Building a glucosylation platform in *E. coli* through Metabolic Engineering

Glycosyltransferases are powerful enzymes for the regioselective glycosylation of various secondary metabolites. Addition of a sugar residue to these molecules greatly alters the solubility, stability or bioactivity which are desirable properties when glycoconjugates are applied as nutraceuticals, therapeutics or cosmetics. A constraint to the use of glycosyltransferases in biocatalysis is the need for activated sugar donors (often nucleotide sugars) which are expensive and rarely available in large quantity. An efficient solution is the use of microbial whole-cell systems that overexpress glycosyltransferases and form their own expensive nucleotide sugars from cheap substrates.

Although the use of these whole-cell systems has shown its vast potential in producing diverse and new to nature glycoconjugates, the conversion rates and titers are often affected by the inefficient nucleotide sugar formation. In this study, we present the development and evaluation of a glucosylation platform in *Escherichia coli* W through Metabolic Engineering. The resulting base strain acts as a versatile host for the selective glucosylation of diverse compounds such as hydroxybenzoic acids or phenylpropanoids. Furthermore, production is coupled to growth via a unique metabolic split mechanism with sucrose as the carbon source for the nucleotide sugar donor. Our metabolically engineered *Escherichia coli* W has been proven to be an efficient producer of numerous glycoconjugates with high production rates.