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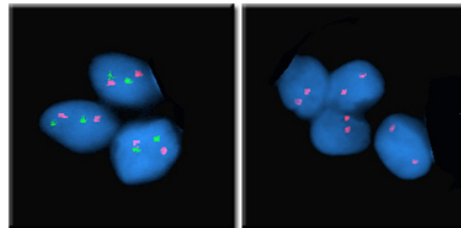
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For our studies of prostate cancer, we are looking at the role of genetic variation in prostate cancer risk. We are currently conducting a series of molecular epidemiological studies in an attempt to identify variants in prostate-related genes that increase an individual's risk for prostate cancer. In collaboration with Dr. Ian Thompson, we are studying three populations (Hispanic Caucasians, non-Hispanic Caucasians and African Americans) gathered from the San Antonio area. We have already identified variations in the several prostate-related genes that increase an individual's risk of prostate cancer. We are now expanding these studies to look for markers of prognosis. This research is funded by the National Cancer Institute. In collaboration with Dr. Donna Lehman, we are looking at the role of copy number variants in prostate cancer risk. The focus is primarily on the Hispanic Caucasian population from South Texas and is funded by the Department of Defense.

In our studies with Dr. Teresa Johnson-Pais, we are using array based comparative genomic hybridization (CGH) to identify regions of loss and gain in prostate cancer specimens. We are currently characterizing these regions for putative tumor suppressor genes and/or oncogenes. Once genes are identified from these regions of loss and gain, we use a cell biology approach to manipulate the expression of these genes in established cell lines.

Paraffin embedded prostate specimen hybridized with a bacterial artificial chromosome that appeared deleted by CGH. Normal adjacent prostate cancer cells are shown on the left while on the right is a tumor with a homozygous deletion of a region of chromosome 18.



Selected Publications:

Shook SJ, Beuten J, Torkko KC, Johnson-Pais TL, Troyer DA, Thompson IM, Leach RJ (2007) Association of RNASEL variants with prostate cancer risk in Hispanic Caucasians and African Americans. *Clin Cancer Res* 70:748-752.

Beuten J, Gelfond JAL, Franke J, Weldon KS, Crandall AC, Johnson-Pais TL, Thompson IM, Leach RJ (2009) Single and multigenic analysis of the association between variants in 12 steroid-hormones metabolism genes and risk of prostate cancer. *Cancer Epidemiol Biomarkers Pre* 18:1869-1980.