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Relationship between genetic distance and heterosis for yield and morphological traits in winter canola (*Brassica napus* L.)

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Abstract Genetic distance among canola cultivars was estimated through multivariate analysis. Thirty cultivars from various sources were analyzed and clustered based upon five morphological characteristics and yield components – crown diameter, number of branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and yield plant^{-1} – and placed in three distinct clusters. Two cultivars from each cluster were selected as parents and 15 partial-diallel inter- and intra-cluster crosses were made between the six selected parents and evaluated at two locations in Michigan in 1990/1991. The association between genetic distance and mid-parent heterosis was investigated. The correlation between genetic distance and heterosis was positive and highly significant for seed yield, number of pods plant^{-1}, and number of seeds pod^{-1}. Clustering, based on yield and yield-component traits, demonstrated that inter-cluster heterosis was greater than intra-cluster heterosis in the majority of cases.

Key words Canola · Heterosis · Genetic distance · Multivariate analysis

Introduction

Historically, the development of hybrid cultivars of corn, sunflower, sorghum and many horticultural species has led to significant increases in seed yield due to the phenomenon of heterosis (Furgala et al. 1979; Duvick 1984; Miller and Kebede 1984). The yield potential of single-cross oilseed rape hybrids (*Brassica napus* L.) has attracted considerable interest from oilseed breeders, seed producers and growers around the world. It has been shown that heterosis, measured as the superiority of hybrids over their mid-parent, is proportional to the genetic distance between their respective parents in bean (Ghaderi et al. 1984), flax (Murty et al. 1965), and mung bean (Ramanujam et al. 1974; Ghaderi et al. 1979). The amount of genetic variability in a population is an important parameter which can be easily measured since it is based on the genetic distance between the parents (Cowen and Frey 1987). Several statistical methods have been used to estimate the genetic distance between two populations using phenotypic data. These include Euclidian (Goodman 1972), principle-component (Adams 1977) and Mahalanobis D^2 (Mahalanobis 1936) techniques, which have been used by different authors (Sneath and Sokal 1973) in a number of crops including okra (Bhatt 1970; Ariyo 1987), wheat (Shamsuddin 1985) and tomato (Jacquard 1974; Balasch et al. 1984).

The objective of the present study was to use multivariate statistics and clustering techniques to group a set of winter canola cultivars based on morphological traits and yield-component data. Using the differences in genetic distance, yield performance and heterosis of F_1 hybrids between and within clusters was compared.

Materials and methods

Thirty cultivars and/or breeding lines of winter canola from different origins and breeding programs were used for this study. Actual pedigrees are not available.

The cultivars were planted for 2 years (1988, 1989) to collect data on morphological traits, yield and yield components. Trials were planted during September 1988 in East Lansing, Michigan, and at Clarksville, Michigan, in 1989. A randomized complete block design with four replications for parental selection and three replications for cross evalution was used. The plot size for parental selection was 6 m by 0.75 m, and each plot consisted of five rows 15-cm apart, whereas, the plots for hybrid evaluation were comprised of single 1.5-m-long rows with a spacing between rows of 30 cm.

Data were collected from eight competitive plants from each plot for crown diameter (mm), leaf length, leaf width, number of branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight, and yield plant^{-1}.

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An analysis of variance was performed to determine whether there was a significant difference among the genotypes for the traits under evaluation. Based on the analysis of variance results, the characteristics, including crown diameter, number of branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and seed yield, were used in estimating the genetic distance. Multivariate analysis was performed using the principle-component (Adams 1977) and clustering techniques (Bhatt 1970), and genotypes were grouped into a number of clusters. The genetic divergence among the genotypes was measured by means of the Euclidian-distance method and six parents were selected to be inlcuded in the crossing program. A half-diallel crossing scheme was conducted between the six selected parents (LD-9430, Cascade, Cobra, Winfield, Ceres, and CC-4) and 15 crosses were made within and between the clusters. Parents and their F_1s were planted at two locations (East Lansing and Clarksville) during September 1990 and data on the same five characteristics used in the clustering analysis were recorded and analyzed. The heterosis of hybrids were estimated on mid-parental values using the following formula: mid-parent heterosis (%) = 100 (F_1 − MP)/MP, where F_1 = hybrid mean and MP = parental mean.

Results and discussion

Genetic distance among the parents

The analysis of variance for morphological traits, yield and yield components, including seed yield plant^{-1}, number of branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and crown diameter, revealed significant differences among the 30 cultivars. The cultivars were grouped into three distinct clusters based on the genetic variation of these characteristics. Two cultivars from each cluster were selected as parents. Cluster 1 included LD-9430 and Cascade, cluster 2 included Cobra and Winfield, and cluster 3 included Ceres and CC-4 (Table 1). The genetic distance between parents was calculated using the Euclidian-distance technique. The distance between parents ranged from 1.104 to 7.497. The minimum distance was between Cobra and Winfield, while the maximum distance was between LD-9430 and Ceres (Table 2).

Relationship between heterosis and genetic diversity

All 15 hybrids exceeded the mid-parent value for seed yield, pods plant^{-1} and seeds pod^{-1} at both locations. The data agree with the findings of Paterniani (1973) in corn and Upadhaya (1967) in barley.

Table 1 Cluster pattern of selected canola cultivars based on their genetic divergence

Cluster	Cultivar	Source
1	LD-9430	Calgene
	Cascade	Cargill
2	Cobra	Calgene
	Winfield	Calgene
3	Ceres	Calgene
	CC-4	Cargill

Table 2 Genetic distance between six canola parents calculated based on six morphological and yield components traits

Parents	Cluster no.1		Cluster no.2		Cluster no.3	
	LD-9430	Cascade	Cobra	Winfield	Ceres	CC-4
CC-4	5.610	4.785	3.341	3.545	2.501	–
Ceres	7.497	6.180	4.592	4.376	–	–
Winfield	4.266	2.927	1.104	–	–	–
Cobra	3.576	2.402	–	–	–	–
Cascade	2.128	–	–	–	–	–
LD-9430	–	–	–	–	–	–

The correlation between heterotic effects for seed yield and parental distance was positive and highly significant for the combined analysis at both locations, $r = 0.70$ (Fig. 1). This positive and significant correlation supports the strong association between heterosis in seed yield and genetic distance between parents in tomato (Khanna and Misra 1977), corn (Moll et al. 1962), and wheat (Shamsuddin 1985). The results showed that parents of the majority of the highest-yielding hybrids belonged to two different clusters. For example, the highest seed yield was obtained by crossing Cobra from cluster 2 and Ceres from cluster 3 (Table 3). Heterosis for the number of pods per plant and seeds pod^{-1} was also highly significant and positively correlated with genetic distance. For example, the maximum percent heterosis was 27.9 for pods plant^{-1} obtained by crossing LD-9430 and Ceres which had a genetic distance of 7.497. The same trend was observed for number of seeds pod^{-1} of the same cross which showed a percent heterosis of 26.7 (Tables 2 and 3). The correlation coefficient ($r = 0.79$) between genetic distance and number of pods plant^{-1} for combined locations was significant.

Fig. 1 Correlation between genetic distance and percent heterosis for yield and yield components combined over two locations

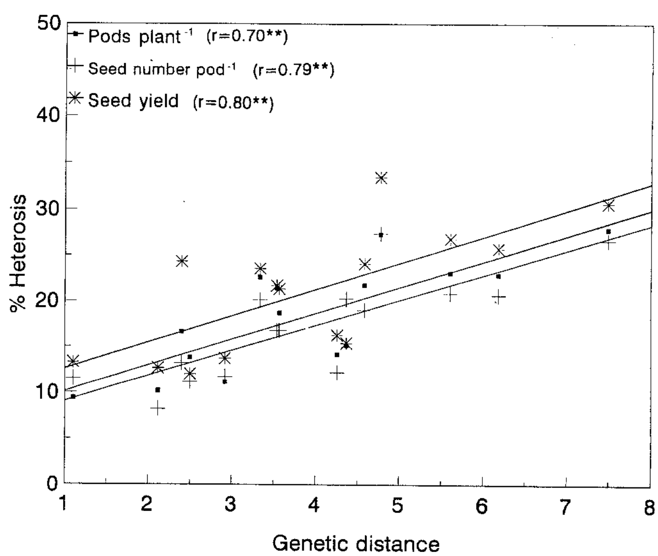

Table 3 Means (% mid-parent heterosis) for three traits in canola parents and crosses combined over locations in Michigan, 1991

Parents and crosses	Cluster	Pod number plant^{-1}	Seed number pod^{-1}	Seed yield (kg ha^{-1})
Parents				
LD-9430	1	140	18	2130
Cascade	1	136	21	2246
Cobra	2	172	26	2512
Winfield	2	158	22	2253
Ceres	3	184	29	2829
CC-4	3	205	28	2634
Intra-cluster crosses				
LD-9430 × Cascade		152 (10.18)	21 (8.21)	2465 (12.66)
Cobra × Winfield		181 (9.41)	27 (11.52)	2698 (13.27)
Ceres × CC-4		221 (13.81)	32 (11.14)	3061 (12.01)
Inter-cluster crosses				
LD-9430 × Cobra		186 (18.72)	25 (16.78)	2816 (21.33)
LD-9430 × Winfield		170 (14.14)	22 (12.20)	2548 (16.27)
LD-9430 × Ceres		207 (27.90)	30 (26.67)	3240 (30.69)
LD-9430 × CC-4		212 (23.08)	27 (20.88)	3022 (26.85)
Cascade × Cobra		180 (16.66)	26 (13.18)	2756 (24.32)
Cascade × Winfield		164 (11.13)	24 (11.72)	2558 (13.70)
Cascade × Ceres		197 (22.91)	30 (20.66)	3178 (25.28)
Cascade × CC-4		217 (27.34)	31 (27.41)	3258 (33.46)
Cobra × Ceres		217 (21.74)	33 (19.04)	3314 (24.10)
Cobra × CC-4		231 (22.63)	32 (20.12)	3181 (23.56)
Winfield × Ceres		197 (15.14)	31 (20.26)	2932 (15.41)
Winfield × CC-4		221 (21.38)	29 (16.79)	2976 (21.70)
LSD (0.05)		30	7	387

From individual and combined locations it is concluded that both pods plant^{-1} and seed number pod^{-1} have a strong association with genetic distance. This association is, therefore, an indication that there was a positive association between seed yield, as deduced from the number of pods plant^{-1}, and seed number pod^{-1}, with the genetic distance. This supports the findings of other researchers in rapeseed (Hutcheson et al. 1981; Grant and Beversdorf 1985) and dry beans (Ghaderi et al. 1984).

Two possible factors could be contributing to a positive association between the genetic distance and heterosis: (1) either the parental distance increases as the result of an increase in the magnitude of any existing dominance, and/or (2) the parental populations differed in the gene frequencies controlling these characters and this difference increased as the distance among the parents becomes greater. For characters such as yield, number of pods, and seed number pod^{-1}, which are inherited quantitatively in canola, the heterotic effect depends on the number of complementary loci and their dominance effects. In order to relate heterosis in a linear fashion with genetic distance, its components, whether alone or in combination, should also respond linearly to the varying distance. A positive correlation of distance with a number of contrasting alleles becomes easy to visualize, as stated in (2) above, when various ds (the deviation of the heterozygote from the mean of the homozygote parents) are mostly positive and this factor alone may be sufficient to explain a positive correlation between heterosis and genetic distance.

Substantial mid-parent heterosis for yield was detected in most combinations and was equivalent in range to the mid-parent heterosis reported for other self-pollinated crops (Gutierrez and Singh 1985; Shamsuddin 1985). High parent heterosis for yield ranged from 7.4 to 9.8% in intracluster crosses verses 3.6–23.7% in inter-cluster crosses, suggesting that efforts directed towards the production of hybrid cultivars in canola are justified. The inter-cluster heterosis was shown to be greater than the intra-cluster heterosis which confirms the findings of Khanna et al. (1977) in tomato and Moll et al. (1962) in corn.

Our results indicate that multivariate statistics and clustering procedures could be adopted to provide the breeder with objective information to help in the selection of the initial parents for a successful single-cross hybrid program. Yield components, including pod plant^{-1} and seed number pod^{-1} in particular, are very important traits to be utilized in a clustering procedure since yield is the ultimate objective within a hybrid breeding program, whereas other characteristics, such as leaf length, leaf width and number of branches plant^{-1} which, as in this study, did not contribute towards making clusters, can be disregarded.

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