

## MWP – Young Researcher Abstract 2025

<p><b>Project title:</b> Large-scale Genome-Wide Association Studies for Specialized Metabolites in Poplar</p>	
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<p><b>Abstract</b> (approx. 200 words):</p> <p>Poplar is an important woody biomass crop and a model of choice for molecular research in trees. Although its genome was sequenced nearly 20 years ago, the structures and biosynthetic pathways of most specialized metabolites—critical for biological processes such as defense and adaptation—remain largely unknown.</p> <p>In the ERC-funded project POPMET, we sequenced the genomes of more than 700 wild <i>Populus nigra</i> accessions using long-read Oxford Nanopore (ONT) sequencing and assembled a high-quality reference genome. Meanwhile, the metabolite profiles of leaves from each accession were analyzed by UHPLC-MS, resulting in over 18,000 detected peaks, corresponding to approximately 4,500 compounds. Using the candidate substrate-product pair (CSPP) algorithm developed in our group, we predicted biosynthetic conversions among 3,500 of these compounds. Genome-wide association studies (GWAS) identified significant associations for more than 3,000 compounds. The functions of enzyme-encoding genes are being validated through enzymatic activity assays and reverse genetic approaches, including CRISPR-Cas9 knockouts in hybrid poplar. Our initial focus is on salicinoids, an important class of defense compounds in poplar.</p> <p>This project will significantly advance our understanding of specialized metabolism in poplar and provide resources for future fundamental research and genome-assisted breeding.</p>	
<p><b>Key words:</b> poplar, metabolite GWAS, long read ONT sequencing, CSPP, salicinoids</p>	