

# Marker assisted breeding of new winter oilseed rape lines (*Brassica napus* L.) with changed seed oil fatty acid composition



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Rapeseed is a worldwide important oil seed crop, used for human nutrition as well as a source of raw material for biofuel production and for chemical and pharmaceutical industry. Oil crop market demands concern, among others, development of new cultivars characterized by the changed seed oil fatty acid composition comprising high oleic and low linolenic acid content, HOLL-type, applied for biofuel production due to its oxidation and thermal stability. At the Plant Breeding and Acclimatization Institute in Poznań, Poland, high oleic HO and low linolenic LL mutant lines were obtained by chemical mutagenesis (Spasibionek, 2006) and improved by introducing into new genetic background. New mutant rapeseed HOLL recombinants were developed. At present, marker assisted breeding, MAB, of HOLL genotypes of good agronomic value is in progress accompanied by screening of segregating populations with the use of allele-specific functional genetic markers.

Phenotyping was done, including:

- seed yield estimation
- % of standard cultivar yield
- % of wintering
- seed oil fatty acid composition by gas-liquid chromatography (Table 1.)



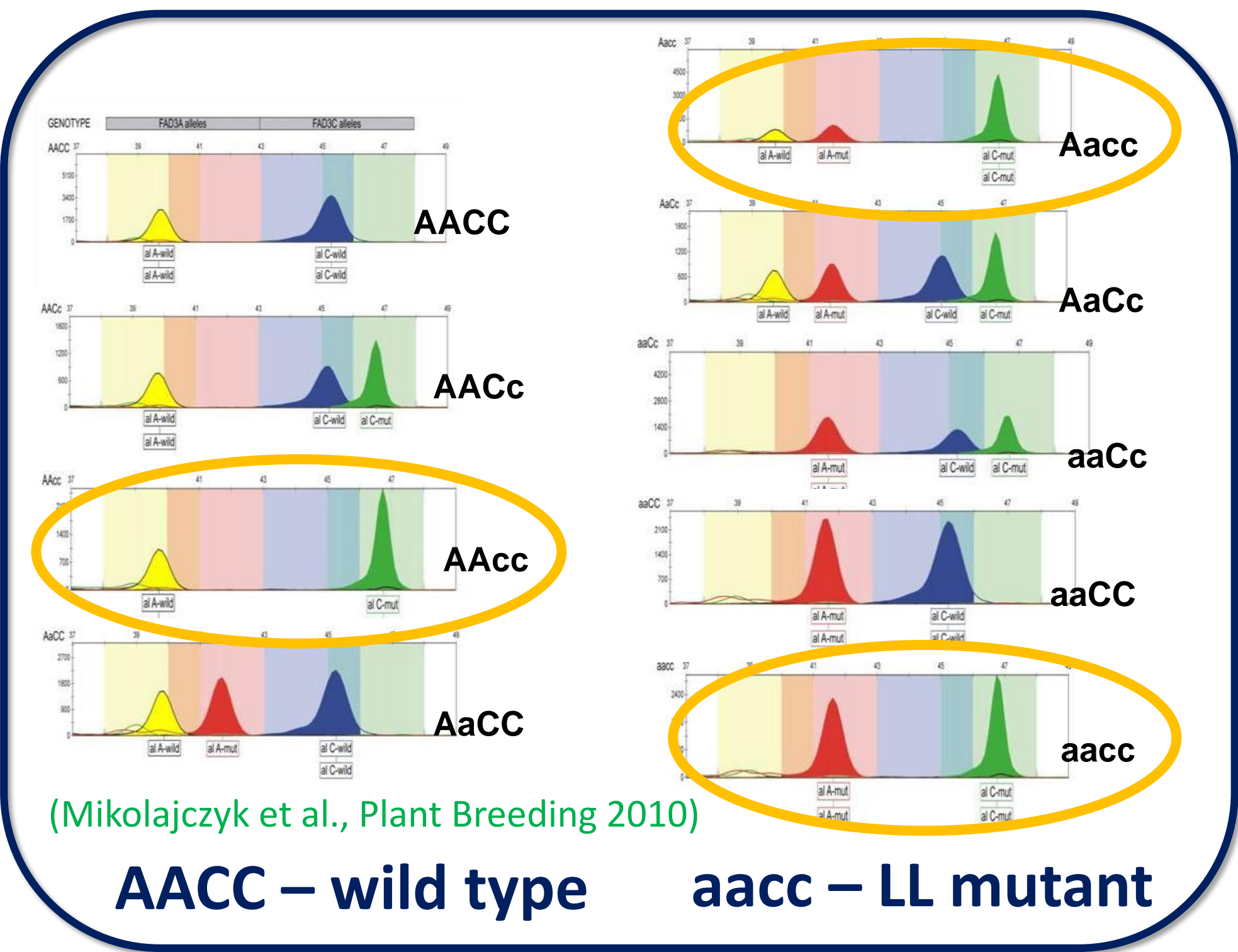
Genotyping with the use of unique SNaPshot assay including allele-specific functional genetic markers was done for precise detection of mutated and wild-type alleles of *FAD3* desaturase genes in the *B. napus* A and C genomes (Mikolajczyk et al., 2010; 2011; Bocianowski et al., 2012) (Table 1.)



Plant object	Seed yield [dt h <sup>-1</sup> ]	% of the standard cultivar seed yield	% of wintering	Fatty acid [%]			Genotyping	
				Oleic C18:1	Linoleic C18:2	Linolenic C18:3	FAD3A allele	FAD3C allele
Standard cultivar								
Monolit	31,1	100,0	68,0	63,7	18,7	9,6	AA	CC
HO and LL mutant lines used for recombination								
LL_M681	13,8	44,4	37,4	66,1	24,0	2,4	aa	cc
HO_M10464	9,2	29,6	76,5	78,8	7,4	7,4	AA	CC
HOLL-type recombinants								
440/15	31,2	100,3	62,3	80,3	9,0	3,8	AA	cc
837/15	14,2	45,6	67,7	77,6	12,7	2,4	aa	cc
878/15	28,3	91,0	50,1	76,6	13,4	2,8	aa	cc
880/15	32,0	102,9	65,5	80,1	9,7	2,7	aa	cc
882/15	29,5	94,8	88,7	76,7	8,3	2,5	aa	cc
888/15	24,2	77,8	72,0	76,8	13,2	3,3	AA	cc
899/15	27,0	86,8	75,6	78,5	10,4	4,4	AA	cc
902/15	22,8	73,3	69,0	78,2	10,7	4,4	AA	cc
F calc.	1,85	-	2,87**	95,30**	125,06**	153,01**		
NIR 0.05	4,49	-	17,69	0,72	0,38	0,27		



Table 1. Genetic gain in improvement of the agronomic value of new HOLL-type mutant rapeseed recombinants recorded by routine phenotyping and SNaPshot



Field trials of HOLL-type recombinants were accompanied by detection of *fad3* desaturase alleles in the A and C genomes of *B. napus*:

## Conclusion

Selection proces using conventional phenotyping and accompanied by MAB with the SNaPshot assay enabled to break linkage between low yield and modified fatty acid composition  
New genotypes with yield and wintering comparable to a standard cultivar and revealing the HOLL genotype were obtained