189. A novel poplar biomass germplasm resource for functional genomics and breeding

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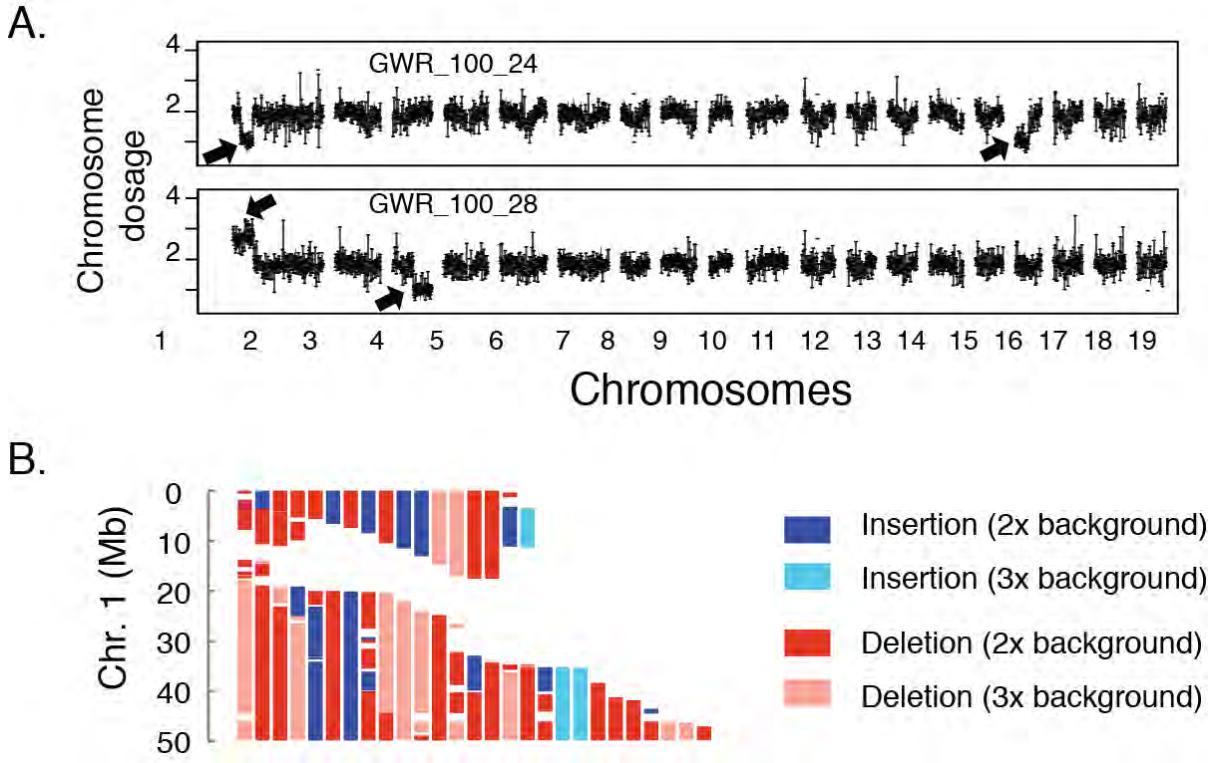
http://comailab.genomecenter.ucdavis.edu/index.php/Poplar
http://www.fs.fed.us/psw/programs/cb/staff/agroover/

Project Goals: We have produced a new population of interspecific poplar hybrids carrying insertions and deletions tiling the entire genome with dosage variation. This unique functional genomics resource can be used to investigate the role of gene dosage in poplar hybrid performance, and to identify and genes that contribute to poplar bioenergy traits. Our specific objectives are 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 will include a population of interspecific poplar hybrids carrying defined dosage variation and extensively characterized trait measurements. Possibly, our germplasm collection also includes cultivars directly usable for bioenergy applications. The approaches and tools developed can be generalized to other poplar hybrids and to germplasm development for other vegetatively-propagated species.

Interspecific hybridization is the most effective method for producing poplar clones for commercial applications, including biomass production. Previous research has shown that commercial F1 hybrids frequently exhibit dosage variation, i.e. variation in the number of pieces or entire chromosomes, and that these variants can have transgressive phenotypes desirable for biomass production. Poplar is an excellent system for studying and exploiting gene dosage because germplasm is propagated vegetatively for research and production, and advanced genome-enabled tools can be directly employed on the actual feedstock.

In the previous funding cycle, we have produced a population of interspecific hybrids carrying dosage lesions. Over 500 seedlings were subjected to high-precision dosage analysis using next-generation sequencing. Insertion and deletions were detected in approximately 55% of the progeny, and varied in length, position and number per individual, cumulatively covering >99% of the genome with an average of 10 dosage lesions (See Figure). Additionally, triploid individuals are also present within the population of dosage variant, which provide an additional layer of dosage variation. Preliminary phenotypic analysis confirmed that dosage variation is well tolerated and that samples with distinct morphological alterations are present within the population.

In this proposal, we will complete the development of this unique resource for the research community and start to use this germplasm as a functional genomics tool. Using precise phenotypic data, gene dosage information as well as associated gene expression information, we will investigate the role of gene dosage in poplar hybrid performance and identify chromosomal regions and genes that contribute to poplar bioenergy traits. Our efforts will add new, useful and unique tools that have both functional and practical applications for poplar breeding and is widely applicable to other biomass crops such as switchgrass, alfalfa, willow, and miscanthus.



Detection and characterization of dosage variants. A. For each sample, sequencing reads were aligned to the reference sequences and sorted into consecutive bins of 100 kbs, along the 19 chromosomes of the poplar genome (v3.0). Two different samples are represented here. Changes up or down in chromosome dosage correspond to the presence of an additional copy (insertion) or the deletion of a copy of a particular chromosome fragment, respectively (arrows). B. Lesions identified so far 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 carries up to 10 lesions. Deletions are most common (red and pink) but insertions are observed as well (blue). Background ploidy (2x or 3x) is indicated as well.

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