A population of copy number variants for poplar functional genomics.

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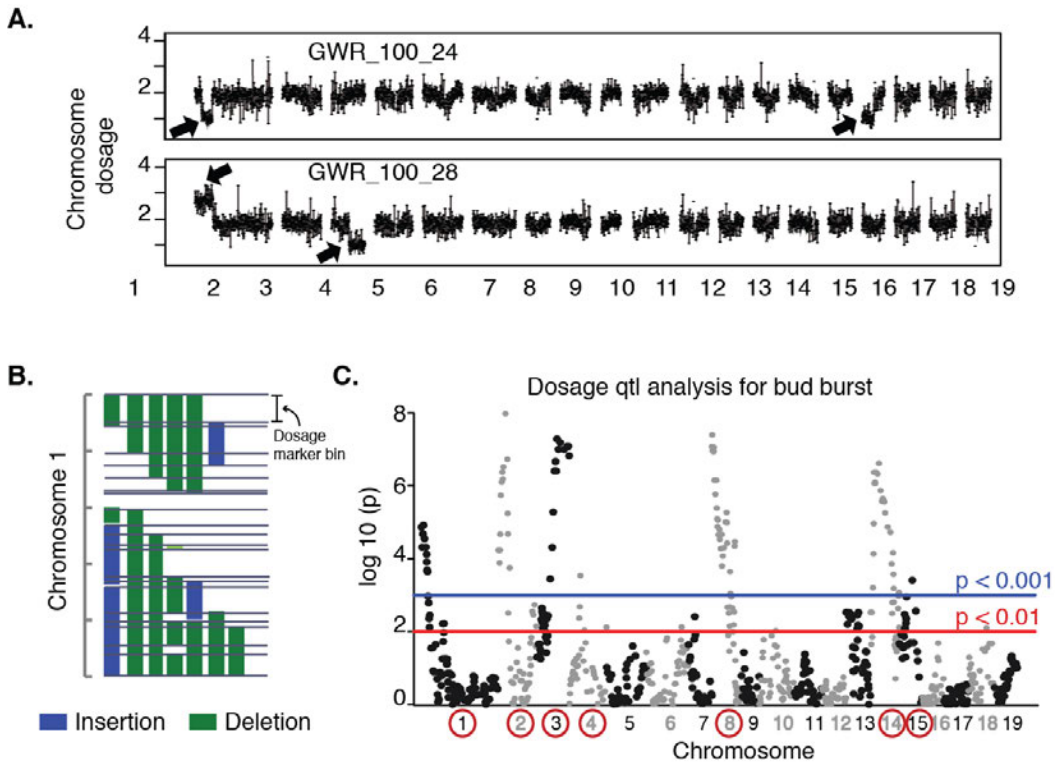
http://comailab.genomecenter.ucdavis.edu/index.php/Poplar
http://www.fs.fed.us/psw/programs/cb/staff/agroover/

Changes in gene dosage can affect gene function in multiple ways, and inducing dosage mutations (insertions and deletions) is a powerful approach to rapidly create wide phenotypic variation. We have produced and characterized a population of interspecific poplar hybrids carrying insertions and deletions tiling the entire genome multiple times. We are using this resource to identify genes that contribute to specific traits, initially focusing on poplar bioenergy traits. For this funding cycle, our specific objectives were to i) finish characterize and maintain this resource ii) investigate the phenotypic effects of dosage change and iii) exploit the indel germplasm for functional genomics. Outputs include a population of interspecific poplar hybrids carrying defined dosage variation and extensively characterized trait measurements, and possibly cultivars directly usable for bioenergy applications. The approach and tools developed here can be easily applied to other vegetatively-propagated species.

Poplar breeding is predominantly based on interspecific hybridization, harnessing the advantage of hybrid vigor. The resulting F1 hybrids frequently exhibit dosage variation, either in the form of whole genome duplication (triploidy) or in the form of copy number variation of pieces of, or entire chromosomes (aneuploidy). These variants can have transgressive phenotypes, sometimes desirable for biomass production or other characteristics of interest. Inducing large-scale copy number variation is therefore a rapid method for creating new variants. This approach is rarely used in sexual species because the resulting variation is often meiotically unstable but in clonally propagated species, such as the fast growing tree genus *Populus*, it holds many advantages. Using gamma irradiation of pollen grains, we have created a population of ~800 interspecific F1 sibling that vary in their chromosomal composition. We have found that approximately 50% of them carry at least one large-scale insertions or deletions (Henry et al, 2015). Phenotypic analysis confirmed that dosage variation is overall well tolerated and samples with distinct morphological alterations are present within the population.

We are completing the development of this unique resource for the research community and have started to use this germplasm as a functional genomics tool. Using precise phenotypic data, gene dosage information, and soon, associated gene expression information, we are investigating the role of gene dosage in poplar hybrid performance. By looking at the association between trait value and copy number across the genome, we are able to identify dosage qtls that contribute to a variety of quantitative traits (see Figure). We have so far focused primarily on phenotypic traits related to biomass production, leaf morphology and wood properties but have also started to acquire information about other traits such as drought or biotic stress tolerance and the population is available for other measurements as desired. Our population provides a powerful platform for both understanding gene function and the effect of gene dosage on phenotypes and

on poplar hybrid performance. This resource is publicly available for others to investigate specific traits of interest.



Identification of dosage qtls. A. For each F1 interspecific hybrid individual, the presence of an additional copy (insertion) or the deletion of a copy of a particular chromosome fragment was identified by detecting changes up or down in sequence coverage (arrows). **B.** Subset of lesions identified on chromosome 1. Lesions are tiled across the length of the chromosome. Dosage lesions vary in length (up to a whole chromosome) and a single individual carried up to 10 lesions. Deletions were most common but insertions were observed as well. For dosage qtl analysis (C), dosage markers were defined based on lesion boundaries. **C.** Dosage qtl analysis identified regions of the genomes for which copy number is associated with trait value. In this particular case, the timing of bud burst was recorded and found to be strongly associated with loci on 7 different chromosomes.

References

1. Henry IM, Zinkgraf MS, Groover AT, and Comai L. A System for Dosage-Based Functional Genomics in Poplar. Plant Cell **2015,** 27:2370-2383.

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