

EFFICIENCY OF EARLY GENERATION SELECTION IN SPRING CANOLA (*BRASSICA NAPUS* L.).

J. BROWN, D.A. ERICKSON, J.B. DAVIS and A.P. BROWN.

Department of Plant, Soil and Entomological Sciences, University of Idaho, Moscow, ID 83844-2339, U.S.A.

ABSTRACT

Family bulk performance of 56 spring canola crosses were examined from F_1 , F_2 and F_3 generations. Correlations coefficients obtained between different generations indicated that selection for yield was very ineffective at F_1 or F_2 and that selection for oil content using F_1 glasshouse plants would have an effect worse than random. However, selection for other characters, could effectively be carried out on glasshouse F_1 or field F_2 family bulks. The inefficiency of selection for yield and oil content was due to large genotype x environment effects rather than large dominant genetic variance compared to additive genetic effects. Inspection of data from F_3 family means and within family variance suggest that the use of cross prediction methods could increase early generation selection efficiency in canola breeding.

INTRODUCTION

Plant breeding is a two stage operation; genetic variation is generated and selection is carried out within the resulting population to identify desirable recombinants. The latter of these two operations, the selection stage, is the topic of this paper. In the early generations of selection the number of genotypic lines to be evaluated can be large and the amount of planting material available for testing is small. Therefore these early evaluations are most often performed at one location and the influence of genotype x environment interactions can not be determined. In addition, selection is often carried out on highly heterozygous populations where the true genotype can be masked in the phenotype by dominant effects.

Response to selection is given by: $R = i\sigma_p h^2_n$, where i is a function of the intensity of selection, σ_p is the phenotypic standard deviation of genotypes and h^2_n is the narrow sense heritability. Irrespective of selection intensity, little, or no, gain from selection will be achieved if no phenotypic variation between individuals exists and/or the heritability of the character being selected is low or zero.

Thus far, there have been few studies on the efficiency of selection in spring canola (*Brassica napus* L.). This paper examines the repeatability of progeny performance in a canola breeding program and attempts to identify areas where the efficiency of selection could be increased and hence add to the effectiveness of cultivar development.

MATERIAL AND METHODS

In 1992, 56 parent cross combinations were taken at random for examination in this study. F_1 seed from each of these crosses were planted in a two replicate

randomized complete block design in the glasshouse. All 56 F_2 families were planted in a two replicate randomized block design at a single location in 1993. Prior to harvest, a random sample of 16 plants were harvested by hand from each family. Seed from each plant was individually thrashed and kept separate to be planted a single plant row the following year. The remaining bulk seed was harvested using a Hege small plot combine.

Progeny from each F_2 bulk population grown in 1993 were planted as F_3 population bulks at two locations in 1994. In addition, each of the 56 crosses were represented at a different location in single plant rows. The 16 single plant rows from each cross were planted in a nested design with two replicates with each family represented by eight plots within each main plot.

To examine the relative importance of additive genetic variance (**A**) compared to dominant genetic variance (**D**), seed was produced from an 8x8 half diallel crossing design, including selfs. The eight parents and 28 F_2 progeny were grown in a completely randomized block design with four replicates at a single location.

The following variates were recorded on all trials: days to flowering; plant height at maturity; a visual assessment of "breeders' preference"; seed yield and oil content (using a Nuclear Magnetic Resonance Analyzer).

RESULTS AND DISCUSSION

The efficiency of selection based on the performance of F_1 and F_2 progeny grown in field trials was examined by correlation between these generations and the F_3 stage (Table 1). All correlation coefficients for seed yield were not significantly greater than zero. A negative relationship was found between oil content from F_1 families in the glasshouse and both field generations. However, a significant correlation was found between oil content at F_2 and F_3 . In general, a greater association was found between the other characters. Greatest repeatability of performance was found for days to flowering. In general there was greater repeatability for all characters between F_2 and F_3 than between F_1 and either generation. Therefore, selection would not be effective for yield at either the F_1 or F_2 stage, and selection for oil content using glasshouse F_1 families would be worse than a random reduction in progeny number.

Low selection efficiency is related to, phenotypic variation (σ_p^2) and narrow-sense heritability (h_n^2). Within the crosses examined, ample phenotypic variation was observed. Therefore, the lack of relationship between generations must be the result of low values of h_n^2 . Narrow-sense heritability (h_n^2) is the proportion of total phenotypic variation that is accounted for by additive genetics variance (**A**) and is derived from the equation: $h_n^2 = A/(A+D+E)$, where: **A** is additive genetic variance, **D** is dominant genetic variance and **E** is error variance.

If h_n^2 is small, then either **D** is large compared to **A**, or **E** is large compared to **A**. Analyses of variance on F_2 families from a half diallel were carried out to examine the relative magnitude of **A** to **D**. In these analyses the effect of genotypes were partitioned into additive effects (**a**), directional dominance (**b₁**), non-directional dominance (**b₂**) and a remainder effect (**b₃**). Non-additive/dominance effects (**b₃**) accounted for greatest variation in plant height. For all other characters examined,

however, additive effects accounted for greatest variation and in all instances additive genetic variation exceeded dominant genetic variation

Table 1. Correlation coefficients of seed yield, % oil content, days to flower start, plant height and breeders' preference between different generations (F_1 , F_2 and F_3 family bulks).

Comparison	Seed yield	% oil content	Flower start	Plant height	Breeders' preference
$F_1 \text{ v } F_2$	0.05	-0.02	0.36**	0.36**	0.10
$F_1 \text{ v } F_3$	0.19	-0.09	0.40***	0.22	0.16
$F_2 \text{ v } F_3$	0.08	0.24*	0.60***	0.36**	0.62***

* = $0.01 < P < 0.05$; ** = $0.001 < P < 0.01$; *** = $P < 0.001$.

The ability to estimate h^2_n values from mid-parent/offspring regression is one advantage of including the parental self in diallel designs. All h^2_n values for all traits were moderate to high. This suggests that selection efficiency should be considerably higher than the relationship between generations suggest. Note that the diallel analyses were carried out using data collected from a single location and year therefore, no genotype x environment (GxE) component exists in the error term (E). The effect of GxE was examined by correlating performance of the 56 F_3 families when grown at two locations. Correlation coefficients obtained between the two sites for days to flower start, plant height and breeders' preference were all significant and moderate to large. The highest yielding families at one location were, however, lowest yielding at the other site shown by a negative correlation relationship. Similarly oil content showed poor repeatability between locations indicating that GxE is a major factor in the poor efficiency of selection earlier observed. It is difficult to imagine how it would be possible to evaluate the many individuals in a the early stages of a breeding program at many locations. However, some account needs to be made for GxE in order to increase the efficiency of selection.

The performance of F_3 single plant rows was compared to that from the F_3 bulk families grown at two locations using correlation. Correlation coefficients were obtained based on the average performance of the 16 single plant rows and also based the family mean and within family genetic variance. In every trait the addition of σ^2_g increased the coefficient.

CONCLUSIONS

Selection for yield or oil content at the early generation stages of a spring canola breeding program was very ineffective. However, selection for other traits was more effective. Low h^2_n values were caused by large GxE interactions rather than a predominance of dominant effects over additive genetic variation. Estimating the potential of a cross based on the additive genetic mean and additive genetic variance could increase the efficiency of selection. A number of researchers have found increased selection efficiency using cross prediction based on progeny mean and variance. The use of such prediction methods could increase the efficiency of early generation selection in canola breeding.