

Development of Microfluidic Devices Interfaced to Mass Spectrometry

Introduction

Over the last decade, mass spectrometry has evolved into a primary tool for proteomics. In general, isolating and characterizing a specific protein in any biological medium has been approached by separation steps in order to facilitate the interpretation of the MS spectra. The isolated protein is prepared into shorter peptides by proteolysis with trypsin, followed by identification using mass spectrometry and data base searching. Although these proteomic methods using mass spectrometry have helped scientists to analyze protein accurately and efficiently, the sample preparation step such as digestion, separation, and preparation are still very time consuming. Also, high sensitivity with lower sample consumption and higher sequence coverage of proteins are tremendous analytical challenge of proteomic studies. Microfluidic chips can be realized due to success in microfabrication of substrate. This chip has advantages of improved portability due to miniaturization, reduced sample and reagent consumption, and the accelerated speed of reaction and analysis for high-throughput screening.

The goal of my study is to develop an automated digestion, separation and droplet deposition microfluidic chip for MALDI-TOF MS. This goal will be completed by Dr. Murray group, CAMD, and CBMM.