# Simulating the Effect of Experimental Design on Recombination Dow AgroSciences



Cherie Ochsenfeld, Carol Powers, and Jan Erik Backlund

#### Introduction

The ability to fine map quantitative trait loci is essential to effectively locate narrow regions of the genome associated with important agronomic traits for use in germplasm improvement. In Canola it is especially challenging to apply fine mapping methodologies due to the lack of polymorphic markers between breeding lines. The low polymorphism rate limits the number of recombination events that can be observed in the experimental population, which is an important determinant in the statistical power of quantitative mapping methods. A popular experimental population for use in fine mapping is recombinant inbred advanced intercross lines (RIAIL), which improves power through the accumulation of recombination events from multiple rounds of random mating followed by inbreeding. However, due to the low polymorphism rate in Canola. this improvement could be limited. One strategy to introduce additional polymorphic markers in the design is to incorporate multiple parental lines. In this study, a multiple parent extension of the RIAIL design is explored empirically to quantify if additional resolution that can be obtained for fine mapping experiments using Canola as a model organism.

#### **Simulation Design**

\*A simulated map was used with markers placed 10 cM apart on each of the 19 chromosomes in Canola.

\*Each marker was assumed to be polymorphic among all the parental lines.

The number of parental lines were random mated and varied between 2 and 8.

The number of F1 progeny generated was varied and they were randomly intermated for 0 to 4 additional generations.

\*During random mating, individuals had a 10% probability of self-mating.

\*In the initial self-mating generation, lines were selfmated multiple times to generate a total of 16 lines.

\*The 16 lines were subsequently self-mated for an additional 7 generations.

## Results

\*Figures 1 and 2 display the results from the 16 progeny at the last self-mating generation in the 45 different RIAIL experimental designs that differed in the number of parental lines, number of random mating generations, and number of progenv in the F1 generation.

\*The results from a traditional RIL experiment are provided as a basis for comparisons.

\*Bars of the same color represent designs requiring the same length of time to generate the population. Each change in the bar color represents a increase of a single breeding generation.







Figure 2: The mean bin width in *cM* in the resulting 16 inbred lines.

### Discussion

Increase in mapping power occurs when the number of parental lines and number of random mating generations are increased.

\*Bins become more consistent in size as the number of random generations increased.

\*When no random mating is applied, increasing the number of parents does not make a significant difference in power.

Increasing the number of F1 progeny results in insignificant improvements in the both bin size and number.

The effect of the number of random generations was increased in designs that included more parental lines. For example: increasing the number of random breeding generations from 0 to 4 results in approximately double the number of bins for 8 parents and only ~25% increase for the 2 parent designs.

\*The less polymorphism that exists between the parents will result in a smaller improvement in power.

Improvement in power coupled with reduced genotyping costs and a gain in repeatability of mapping experiments makes a multi-parent RIAIL design a valid option for fine mapping of QTL.

## References

Darvasi, A. & Soller, M. (1995), 'Advanced intercross lines, an experimental population for fine genetic mapping', Genetics 141, 1199-1207.

♦Valdar, W., Flint, J. & Mott, R. (2003), 'QTL finemapping with recombinant-inbred heterogeneous stocks and in-vitro heterogeneous stocks', Mammalian Genome 14, 830-838.

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