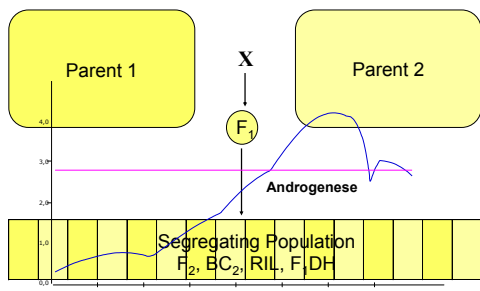




# Development of intervarietal substitution lines in oilseed rape (*B. napus* L.)

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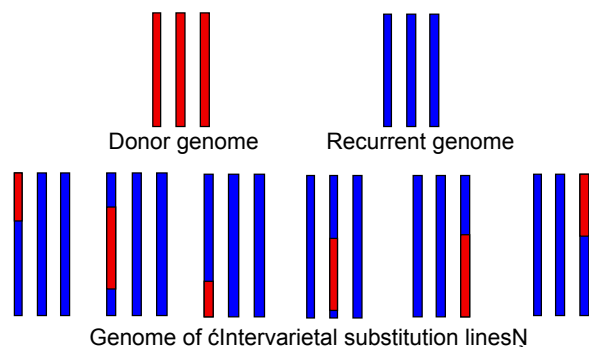
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## QTL mapping in segregating populations

QTL mapping in segregating populations has a number of drawbacks:

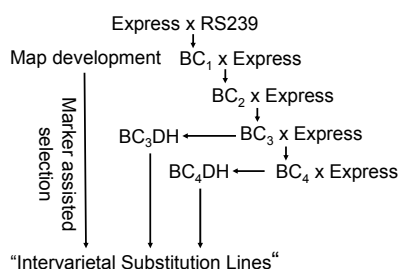
- Low power of detection, large populations of several hundred genotypes are required.
- Large confidence intervals for QTL positions in the range of several cM up to several 10's of cM.
- Further characterisation of mapped QTL is difficult because for each experiment the whole population has to be tested.



## Intervarietal substitution lines

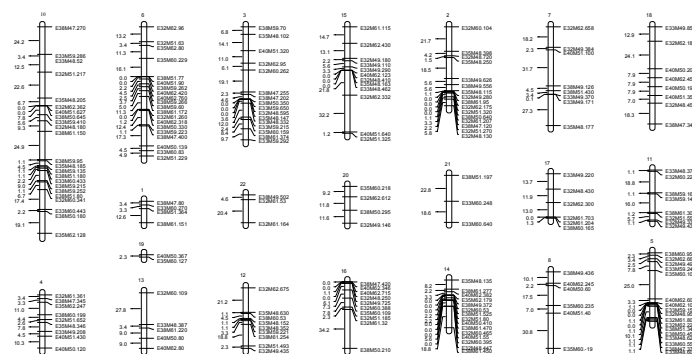
Alternative to QTL mapping in segregating population, QTL can be mapped using sets of intervarietal substitution lines where each line contains just one distinct segment of a donor genome. Using substitution lines has a number of advantages:

- higher power of detection
- a limited number of 50 - 100 lines is sufficient for QTL mapping
- QTL can be fine mapped by subdividing a donor segment in backcrosses with the recurrent parent
- After detection, a QTL can be further characterised by just testing the line that showed the QTL effect.



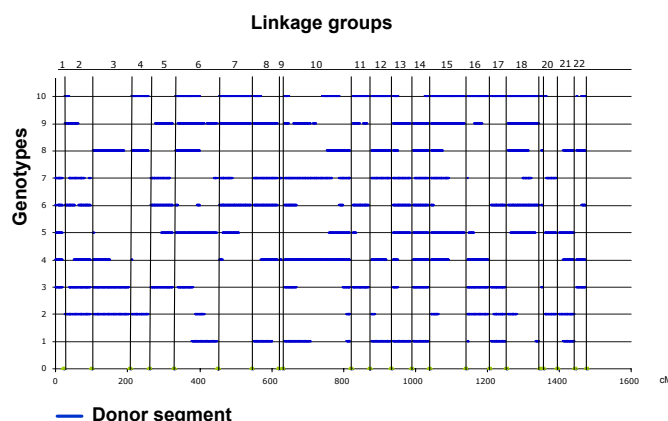
## Development of substitution lines

Substitution lines are developed by Marker Assisted Selection (MAS) in a recurrent backcross program. We are developing a set of intervarietal substitution lines from a cross between the resynthesized rapeseed 'R239' and the winter rapeseed variety 'Express'. The development of the substitution lines is currently in BC<sub>3</sub>.



## Genetic map for Marker assisted selection

A genetic map was developed in the BC<sub>1</sub> generation using AFLP markers. The map comprises 206 markers distributed on 22 linkage groups covering 1327 cM of the rapeseed genome.



## Genotypes of selected BC<sub>1</sub> plants

In each generation a set of genotypes will be selected with:

- As large as possible individual donor segments collectively covering the whole mapped genome
- As high a proportion of recurrent parent genome per line as possible

In the plants selected in BC<sub>1</sub> each linkage group is represented at least in one genotype by a full-length donor segment.

## MAS during the development of intervarietal substitution lines

Generation	Population size	Mean genome coverage by donor segments [cM]		No. of sel. plants	Mean genome coverage by donor seg. in selected plants [cM]
		Observed	Expected		
BC <sub>1</sub>	90	683	663	10	603
BC <sub>2</sub>	273	327	332	18	269
BC <sub>3</sub>	100 <sup>1</sup>	125	135	-	-

<sup>1</sup>partial population

In a recurrent backcross program it is expected that the extent of the genome still covered by donor segments is halved per generation. The average coverage actually observed in BC<sub>1</sub> to BC<sub>3</sub> closely agrees with this expectation. In BC<sub>1</sub> and BC<sub>2</sub> plants could be selected with a smaller than average fraction of donor genome despite the fact that sets of genotypes were selected in which most linkage groups were represented by full length donor segments in at least 1 to 2 plants.

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