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Researchers identify 'regulatory' genetic sequences that may predict risk for prostate cancer

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Researchers at the Keck School of Medicine of the University of Southern California (USC) have identified a novel genetic mechanism that may govern an individual's risk of developing prostate cancer.

The findings, published today in the *Public Library of Science (PLoS) Genetics* journal, found mechanisms involved in cancer-associated sites in areas where no genes are present (gene 'deserts') at a chromosomal region called 8q24. The new findings show that some of these sites have embedded regulatory sequences that act as enhancers of gene expression, modulated by genetic variation, or single nucleotide polymorphisms (SNPs).

The two-year study, conducted by researchers from USC, Harvard University and the Weizmann Institute of Tel Aviv, Israel, found novel functions of SNPs in areas where no genes were present. They found how the SNPs are able to modulate genetic expression even while they were near no genes. SNPs denote a modest increase in risk for certain diseases; in this particular chromosomal area, the SNPs appear to be influencing gene expression for prostate (and other) cancer 'at a genetic distance'.

"The real contribution of this discovery is that we get a feel for a previously unappreciated mechanism that may be a predisposition to this disease," said Gerhard (Gerry) Coetzee, Ph.D., professor of urology and

preventive medicine at the Keck School of Medicine and principal investigator on the study. "We have unearthed a new way to understand the risk for prostate cancer."

The study was prompted by discrepancies in prostate cancer risk among ethnic groups. Currently, risk factors for prostate cancer are governed by age, and a disproportionate increased risk chiefly among African-American men, with Caucasian men following and Asian men last. This gene 'desert' featuring versions of particular SNPs are found more often in African-American men and may explain their increased risk for the disease.

More information: Li Jia, Gilad Landan, Mark Pomerantz, Rami Jaschek, Paula Herman, David Reich, Chunli Yan, Omar Khalid, Phil Kantoff, William Oh, J. Robert Manak, Benjamin P Berman, Brian E Henderson, Baruch Frenkel, Christopher A Haiman, Matthew Freedman, Amos Tanay, Gerhard A Coetzee Functional Enhancers at the Gene-Poor 8q24 Cancer-Linked Locus, PLoS Genetics 2009 14 Aug 2009.

Source: University of Southern California (news : web)