Are We Ready to Use the Omics Strategies for Precision Medicine?

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It was nearing the end of summer on a rainy day when the editorial board members of the *International Neurourology Journal* (INJ) met and discussed publishing a special issue. We decided to introduce and summarize recent advances in multiomic approaches to better understand bladder diseases and beyond.

The recently implemented "Precision Medicine Initiative" has enabled great advances in personalized healthcare. In recent years, the explosive growth of individual whole genomes has led to a greater systematic understanding of the variety of important and essential factors in cellular mechanics, such as transcriptomes, proteomes, and metabolomes. With all of this information, what then is the promise of precision medicine? We have found that it will allow us to deepen our biological understanding of a patient's background and needs at the molecular level. This will allow us to tailor our care to provide more proactive, predictive, and precise treatments at a highly targeted level for individuals.

Qualified biomarkers revealed by multiomic approaches are part of a more concentrated effort to provide "personalized advice" with respect to monitoring the severity, progression, and prediction of therapies of diseases. As scientists and physicians, our long-term goals include determination of disease specific biomarkers for accurate diagnosis, continuing improvement of our understanding of the biological basis of disease, and identification of new strategies for patient care. The advanced approaches and expertise we have described here are meant to bring the new capabilities of precision medicine to a wider range of areas through cutting edge technology and novel strategies.

In this special issue, which is titled "Omic Approaches to Understand Bladder Diseases and Beyond," our goals are (1) to update our readers with the current progress of relevant cutting-edge technologies, and (2) to describe the scientific and clinical impacts resulting from these new discoveries.

Of the various proteomic-based technologies in biomedical research, mass spectrometry (MS)-based platforms are one of best for unbiased and targeted proteomic analyses. The first paper in this volume is a review titled "Urine Proteomics in the Era of Mass Spectrometry" by Dr. Ashely Beasley-Green [1] at the National Institute of Standards and Technology (Gaithersburg, MD, USA). It explains a number of advantageous features of MS-based technologies on individual biomarker identification along with their effectiveness when applied to renal disease diagnosis. Urine albumin is a major, biologically noninvasive component used in multiple renal disease measurement technologies. It is shown from this review that amazing results have been achieved in protein identification using multiplexed candidate reference measurement procedures that utilize mass spectrometry and multiple reaction monitoring. These tools permit qualitative assessment of biomarker candidates.

The second article [2] is an informative review by Dr. Sang Tae Park, who was a former trainee at Harvard Medical School and the current CEO and CSO of the Macrogen Clinical Laboratory, Macrogen Corporation (Rockville, MD, USA). It provides a general understanding of next-generation sequencing (NGS) such as the following questions: What types of NGS technologies and platforms are being used? How can NGS be applied in understanding human genetics and genomics? What we can expect in a new era of whole genome sequencing (WGS)?

NGS applications allow for epigenetic studies, whole genome methylation sequencing, and chromatin immunoprecipitation followed by sequencing. He explains these important issues point-by-point and discusses how these technologies can be applied to personalized precision medicine.

Dr. Gangning Liang, Professor of Research in the Department of Urology at the University of Southern California (Los Angeles, CA, USA), who has 20 years of hands-on experience in the field of epigenetics, then talks about his experience in characterizing the roles of DNA methyltransferases and microRNAs during tumorigenesis. His discussion delves into how we can develop novel methods of characterizing epigenetic changes and how to monitor these changes in patients. His article [3] includes detailed information on current research, ranging from somatic genetic aberrations to various epigenetic regulations such as DNA methylation, histone modifications, microRNA regulation, and nucleosome positioning. He also provides evidence suggesting genetic and epigenetic alterations as possible therapeutic targets.

We then switch gears a little bit to the specific diseases that our INJ audience is interested in learning about. The second section answers our questions as to how these cutting edge technologies can be applied to aspects of translation. We invited several more experts in benign urological diseases, such as interstitial cystitis and bladder pain syndrome (IC/BPS), lower urinary tract dysfunction (LUTD), prostate cancer, and gastric cancer.

Dr. Hann-Chorng Kuo et al. at the Buddhist Tzu Chi General Hospital and Tzu Chi University (Hualien, Taiwan) introduces the accumulated efforts to identify potential biomarkers targeting IC/BPS, which is an irritating bladder syndrome and is usually characterized by frequent nocturia as well as bladder pain in patients. He summarized the pathomechanisms of IC/BPS by mapping the heterogeneity of the disease and the concentrated efforts on the potential serum and urinary biomarkers of the disease [4].

Dr. Akihiro Kanematsu, a former trainee at Harvard Medical School/Boston Children's Hospital and a current Associate Professor and a pediatric urologist at Hyogo College of Medicine (Hyogo, Japan), provides a comprehensive review of translational research aimed at elucidating the pathophysiology of pediatric LUTD [5].

In "Racial Differences of Diagnosis and Treatment for Prostate Cancer," Dr. Jong Y. Park, an associate member at the Moffitt Cancer Institute (Tampa, FL, USA), discusses how new gen-

eration omic tools have been adapted for the field of molecular epidemiology. Prostate cancer is the second most common cancer in the U.S. Recent statistics from the American Cancer Society state that an estimated 26,120 deaths will occur in 2016 due to prostate cancer alone. Interestingly, the incident rates and mortality rates of different ethnic groups in the U.S. vary greatly. The causes of these disparities are numerous. In his review, Dr Jong Y. Park et al. compare inequalities at diagnosis and treatment while also considering the genetic susceptibility of different ethnic groups who are affected by prostate cancer. According to his study, there is a positive correlation between high socioeconomic status and survival rate in both African American and Caucasian groups; socioeconomically wealthier groups had more of a chance of detecting prostate cancer at an earlier age with a higher survival rate. In terms of therapy/treatment, it is important to note the relationship between the lower survival rate of African Americans and the fact that African Americans experience treatment delays and postoperative complications more often than Caucasians. The authors also suggest that we need to expand these variables, which affect the differences, in order to better understand the factors of these disparities [6].

It is widely accepted that early prostate cancer detection and treatment can result in a higher survival rate for a patient, but, occasionally might lead to overdiagnosis and overtreatment. The development of precision medicine is therefore a novel tool that enables us to lower the chances of false negatives and false positives while also improving therapies for diseases. A review titled "How Precisely Can Prostate Cancer Be Managed?" by Dr. Liyan Zhung et al. [7], at Lahey Hospital and Medical Center, Tufts University School of Medicine (Burlington, MA, USA) responds to the following questions: who will need a biopsy? a rebiopsy? who are candidates for active surveillance? and who needs adjuvant radiation or hormonal therapy after prostatectomy? In addition to answering these questions, the paper introduces a number of useful diagnostic tools based on genomic screening to give us a better understanding of current tools. It also helps us understand the precision medicine that has been applied to prostate cancer and other cancer treatments.

Dr. Samuel J. Klempner et al. at the Angeles Clinic and Research Institute, and Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center (Los Angeles, CA, USA) discuss the current research being developed on phosphatidylinositol-3-kinase (PI3K) pathway signaling in gastric cancer, the most common cancer among men in Korea [8].

This collection of 8 review articles in this special issue are all

tied together by one common and simple mission: to close our knowledge gap for better patient care. While this gap will not close overnight, it is time to think of basic science, molecular epidemiology, and clinical translation science as utilizing multiomic approaches as strong tools with a mission that can be combined to make greater advances in healthcare.

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