Report from the International Congress on Personalized Health Care (ICPHC)

From screening to therapies: the changing face of science and technology innovation

SCIENTIFIC BREAKTHROUGHS

Candan Hizel, PhD, HDR, Consultant-expert in Genomics for Health Biotechnology & Personalized Medicine

Following the success of the first edition in June 2016, the 2nd International Congress on Personalized Health Care (ICPHC) was held from September 23 to 26, 2018, in Montreal, Quebec (http://www.icphc.org/). Some 250 participants from different countries were updated on recent developments in genomic applications in personalized medicine. Marking the 15th anniversary of the completion of the Human Genome Project, ICPHC 2018 explored 4 major themes: a wide range of "-omics" disciplines, big data–artificial intelligence for "omics," current and future applications of personalized medicine, and public health genomics. Within each theme, high-profile plenary keynote speakers from leading academic and industrial centres presented their forward-looking vision on the implementation of personalized health care through "omics" technologies.

Scientific tracks covered cutting-edge research and innovation in genomics, healthcare technology R&D, and genomic education to reframe translation research from "genome-to-clinic" to "genome-to-society." Personalized medicine is expected to redefine healthcare management and is likely to have a positive impact on public health globally. However, the application and integration of such a medical approach into health systems also raises technological, financial, ethical and legal issues. These questions were explored during the meeting by bringing together researchers, academics, clinicians, ethicists and experts from different

fields to share ideas and pool resources with regard to the development of personalized health care.

The session entitled "From screening to therapies: changing face of science and technology" covered 4 important topics and highlighted the parade of scientific breakthroughs in genomics, informatics and high-throughput technologies that are accelerating the use of personalized medicine in many healthcare domains.

Clinical geneticist Tina Hambuch-Hawks from Invitae in the United States provided the keynote address in this session. She spoke on "Clinical genomics sequencing: a decade of testing, a lifelong relationship," tracing the evolution over the last 10 years of whole-genome sequencing (WGS) as a clinical genetic test for rare diseases, as well as more common, notably different types of cancer. She pointed to 4 particular challenges resulting from the rapid growth in the field: 1) disparities in methods and quality of approaches, 2) the ability to analyze, store and reanalyze large data sets while ensuring security and privacy, 3) keeping up with and accurately communicating our still-incomplete understanding of genomic variation, and 4) the ability of the medical community to integrate this information into practice.

Hambuch-Hawks underscored that with sharp decreases in cost over the past few years, WGS, a comprehensive method for analyzing the complete DNA sequence of an individual's genome, has become a realistic procedure for DNA-guided diagnostics in personalized medicine for cancer, providing fast and accurate detection of mutations. As one example, she pointed to clinically diagnosed BRCA1 and BRCA2 mutations in breast cancer that are identified by WGS. She further pointed out the important advantages of WGS, such as capturing both large and small variants, including single nucleotide polymorphisms (SNPs), insertions/deletions, and copy number variations (CNVs). Standardizing the integration of clinical data with WGS, and data interpretation, is now of critical importance, she stressed, to support personalized medicine.

In her talk entitled "Next-generation sequencing (NGS) and patient pathways: what is the impact on clinical decisions?" health economist Severine Coquerelle from France described multicentric use of NGS platforms in different hospitals in France and their use in adult patients treated for lung cancer, colorectal cancer and melanoma with germinal and somatic mutations. She sees an urgent need to standardize different NGS platforms in order to have positive global impact on healthcare and health economics.

She presented a multicentric observational study conducted in French hospitals working with these platforms that evaluated whether information on mutational profiles modified clinical practice and patient care. They looked at NGS analyses performed on 1213 adult patients in 117 centres between October 2013 and September 2016, treated for lung or colorectal cancer, or melanoma. Patient pathways and referrals were obtained from NGS prescription and interviews with biomolecular biologists and clinicians. While the panels used were relatively homogeneous, they found significant variability in clinical practices, raising questions about treatment equity. Practical difficulties emerged as biologic and clinical databases were not interoperable. Patient stratification, through the use of personalized medicine tools, is supposed to optimize patient care, reduce toxicities and increase the risk-benefit balance, as well as decreasing healthcare costs. This study shows there is much work to be done before these benefits appear.

Charles Dupras, a postdoctoral fellow at the Centre of Genomics and Policy at McGill University in Montreal, delivered a talk entitled "Epigenetics, ethics, law and society," which addressed the impact of epigenetics on society at multiple levels: medical, philosophical, judicial, political and commercial. He discussed the results of a comprehensive literature review of the ethical, legal and social implications of epigenetics, as observed by researchers in social sciences and humanities over the past decade, to provide a multidisciplinary portrait of an emerging field. Epigenetics has developed into an increasingly diversified field of scientific inquiry focused on the molecular mechanisms responsible for variations in gene expression. Researchers are interested in associations between toxic exposures and epigenetic modifications, the relation between certain epigenetic variants and specific diseases, and the possible inter-/transgenerational inheritance of acquired epigenetic traits. Dr. Dupras pointed out that epigenetics plays a crucial role in the interaction of nature vs nurture, the biologization of social factors, and has implications for preventive public health strategies such as cancer management, where epigenetic and chromatin aberrations play important roles in tumour potentiation, pre-conception planning, political theory, legal proceedings, stigmatization and discrimination.

Finally, Professor Yixue Li from the Shanghai Center for Bioinformation Technology in China provided a talk on precision medicine in hepatocellular carcinoma (HCC): from cell line to patients. Over the past few years, his team and collaborators have built the world's largest cell bank of liver cancer cell lines, the Liver Cancer Model Repository (LIMORE). Based on the LIMORE Cell Bank, they have screened out a number of potential disease biomarkers, which can be used for evaluation of the efficacy and prognosis of anti-liver cancer drugs. They have successfully used the LIMORE system to discover a disease biomarker that can be used as a companion to the diagnosis of sorafenib's prognosis and efficacy. Dr. Li highlighted HCC genetic heterogeneity among patients, caused by the accumulation of a series of driver gene mutations that confer on tumour cells a selective growth advantage. Since tumour heterogeneity may pose challenges for delivering precision medicine, he emphasized the importance of identifying driver mutations for more precise targeted therapy for HCC patients. Fifteen years after the Human Genome Project, Dr. Li considers we have entered a "postgenomic" era, which entails an important conceptual shift toward greater emphasis on the prediction and prevention of future health outcomes, such as susceptibility to cancer, and response to health interventions, using personal genomics information.