A Report from
The 2016 AACR Meeting
New Tools, New Discoveries
Meet Christina Curtis, PhD, MSc, the 2016 Grant Recipient

Computational molecular biology. What is it and why does it matter to the TNBC community? Briefly stated and way under simplified, computational molecular biology is an emerging tool that is opening new doors to understanding the biology and behavior of cells. It is also Christina Curtis's special area of expertise. Dr. Curtis, an assistant professor in the school of medicine at Stanford University, is the 2016 recipient of a grant funded by the Triple Negative Breast Cancer Foundation and its partner Carol's Crusade For A Cure Foundation. Her work focuses on developing ways of predicting which cancers are more likely to recur, both in individual patients and in groups of patients with triple negative breast cancer.

"We are interested in using innovative computational and analytic approaches to improve the diagnosis and treatment for cancers," Dr. Curtis says. "Why do some people develop metastatic breast cancer?

Knowing which cancers are likely to recur is critical for many reasons. If you know which tumors are going to behave aggressively, you can treat them more aggressively, early in the process. You can also spare patients with less high risk cancers from treatments that will not help them. Traditionally, decisions about the degree of risk for any patient have been based on the clinical characteristics of the tumor. How big is it? Are there lymph nodes involved? What do the cells look like under the microscope? Those factors are still important but today, the biology and the genetics of any individual cancer are playing an increasingly role in making personalized decisions about treatment.

Dr. Curtis's work begins with doing a genomic analysis of actual tissue acquired in biopsies. She then uses that information to develop a three-dimensional model of the tumor that will behave like the actual cancer cells. She can look at the full range of mutations and see which ones are most likely to produce metastases or resist treatments.

"Our original model was for colon cancer," she says. "We are now applying what we learned to triple negative breast cancer. TNBC is a complex group of tumors with very diverse genomic and molecular profiles. It is also a cancer for which there is truly an urgent need to understand the biology and use that knowledge to improve the outcomes for patients."

One challenge Dr. Curtis faces is getting the tissue for analysis. "We need tissue from both primary and metastatic tumors so we can see how these cells evolve and change, understand what mutations occur during that process. It can be difficult to get the metastatic tissue because many patients don't want to undergo biopsies that don't have any therapeutic benefit, or the metastatic tumors are in hard to biopsy places."

Dr. Curtis promises to keep the TNBC community up to date on the progress of her work. She and her colleagues are at the forefront of a rapidly emerging approach to science that brings together clinicians and experts fields ranging from physics to engineering to high end computing. The result is an array of new tools and new insights that are transforming the way we understand and treat cancers.