GENOMIC PROFILING OF PROSTATE CANCER

A new study published in *Cancer Cell* reports a comprehensive analysis of genomic alterations in human prostate cancer. In other cancers, genomic profiling has enabled implementation of molecular classification schemes and the identification of new drug targets. "Prostate cancer has lagged behind these other cancers because it is more challenging—with smaller tumors, and lots of normal stroma admixed with tumor tissue," observes Charles Sawyers, who worked on the paper. "We took this challenge on several years ago because there is a huge need for this kind of information in this disease."

The investigators used a range of genomic technologies to measure DNA copy number, messenger RNA and microRNA expression in 218 prostate cancer tumors, as well as mutation status in 157 genes of high interest. Computational biology techniques were then used to integrate the results among platforms, and identify common genomic alterations linked to clinical outcomes. The researchers' data are freely available at <http://cbio.mskcc.org/prostate-portal/>.

Sawyers identifies three main findings from the group's work. First, *NCOA2* (which encodes nuclear receptor cofactor 2, a known androgen receptor coactivator) is amplified or mutated in a subset of primary tumors. Second, the *TMPRSS2-ERG* gene fusion is associated with a novel prostate-specific deletion at chromosome 3p14, which is likely to contain an important tumor suppressor gene. Finally, global analysis showed alterations in DNA copy number to be linked with clinical outcome.

The investigators are now studying *NCOA2* and three candidate genes on 3p14. They are also aiming to validate the association between copy number and prognosis, with a view to developing a DNA test that can be run on a biopsy specimen. Such a test might offer robust risk stratification, similar to the current standards for other malignancies such as breast cancer.

Nick Groves-Kirkby

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RESEARCH HIGHLIGHTS