Establishment of cell-to-cell heterogeneity is essential to the formation of all the different kinds of tissues that are required for normal development of the vertebrate embryo. For instance, in the South African clawed frog (Xenopus laevis), a powerful animal model in cell and developmental biology, distinct cells of the 16-cell embryo are known to give rise to specific tissues later in development. Measurements of transcripts and metabolites revealed that molecular differences exist between cells with different fates of the 16-cell frog embryo. However, no information is yet available on how proteins are distributed between cells of the early developing embryo when fate specification begins. The limitation has been due to a lack of sufficiently sensitive mass spectrometry (MS)-based approaches for single-cell analysis.

My research is focused on developing such MS-based analytical tools to enable the characterization of proteins in individual embryonic cells. First, we developed a capillary electrophoresis (CE) electrospray ionization (ESI) platform to allow minute amounts of peptides to be separated and then detected by a high-resolution mass spectrometer (HRMS). This CE-ESI-HRMS system enabled attomoles level limit of detection and was quantitative across 4–5 log-order in concentration for standard peptides. It also provided reproducible peptide separation from complex protein digests of X. laevis embryos even across 7 days of experiments. By adapting multiplexed quantification to CE-ESI-HRMS, we quantified proteomic differences between neural-, epidermal-, and hindgut-fated single cells in the 16-cell X. laevis embryo, providing the first example of proteomic cell heterogeneity in the vertebrate embryo. To extend these measurements to progressively smaller cells as the embryo develops, we integrated capillary microsampling to CE-ESI-HRMS. Microprobe CE-ESI-HRMS was validated using the 1-cell embryo where known intracellular heterogeneity exists between the animal and vegetal poles of the embryo. Last, we applied our technology to the temporal analysis of neural-tissue fated cell clones across successive stages of the developing embryo. By quantifying ~400 proteins in total, we uncovered proteomic changes as the precursor cell established a clone. The tools that were developed in my research enabled both spatial and temporal proteomic analysis of individual cells in X. laevis, raising a potential to study cell molecular mechanisms underlying normal and diseased development.

Bio
Camille Lombard-Banek obtained a MSc in Chemical Engineering from Ecole Nationale Supérieure de Chimie de Lille (ENSCL, France) followed by a MSc in Chemistry from the University of Toledo, OH. Her research entails the development of microanalytical HRMS to enable the proteomic analysis of single embryonic cells. Her work has resulted in 5 peer-reviewed publications with 1 featured on the cover page, 3 manuscripts in progress, and ~30 presentations at (inter)national conferences.

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Friday, November 10, 2017
SEH B1220
2:00 - 3:00 p.m.
Refreshments will be served at 1:45 p.m.