Susan G. Komen
Research Grants – Fiscal Year 2014

This research grant was approved by Komen's national board of directors for FY2014 Research Programs funding. This grant will be funded upon the execution of grant agreements between Komen and the grantee institutions.

Drivers and therapeutic targets in mucinous carcinomas of the breast

Investigator(s): Salvatore Piscuoglio, Ph.D.; Britta Weigelt, Ph.D. (Mentor)
Lead Organization: Memorial Sloan-Kettering Cancer Center
Grant Mechanism: PDF Basic and Translational **Grant ID:** PDF14298348

Public Abstract:
Breast cancer, the most common type of cancer in women in the US, is classified by pathologists into different types based on the size, form and shape of the cancers cells when assessed under the microscope. The common breast cancer type, the ductal type, accounts for ~75% of all breast cancers. Mucinous cancer is one of the 21 rare types of the disease and accounts for 2% of all breast cancers, meaning that approximately 4,600 women will be diagnosed with this disease in the USA in 2013. This tumor type is characterized by large amount of mucous, in which the tumor cells are floating. Mucinous breast cancers are usually hormone-sensitive, and whilst patients with this tumor type were long thought to have a more favorable prognosis than those with ductal types cancers, recent studies have suggested that the prognosis may in fact be worse when compared to patients with ductal type cancers of the same hormone receptor status. Despite the use of molecular technologies to understand the biology of breast cancers, rare types of the disease, such as mucinous cancers, have largely been neglected. The few analyses performed by our group and others, however, have provided evidence to suggest that mucinous tumors lack molecular alterations and gene mutations that are characteristic of hormone-sensitive ductal type cancers. Nevertheless, treatment decisions for patients of mucinous carcinomas are based on the same parameters used for patients with the common type of the disease. In this project, we will analyze a unique series of frozen mucinous tumors using cutting-edge sequencing technologies and state-of-the-art computer-based approaches to i) determine all gene alterations these tumors harbor, ii) to compare them with the gene aberrations found in the common types of breast cancer, and iii) to define those gene alterations that mucinous breast cancers are likely to depend upon for their malignant behavior. We will then use models of breast cancer in the laboratory to determine which of the gene alterations identified in mucinous cancers make the cells malignant or are required for breast cancer cells to survive. We will also investigate whether cancer cells with the genetic aberrations identified are sensitive to specific therapeutic agents both alone and in combination with hormone therapy. This project will provide a comprehensive characterization of the landscape of genetic aberrations of mucinous breast cancers, and may lead to the identification of novel treatment approaches tailored specifically to women with this rare breast cancer type. This knowledge will bring us a step closer to the realization of the potentials of precision medicine for mucinous breast cancer patients, and to a potential reduction in breast cancer morbidity and mortality.