of data was done according to the model of Hayman (1954a, 1954b, 1958), The relationships between the variance (Vr) and the parent-offspring covariance (Wr) of the members of the same half –sib family (array) were used to test the assumptions of the additive-dominance model of gene actions. When the model fits the data collected the regression coefficient of Wr on Vr must be not different from unity and the variance of Wr-Vr values over arrays must be not significant when compared with the variance over replicated blocks. If both tests were satisfied, the genetic components of variance, the degree of dominance (H/D) and the narrow sense heritability (h2) were calculated (Mather and Jinks, 1971).

Genetic and phenotypic correlations were calculated using the covariance analysis (Falconer, 1967).

Results and Discussion

Genetic variability as it results from the analysis of variance reported in Tab.1, is an important component of variation for all the analysed characters (significance of "a" and/or "b"). It is interesting to notice how the genetic control of the same character changes with plant development.

Duration of phenological phases

The results synthesised in Tab.1 indicate that the genetic variability for the duration of the vegetative phase (V-R1) and the flower differentiation phase (R1-R5) is determined by the additive genetic effects (significance of “a”), while the genetic control of the grain filling duration (R5-R9) is based on the dominance effects of allelic interactions (significance of “b”). The relationships between Wr and Vr (Tab. 2 and Tab. 3) satisfy the assumptions of the genetic model for the three characters (see Materials and Methods). The analysis of genetic components (Tab. 4) indicate that heritability is very high only for the first two phases, in agreement with the importance of additive effects.

Tab.1: Analysis of variance of diallel tables ("**": P=0,1; "*":P=0,5)

Source	d.f.	Mean squares									
		V-R1	L.A1	D.M1	R1-R5	L.A2	D.M2	R5-R9	D.M3	S.YL	H.IN	OIL
a	10	432,2**	234,3**	72,4*	745,3*	652,2**	865,4**	84,2	54,8	544,5**	89,2	322,1**
b	55	15,7	97,8*	88,2**	20,5	137,1**	227,7**	425,3**	905,6**	415,2**	401,8**	291,3*
b1	1	23,2	63,5	121,2	23,7	187,4*	210,2*	432,6*	653,1**	755,7*	326,8*	214,9
b2	10	19,1	89,2	98,3*	15,9	153,2*	154,3	539,4**	568,4*	692,5*	244,1	310,4**
b3	44	14,7	100,5	85,2*	21,5	132,3*	244,8*	399,2*	987,3**	344,5*	439,4*	289,3*
c	10	11,3	21,3	0,7	16,7	23,6	31,2	54,2	122,3	77,9	114,6	80,2
d	45	17,3	18,3	0,4	21,3	12,5	10,6	16,8	45,3	54,6	64,6	43,8
Blocks	2	6,9	15,7	1,9	14,3	17,3	21,2	21,4	43,5	33,7	11,4	7,8
Bxa	20	11,5	7,3	2,4	11,2	15,9	14,3	23,8	22,9	24,8	18,4	5,6
Bxb	110	8,6	10,2	7,7	8,3	11,0	9,6	15,5	27,8	28,8	7,7	9,6
Bxb1	2	8,4	7,5	10,2	11,2	13,5	20,3	31,2	32,1	28,3	9,3	3,5
Bxb2	20	4,6	8,9	8,2	7,9	17,3	18,2	22,9	45,7	11,5	5,6	7,9
Bxb3	88	9,5	10,5	7,5	8,3	9,5	7,4	13,5	23,6	32,7	8,1	10,1
Bxc	20	11,2	5,3	7,3	4,7	11,4	4,4	7,5	22,1	12,8	7,8	7,8
Bxd	90	9,5	4,2	5,4	2,5	16,3	9,2	9,1	31,4	9,4	3,6	11,5

Tab.2 :Analysis of variance of (Wr+Vr) and (Wr-Vr) values.

Source	d.f.	Mean squares									
		V-R1	L.A1	D.M1	R1-R5	L.A2	D.M2	R5-R9	D.M3	S.YL	H.IN	OIL
(Wr+Vr)												
Arrays	10	43.23	35.67	65.17	34.65	473.34**	752.73**	495.57**	154.23*	321.23*	98.45*	77.94
Replicates	22	21.32	11.32	43.56	24.45	14.58	45.34	24.69	25.95	37.46	12.76	39.65
(Wr-Vr)												
Arrays	10	14.22	7.43	11.32	0.65	23.87	41.34	40.10	71.02	34.87	67.56	34.67
Replicates	22	9.54	3.57	7.21	0.45	8.54	24.65	43.49	53.23	17.65	23.95	9.45

Tab.3: Wr on Vr joint regression coefficient (b); Standard Error (S.E.), "t" test from zero t(0) and "t" test from unity t(1)

	Mean squares										
	V-R1	L.A1	D.M1	R1-R5	L.A2	D.M2	R5-R9	D.M3	S.YL	H.IN	OIL
b	0.742	0.812	0.543	0.791	0.821	0.919	0.891	0.297	0.654	0.829	0.451
S.E.	0.236	0.134	0.145	0.231	0.132	0.212	0.176	0.291	0.145	0.167	0,112
t (0)	8.243**	7.348**	9.657**	7,342**	8.913**	7.945**	7.179**	3.793	6.285**	5.159*	5.341*
t (1)	1.341	1.487	2.712	1.853	1.540	0.177	0.324	7.823**	2.257	0.793	0.765

Leaf area **(L.A1, L.A2)**

The analysis of variance for data collected at the end of the first phase (Tab. 1) shows the significance of "a"' and "b", furthermore, since the significance of "b" is not confirmed by heterogeneity of the Wr+Vr analysis, additive genetic effects are the major source of genetic variability (Tab. 4). At flowering the dominance effects of allelic interactions is the most

important source of genetic variability, a similar result was found by Skoric (1974). The relationships between Wr and Vr are in agreement with the importance of dominance deviations (heterogeneity of Wr + Vr analysis in Tab. 2) and indicate that data fit the genetic model as it results from the homogeneity of Wr-Vr analysis (Tab. 2) and from the regression coefficient of Wr on Vr significantly different from zero and not different from unity (Tab. 3).

The analysis of the variation components reported in Tab. 4 indicates that phenotypic selection may be useful to improve the development of leaf area at the stage of visible head (heritability of 62%) but this method cannot be used for the same character at flowering when heritability is very poor. However considering that directional effects are significant ("b1" in Tab. 1) other information may be obtained: the correlation between Wr+Vr values of half sib families and the phenotypic values of common parents reflects the dominance direction; in this case the value is -0.94 (data not reported) indicating that the dominant alleles increase the character.

Dry matter production **(D.M1, D.M2, D.M3)**

At the end of the first phase the variability is significant only for half sib families ("a" in Tab.1), dominance deviations become consistent at flowering as they result from the significance of "b" in Tab.1 and from the heterogeneity of Wr+Vr analysis in Tab.2. At the end of the ontogenetic cycle, the character shows a variability that does not fit the additive-dominance model of inheritance, the regression coefficient of Wr on Vr is in fact significantly different from unity (Tab.3). These results, in agreement with the heritability which is high only when the first two phases of plant development are considered, indicate that the genetic control of dry matter production is more complex at the end of the ontogenetic cycle when other sources of variability become important.

Tab.4: Estimates of genetic variation components

	V-R1	L.A1	D.M1	R1-R5	L.A2	D.M2	R5-R9	D.M3	S.YL	H.IN	OIL
D	7.98	97.3	709.4	11.3	87.3	546.8	23.97	316.9	543.6	11.1	23.9
H1	2.34	62.1	213.6	0.13	657.2	772.5	62.71	218.3	867.1	28.9	34.7
H2	2.37	45.7	164.3	0.75	645.7	814.6	52.65	518.0	367.9	38.1	23.1
F	4.05	15.1	231.3	0.23	25.6	164.3	31.75	51.3	23.8	1.8	0.65
E	2.51	13.3	37.4	0.57	99.5	215.4	7..35	79.1	172.8	38.8	30.3
H1/D	0.62	0.72	0.54	0.32	1.97	1.21	1..59	0.39	1.79	1.42	0.54
h2	0.73	0.62	0.62	0.74	0.23	0.45	0.06	0.15	0.21	0.08	0.18

Seed yield, oil content and harvest index **(S.YL, OIL, H.IN).**

Considering first seed yield, both additive and non-additive variance appear to be important (significance of "a" and “b” in Tab.1). The results reported in Tab.2 indicate that the non-additive source of variation is determined by dominance effect of allelic interactions (homogeneity of Wr-Vr analysis and heterogenity of Wr + Vr analysis). The dominance degree (H1/D) is 1.79 indicating the presence of overdominance, while heritability is 0.21 (Tab.4).

The additive effects are the major component of variation for the oil content (significance of "a" in Tab.1) in agreement with heritability that results 0.18.

The ratio of seed yield and total dry matter, is an important index known as harvest index. In this case the dominance deviation effects are the major part of genetic variability, significance of "b" in Tab.1, this result is confirmed by the heterogeneity of Wr+Vr analysis (Tab.2) and it is in agreement with the Wr on Vr regression coefficient (Tab.3), not different from unity (absence of non-allelic interaction).

Genetic and phenotypic correlations

The results synthesised in Tab.5 indicate that seed yield is positively and strongly correlated with leaf area development and dry matter production in the first and second phase of the ontogenetic cycle. It is interesting to notice also that the genetic correlation between the seed yield and the increment of dry matter production during grain filling is negative. Photosynthetic activity during the first two phases, when flower differentiation is setting, seems to be more important than the activity after flowering even if in the third phase the grain filling is realised. This result may be explained by taking into account that grain filling is carried out by both redistribution of assimilates from storage sites and assimilation after flowering (Blanchet and Merrien, 1982; Hall et al., 1989). The first seems to be more important than the second.

Tab.5: Phenotypic (upper triangle) and genetic (lower triangle) correlations

	V-R1	L.A1	D.M1	R1-R5	L.A2	D.M2	R5-R9	D.M3	S.YL	H.IN	OIL
UI-RI	-	0.45	0.39	0.23	0.42	0.42	-0.12	0.21	0.41	0.32	0.52
L.AI	0.46	-	0.85	0.66	0.68	0.62	0.34	-0.17	0.77	0.43	0.69
D.M1	0.41	0.89	-	0.84	0.72	0.70	0.41	-0.11	0.71	0.15	0.74
R1-R5	0.39	0.91	0.90	-	0.73	0.71	-0.11	-0.34	0.39	0.25	0.34
L.A2	0.77	0.87	0.84	0,91	-	0.92	0.42	0.23	0.86	0.46	0.75
D.M2	0.81	0.85	0.73	0.82	0.91	-	0.35	0.43	0.90	0.29	0.67
R5-R9	0.04	0.17	0.17	0.21	0.21	-0.12	-	0.46	0.51	0.39	0.56
D.M3	-0.15	-0.42	-0.44	-0.19	-0.35	-0.34	0.13	-	0.32	0.23	0.75
S.YL	0.72	0.87	0.88	0.83	0.92	0.87	0.21	-0.34	-	0.61	0.64
H.IN	0.63	0.32	0.35	0.29	0.69	0.72	-0.20	0.12	0.62	-	0.23
OIL	0.74	0.70	0.87	0.60	0.82	0.81	0.51	0.61	0.71	0.44	-

Conclusions

The results obtained indicate that genetic variability is important for all the analysed characters. Genetic control becomes more complex approaching the end of the ontogenetic cycle, when the unfixable component of variation becomes the major part of genetic variability. This is the case of seed yield, oil content, dry matter production during the phase of grain filling and harvest index.

The high genetic correlations among seed yield, oil content and physiological traits such as leaf area development and dry matter production indicate that these characters are important limiting factors by which the efficiency of plant assimilation may be evaluated. Considering the high heritability of these characters especially during the first phases of plant development, their use in early screening may be useful when a large amount of hybrid combinations are included in selection programs.

References

Blanchet, R. and Merrien, A. 1982 - Influence of water supply on assimilation, yield component and oil -protein production of sunflower. Proc. of Workshop Sunflower. E.E.C. Plant protein programme, 185-201, Athens.

Cecconi, E, Pugliesi, C., Baroncelli, S. and Rocca M., 1987 - Genetic analysis for some agronomical characters of a sunflower *(Helianthus annuus L.)* diallel cros. Helia, 10:21-27.

Chervet, B. and Vear, E 1990 - Study of the relationship between sunflower earliness and yield, oil content, development and morphology. Agronomic, 10:51-56.

Cukadar O.B and Miller J.F. 1996 – Inheritance and combining ability of the stay green trait in sunflower. Proc of the 14th Int. Sunflower Conf. Pechino China 12-20 June:218-223

Dominiquez Gimenez, J. and Fernandez Martinez, J. 1987 - Evaluation of inbred testers in sunflower hybrid breeding. Helia, 10:15-19.

Falconer, D.S. 1967 - Introduction to Quantitative Genetics. The Ronald Press Company, New York.

Fick, G.N. 1978 - Breeding and Genetics. In Carter J.F., (ed.), Sunflower Science and Technology, A. Soc. of Agron., Madison, Wise., 279-328.
Hall, A.J., Connor, D.J. and Whitfield, D.M. 1989 - Contribution of pre-anthesis assimilates to grain filling in irrigated and waterstressed sunflower crops. 1 Estimates using labelled carbon. Field Crop Res., 20:95-112.
Hayman, B.I. 1954a - The analysis of variance of diallel tables. Biometrics, 10:235-244.
Hayman, B.I. 1954b - The theory and analysis of diallel crosses 1. Genetics, 39:787-805.
Hayman, B.I. 1958 - The separation of epistatic from additive and dominance variation in generation means. Heredity, 12:371-390.
Mather, K. and Jinks I.L. 1971 - Biometrical Genetics. Second ed. Champan and Hall, London.
Merrien A. 1992- Some aspects of sunflower crops physiology. In: Proc of 13th Int. Sunflower Conf. Vol.1 Pisa Italy: 481-498
Miller, J.F. Hammond, J. and Roath, W.W. 1980 - Comparison of inbred vs. single-cross testers and estimation of genetic effects in sunflower. Crop Science, 20:703-706.
Pistolesi, G., Cecconi, E, Baroncelli, S. and Rocca, M. 1986 - Stressing sunflower *(Helianthus annuus L.)* plants as a method for speeding breeding techniques. Z. Pflanzenzuchtg, 96:90-93.
Schneiter, A.A. and Miller, J.F. 1981 - Description of sunflower growth stages. Crop Science, 21:901-903.
Skoric, D. 1974 - Correlation among the most important characters of sunflower in F1 generation. Proc. of the Xl° Int. Sunf. Conf., Vol 11:683-689, Mar del Plata.
Vannozzi G.P., Baldini M. Gomez-Sanchez D. 1999 – Agronomic traits useful in sunflower breeding for drought resistence. Helia 22:97-124