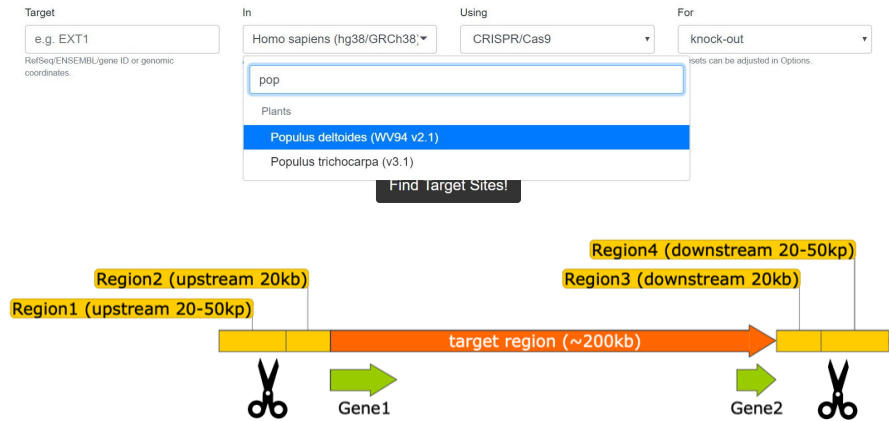


## Background

CRISPR/Cas-based gene editing technology has become a very useful tool for functional genomics research in both plants and animals. One of the major challenges of this technology is to design guide RNAs (gRNAs) that have high on-target activities, and few to zero off-target binding sites in the target genome. Recently, tremendous efforts have been put into the development of software for improved gRNA design. However, most of these software programs are limited to use with a few model organisms, especially animal species. CHOPCHOP software developed by Harvard University is one of the best web platforms for gRNA design. Unfortunately, poplar (*Populus spp.*) genomes have not been included in this platform. To address this challenge, we have collaborated with Harvard University to make CHOPCHOP available for designing gRNAs targeting genes or non-genic regions in poplar.



## Highlights

- Genome-wide gRNA design capability for both *P. trichocarpa* and *P. deltoides* has been built into the CHOPCHOP web platform (<https://chopchop.cbu.uib.no/>).
- The CHOPCHOP web platform has been used to design gRNAs for Cas9-assisted sequencing of large chromosomal regions in *P. trichocarpa* and CRISPR/Cas9-mediated knockout of genes in *P. deltoides*.

## Significance

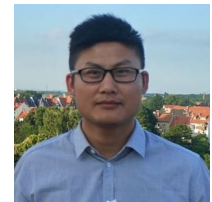
This new CRISPR web toolbox for genome-wide gRNA design in poplar will greatly accelerate efforts in CBI and around the world to perform CRISPR/Cas-mediated genomics research in poplar.



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