

Characterization of the willow sex determination system

Background

- Most plants produce both male and female flowers on the same individual.
- Important biofuel/bioprocess feedstocks like *Populus* and *Salix* have separate sexes, but the molecular underpinnings of sex determination are poorly understood.

Approach

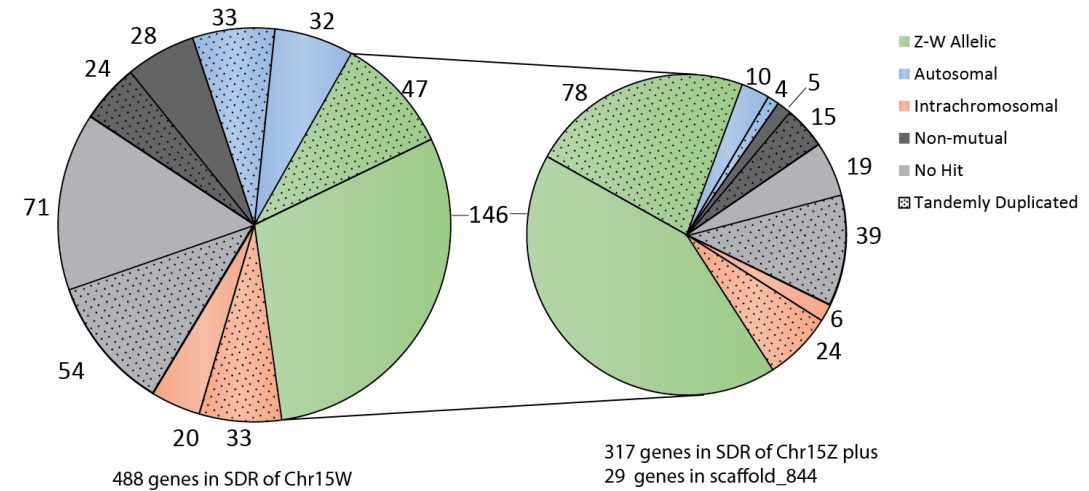
- High-quality *Salix purpurea* genomes of a male and female genotypes were sequenced by JGI and assembled by Hudson/Alpha.
- The sex determination region was identified by contrasting male and female genomes to identify sequences that only occur in one sex. This region was then assembled using dense genetic mapping.

Outcome

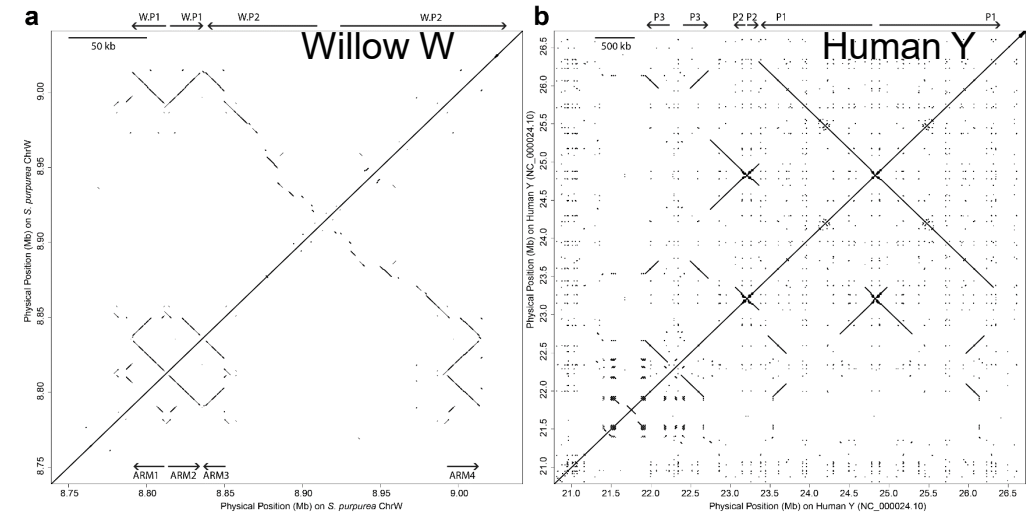
- Sex-specific sequences only occurred in females, indicating a ZW sex determination system.
- The sex determination region is 6.8 Mb in size and contains 171 genes that do not occur on the Z, many of which were transposed from other chromosomes.
- A subset of the genes are arranged in a palindromic repeat structure that is similar to prominent features that occur on mammalian Y chromosomes.

Significance

- Understanding sex determination is important for feedstock improvement because this enables control of flowering, which is important for both breeding objectives as well as biosafety of genetically engineered organisms.



Comparison gene content of Z and W sex chromosomes in Willow



Dot plot comparing sex chromosomes to themselves. Lines perpendicular to the diagonal represent inverted repeats.