

**P011** Characterization of meiotic recombination hotspots in *Arabidopsis thaliana*

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During the last decade, there has been considerable interest in studying meiotic recombination at the hotspot level in yeasts and mammals.

In plants still, little is known about the fine-scale distribution of meiotic recombination events along chromosomes.

Segregation analysis of an *Arabidopsis thaliana* F2 progeny allowed us to build a detailed recombination map of the whole chromosome 4: 1171 crossovers were located in 70 intervals, with an average length of 209 kilobases. The crossover rates varied significantly along the chromosome, from 0 to 20 cM/Mb, with a chromosome average of 4,6 cM/Mb

Further study of regions having high crossover rates led to the identification of meiotic recombination “hotspots” in small fragments of few kilobases.

In order to characterize precisely these hotspots, we have developed a molecular assay, allowing to identify single recombination events that arise during male meiosis in *Arabidopsis thaliana*. This approach relies on single-molecule, allele-specific PCR amplification of recombinant molecules present in pollen genomic DNA.

This “pollen typing” analysis was initiated for three hotspots. Preliminary results provide evidences that these hotspots are not necessary equally ‘hot’ in male and female meiosis.