

- Technology Presentation (5) -



Jack P. Wang, Ph.D.

Strategic Engineering of *Populus* For Bioenergy and Bioproducts Through Multi-Omics Integration in Lignin Biosynthesis

Abstract:

Multi-omics integrative analysis of lignin biosynthesis can advance the strategic engineering of wood for bioenergy and bioproducts. Lignin is polymerized from three monomers (monolignols) produced by a grid-like pathway. The pathway in wood formation of *Populus trichocarpa* has at least 21 genes, encoding enzymes that mediate 37 reactions on 24 metabolites, leading to lignin and affecting wood properties. We perturb these 21 pathway genes and integrated transcriptomic, proteomic, fluxomic and phenomic data from 221 lines selected from ~2,000 transgenics. Stem xylem of the transgenics and wildtype were analyzed by 239 full transcriptomes and 239 proteomes to regress the abundances of transcripts and proteins. Using recombinant proteins from the 21 monolignol pathway genes, we determined 207 reaction and inhibition enzyme kinetic parameters to predict the effects of protein abundances on pathway metabolic-fluxes and metabolite concentrations. To determine the effects of metabolic-fluxes and metabolite concentrations on lignin and wood properties, we quantified the chemical composition of 220 wood samples, and 76 lignin samples using 2D HSQC NMR for lignin composition and structures. We measured the growth of 221 lines, the mechanical strength of 416 wood samples, the density of 213 wood samples, and tested 236 wood samples for saccharification efficiency. All these data were then systematically integrated to describe the transduction of biological information from the 21 monolignol genes through transcripts, proteins, metabolic-fluxes, and metabolite concentrations, leading to 25 economically and ecologically important traits, including lignin, tree-growth, density, strength, and biofuel production. The analysis then predicts improvements in any of these 25 traits individually or in combinations, through engineering expression of specific monolignol genes. The analysis may lead to greater understanding of other pathways for improved growth and adaptation.

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Biography:

Jack P. Wang is Assistant Professor and Director of the Forest Biotechnology Group in the Department of Forestry and Environmental Resources at North Carolina State University. Dr. Wang earned a B.S. in Biology and Chemistry from Waikato University, New Zealand in 2006, and a Ph.D. at North Carolina State University in 2012. Dr. Wang is a molecular geneticist focusing on the systems and integrative multi-omics analysis of forest tree metabolism for growth, development, and defense against biotic and abiotic stresses. Some highlights of his research include an unprecedented quantitative systems analysis of lignin biosynthesis in wood formation with important implications for bioenergy and bioproducts; demonstrating protein phosphorylation as an on/off switch for AldOMT, a central enzyme in monolignol biosynthesis; characterizing the hetero-tetrameric 4CL enzyme complex formation, regulation and numerical modeling; and establishing a proteomics-based predictive kinetic metabolic-flux (PKMF) model of the monolignol pathway. This PKMF model predicts how monolignol pathway enzymes affect lignin content and composition, explains a long-standing paradox regarding the regulation of monolignol subunit ratios in lignin, and reveals novel mechanisms involved in the regulation of lignin biosynthesis.

Publications (selected):

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- 6) Wang JP, *et al.* *Current Opinion in Biotechnology* 56:187-192 (2019).
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- 12) Shi R, *et al.* *Planta* 245:927-938 (2017).
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