Genotypic variation for saturated fatty acid content of Victorian canola

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Abstract

Palmitic, stearic and arachidic acid make up total saturated fatty acid in canola and are routinely evaluated in the Victorian canola breeding program. Saturated fatty acid content is dependent on genotype, seasonal growing conditions, and their interaction. To better understand those factors that influence genotypic expression for individual saturated fatty acid contents in canola, data from advanced breeding experiments conducted between 1998 and 2001 across Victorian sites were analysed to estimate genetic parameters important in selection of saturated fatty acid content in a breeding program. Palmitic and stearic acid had broad–sense heritabilities between 0.82 and 0.94 in mid-maturing genotypes and 0.41 to 0.91 in early-maturing genotypes. The individual saturated fatty acid contents varied significantly ($P<0.01$) both among genotypes and across environments, while genotype × environment interactions were reflected in changes in genotype variance and ranking suggesting that genotypes do not perform similarly across environments. Therefore selection of a superior genotype for total saturated fatty acid composition may not correlate well from one environment to another. Development of canola genotypes with low saturated fatty acid content may be accomplished through evaluation and selection in environments contrasting for temperatures during pod-fill.

Keywords: heritability, palmitic, stearic, genotype × environment

Introduction

Canola (*B. napus*) is considered a healthy oil, as it is high in monounsaturated fatty acids, and low in saturated fatty acids. The saturated fatty acids are palmitic acid (16:0), stearic acid (18:0) and arachidic acid (20:0). Australian canola averages nearly 7% saturated fatty acids with palmitic and stearic acid the major saturated fatty acid. Genetic reductions of both palmitic and stearic acid content would lower the total saturated fat content of canola and increase its reputation as a superior, healthy edible oil. Estimates of genetic parameters for saturated fatty acid content in *Brassica* crops are uncommon in the literature. Inheritance of these traits has been identified from accumulated experience, rather than from a rigorous analysis of genotype data from several canola growing environments. Improved selection strategies for reduced saturated fatty acid content would be better achieved through a sound knowledge of genetic and environmental factors affecting these fatty acid components under Australian growing conditions. The objective of this study is to estimate genetic parameters for individual saturated fatty acid content in canola oil from three years of advanced breeding experiments conducted across the major canola producing regions of Victoria, Australia.

Materials and methods

Data on saturated fatty acid content were derived from advanced breeding experiments conducted by Department of Primary Industries, Horsham, Victoria between 1998 and 2001. These data were obtained on experiments containing both released cultivars and unreleased breeding lines. Two data sets were evaluated and designated as mid and early season experiments based on maturity of the genotypes. The mid-season data set included 8 genotypes grown in 14 environments. The second data set, included 8 early-season genotypes grown in 9 environments. The environments were obtained by a combination of location and presence/absence of irrigation. The experimental design in each environment was a randomised complete block with three replications.

Seed samples were analysed for fatty acid composition. Total saturated fatty acid composition level was defined as the sum of palmitic, stearic and

arachidic acid in the oil. However, this paper focuses its discussion on palmitic and stearic acid which are the principal saturated fatty acids in canola. A linear model to describe the phenotypic performance of genotypes was determined and included two factors: genotypes and environments (location-year combination). A random model was assumed and means and variance components for genotypes, environments, genotype × environment were estimated using the ANOVA and REML algorithm in GENSTAT.

For all measured traits, intraclass correlation coefficients (also known as broad-sense heritabilities), were calculated across all environments as ratios of estimates of these genotypic variances to phenotypic variances (Kempthorne 1957). Phenotypic and genotypic correlations between fatty acid components were calculated on genotype means across environments using GENSTAT. Daily ambient temperatures at each environment were used to characterise the thermal conditions during seed filling. The temperature stress index (TSI) used was calculated using the formula: Temperature Stress Index = $\sum[T_{max} - 25]$, where T_{max} is the daily maximum ambient temperature from flowering to either 20 or 40 days after flowering.

Results

Saturated fatty acid contents were generally smaller in canola grown in mid-season (fewer days with high temperatures above 25ºC) than early-season environments. For the mid-season genotype experiments, environmental effects were significant (P<0.01) for individual fatty acids. Palmitic acid content ranged from 3.8% at Horsham in 1999 to a high of 4.4% at Katamatitie in 1998 and averaged 4.1% across 14 environments. Mean stearic acid content was high at Kerang in 1998 (2.2%) and low at Horsham in 2000 (1.6 %). Variation in total saturated fatty acid content was evident, with a range of 6.1% at Horsham in 2000 to 7.1% at Katamatite in 1998. Seasonal effects were large, with a much larger proportion of total saturated fatty acid in 1998 than in 1999 (lower rainfall). Rainfall calculated for 40 days after flowering, explained a significant (P<0.01) proportion of the environmental variation for the palmitic acid content of mid-season genotypes.

For early-season genotype experiments, significant differences (P<0.01) were observed for saturated fatty acid contents across environments. Palmitic acid content ranged from 4.0% (Diggora 1998) to 4.5% (Horsham 2000) whilst stearic acid ranged from 2.0% at Horsham to 2.4% at Walpeup in 1999. Total saturated fatty acid content was greatest at Walpeup and smallest at Horsham in 1999 (7.3 versus. 6.7%). For early-season genotypes, TSI was more effective than rainfall in explaining fatty acid content variation between environments.

The phenotypic correlation for palmitic and stearic acid was strong for mid-season genotypes (Table 43). However, there were positive and comparatively low genetic correlations for these fatty acids in both mid-season and early-season genotypes. Higher contents in oleic acid were generally associated with lower levels of palmitic acid for mid-maturing genotypes.

For all characters, the environmental variance exceeded the genotypic variance component (Table 44), indicating the importance of environmental factors in controlling phenotypic variation for these characters in southern Australia. Single-plot heritability estimates ranged from 0.41 for stearic acid in early-season genotypes to 0.94 for the same character in mid-season genotypes. Genotype × environment interactions were significant (P<0.01) for all saturated fatty acid contents. For each of these characters, the interaction variance was of similar magnitude, or greater than, the genotype variance.

Table 43: Genotypic and phenotypic (italic) correlation coefficients among all saturated fatty acids for oil from mature seed of eight, mid- and early-maturing canola lines evaluated in 14 and 9 environments, respectively.

Fatty acid	Palmitic	Stearic	Arachidic	Total saturated fatty acid	Oleic
Mid-season					
Palmitic	-	0.15	-0.31	0.67	-0.80
Stearic	*0.58*	-	0.81	0.84	-0.23
Arachidic	*-0.24*	*0.21*	-	0.46	-0.06
Total saturated fatty acid	*0.89*	*0.88*	*-0.16*	-	-0.61
Oleic	*-0.23*	*0.24*	*0.06*	*0.01*	-
Early-season					
Palmitic	-	0.19	-0.14	0.81	-0.48
Stearic	*-0.14*	-	0.30	0.72	0.20
Arachidic	*-0.26*	*0.48*	-	0.19	0.48
Total saturated fatty acid	*0.79*	*0.48*	*0.17*	-	-0.18
Oleic	*-0.60*	*0.37*	*0.39*	*-0.29*	-

Table 44: Genotype, genotype × environment and residual component estimates, and heritability for palmitic, stearic, arachidic acid, and total saturated fatty acid contents of oil sampled from eight, mid- and early-maturing canola cultivars evaluated in 14 and 9 environments, respectively.

Parameter	Palmitic	Stearic	Arachidic	Total saturated fatty acid
Mid-season				
σ^2G	0.005 ± 0.004	0.008 ± 0.005	0.000 ± 0.000	0.018 ± 0.012
σ^2E	0.025 ± 0.112	0.036 ± 0.016	0.001 ± 0.001	0.101 ± 0.042
σ^2GE	0.010 ± 0.003	0.006 ± 0.001	0.000 ± 0.001	0.029 ± 0.007
Residual	0.018 ± 0.002	0.004 ± 0.001	0.000 ± 0.000	0.020 ± 0.003
σ^2GE/σ^2G G	1.94	0.75	2.00	1.65
h^2	0.82 ± 0.11	0.94 ± 0.04	0.84 ± 0.10	0.87 ± 0.08
Early-season				
σ^2G	0.010 ± 0.008	0.001 ± 0.002	0.000 ± 0.000	0.007 ± 0.009
σ^2E	0.034 ± 0.020	0.012 ± 0.007	0.002 ± 0.000	0.032 ± 0.022
σ^2GE	0.027 ± 0.006	0.013 ± 0.003	0.000 ± 0.000	0.066 ± 0.015
Error	0.005 ± 0.001	0.008 ± 0.001	0.000 ± 0.000	0.014 ± 0.002
σ^2GE/σ^2G	2.59	10.75	0.50	8.85
h^2	0.77 ± 0.14	0.41 ± 0.39	0.92 ± 0.05	0.49 ± 0.33

Discussion

These results indicate that differences in environment have the greatest influence on variation in saturated fatty acid content of canola. This information is useful in determining areas most reliable for producing canola with lower saturates allowing new Australian cultivars to meet more stringent world standards. The stress index for the first 20 days (data not presented) after flowering was particularly useful for explaining variation in the proportion of palmitic acid across environments suggesting that higher temperatures have a greater effect early in pod-filling for this character.

Associations among traits have important implications to both the marketing and selection of canola oil quality. Genetic correlations between palmitic and stearic acid were small despite the fact that these are synthesised sequentially in the biosynthetic pathway. High heritabilities suggest that individual selection for these characters should lead to genetic gain in a breeding program. For stearic acid, the heritability for early season was moderate even though the environmental variance was greater than the genotype variance. This possibly indicates that factors in the environment, such as rainfall and temperature have a major influence on this character. Large genotype × environment interactions indicate the need for separate strategies in defining the causes of the interactions, such as appropriate sampling of the target population of environments, and identifying genotypes with desirable quality characteristics in specific types of environments. As only eight albeit random genotypes were used in our experiments, caution should be used in examining the results. However, as cultivars of differing genetic background were grown over a wide range of southern Australia environments, the results strongly indicate that the saturated fatty acid content of a genotype is dependent on the environment where the grain is produced.

References

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