^{13}C flux analysis of metabolic pathophysiology in cells and *in vivo* mouse models

^{13}C metabolic flux analysis (MFA) is the gold standard approach for quantifying rates of biochemical reactions inside living cells. It has been widely applied to debottleneck the metabolism of industrial host organisms, but it is now being increasingly used to investigate metabolic phenotypes of human disease models. As examples of the latter, my group has applied ^{13}C MFA to quantitatively map the metabolic alterations that occur in liver cells exposed to toxic levels of free fatty acids (FFAs) and to elucidate the role of the *G6PC2* gene in controlling glucose metabolism in pancreatic islets. I will discuss these studies as well as my lab's ongoing work to develop an *in vivo* ^{2}H/^{13}C MFA approach to simultaneously assess multiple gluconeogenic, CAC, and anaplerotic fluxes in the livers of conscious, unstressed mice. Our goal is to establish a scalable *in vivo* MFA platform that can be used to examine liver metabolic phenotypes in mouse disease models and to test specific hypotheses suggested by our *in vitro* studies.