BREEDING OF HIGH-ERUCIC ACID RAPESEED BY MEANS OF *BRASSICA NAPUS* RESYNTHESIS

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ABSTRACT

High-erucic rapeseed (*Brassica napus*) has been resynthesized through interspecific hybridization using *B. rapa* and *B. oleracea* genotypes bearing the most effective alleles for erucic acid (C22:1) synthesis as parents. Cross efficiency has been increased by using ovule culture *in vitro*. The hybrid offspring display desirable variation in the content of major fatty acids. In order to study inheritance intraspecific crosses have been carried out between double-low spring rapeseed cultivars and resynthesized high-erucic genotypes containing 55-60 % C22:1 in their seed oil. The observed segregation ratio in the F_2 progeny confirmed the hypothesis that synthesis of erucic acid in resynthesized *B. napus* is controlled by a two gene-pair system acting in an additive manner. A single effective allele has been calculated to contribute about 16 to 17% C22:1.

INTRODUCTION

In the past few years interest has grown to produce high erucic acid oils, which can be used in a wide array of industrial applications (1). Although other potential candidates for erucic acid production, namely crambe (*Crambe abyssinica*) or yellow mustard (*Sinapis alba*), have the advantage that they would not interfere with double-low rapeseed production in Europe, the development of industrial rapeseed with an erucic acid content as high as 60% is considered to be the most promising route due to its higher yield and oil content (2).

EXPERIMENTAL

Development of novel rapeseed germplasm via resynthesis

Most of the traditional rapeseed cultivars possess an erucic acid content ranging from 45 to 50%. In contrast, cauliflowers (*B. oleracea* convar. *botrytis* var. *botrytis*) were found containing a maximum of approx. 60-63% C22:1 in their seed oil. In order to create new germplasm with increased erucic acid content interspecific crosses were carried out between several cauliflower cultivars and 'Yellow sarson' (*B. rapa* ssp. *trilocularis*) following a protocol for embryo rescue described previously (3). The amphihaploid hybrid plants were propagated *in vitro* through secondary shoots which were rooted and further cultivated in the greenhouse. After colchicine treatment chimeric C_0 plants with fertile sectors were isolated for seed production. The C_1 progeny was analyzed for seedoil quality. Table 1 shows that the fatty acid variation found in the parents on single-seed basis has been successfully transferred into the resynthesized rapeseed lines, too.

TABLE 1. Fatty acid variation found in offspring lines (C_1) derived from reciprocal crosses between *B. oleracea* (cauliflower K2256) and *B. rapa* ('Yellow sarson')

	n*	Fatty acids (% of total)					
		C18:1	C18:2	C18:3	C20:1	C22:1	
		5.9	9.1	4.8	1.8	49.7	min
Cauliflower 'K 2256'	38	10.8	11.2	7.4	4.1	57.5	mean
		15.9	14.2	11.8	6.9	60.5	max
		8.8	6.7	4.9	4.6	50.2	min
Yellow sarson 'YS'	64	13.4	9.1	6.5	7.6	56.2	mean
		18.2	12.4	8.1	11.1	61.6	max
		7.2	7.9	3.3	3.7	53.3	min
'K 2256' x 'YS'	53	12.7	10.9	5.7	5.4	57.0	mean
		17.9	13.3	11.7	7.2	60.0	max
		9.2	7.6	2.6	3.5	51.7	min
'YS' x K 2256'	69	14.9	10.0	4.7	6.3	56.4	mean
		20.3	13.1	7.9	9.4	60.7	max

* number of half seeds (parental genotypes) and seed samples (offspring lines) analysed, respectively.

Fatty acid inheritance in resynthesized rapeseed

B. napus crosses were made between resynthesized high-erucic lines (about 57% C22:1) and Canadian double-low spring type cultivars aiming in genetic studies. The F_1 plants were grown in the field and selfed to yield F_2 seeds which were analysed by using the half-seed method. In Figure 1 (top) erucic acid content of the F_2 single half seeds is plotted against both oleic and eicosenoic acid content. In accordance to the model of digenic control described earlier (4-6) five distinct phenotypic classes could be identified representing genotypes with none allele (eeee), one allele (Eeee) and with 2 (EEee), 3 (EEEe) or 4 alleles (EEEE) determining erucic acid content, respectively. Figure 1 (bottom) shows that the data obtained for single F_2 seeds fit the expected 1:4:6:4:1 segregation ratio very well. Further, the contribution of a single allele was calculated by dividing the C22:1 mean value of each phenotype class by the number of alleles. In resynthesized rapeseed the effective erucic acid genes (E) have an allelic contribution of ca. 16 to 17% C22:1. This is a novelty for spring rapeseed as compared to previous studies, in which a level of about 9-10% C22:1 per allele was obtained (4,6).

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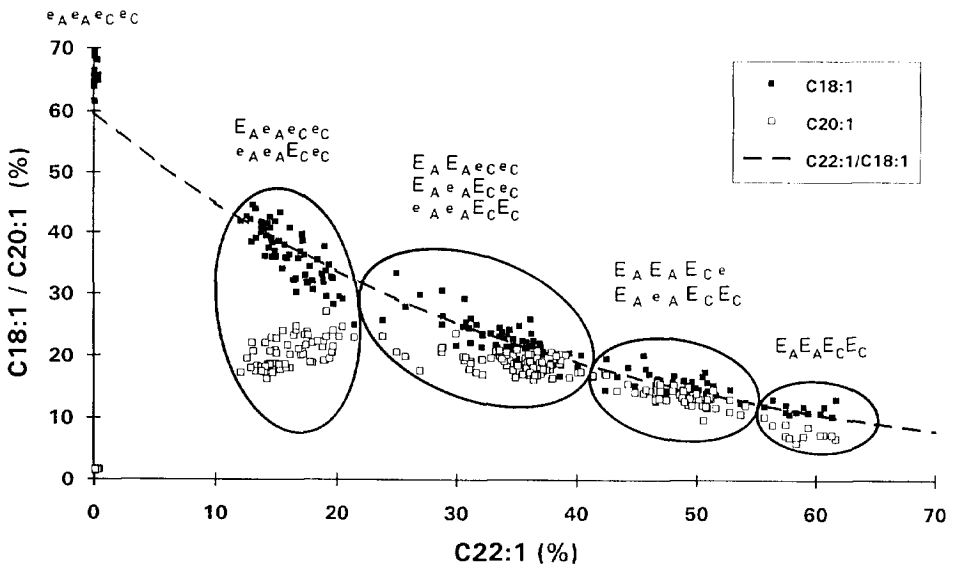

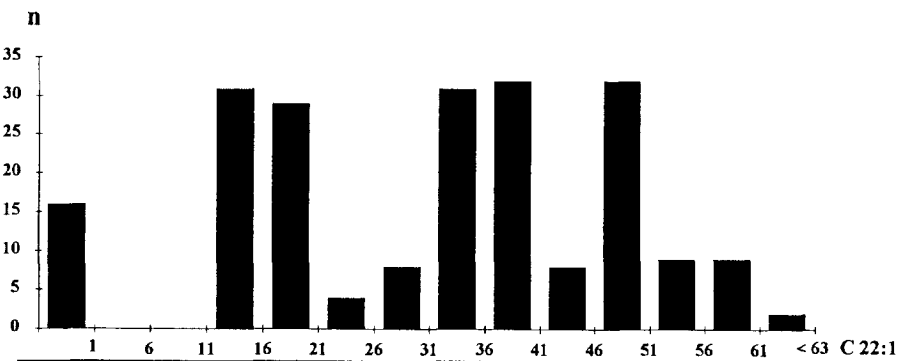

	16.1 %	17.2 %	16.2 %	14.8 %	1)
1 :	4 :	6 :	4 :	1	2)
eeee	Eeee	EEee	EEEe	EEEE	3)

FIGURE 1. Genetic interpretation of erucic acid content in the *B. napus* cross between double-low cultivar 'Profit' and resynthesized high-erucic line '91a'; n= number of F_2 single half seeds, 1) allelic contribution, 2) segregation ratio, 3) erucic acid genotype.