

Public/Lay Abstract:

Breast cancer cells can escape from the primary tumor and travel to distant sites. After arrival at a distant site, these cells can grow to form metastatic lesions that may ultimately kill the patient. Metastatic disease is responsible for nearly 90% of all breast cancer-related deaths. It is estimated that there are currently over 155,000 patients living with metastatic breast cancer in the United States. Despite this overwhelming burden of metastatic disease, cancer researchers do not typically have access to metastatic tumor tissue obtained from patients. In order to improve therapy for patients with metastatic breast cancer, it is critical to understand the genomic changes and cellular phenotypes of metastatic tumors that ultimately become lethal. Cell lines and animal models can provide valuable information to researchers, however, it is crucial that scientists also have access to patient-derived metastatic tumor tissue.

Obtaining metastatic tissue from living patients for research purposes poses a significant challenge. Breast cancer often metastasizes to sites that are technically challenging to biopsy, and procedures that access these sites can be associated with significant risks to the patient. When metastatic tissue is biopsied in the setting of clinical care, specimens are often small and must be reserved for clinical diagnostic purposes. Because of these limitations, most researchers are unable to study end-stage metastases that result in patient death.

One potential solution is to collect metastatic tumor tissue from patients after they have passed away. The medical autopsy is a traditional tool that pathologists have used for centuries; when coupled with modern advances in genomics, it is an exceptional method for studying the metastatic process. Post-mortem examination allows for the collection of breast cancer metastases from multiple body sites (e.g. bone, liver, lung, brain) in the same patient that can then be banked and studied using a variety of methods.

The primary objective of this study is to establish a tissue donation program for biobanking of breast cancer metastases collected during autopsy. A subset of the collected tissue will be used for gene expression profiling using NanoString technology. Specifically, we plan to identify genes whose expression is significantly altered in advanced metastatic breast cancer when compared to the patient's primary tumor. We will also compare gene expression between breast cancer metastases at different sites within an individual in order to identify changes in the tumor cells associated with metastatic growth in different environments. The results of these studies will lead to an enhanced understanding of metastatic disease, and may lead to the identification of novel therapeutic targets that may ultimately improve treatment for patients with metastatic breast cancer.