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Quantitative immunofluoresence profiling of therapy-relevant protein biomarkers for stratification of breast cancer patients

Hallgeir Rui
Thomas Jefferson University, USA

Abstract

Breast cancer is a diverse group of malignancies with greatly different responsiveness to current therapeutic agents. A key goal of molecular characterization of breast cancer is to identify subtypes with increased likelihood of responding to existing or emerging drugs or their combinations. Extensive molecular subtyping of breast cancer has been achieved based on mRNA profiling of tumor extracts. Nonetheless, the value of mRNA analyses is diminished by 1) overall poor correlation between mRNA and protein levels, and 2) assay variability due to uncontrollable variation in mRNA contributed from inconsistent ratios of carcinoma cells, stromal fibroblasts, leukocytes and endothelial cells sampled in tumor extracts. We present our ongoing consortium efforts to map breast cancer subtypes at high resolution based on expression levels of druggable target proteins within carcinoma cells of a panel of 5,000 untreated primary breast cancer specimens using quantitative in situ immunofluorescence-based methods. Progress with analysis of prolactin-receptor-Jak-Stat pathway profiling will be highlighted using complementary quantitative immunofluorescence technologies. Utility of resulting protein-based breast cancer subclassification maps for rational recruitment of patients into biomarker-driven, adaptive clinical trials will be discussed.

Biography

Hallgeir Rui holds the position of Professor of Cancer Biology, Medical Oncology and Pathology at Thomas Jefferson University, Philadelphia, PA. He serves as the Scientific Director of the Jefferson Breast Care Center and is the Leader of Kimmel Cancer Center's Biology of Breast Cancer Program. Dr. Rui is also Director of the Pathology Translational Research core facility. Dr. Rui holds several patents including high-density tissue arraying technology. Dr. Rui is the PI of a $6.7 million Komen Promise Grant to classify malignant breast tumors based on expression of druggable target proteins for improved personalized cancer care.