MedicalXpress

Researchers make progress in genomic classification of bladder cancers

February 19 2016

The ability to map the human genome has transformed how scientists and researchers classify various cancers. In the past, cancer cells were examined through a microscope and their appearance, often enhanced with dyes or other agents, was used to categorize the type of cancer. Now, it is possible to extract the DNA or RNA from these cells and establish a classification according to the type and quantity of mutations, active and inactive genes, and other molecular characteristics. An article in the current issue of *Bladder Cancer* reports the results of a consensus meeting of experts in the field and describes the recent efforts to classify bladder cancers.

Investigators from seven centers of excellence from around the world met at the Spanish National Cancer Research Centre-CNIO (Madrid, Spain) in 2015. Each group, having proposed a genome-based molecular taxonomy of urothelial bladder cancer (UBC), recognized the value of an agreement that could then help facilitate progress in the field and stimulate collaboration.

Lead author of the consensus document Seth P. Lerner, MD, Editor-in-Chief of Bladder Cancer, and Professor of Urology, Scott Department of Urology, Baylor College of Medicine, Houston, explained, "The need to reach consensus about the UBC subtypes and how they can be best defined is important in at least two different areas: first, to achieve an improved understanding of the underlying biology; second, using this information to stratify patients with the aim of improving management, based either on differences in outcome or in response to therapy. The

latter aspect concerns both standard and novel, targeted therapies towards precision medicine."

Genomic sequencing of breast cancers in the early 2000s pioneered efforts to classify cancers by their genome. The Cancer Genome Atlas (TCGA) and the International Cancer Genome Consortium (ICGC) projects are now driving the classification to all tumor types. Because UBC has been a relative latecomer to these studies, many of the research groups felt the need to rationalize the methods and taxonomies being proposed so that the community could benefit at this early stage.

The document summarizes the status at TCGA, Lund University (Sweden), The University of North Carolina (USA), Baylor College of Medicine (USA), the MD Anderson Cancer Center (USA), the CIT Consortium (France), and Spanish National Cancer Research Centre-CNIO (Spain).

Although there are five separate classification methods being used worldwide, the consensus meeting determined that a subgroup of invasive bladder cancers can be identified according to four genes, two expressed positively (KRT5/6 and KRT14) and two suppressed (FOXA1 and GATA3). This group appears to be consistently associated with a poor prognosis. Francisco X. Real, MD, PhD, of the Spanish National Cancer Research Centre, recommended that "Future studies should refine this molecular definition, determine the optimal techniques that can be applied for tumor classification, as well as clinical-pathological and etiological associations."

The group also proposed naming conventions for some types of UBCs, as well as changes to other designations of specific tumor types that would make it easier for research groups to present their findings using a consistent nomenclature. Future meetings will be convened to update the consensus evidence and to develop strategies for future collaboration,

ultimately improving patient care and outcomes.

More information: Seth P. Lerner et al. Bladder Cancer Molecular Taxonomy: Summary from a Consensus Meeting, *Bladder Cancer* (2016). DOI: 10.3233/BLC-150037

Provided by IOS Press