Global profiling of metabolites, the small molecules produced by living things, provides one of the most powerful strategies for learning about gene and protein functions. This approach, known as metabolomics, is generating information that will serve as the foundation for engineering of plants and microbes to produce renewable feedstocks for high-value biochemicals and biofuels. Metabolite profiles also are important indicators of health and disease, and many metabolites serve important signaling functions that regulate physiological states ranging from inflammation to resolution of tissue damage.

Research in the Jones laboratory is driven by a desire to understand how genetics and environment combine to influence biological chemistry by: (1) developing analytical and biochemical tools for deep profiling and spatial localization of specialized metabolites, (2) developing experimental and data mining approaches to accelerate discoveries of natural products in plants and the genes involved in their accumulation, (3) deployment of mass spectrometry measurements of human exposures to nutrients, toxins, and endogenous metabolites that drive epigenetic regulation of factors that influence disease (and may be inheritable traits), and (4) measurements of small molecule biomarkers whose levels reflect the effectiveness of disease treatments.

Many plants accumulate large quantities of bioactive phytochemicals and are prolific biochemical factories. Our laboratory has pioneered rapid metabolite profiling protocols based on ultrahigh performance liquid chromatography (UHPLC) coupled to high-resolution time-of-flight mass spectrometry (MS). By employing rapid gradients and by multiplexing collision potentials across a lens between the mass spectrometer ion source and mass analyzer, ~500 metabolites are measured in a 5-minute analysis. This allows for large-scale screening of genetic variants to guide gene function discoveries. Ongoing research involves labeling metabolites using $^{13}$C to investigate metabolic dynamics coupled with elucidation of metabolite structures using MS and NMR.

We also investigate whether inflammatory, anti-inflammatory, and analgesic metabolite biomarkers in the blood and urine of human patients indicate mechanisms underlying the effectiveness of various treatments of traumatic brain injury. In addition, since more diseases are associated with environment and lifestyle than specific genetic factors, our lab is adapting our analytical methods to investigate the exposome, which is the entire range of molecules (e.g. from foods, environment, gut microbes) to which individuals are exposed.

Selected Publications

- Comparative structural profiling of trichome specialized metabolites in tomato (Solanum lycopersicum) and S. habrochaites: acylsugar profiles revealed by UHPLC/MS and NMR, B. Ghosh, T. C. Westbrook, and A. D. Jones, Metabolomics 2014, 10, 496-507.