SELECTION ON POLLEN FOR RAPESEED OIL QUALITY IN POLYUNSATURATED FATTY ACIDS.

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ABSTRACT

Correlation between fatty acid composition of pollen and that of seeds was studied in *B.napus*. It has been shown that: i) The same simple and rapid method can be applied to determine seed and pollen fatty acid composition. ii) Early breeding for low α-linolenic acid content in rapeseed oil is efficient on pollen and can be used to accelerate breeding programs.

INTRODUCTION

The utilisation of a destructive method for oilseed fatty acid (FA) analysis and the lack of biochemical or molecular markers for a specific C18 FA composition of rapeseed oil hinder early breeding for this character, especially for a low α-linolenic acid (C18:3) content. As a consequence, this selection must concern a non vital organ or a part of organ that accumulate storage lipids, such as seeds. Evans (1988) had shown strong correlations between the C18:3 content of seed and that of polar lipids (membrane) and neutral lipid (storage) of intern and extern pollen. This paper describes the results of experiments designed to evaluate correlations between whole pollen and seeds for C18:3 content and for Linolenic Desaturation Ratio (LDR).

EXPERIMENTAL

Two spring rapeseed lines have been crossed to produce F1 seeds: Stellar, containing 3% of C18:3 and Drakkar, containing 9% of C18:3. Microspores from a single F1 plant were cultured to provide doubled haploid plants (DH). Seeds from DH plants were obtained in 3 different environmental conditions (1 to 3 replications). Open flowers were simply shaked over a glass tube to collect the mature pollen in the third environmental condition (3 replications). The same methods of extraction, esterification and fatty acid methyl esters (FAMES) analysis were applied on pollen and seeds. The samples were crushed in a solution containing 0.5% NaOH; MeOH/isooctane (5:1). After 20mn at 20°C, the FAMES were extracted by adding isooctane/IsoPropanol (9:1) and finally separated by gas chromatography on capillary column. The fatty acid content is given in percent of total fatty acids and the LDR is also calculated (%C18:3x100 / %C18:3 + %C18:2) (Pleines,1989).
Figure 1 shows the regression curves:

A: Pollen C18:3 content (mean on 3 replications) as a function of seed C18:3 content (mean on the 3 environmental conditions)

B: Pollen LDR (mean on 3 replications) as a function of seed LDR (mean on the 3 environmental conditions).

Fitted functions of these curves are Gompertz functions (Berger,1981) given by the following equations:

$$\mathbf{A}: \; y = 59.3\, e^{-1.42}\,(e^{-0.32x})$$

$$\mathbf{B}: \; y = 92.6\, e^{-1.58}\,(e^{-0.11x})$$

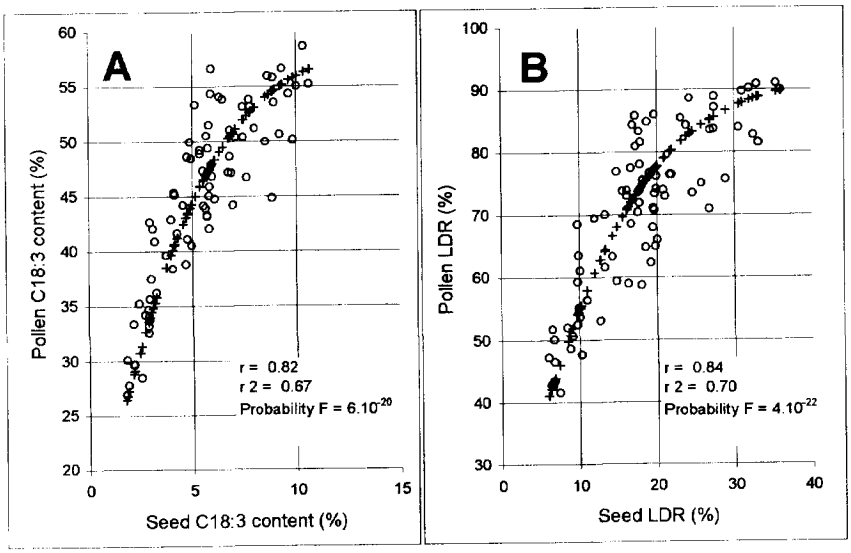

Figure 1: Regression curves for C18:3 content and LDR ratio between seeds and pollen of doubled haploid plants derived from the cross Stellar x Drakkar.

Regression statistics (r, adjusted r^2, residues, F test) are slightly better for LDR rather than for C18:3 content. So LDR could be preferred to the only C18:3 content when screening for C18:3 in breeding programs. Though, this screening method seems to be more efficient to select low C18:3 lines than high C18:3 ones (residues increase for high C18:3 lines).

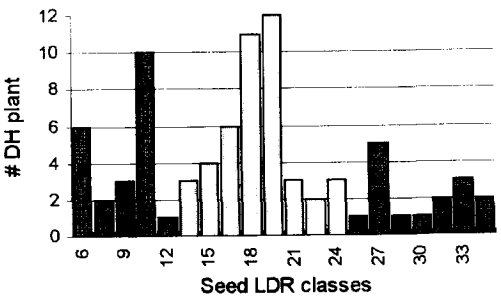

Figure 2.A: Seed segregation diagram of the DH population.

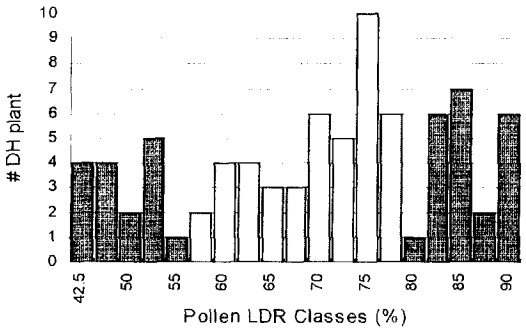

Figure 2.B: Pollen segregation diagram of the DH population.

Seed and pollen segregation diagrams of the DH population were compared (Figure 2). 3 classes can be visualised. In the seeds, the first class corresponding to homozygous low C18:3 lines (22.6 % of the DH population compare to 25%, expected frequency on the hypothesis of 2 genes controlling the C18:3 content) is clearly individualised. It is the same for pollen LDR (26.2 % of the DH population compare to 25%). Selection on pollen for low C18:3 content gives nearly the same set of genotypes as selection on seeds applied at the same generation.

The results obtained show that the pollen C18 polyunsaturated FA composition can be used as an early valuer of seed C18 polyunsaturated FA composition.

This method of early selection on pollen can specify the results obtained by half-seed selection just before the application of cross programs. It allows to select for C18:3 content on microspore-derived doubled haploid. Studies are under way on different progenies, especially F2 and backcross, to evaluated the efficiency of such a method in breeding low C18:3 lines in greenhouse and field conditions.

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