

Mass Spectrometry (MS) offers high sensitivity, specificity, wide molecular coverage, relative quantitation, and structural identification capabilities. It has become an indispensable tool for single-cell proteomics and metabolomics. The Picosecond Infrared Laser-coupled Mass Spectrometry (PIRL-MS), pioneered by the Miller group, has already demonstrated that it is a powerful tool for studying proteins within tissue. Conventional methods, such as fluorescence imaging, can only capture a sliver of the available information. In contrast, PIRL can ablate micron-scale voxels from tissue, extracting fully intact and ionized biomolecular species subsequently detected by MS. Our ongoing research is focused on optimizing the collection and transmission of ablated species to the mass spectrometer, striving for a 100% efficiency rate. PIRL-MS in the space charge free ion collection limit will be capable of single molecule detection for which we have demonstrated that the entire molecular signature of tissue is conserved.

This project will be the first in a series of studies to demonstrate a new method of mass spectrometry imaging for high spatial resolution of detecting proteins in biological samples. Our early results show sub-cellular capabilities for assigning complex MS spectra. The goal is to further identify sub-cellular proteomics to map biochemical pathways with an emphasis on correlating molecular expression to healing as a key example of cell functions and mutability.