

# Hotspots and sex-biased recombination in *Populus trichocarpa*

## Background

- Quantitative trait locus (QTL) mapping of feedstock-relevant phenotypes offers genetic markers for the accelerated domestication of poplar. Most traits of interest show quantitative inheritance, and this complicates the breeding process. Therefore, fine-scale characterization of meiotic recombination patterns is imperative to long-term success of natural and artificial selection in a successful breeding program for trees.

## Approach

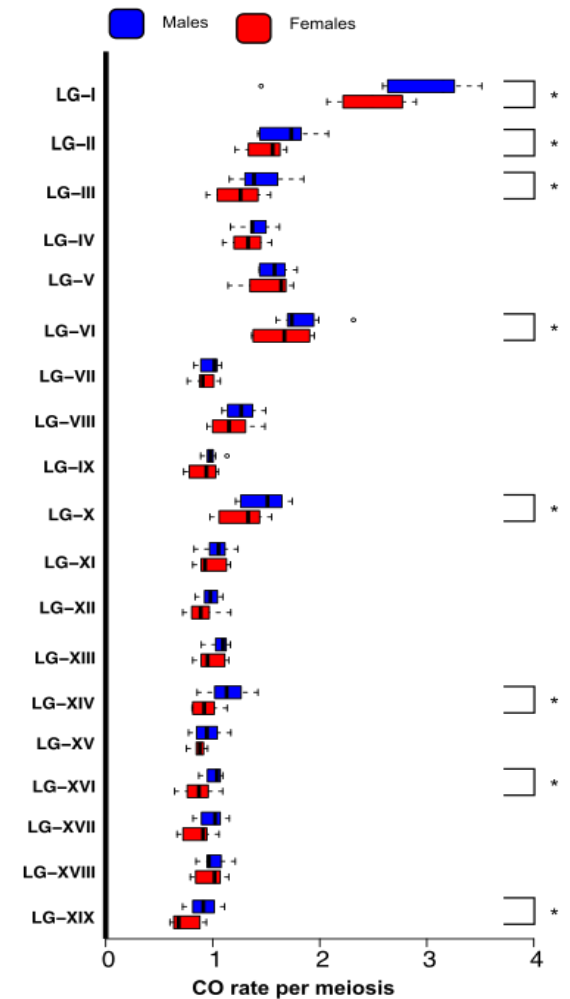
- Dense genetic mapping and haplotype reconstruction were used to estimate recombination for a full factorial *Populus trichocarpa* cross of 7 males and 7 females. Genomes of the resulting 49 full-sib families (N=829 offspring) were re-sequenced, and high-fidelity biallelic SNP/INDELs and pedigree information were used to ascertain allelic phase and impute progeny genotypes to recover gametic haplotypes.

## Results

- High density framework genetic maps were produced for 14 individuals representing each sex. The improved accuracy of genetic maps can be highlighted based on high concordance between genetic and physical positions. There was considerable variation in recombination rate among individuals.
- One of our most striking findings was the higher rates of sex-biased recombination in male parents compared to females in 9 out of 19 linkage groups (**Figure**).
- We identified candidate recombination cross-over (CO) hotspots spread throughout the genome. These are associated with several DNA sequence enriched motifs that showed striking similarity to motifs associated with CO's in maize, *Arabidopsis* and tomato.

## Significance

- Genome-wide recombination landscape and patterns of inheritance were presented at a finer scale previously unachieved for *Populus*. The phased haplotypes and recombination rate estimates will be useful for refining ongoing genomic selection models. These findings will aid studies about evolutionary history and adaptive potential of trees for perennial propagation, wood formation and other useful traits.



Broad to fine scale CO count differences between sexes: a) CO rate per chromosome per meiosis in males (blue) vs. females (red).

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