

Research Topics – Goodison group

Breast tumor progression

NIH-funded program (\$1,200,000 – 5 years) to develop metastasis models and to use these models to identify genes which drive, or suppress metastatic sufficiency. Molecular techniques including subtractive immunization, representational difference analysis, proteomic and transcriptome gene expression profiling are being employed to identify genes/antigens that confer metastatic sufficiency upon human breast tumor cells. Specific genes that are functionally involved in metastasis and their role in molecular networks are being identified through genetic manipulation and in vitro and in vivo assays. Genes confirmed to influence metastatic efficiency will be used to develop marker sets for detection and/or therapeutic development.

Urologic cancer detection

Florida State funded program (\$500,000 - 3 years) to develop non-invasive, molecular assays for the early detection of bladder cancer. Gene expression microarrays are being used to profile exfoliated urothelia from patients of known disease status. Data will be used to identify biomarkers which may have utility on the development of urine tests. A previous NIH-funded program to profile prostate cancer is ongoing at the level of biomarker validation.

The Telomerase enzyme in tumor cell immortalization

We have published multiple articles on the utility of the enzyme telomerase as a biomarker for cancer. These have employed enzyme activity assays, qPCR analyses and most recently, antibody-mediated evaluations. We are also investigating the mechanisms by which telomerase ‘immortalizes’ cells, and how specific component isoforms function in telomere maintenance and cell cycle regulation.

Disease biomarkers

Several other biomarker studies are ongoing in collaboration with colleagues at the University of Florida. Potential biomarkers are being screened and evaluated in prostate and breast tissue specimens. Current studies include proteomic screening, CGH-array, pyrosequencing, statistical meta-analysis methodology, microarray applications.