RELATIONSHIPS BETWEEN ENZYMATIC POLYMORPHISM AND HETEROSIS IN CULTIVATED SUNFLOWER POPULATIONS.

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Summary:

Analysis of combining abilities against 4 testors were performed on 124 populations from various origins on yield, seeds water content and seeds oil content. Isoenzymatic systems were studied too, on 39 of these populations (MDH, PGD, PGI, PGM, ACO, ADH2, GOT, LAP, EST). Genetic structure was studied both on combining values and allelic frequencies. A group structure was shown on French, Moroccan and Russian populations who were the majority. The MDH, PGI et PGD systems appear to provide the best discrimination on SCA against the 4 testors. EST and PGI systems are slack linked with GCA of populations.

Introduction:

Sunflower populations from 10 different countries over the world (see table 1) were crossed against 4 Cms testors lines differing in their genetic origins and agronomic characteristics. Hybrids resulting from these crosses were tested as part of a network named PROTOURNESOL that involves INRA and 18 french companies of sunflower breeding. The experimental design used was a lattice with 2 replicates of 100 plants in 3 geographical places. Yield was estimated by a pondered mean coefficient (PMC). This coefficient gives a lesser weight to experiments having the biggest coefficients of variation.

$$PMC = (1/K) \quad \Sigma_{1,K} \left[(X_k - T_k) \; / \; \sqrt{ [(\sigma_e^2(k)/n_k)*(1+(1/n_t))] } \right]$$

With:

K = trial location number.

k = trial location index.

n_t = number of controls.

X_k = mean yield in trial location k.

T_k = average control yield in trial location k.

n_k = number of replications in trial location k.

Populations were analysed too, on nine polymorphic isoenzymatic systems. These systems were MDH (malate dehydrogenase), PGD (phospho-gluconate dehydrogenase), PGI (phosphoglucoisomerase), PGM (phosphoglucomutase), ACO (aconitase hydratase), ADH2 (alcohol dehydrogenase), GOT (glutamate Oxaloacetate transaminase), LAP (leucine amino peptidase) and EST (esterases). Analysis were made on forty seeds of each population.

Structure of Specific combining abilities:

Combining abilities were computed from analysis of the variance of the linear model on seed yield, seed water content and seed oil content. General (GCA) and Specific (SCA) effects are significant at 1% level (test of Fisher).

The SCA can be correlated amongst each other therefore they were studied using the method of Mandel (Mandel 1971) that allows one to examine an interaction with a discriminate method, similar to a Principal Component Analysis (PCA). We thus obtained three independent principal components. The two first components represent a percentage of the total inertia that is respectively 84%, 75% and 87% for the 3 characteristics studied. The figures 1, 2 and 3 which result from Mandel analysis reveals a structure according to the geographical origin of populations.

Structure of enzymatic polymorphism:

We found in allelic frequencies a various polymorphism level according to enzymatic systems. Most of them have a major allele like MDH(b), PGI(a), PGM(b), ADH2(a), GOT(b) and LAP(b) whose mean frequency in all the populations is at least 0.75. ACO and EST systems are the most polymorphic. Some systems have rare alleles like PGM(c), ACO(a), ADH2(c), GOT(c), LAP(c). When several populations have one of this rare allele one notice than they have different geographical origin. Therefore one can suppose that recombinations happen between these populations or that they had common ancestors. We notice too, that the M23 population has 80% of the rare allele ADH2(c).

In order to found a structure of enzymatic polymorphism we compute a Component Principal Analysis (CPA) on allelic frequencies. Allelic frequencies are used as variables and sunflower populations as individuals of the CPA.

Explained cumulative per cent of the variation for the 5 primes components are 18.7%, 34.9%, 49.5%, 60.5% and 68.8%.

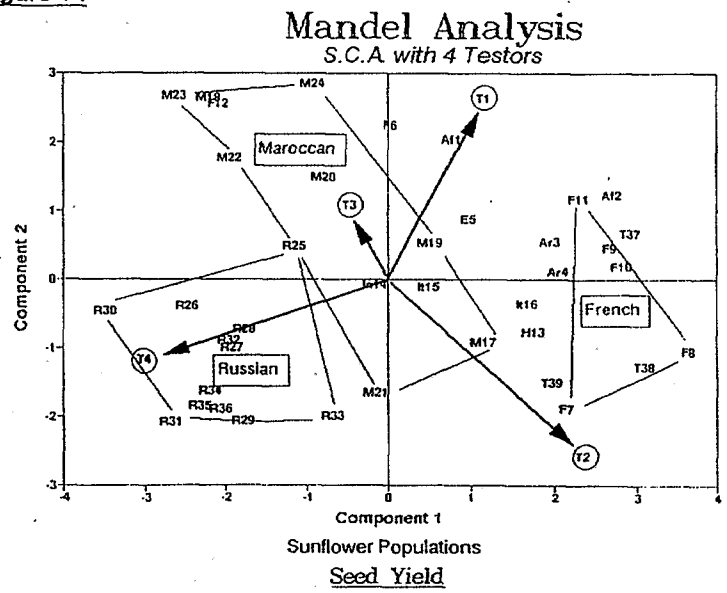
Study of variables (see figure 4) shows that the first axis is determined by MDH system with allele (b) opposite to allele (a), and with a lower contribution by LAP system (allele (b) opposite to allele (a)) and GOT system (allele (b) opposite to allele (c)). The second axis is determined by PGI system (allele (a) opposite to allele (b)) and PGD system (allele (b) opposite to allele (a)).

Study of individuals show a structure according to geographic origins of populations. Indeed axis 1 separate Moroccan, French and Russian populations (except M23 and R31 populations). This clustering is essentially determined by MDH, GOT and LAP systems.

Table 1: Code and origin of populations

Code	Origin
Af1 to Af2	Africa
Ar3 to Ar4	Argentina
E5	Egypt
F6 to F12	France
H13	Hungary
In14	India
It15 to It16	Italy
M17 to M24	Marocco
R25 to R36	Russia
Tr37 to Tr39	Turkey

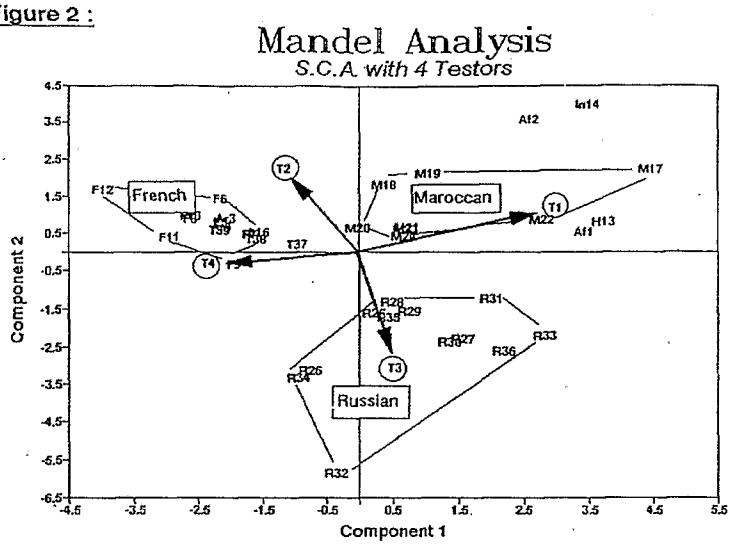
Figure 1 :



Sunflower Populations

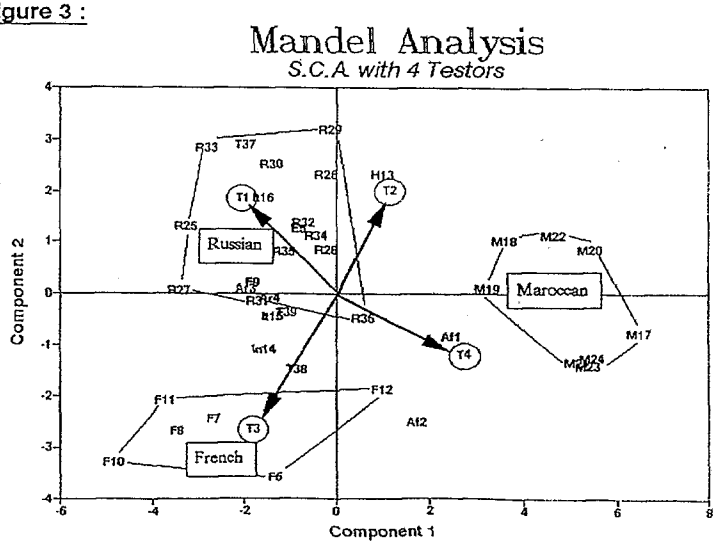
Seed Yield

Figure 2 :



Sunflower Populations
Seed Water Content

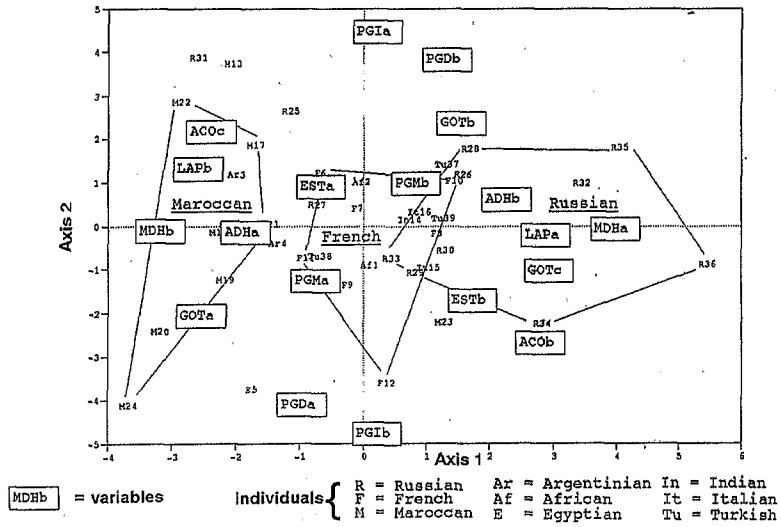
Figure 3 :



Sunflower Populations
Seed Oil Content

Figure 4 :

CPA on allelic frequencies of nine enzymatic systems



Conclusion:

A between population structure according to geographic origins was shown both in Mandel analysis based on specific combining abilities and in the study of polymorphism by enzymatic approach. One can suppose that a direct relationship between phenotypic and molecular polymorphism may be studied in order to determine predictors of heterosis in sunflower.

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