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LincRNA Dependent Regulation in Breast Cancer Metastasis

Investigator(s): Grace Zheng, M.D., Ph.D.; Howard Chang, M.D., Ph.D. (Mentor)

Stanford University, CA

Awarded: $180,000.00

Grant Mechanism: Postdoctoral Fellowship

Public Abstract:

Most deaths from breast cancer are due to metastasis as aggressive cancer cells can survive in many different conditions. To better understand breast cancer metastasis, scientists have focused on studying the differences in cancerous and healthy cells at the level of proteins. However, only 2% of our genome codes for proteins. Recent research has shown that the rest of the genome, previously considered junk, has an important regulatory role in all aspects of cellular function, including cancer. One such gene is highly abundant in breast tumors, and its level is a significant predictor of subsequent metastasis. Here, we propose to understand the mechanistic role of this gene in directing breast cancer metastasis. Specifically, we will address two questions: 1) Which part of the gene is important in directing breast cancer metastasis? 2) How does this gene direct metastasis? Our study will provide the first mechanistic relationship between the “junk” part of the genome and breast cancer metastasis. This insight will be invaluable in generating new therapies for breast cancer, and will provide foundational concepts and technologies that are applicable to explore the roles of other “junk” part of the genome in breast cancer.