

Global Summit on
Plant Science

September 21-23, 2015 San Antonio, USA

Some unexpected features of the *Populus* genome

Gerald A Tuskan

Oak Ridge National Laboratory, USA

A genome is hierarchal summation of historic duplications, rearrangements and mutational events that descend from an ancestral progenitor. In a practical manner, a genome, in the context of high-throughput sequencing is a computational representation of actual linear sequences of nucleotides depicted as a pseudomolecule. Genome expansion, through whole-genome duplication events followed by rearrangements and mutations leads to predictable, conserved functions across plant and animal taxa. Summed across many distantly related genomes we can then build hierarchal models of incremental gene expansion that are used to project function into annotated gene space. This approach has served us well in the areas of comparative genomics, transcript and proteomic analyses and taxonomic classifications. There are, however, unusual and non-iconoclastic genomic features that appear conserved across taxa and may have arisen outside of incremental accumulation of small mutations. We have used a deep SNP and INDEL library in *Populus* for the discovery of novel genes/proteins using GWAS approaches. These features include: Cryptic genes and gene structures, horizontal gene transfer and gene/motif cooption and de novo gene formation. Transient and stable transformation, co-evolution and co-expression network analyses and pharmacological experiments have been used to validate hypothesized functions. Phenotypic examples related to callus formation, bark texture and lignin deposition within the cell wall will be presented.

Biography

Gerald A Tuskan holds a dual appointment as Group Lead for Plant Genomics Group at Oak Ridge National Laboratory and Co-lead for the Plant Genomics Program at the Department of Energy Joint Genome Institute. He has over 25-years of experience leading and working with DOE on the development of bio-energy feed-stocks. He is currently the Activity Lead for the DOE BioEnergy Science Center *Populus* team and is co-lead PI on DOE Plant-Microbe Interactions project. His research focuses on the accelerated domestication of *Populus* through direct genetic manipulation of targeted genes and gene families with focus on cell wall biosynthesis.

tuskanga@ornl.gov

Notes: