

Studies show that a dynamic relationship exists between the humoral immune response and breast cancer cells; however it is unclear whether B cells contribute by eliminating tumors or promoting their growth. B cells from different sources within the same body must be analyzed to resolve the question of where anti-tumor B cells reside. We have identified tumor derived antibody targets using the SEREX (serological analysis of recombinantly expressed cDNA libraries) method and developed phage displayed antibody libraries derived from various tissue sites within the same patient to determine the best source of tumor binding antibodies and to better characterize the oligoclonal humoral response to breast cancer antigens. This project can provide answers to the question of where anti-tumor B cells reside in patients. Specifically, it will determine which tissue source yields the best source of tumor binding immunoglobulin RNA by addressing the problem from three different approaches: the B cell target, the antibody binding to this target, and the genetic lineage of B cells in these locations.