Profiling prostate cancer

June 24 2010

A large scale genetic analysis of multiple prostate cancer samples, published online by Cell Press on June 24th in the journal *Cancer Cell*, is providing exciting new insight into the disease and may lead to more effective treatment strategies. In addition, the freely available genetic and clinical outcome data obtained in the study represents a valuable public resource for the cancer research community.

Prostate cancer is clinically diverse with some patients developing fatal metastatic disease within a couple of years and others living for decades. This suggests that prostate tumors may have a substantial underlying genetic diversity. Although large-scale genomic characterization projects have provided helpful insight into the molecular classification of many other types of cancer, similar studies of prostate cancer have proven to be more of a challenge.

"Our current knowledge of prostate cancer genomes is largely based on small groups of patients," says senior study author, Dr. Charles Sawyers from Memorial Sloan-Kettering Cancer Center. "To obtain a more comprehensive picture of prostate cancer genomics, we adopted an integrated comprehensive approach to analyze 218 primary and metastatic prostate cancer as well as 12 cell lines."

Dr. Sawyers and colleagues found that an integrative analysis revealed a much higher frequency of alterations in the androgen receptor pathway than previously suspected, including amplification or mutation of the NCOA2 gene, an amplifier of androgen receptor output. Importantly, the pattern of DNA copy number alterations defined subsets of low- and

high-risk disease in primary samples, raising the possibility of a test that could predict who needs aggressive therapy versus watchful waiting.

"Taken together, our findings clarify the role of several known cancer pathways in prostate cancer, implicate several new ones, and provide a blueprint for clinical development of pathway inhibitors," says Dr. Sawyers.

All the data obtained in the study was made available through an easily accessible web-based application. "The high prevalence of prostate cancer, which is the most common malignancy in males, and the relative paucity of large comprehensive genomic datasets in the disease make this a unique public resource for the cancer research community," concludes Dr. Sawyers.

More information: Taylor et al.: “Integrative genomic profiling of human prostate cancer.” Publishing in Cancer Cell 18, 1, July 13, 2010. www.cancercell.org

Provided by Cell Press