The inheritance of erucic acid content in summer rapeseed (*Brassica napus* L.)

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ABSTRACT

Two zero erucic acid cultivars were crossed with four cultivars containing various levels of erucic acid (4.6% to 46.5%) including reciprocals. The erucic acid content of F_1's and their reciprocals was intermediate between the parents indicating embryonic control of erucic acid and absence of maternal effect in inheritance of erucic acid in B. napus. Erucic acid content of F2 seeds segregated in to 5 classes <2%, 2-16%, 16-32%, 32-44% and >44% erucic acid with a ratio of 1:4:6:4:1. Backcrosses seeds (BC1) derived from the F1 (zero erucic acid parents, segregated into three classes (<2%, 2-16% and 16-32% erucic acid) with a ratio of 1:2:1. On the other hand, backcross seeds (BC2) derived from F1 (high erucic acid parent segregated into three classes (16-32%, 32-44% and >44% erucic acid) with a ratio of 1:2:1. The segregation patterns indicated that erucic acid content in *B. napus* was governed by two independent genes interacting in an additive manner. Pooled data analysis also confirmed above results.

Key words: rapeseed, erucic acid, inheritace

Introduction

An important characteristic of rapeseed-mustard oil is the presence of erucic acid, which is associated mainly with plants of *Brassica* genus. Finding of plants almost completely free of erucic acid in summer rape (*B.napus*) made it possible to improve the quality of rape oil (Stefansson et al. 1961). Digenic inheritance of erucic acid confirmed in *B. juncea* (Kirk and Hurlstone 1983) and in *B. carinata* (Getinet et al. 1996). Krzymanski and Downey (1969) suggested that one gene pair governs the level of erucic acid and each allele contributes approximately 3.5% erucic acid to the seed in winter rapeseed. Jonsson (1977a) reported that in rape (*B. napus*) erucic acid content controlled by alleles at one, one or two and two loci for 5-10%, 10-35% and more than 35% erucic acid levels, respectively. Multiple alleles at each locus have been reported in inheritance of erucic acid (Krzymanski and Downey 1969, Jonsson 1977a, b, 1978, Liu and Liu 1987). This study had as its objective the determination of the inheritance of erucic acid in segregation populations derived from crosses between zero and high erucic acid parents in *B. napus*.

Materials and methods

Experimental material for this study were 6 genotypes of *B. napus* including two zero erucic acid (Hyola401 and GSC3A00) and four cultivars with various level of erucic acid from 4.56 up to 46.5 viz. TERI(OE)R-983 (4.56%), HNS-9802 (13.13%), HNS-9801 (33.71%) and NPN-01 (46.5%). All the cross combinations have been made between two zero erucic acid parents and other cultivars (including reciprocals). Two F_1's (Hyola401 $\times$ NPN-01 and GSC3A00 $\times$ NPN-01) out of 18 F_1's and reciprocals selected and were crossed with their corresponding parents to develop BC_1 ($F_1 \times$ zero erucic acid parent) and BC_2 ($F_1 \times$ high erucic acid parent) progeny. From segregation populations (F_2 and Backcrosses) of two selected F_1's (Hyola401 $\times$ NPN-01 and GSC3A00 $\times$ NPN-01) 440 individual seeds analyzed for fatty acid composition by single seed technique. Instrument used for fatty acid analysis was gas chromatograph (HP 5890 Series II) with capillary column at 250 ºC, detector at 280 ºC and injector at 260 ºC.

Results

The erucic acids content of F_1's and reciprocals resulting from the crosses between zero erucic acid and other parents having different levels of erucic acid revealed that the amount of erucic acid in F_1's and reciprocals was about intermediate.The frequency distribution of F_2 generation for both crosses (HYOLA401×NPN-01and GSC3A"00"×NPN-01) were separated into five classes consisting of seeds with erucic acid contents of <2%, 2-16%, 16-32%, 32-44% and >44%. Frequency distribution of BC_1 were separated into three classes including <2%, 2-16% and 16-32% erucic acid contents. These three classes for BC_2 were 16-32%, 32-44% and >44%. In HYOLA401×NPN-01cross the erucic acid content of 128 F_2 single seeds was classified in five classes (Table.1). The chi-square test revealed that 2 genes with additive effects controlled inheritance of erucic acid in these cultivars. In the BC_1 (HYOLA401×NPN-01) ×HYOLA401 and BC_2 (HYOLA401×NPN-01)×NPN-01 erucic acid content of 64 and 60 single seeds classified into three classes, respectively. Test of goodness of fit for these backcrosses were non-significant, so these generations confirmed digenic hypothesis with additive effect. In GSC3A"00"×NPN-01 in BC_2 (GSC3A"00"×NPN-01)×NPN-01 test of goodness of fit for observed ratios was significant for this generation. So segregation ratios of erucic acid in this generation did not confirm digenic hypothesis. The results of pooled data analysis were same as results of second cross (Table. 1).

Table. 1Number of F_2 and backcrosses single seeds in different erucic acid classes with chi-square values and probabilities for goodness of fit for two crosses and pooled data of *B. napus*.

Crosses and generations	No. of seeds with % erucic acid					Expected ratio	χ^2 value	Prob.
	<2	2-16	16-32	32-44	44			
(Hyola401×NPN-01)								
F_2	5	35	47	30	11	1:4:6:4:1	2.677	0.75-0.50
(F_1×P_1)	15	32	17	---	---	1:2:1	0.125	095-0.90
(F_1×P_2)	---	---	20	30	10	1:2:1	3.333	0.25-0.10
(GSC3A "00"×NPN-01)								
F_2	7	28	40	17	4	1:4:6:4:1	3.986	0.50-0.25
(F_1×P_1)	9	24	15	---	---	1:2:1	1.500	0.50-0.25
(F_1×P_2)	---	---	23	15	6	1:2:1	17.591	0.00
Pooled								
F_2	12	63	87	47	15	1:4:6:4:1	2.79	0.75-0.50
(F_1×P_1)	24	56	32	---	---	1:2:1	1.14	0.75-0.50
(F_1×P_2)	---	---	43	45	16	1:2:1	15.9	0.00

Discussion and conclusion

Intermediate levels of erucic acid in F_1seeds of crosses indicated that erucic acid was controlled by the genotype of the developing embryo and not the female sporophyte. This also indicated that genes involving inheritance of erucic acid had little or no dominance effect (additive effect). Similar observations has been reported in *B. napus* (Kondra and Stefansson 1965, Anand and Downey 1981), *B. juncea* (Kirk and Hurlstone 1983) and in *B. carinata* (Getinet et al. 1996). The 1:4: 6: 4:1 segregation ratio in F_2 seeds in two crosses indicated that erucic acid content in Hyola401, GSC3A00 and NPN-01 was controlled by two genes with additive effects. Two gene inheritance model were supported by segregation patterns observed in backcross seeds derived from the backcross to zero erucic acid. The segregation of seeds with four alleles for erucic acid at 1: 2: 1 ratio could not be fulfill in backcross to high erucic acid in GSC3A00×NPN-01. Symbol e represented the allele for no erucic acid as suggested by Krzymanski and Downey (1969). Thus the genotype of zero erucic acid parents (Hyola401 and GSC3A00) designated as $e_1e_1e_2e_2$, high erucic acid parent (NPN-01) as $E_1E_1E_2E_2$ and F_1 as $E_1e_1E_2e_2$ (Table.2). Erucic acid content in genotypes having one E allele (E_1 or E_2) were about 9% and with increasing number of E allele to 2 and 3 about 15% erucic acid increased for each allele. Adding fourth E allele increased 7-11% erucic acid in corresponding genotypes. Krzymanski and Downey (1969) described that there are at least five alleles governing the level of erucic acid and depicted these alleles by the symbols e , E^a ,E^b ,E^c and E^d with each controlling the synthesis of 0, 10, 15, 30 and 3.5 per cent of erucic acid content respectively.

Table 2. Expected genotypes, ratios and mean of erucic acid per cent of F_2 for Hyola401×NPN-01 and GSC3A00×NPN-01 and pooled data.

Genotype	Mean of erucic acid (%)			Expected F_2 ratio
	Hyola401×NPN-01	GSC3A00×NPN-01	Pooled	
$e_1e_1e_2e_2$	0.76	1.06	0.93	1
$E_1e_1e_2e_2$ $e_1e_1E_2e_2$ $E_1E_1e_2e_2$	9.58	9.65	9.61	4
$E_1e_1E_2e_2$ $e_1e_1E_2E_2$	24.74	23.55	24.19	6
$e_1E_1E_2E_2$ $E_1E_1E_2e_2$	39.24	38.34	38.91	4
$E_1E_1E_2E_2$	46.46	49.58	47.29	1

In present investigation alleles E_1 and E_2 are equal to E^a and E^b that reported already. *Brassica napus* is an amphidiploid containing the genomes of *B. campestris* (AA) and *B. oleracea* (CC). Interspecific hybridization of *B. napus* with zero erucic acid *B. campestris* revealed that the allele E^a is located on C genome chromosomes (Anand and Downey 1981).

High seed yield and number of desirable characters is found in materials with a high erucic acid content. For improvement of erucic acid content in these cultivars, oil quality breeding point of view, transfer of genes responsible for low erucic acid content could be done easily by selection in segregation populations through half seed technique or carry out simple backcrossing with low erucic acid progeny identified through half seed technique.

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