Development of intervarietal substitution lines in oilseed rape (*B. napus L.)*

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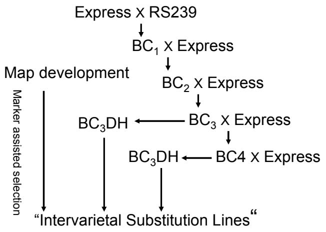
Introduction

Due to the introgression of undetected inferior gene the pedegree breeding is becoming less informative to detect the gene of interest. However, substitution lines will help us to have a complimentary segment of the whole donor genome within the genetic background of the recurrent parents divided into each single lines holding the donor segment on their respective linkage groups.The objective of this study is to develop intervarietal substitution lines from two rapeseed varieties having different quality traits and to examine the segregation of the donor segment in the backcrossing.

Material and Methods

Express 24 (E24), a short high yielding variety, was used as a recurrent parent and the resyntesised rapeseed RS 239, artificially synthesised from *Brassica olereacea* and *Brassica rapa*, was used as a donor plant. By crossing RS239 and E24, F1 generation was obtained and then F1 plants were crossed back to the recurrent parent E24.

Figure 1: Scheme for development of intervarietal substitution lines



Express X RS239

BC_1 X Express

Map development

BC_2 X Express

BC_3DH ← BC_3 X Express

BC_3DH ← BC4 X Express

Marker assisted selection

"Intervarietal Substitution Lines"

Result

Both donor and recurrent segments were analysed for all offspring in BC_1 and BC_2 obtained after backcrossing to E24 and marker assisted selection was undertaken based on 23 primers combination using AFLP marker. According to our map the total genome length is 1327,1 cm, divided in to 22 linkage

Table 2 depicts the expected and observed mean of the donor segment in BC_1 and BC_2, the observed donor segment shows low deviation from the expected in both of the backcrossing, however, it was possible to select the whole donor segment in BC_2 for 19 of the 22 linkage groups that made possible due to intense MAS of the mapping population.

Figure 2: AFLP map for crossing of resynthese RS239 x Express

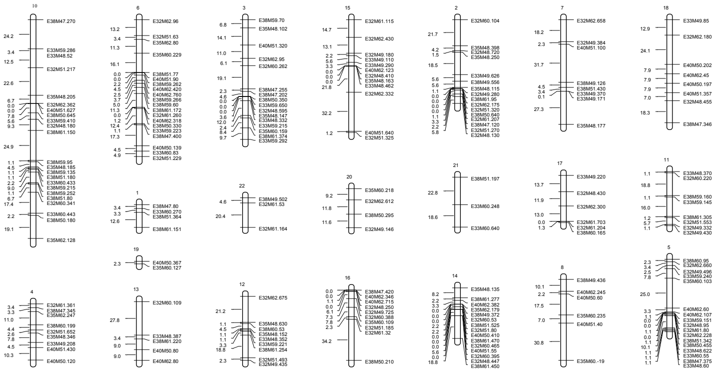


Table 1: Distribution of donor segments for 10 selected lines in BC_1 across the linkage groups

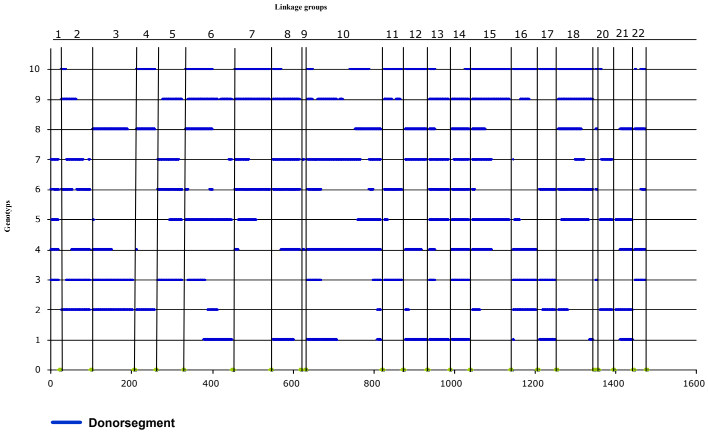


Table 2: The Length of donor segment in backcrossing 1 & 2

No. of	Total Pop.	Selected	Mean of donor segments in cM	
Backcrossing	of MAS	lines	Expected	Observed
BC_1	90	10	663,6 (50%)	629,0 (47%)
BC_2	285	18	331,8 (25%)	255,4 (19%)

Table 3: Distribution of donor segments for 18 selected lines in BC_2 across the linkage groups

Genotyps	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Lin. gr.1	🟥 1		🟨 2		🟩 1	🟩 1				🟩 1		🟩 1						🟩 1
2		🟥 1			🟩 1	🟨 1			🟨 1	🟩 1	🟨 2		🟨 1		🟥 1	🟨 1		🟩 1
3		🟨 1	🟥 1	🟨 1						🟨 1		🟨 1		🟨 1		🟩 1	🟩 1	🟨 1
4	🟨 1			🟥 1			🟨 1	🟨 1		🟨 1						🟨 2	🟨 1	
5			🟩 1		🟥 1					🟨 1	🟨 1	🟨 1			🟨 1			
U. h. 6						🟩 1		🟨 1	🟨 1			🟨 1	🟨 1					
L. h. 6		🟨 2	🟨 1	🟨 1	🟨 2	🟨 1	🟩 1					🟨 2		🟨 1	🟨 1	🟨 1	🟨 1	
7		🟨 1			🟨 1			🟥 1	🟨 1									🟨 1
8	🟨 1	🟨 1			🟨 1		🟩 1		🟥 1				🟨 1	🟨 1	🟨 1			
9	🟨 1	🟥 1																🟥 1
10			🟨 1	🟨 1									🟨 1	🟨 1	🟨 1		🟨 1	
U. h. 10										🟩 1	🟨 1							
Mid. 10																		🟩 1
L. h. 10	🟩 1						🟨 1				🟨 1							
11			🟩 1					🟨 1		🟨 1	🟥 1	🟨 1						
12	🟨 1	🟥 1					🟥 1						🟨 1	🟨 1		🟨 1	🟨 1	🟩 1
13	🟨 1				🟥 1	🟥 1	🟨 1		🟥 1		🟨 1	🟩 2					🟨 1	
14	🟥 1		🟥 1		🟥 1	🟨 1	🟨 1	🟨 1	🟥 1		🟨 2	🟨 1			🟨 2			🟨 1
15				🟨 1		🟩 1		🟨 2	🟨 1					🟨 1	🟨 1		🟨 1	🟨 1
U. h. 15				🟨								🟩 1						
L. h. 15													🟩 1					
16	🟨 1	🟨 1	🟩 1			🟨 1	🟨 1	🟩 1			🟩 1		🟩 1	🟥 1		🟨 1		🟨 1
17					🟨 1		🟨 1		🟨 1				🟩 1		🟥 1	🟨 1		
18		🟨 1		🟨 1	🟨 1			🟨 1	🟥 1			🟨 1	🟨 1				🟨 1	
19			🟥 1					🟥 1										
20					🟨 1					🟨 1				🟨 1		🟥 1		
21						🟩 1	🟩 1			🟨 1		🟥 1		🟨 1			🟨 1	
22		🟩 1	🟨 1		🟨 1						🟨 1						🟥 1	🟥 1
No. of segments	9	11	11	6	13	9	10	10	9	9	11	13	9	9	9	9	10	11

** 🟥 Whole donor segment 🟩 Half donor segment 🟨 short donor segment

Table 4: Comparison of donor segment in BC_1 and BC_2

	BC_1			BC_2		
	Min.	Max.	Mean	Min.	Max.	Mean
Donor segment RS 239 in cM	433,3	737	629	158	368	255
Recombination	6	18	10	6	14	10

Discussion

Development of intervarietal substitution was successfully developed for tomato, *Lycopersicon pennellii*, and *L. esculentum* in only two backcrossing (Eshed and Zemir, 1995). The oil rape seed has 19 chromosome compared to 12 in tomato, although development of a substitution line could also be done in the oil rape seed, more generation of backcrossing is needed to discard unnecessary donor segments distributed across 22 linkage groups to achieve a defined intervarietal substitution lines.

Literature

Eshed, Y.; Zamir, D. (1995). An introgression line population of *Lycopersicon pennellii* in the cultivated tomato enables the identification and fine mapping of yield-associated QTL. Genetics 141:1147-1162

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