

The *populus* was selected as the first tree with the genome to be sequenced, mainly due to its small genome size, the wide deployment worldwide (30+ species), and its short juvenile period. Its rich content of cellulose, which is one of the most important source for biofuel. A female clone of *P. trichocarpa* was chosen to be sequenced.

The current assembly of *Populus* genome is release 1.0, whose small insert end-sequence coverage is 7.5X, and it was released in June 2004. It consists of 22,012 sequences (including the 19 chromosomes) and the total length is 485,510,911 bps. The data was downloaded from [the official site of the *Populus trichocarpa* genome sequencing project](#). The latest version of the genome can be found at the [Poplar Genome Project](#) at JGI Eukaryotic Genomics.

Duplication regions introduce significant difficulties into the correct assembling of sequence contigs. For example, ~45% of the 75.2-Mbp segmental duplication regions in the initial assembly of the Norway Rat genome lacked chromosome assignment [1]. We identified all the repetitive elements in the *populus* genome. We further assign each of them as different classes of repetitive elements, including DNA transposons, RNA retrotransposons, Miniature Inverted-repeat Transposable Elements (MITE), Simple Sequence Repeats (SSR), and Segmental Duplications (SD), etc.

We organized the annotations into this easily browsable, searchable, and blastable database, *RepPop*, for the whole community. If you have any questions, please find the contact information in the [Contact](#) section.

We also provided a Wiki interface for the whole community to curate the annotations in this database at:

<http://csbl.bmb.uga.edu/~ffzhou/RepPopWiki/>

References:

[1] Tuzun, E., et tal. [Recent segmental duplications in the working draft assembly of the brown norway rat](#). *Genome Research*, 2004.