

The identification and molecular
mapping of major candidate
genes and QTL involved in the
fatty acid desaturation pathway
in *Brassica napus*

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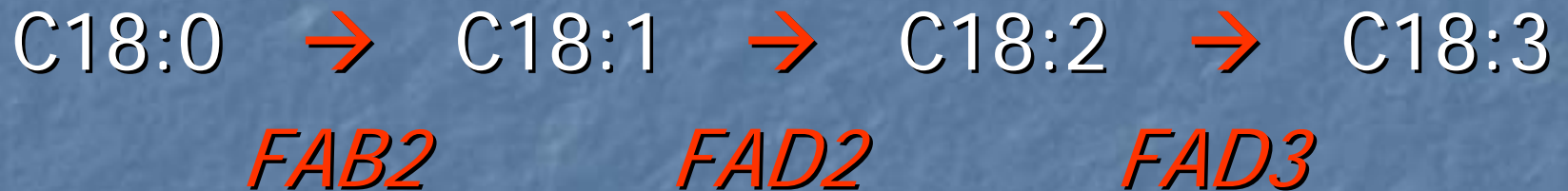
Rapeseed oil is composed of a variety of fatty acids

- The fatty acid composition of rapeseed oil determines the fitness of the oil for its many end-uses.
- Three fatty acid constituents of rapeseed oil are:
 - Oleic acid (C18:1)
 - Linoleic acid (C18:2)
 - Linolenic acid (C18:3)

Why are these fatty acids important?

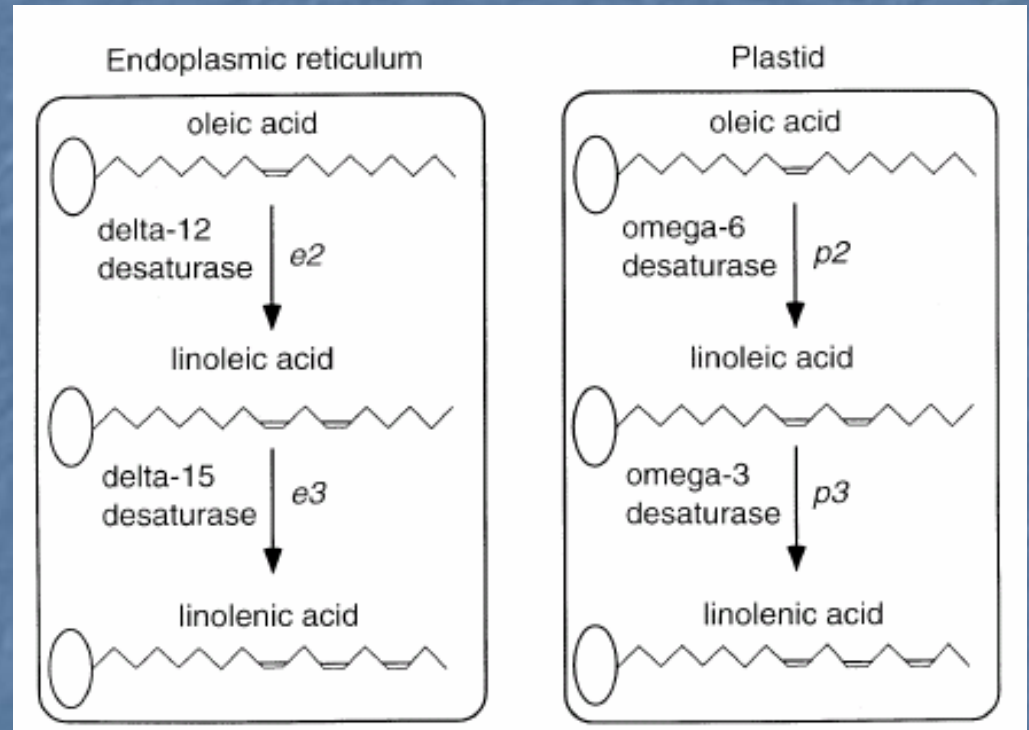
- Polyunsaturated fatty acids (PUFAs) are dietary essentials and are thought to provide a number of specific health benefits.
- But PUFAs are prone to rancidity at high temperatures.

A focus on the fatty acid desaturation pathway



Fatty acid biosynthesis and parallel pathways

Illustration of two biosynthetic pathways for the desaturation of fatty acids from oleic acid (C18:1)



(from Scheffler et al. 1997)

A candidate gene approach

- *Arabidopsis*-based probes for:

FAB2, FAD2 and FAD3

were hybridised to two *B. napus* BAC libraries: JBnY and JBnB.

- Sub-cloning was used to increase sequence availability for BACs.

A candidate gene approach

- Sub-clone sequences/BAC-end sequences were used to design molecular markers linked to candidate genes.
- Marker analysis was conducted in:
 - *B. napus* mapping population 'Q' (re-synthesised *B. napus* x cultivar Tapidor)
 - *B. napus* mapping population 'TN' (cultivar Tapidor x cultivar Ningyou)

Mapping positions of confirmed fatty acid gene homologues

- *FAB2*: A3 (Q), C3 (Q) (TBC)
- *FAD2*: A5 (Q), C1 (Q)
- *FAD3*: C3 (Q), C4 (1 of 2) (Q),
C4 (2 of 2) (Q)
- *FAE1*: A8 (Q), C3 (Q & TN)

Two-directional whole-homologue sequencing (by primer walking) for the above *FAD2*, *FAD3* and *FAE1* homologues is nearing completion.

Three annual 'Q' field trials have been grown to identify QTL for total seed oil content, constituent fatty acids and fatty acid ratios



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