

Neish Young Investigator Awardee



Xu (Sirius) Li is an Assistant Professor at the Plants for Human Health Institute, North Carolina State University. Before joining NCSU in 2011, he worked as a postdoc in Clint Chapple's laboratory at Purdue University. He received his PhD degree in biochemistry in 2005 from Iowa State University where he was awarded a Plant Science Institute Fellowship. He obtained a BS degree in plant molecular and developmental biology, and a MS degree in plant physiology, both from Peking University in China. Dr. Li's research focuses on plant specialized (secondary) metabolism. He has been developing an integrated metabolomics, genetics, and genomics platform for discovery of plant metabolic pathways using the model plant *Arabidopsis thaliana*. His long-term goal is to apply this platform to understand the biosynthesis of health-promoting phytochemicals and to manipulate metabolic pathways in crops, vegetables, and fruits to enhance their values for human health.

[S1-4] Identification of a residue responsible for UDP-sugar donor selectivity of a dihydroxybenzoic acid glycosyltransferase from *Arabidopsis* natural accessions

Han-Yi Chen^{1,2}, Xu Li^{1,2}

¹Plants for Human Health Institute, North Carolina State University, Kannapolis, NC, USA

²Plant and Microbial Biology, North Carolina State University, Raleigh, NC, USA

UDP glycosyltransferase plays a major role in the diversity, reactivity, and regulation of plant specialized metabolites by catalyzing the transfer of the sugar moiety from activated UDP-sugars to various acceptors. *Arabidopsis* UGT89A2 was previously identified from a genome-wide association study as a key factor that controls the differential accumulation of dihydroxybenzoic acid (DHBA) glycosides in distinct *Arabidopsis* natural accessions, including Col-0 and C24. The *in vitro* enzyme assays indicate that these distinct metabolic phenotypes reflect the divergence of UGT89A2 enzyme properties in the Col-0 and C24 accessions. UGT89A2 from Col-0 is highly selective toward UDP-xylose as the sugar donor, and the isoform from C24 can utilize both UDP-glucose and UDP-xylose but with a higher affinity to the glucose donor. The sequences of the two isozymes only differ at six amino acid residues. Examination of these amino acid residues in more natural accessions revealed a strong correlation between the amino acid polymorphism at the position 153 and the DHBA glycoside accumulation pattern. Site-directed mutagenesis that swapped residue 153 between UGT89A2 from Col-0 and C24 reversed the UDP-sugar preferences, indicating that the residue 153 plays an important role in determining sugar donor specificity of UGT89A2. This study provides insight into the key amino acid changes that confer sugar donor selectivity on UGTs, and demonstrates the usefulness of natural variation in understanding structure-function relationship of enzymes involved in specialized metabolism.