

GENOTYPE-ENVIRONMENT INTERACTIONS OF YIELD COMPONENTS IN  
*BRASSICA NAPUS* L.

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## ABSTRACT

Studies on the relationships of seed yield, seed set per pod, 1000 seed weight and their responses to environments in *Brassica napus* L. indicated that seed weight had a higher positive relationship to seed yield than seed set per pod when evaluated over locations. However, the relationships of these traits were genotype, and environment-dependent and could not be simply defined. The estimated heritability was 0.7835 for seed set per pod, 0.6547 for 1000 seed weight, and 0.6726 for seed yield. It was concluded that direct selection over years and locations was the most effective and economical method for estimating seed yield.

## INTRODUCTION

*Brassica napus* L. is a major canola species in western Canada as well as many other regions in the world. Breeding for high seed yield is a major breeding objective of this crop. The use of indirect selection from yield components, i.e. pod number, seed weight, seed number per pod, has been previously reported (Andersson and Olsson, 1961; Thurling, 1974, 1991; Seiffert and Boelcke, 1977; Shabana et al 1990; Grosse et al 1992). However, the relationships between seed yield and its components are subject to environmental effects. Therefore, such relationships have not been clearly defined and successfully applied to breeding programs. The present study provides information on the interrelationships between seed yield, seed number per pod and seed weight, and to investigate the genotype x environment interactions of these traits in a canola -growing region of western Canada.

## MATERIALS AND METHODS

Seven spring type *B. napus* genotypes, Alto, G3, G4, LPHIPR, GD, HIOIL, HIYLD were tested in 1993 and 1994 at three locations, Edmonton Research Station, Ellerslie and Kelsey, Alberta, Canada. The experiment was conducted in an RCB design with three replications. Seed set in each pod was determined on five pods on the main raceme of each of five random plants of each genotype when the developing and aborted seeds could be clearly differentiated in the pods. Total seed yield was recorded after harvest and one thousand seed weight was determined from the bulk seed sample. The data were analyzed by ANOVA, correlation and stepwise regression, and the heritability of each trait was estimated using the model of Comstock and Moll (1963).

## RESULTS AND DISCUSSION

1. Environmental effects on seed set per pod, 1000 seed weight and seed yield and heritability estimates: Analysis of variance revealed significant interaction of genotype x year for all three traits (Table 1). In contrast, no trait showed significant genotype x location interaction. It appeared that these traits were more sensitive to seasonal than to location variations. Thus, evaluation of these traits over seasons seemed to be more critical. It should be mentioned, however, that two of the three locations involved were in close proximity, therefore, the environmental conditions of these two locations might be similar. Studies involving more diverse locations should furnish more information.

Based on the information in Table 1, estimated heritability was 0.7835 for seed set per pod, 0.6547 for 1000 seed weight, and 0.6726 for seed yield respectively. The heritabilities of these traits were relatively high despite the high genotype x year interactions. It should be noted (Table 1) that no trait showed significant variation at the 5% level due to genotype, which may be due to the limited genotypes investigated. Even higher heritabilities may be expected in a breeding program since there are usually more genetically diverse genotypes involved. Since the genotypes tested were mainly doubled haploid lines or the established cultivar, the heritabilities estimated mainly included the additive and additive by

Table 1. Analysis of variance of seed set per pod, 1000 seed weight, and seed yield, of seven *B. napus* genotypes tested over two years at three locations

Source of variation	DF	Seed set per pod		1000 seed weight		Seed yield	
		MS	F	MS	F	MS	F
Genotype (G)	6	89.159	4.618	5.085	2.985	291.383	3.053
G x Year (Y)	6	21.497	3.162 *	1.666	8.816 **	82.732	3.747 *
G x Location (L)	12	4.606	0.678	0.279	1.475	34.972	1.576
G x Y x L	12	6.798	0.983	0.189	4.527 **	22.082	1.036
Error	72	6.909		0.042		21.325	

\* Denotes significant at 5%; \*\* Denotes significant at 1%

additive gene effects, suggesting that selection for each of these traits would be effective in breeding programs. This is particularly true in breeding programs using the doubled haploid approach.

2). Regression of seed yield on seed set per pod and 1000 seed weight: Linear regression of seed yield on seed set per pod and 1000 seed weight (Table 2) clearly indicated that seed yield was genotype dependent, and that the magnitude of such composition also varied from year to year. A generally higher association of seed yield to 1000 seed weight than to seed set per pod was also observed in both years. However, high yield was the result of both a greater number of seeds per pod and heavier seeds, as well as other yield contributing factors. This was supported by the fact that HIYLD, Alto and HIOIL, which had the highest seed yields over years and locations (data not shown), all had high positive association to both seed set per pod and seed weight. In contrast, other genotypes had either no relationship between yield and the two yield components or a positive relationship to only one of them. However, even for these high yielding genotypes, the contribution to seed yield from seed set per pod and seed weight was no more than 60% (data not shown), suggesting other factors such as plants per unit area and effective pods per plant must also play a role in total seed yield.

When seed yield was regressed on seed set per pod, and seed weight on individual locations, no apparent association was found for HIYLD although this genotype consistently had the highest seed yield over two years and three locations (data not shown). This suggests that seed yield cannot be simply evaluated from the seed number per pod and seed weight, particularly if the trial is conducted at a single location. Simple selection for these two traits alone at a single location is very unlikely to effectively improve seed yield.

3). Correlation between seed yield, seed set per pod and 1000 seed weight: Phenotypic correlation coefficients of the three traits for individual genotypes at individual years and locations as well as years combined showed that the relationship and the degree of association between them varied, depending on genotype, year and location involved (data not shown). There was no consistent relationship between these traits when they were evaluated from a single location. Thus, it may be possible to improve both seed set per pod and seed weight without negative effects on one or the other, however, they have to be selected simultaneously. Simple selection for one trait alone is very unlikely to improve the other.

The results from the present study demonstrate that seed yield, seed number per pod, and seed weight are very complex traits highly influenced by both genotype and environments. Although seed weight appears in general to have a higher positive relationship to seed yield, the relationships of these traits cannot be simply defined on the bases of limited year and location studies. In addition, the contribution to seed yield from either seed set per pod, or seed weight, or the combination of the two is also limited. There is a delicate balance between seed yield and its contributing factors. The importance of this conclusion is that selection for seed yield in most, if not all, breeding programs is first made in a centrally located experimental station and potential lines are then tested over locations and seasons. The sensitivity of yield, its components or their relationships to the environment will be misleading if too much emphasis is given to yield components. Furthermore, the relationships of seed yield and its components, to be properly evaluated and applied to breeding programs, have to be based on multiple locations and seasonal tests. Such tests will inevitably increase the cost. Considering the limited resources, it appears that breeding programs for yield improvement should continue to rely on the direct selection.

TABLE 2. Regression of seed yield on seed set per pod and 1000 seed weight of *B. napus* genotypes in 1993, 1994 and years combined

	Intercept			Seed set per pod			1000 seed weight		
	Estimate	F	Pr>F	Estimate	F	Pr>F	Estimate	F	Pr>F
1993									
Alto	-53.372	7.98	0.026				19.564	16.90	0.005
GD	No significant relationship at Pr>F = 0.15								
G3	No significant relationship at Pr>F = 0.15								
G4	32.377	4.98	0.061				12.930	14.93	0.006
HIOIL	-38.534	5.74	0.048				17.992	16.27	0.005
HIYLD	-54.236	3.96	0.087	2.613	9.61	0.017			
LPHIPR	-35.683	8.73	0.021				15.055	24.44	0.002
1994									
Alto	-51.625	2.71	0.144				22.827	6.50	0.038
GD	-22.370	2.04	0.196	1.433	8.36	0.023			
G3	No significant relationship at Pr>F = 0.15								
G4	-66.452	2.15	0.186				21.121	3.63	0.098
HIOIL	-51.542	2.25	0.178				23.640	4.95	0.061
HIYLD	-134.193	7.18	0.037	2.069	2.82	0.144	28.372	7.85	0.031
LPHIPR	-48.885	5.24	0.056				20.966	11.95	0.011
Years combined									
Alto	-56.754	6.52	0.022	1.788	8.98	0.009	7.772	3.30	0.089
GD	9.916	0.50	0.492	0.762	4.95	0.042	-2.985	4.08	0.062
G3	No significant relationship at Pr>F = 0.15								
G4	-37.716	7.60	0.014				14.13	18.96	0.005
HIOIL	-45.178	7.47	0.015	1.183	4.15	0.060	11.184	5.77	0.030
HIYLD	-80.116	11.33	0.042	2.194	12.71	0.003	10.638	8.34	0.011
LPHIPR	-35.780	4.57	0.050	0.784	2.59	0.128	10.153	8.76	0.010

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