INHERITANCE OF GLUCOSINOLATES IN OILSEED RAPE

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ABSTRACT

The inheritance of individual and total glucosinolate concentrations in seeds of oilseed rape was investigated. The investigation was based on MECC analysis of 584 plants from the basic generations of a cross between a double low spring rape cultivar and an artificially synthesized Brassica napus. All glucosinolates present in the seed extracts were recorded, but only the results for progoitrin and total glucosinolate concentrations will be presented here. An additive-dominance model adequately explained the action of those genes controlling progoitrin accumulation in the seeds, but for total glucosinolates epistatic effects were also detected. Recombinant inbred lines offered a better prospect for reducing total glucosinolate and progoitrin concentrations than second cycle hybrids.

INTRODUCTION

Glucosinolates form a group of natural products, with well-defined structures and properties, which occur in all plants of the order Capparales and in a few other plants (Sørensen, 1990). Glucosinolates, and especially their transformation products, are responsible for many of the beneficial and harmful properties of glucosinolate containing plants. These properties vary with the type of glucosinolates, and include the negative effects glucosinolate products have on the technically and economically important oils and proteins from oilseed rape (Sørensen, 1990).

Biosynthetic, glucosinolates are formed in the plants with amino acids as precursor. Approximately 30 glucosinolates occur in oilseed rape, for which Trp, Phe and Met are the amino acid precursors used in the biosynthetic sequences, comprising a series of several individual steps, still with some details unknown (Lethenborg et al., 1994).

The aim of this work is to obtain specific information on the complicated inheritance of glucosinolates (Lethenborg et al., 1994; Magrath et al., 1994; Rucker and Rudloff, 1991; and refs. cited therein), so that the breeder can develop high quality oilseed rape cultivars which fulfill the requirements for the various applications of this crop.

EXPERIMENTAL

The parents used in the crosses were an artificially synthesized Brassica napus (P_1)and a double low B. napus spring rape cultivar, Jaguar (P_2)(Lethenborg et al., 1994). The artificial B. napus was generated by crossing B. alboglabra (CC genome donor) and B. campestris cv. Yellow Sarson (AA genome donor). Parents were crossed reciprocally, while F_1 plants were selfed and backcrossed to both parents, after which the individual plants were bagged. Mature seeds were harvested from parental, F_1, F_2 and first backcross generations, and analysed for individual glucosinolates using micellar electrokinetic capillary chromatography (MECC) as described elsewhere (Lethenborg et al., 1994).

RESULTS AND DISCUSSION

Progoitrin is the main component of the total for all generations apart from P_2 (Table 1a). For both characters the F_1 is significantly greater than the higher parent, giving rise to positive heterosis, which will be of little value in developing low glucosinolate material from this cross.

TABLE 1. (a) generation means (μmol/gseed) and (b) individual scaling tests for (i) progoitrin and (ii) total glucosinolate concentrations.

a			b		
Generation	(i)	(ii)	Test	(i)	(ii)
P_1	0·00 ± 0·000	112·87 ± 4·190	A	5·90 ± 3·990	-68·52 ± 7·081***
P_2	6·65 ± 0·613	13·77 ± 0·801			
F_1	77·75 ± 2·745	133·59 ± 3·586	B	2·61 ± 4·835	-19·06 ± 5·144***
F_2	43·21 ± 2·055	81·41 ± 2·596			
B_1	40·18 ± 1·990	88·97 ± 2.221	C	10·69 ± 9·904	-68·17 ± 13·321***
B_2	45·15 ± 1·415	64·15 ± 1·800			

Throughout *P = 0·05 - 0·01, **P = 0·01 - 0·001, ***P = <0·001

Individual scaling tests (Mather and Jinks, 1982) applied to the segregating generations of both characters reveal that an additive dominance model of gene action suffices for progoitrin, but total glucosinolates display a more complex pattern of inheritance, requiring a model which includes non-allelic interactions (Table 1b). Joint scaling tests conducted on both characters confirm these conclusions (Table 2).

From the information supplied in Tables 1a and 2 the proportion of recombinant inbred lines expected either to be free of progoitrin or to have a total glucosinolate concentration equal to or below that of Jaguar has been calculated (Mather and Jinks, 1982). The predicted values are 44.2% and 2.2%, respectively. For second cycle hybrids (Toledo, Poomi and Jinks, 1984), generated by intercrossing the recombinant inbred lines at random, the corresponding values are 2.2% and 0.54%, both appreciably lower than those for recombinant inbred lines (Tables 2).

Total glucosinolate concentration clearly has a more complex pattern of inheritance than progoitrin in this cross. The breeder would therefore have a better prospect of producing rape cultivars from this material with a low level of glucosinolates if he focused on reducing progoitrin concentration. The development of high quality rape cultivars requires rape with an acceptable low level of glucosinolates allied to an appropriate relative composition of the individual glucosinolates.

TABLE 2. Estimates of the components of generation means and variances for (i) progoitrin and (ii) total glucosinolate, together with the percentage of recombinant inbred lines and second cycle hybrids expected either to be free of progoitrin or have a total glucosinolate level ≤ Jaguar.

Parameter	(i)	(ii)
m	3·40 ± 0·306***	82·62 ± 12·015***
Σa	3·40 ± 0·306***	49·55 ± 2·132***
Σd	77·50 ± 1·714***	-55·84 ± 27·844*
Σaa		-19·31 ± 11·827
Σad		-49·46 ± 7·132***
Σdd		106·79 ± 17·514***
$\chi^2_{[3]}$	2·506 NS	—
Σa^2	567·655	1165·201
Σd^2	726·369	494·796
% recombinant inbred lines	44·20	2·20
% second cycle hybrids	2·20	0·54

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