TOWARDS A POPLAR BIOMASS PROTEIN-PROTEIN INTERACTOME

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Interactions between proteins are central to nearly all biological functions. We are identifying and mapping *Populus* protein-protein interactions relevant to woody biomass formation by focusing on proteins that are coexpressed in developing secondary xylem. Through integration with other 'omics data, this high-confidence wood interactome will provide a solid framework for identifying key regulators of wood formation and biomass accumulation and for designing strategies to alter biomass traits. We cloned 374 members of the poplar biomass ORFeome for use in indentifying biomass protein-protein interactions. These biomass ORFs encode a variety of protein classes, such as proteins involved in cell-wall synthesis and signal transduction as well as proteins of unknown function. Completion of yeast two-hybrid (Y2H) binary assays involving over 300 biomass ORFeome members has identified 11 interaction pairs. 60 biomass ORFeome members are being used as bait proteins for an Y2H screen with a poplar xylem cDNA prey library. Nine bait proteins have be completely through the screening process with 43 unique high-confidence protein-protein interactions identified. Methods and results from these Y2H screens as well as diagrams of identified biomass protein interaction modules are available at our project website (http://xylome.vbi.vt.edu/index.html). In addition, functional analyses *in planta* of selected interacting proteins can provide valuable insight regarding new strategies for regulating woody biomass production. Thus, we have begun to functionally characterize select interacting pairs in both Arabidopsis and poplar by ectopically expressing or suppressing genes singly and in combination. Co-overexpression of interacting proteins PB15 (ROP-GTPase) and PB129 (DUF620) in Arabidopsis resulted in expanded interfascicular regions containing enlarged fibers compared to fibers in normal interfascicular regions of the inflorescence stem. Notably, this phenotype was not observed in transgenics overexpressing just one of these genes, showing the potential of interactome data to be translated into alteration of wood phenotypes.