

GENETIC DIVERSITY AND HYBRID PERFORMANCE IN EUROPEAN WINTER OILSEED RAPE (*BRASSICA NAPUS* L.).

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ABSTRACT

Genetic distances were estimated between 64 oilseed rape varieties by RFLP analysis. Within the winter types cluster analysis indicated seven divergent groups, presenting the first base of gene pools for hybrid breeding in winter rape. Seed yield performance of 22 experimental hybrids significantly exceeded the yield of their parents by an average of 16,9 %. The correlation between heterosis of F₁ hybrids and the genetic distances of their parental lines was determined to $r=0.72$.

INTRODUCTION

The high levels of heterosis reported for oilseed rape hybrids (Grosse et al. 1992) and the available stable system for pollination control from INRA (France) accelerated the development of hybrid breeding systems for rapeseed. The effective utilization of heterosis requires complementing gene pools, providing for high yield of crosses between the pools. In contrast to maize, such gene pools are not yet available in rapeseed. In the past, the development of such gene pools requires test crosses. Today, genetic distance estimate by molecular marker techniques, e.g. RFLPs, offer an efficient alternative, if the genetic distance of parental lines is highly correlated with heterosis of the hybrids (Smith et al. 1991). Our interest has been (1) to evaluate the utility of RFLPs in distinguishing genetically divergent groups in the existing rapeseed materials and (2) to determine possible correlations between genetic distances and heterosis in crosses between breeding lines.

EXPERIMENTAL

Plant materials and RFLP analyses

A collection of 64 rapeseed varieties and breeding lines, comprising 61 winter- and 3 spring types was examined. To conform to hybrid breeding, each variety was represented by a single plant and its selfed progeny. Following a factorial crossing plan (4 x 6), the same single plants of ten lines were crossed by hand. Yield performance of these 22 experimental hybrids and their parents was determined in field trials at three locations in the growing season 1993/1994. Using the restriction enzymes EcoRI and HindIII, the RFLP analyses were performed by standard protocols (Maniatis et al. 1989). Distance values were calculated according to Dice (Dice 1945) and cluster analysis was applied using the UPGMA algorithm.

Clustering and correlations

Hybridization of 176 DNA probes revealed 226 probe/enzym combinations with a total of 841 scorable polymorphisms. The estimated genetic distances varied from 0.02 (lines 39 and 40) to 0.55 (lines 27 and 42). Cluster analysis clearly divided the analysed

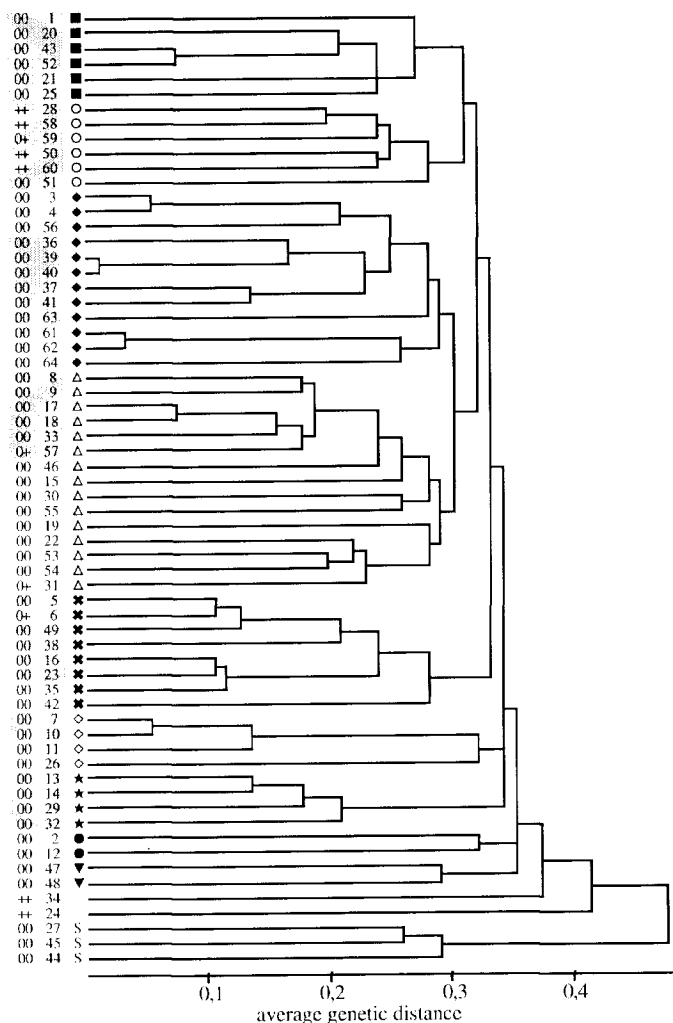


FIGURE 1: Dendrogram of 64 rapeseed genotypes clustered by UPGMA based on genetic distance estimates of 841 RFLPs according to Dice (1945). Identified groups are marked with different symbols and 'coregroups' are underlined in grey. '0' and '+' indicates low and high seed contents, respectively, of erucic acid and glucosinolates.

materials in spring- and winter types. The winter types were further divided into nine subgroups (Fig. 1) and distances between these groups ranged from 0.28 to 0.34 whereas the average estimate within each group was 0.24. Two lines, the Dutch landrace 'Mansholt's Hamburger Raps' (34) and the Asiatic line 'Italy' (24) clustered to none of the identified groups. Comparisons of 20 dendrograms derived from randomly selected probe sets with 350 fragments each revealed a total of 37 winter genotypes which consistently clustered in seven 'core groups' (Fig. 1). Depending on the actual probe set, genotypes clustering outside the core groups frequently changed positions in the dendrograms. An additional analysis of a larger set of genotypes comprising 142 winter types using a selected probe set of 71 well hybridizing and easy to score probe/enzyme combinations confirmed the identification of these groups by clustering additional lines to them.

All 22 tested hybrids significantly exceeded the yield of their parents (401 g/m²) by an average of 16,9 % ($p \leq 0.05$) and the yield of the standard 'Idol' by 15,0% ($p \leq 0.05$). The estimated heterosis to the mean seed yield of the parents ranged from -3.9 % for the F₁-hybrid of the lines 41 and 37, clustering in group 'F' to 27,4 % for the hybrid of line 17 (group C) and line 37 (group F). Similar values were determined for oil-yield (g oil/m²) and plant length (cm). In all cases the lowest heterosis was estimated for crosses within the identified groups and the highest for crosses between single members of different groups. All calculated correlations between the heterosis of determined traits and the estimated distance values were highly significant ($p \leq 0.01$) and ranged from $r = 0.71$ for oil-yield to $r = 0.73$ for plant length (Tab.1). Also the estimation of the distance values with the selected set of 71 probes amounted to correlation values of $r = 0.72$.

TABLE 1: Correlations between the heterosis of 22 F₁-hybrids and the genetic distances of their parental lines estimated with two RFLP data sets.

Traits	Total probe set (841 polymorphisms)	Selected probe set (296 polymorphisms)
seed yield (g/m ²)	0.72*	0.72*
oil-yield (g oil/m ²)	0.71*	0.73*
plant height (cm)	0.73*	0.69*

* = significant at $p \leq 0.01$

Both, the clustering and the high correlations between heterosis and genetic distances underline the suitability of molecular markers for assisting hybrid breeding of rapeseed. The present RFLP data enable to distinguish several consistent groups of genotypes and to allocate additional lines to them. These groups represent likely candidates for the development of divergent gene pools. Furthermore, for the present development of F₁ hybrids, the high correlations between heterosis and genetic distances confirm the apply of distance values as a criteria for the selection of promising parental lines.

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