

Rare cancer stem cells (CSCs) are hypothesized to contribute to therapeutic resistance and metastases, resulting in recurrence and poor prognosis in breast cancer, a disease that is the 2nd leading cause of death in women. Despite their significance, CSCs are extremely difficult to investigate, because of their rarity. What studies there are have been show that CSCs are inextricably linked to the epithelial-mesenchymal transition (EMT) and the understudied mesenchymal-epithelial transition (MET), a spectrum of phenotypes that enable the survival of a subset of tumor cells as they confront obstacles in the metastatic cascade. CSCs, EMT, and MET cells all exist on a spectrum, with cells rarely at either end point of the spectrum.

The goal of our project is to use an innovative technology—high-throughput DNA-directed patterning—to present spatially and temporally solid-phase cues and cells known to be present in the breast tumor microenvironment (TME) in order to generate, with great control, rare and specific CSC and EMT/MET transitional phenotypes. Among the advantages of high-throughput DNA-directed patterning is that it allows for high-spatial precision, combinatorial patterning with a high number of replicates. We will use our patterning method study the overlap among these phenotypes as they respond, in real time, to analogous cues and TME cells (adipocytes, immune cells, cancer-associated fibroblasts, tumor-associated macrophages, vascular cells, etc.).