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Published in:
The FASEB Journal

Published: 01/07/2021

Document Version:
Final Published version, also known as Publisher's PDF, Publisher's Final version or Version of Record

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Publication record in CityU Scholars:
Go to record

Published version (DOI):
10.1096/fj.202100317

Publication details:
Chan, K. H. K., Hsu, Y-H., Yang, X., Goto, A., & Chen, B. H. (2021). The 2020 FASEB virtual Catalyst Conference on Integrative Approach for Complex Diseases Prevention and Management and Beyond, December 16, 2020. *The FASEB Journal*, *35*(7), [e21500]. https://doi.org/10.1096/fj.202100317

Received: 18 February 2021 | Accepted: 18 February 2021

DOI: 10.1096/fj.202100317

MEETING REPORT

THE FASEB JOURNAL

The 2020 FASEB virtual Catalyst Conference on Integrative Approach for Complex Diseases Prevention and Management and Beyond, December 16, 2020

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The first Federation of American Societies for Experimental Biology (FASEB) virtual Catalyst Conference (CC), Integrative Approach for Complex Diseases Prevention and Management and Beyond, was held on December 16, 2020. The conference focused on several disease-driven approaches, including multiomics and molecular and genetic epidemiology, which have been applied to dissect the pathophysiological and etiological mechanism of a wide range of health conditions from musculoskeletal diseases, cardiometabolic diseases, and cancers to aging. There were four invited presentations and two keynote speakers over about half a day.

This CC was organized based on the following rationale. Both hypothesis-driven and data-driven approaches that integrate the recent developments in biotechnology have been employed to scrutinize the etiologic and molecular mechanisms of many different complex diseases and to provide insights for diseases or mortality classification and stratification. These studies have shed light on the prevention and management of these diseases and beyond. This first conference among the virtual CC series aimed to present and discuss cutting-edge methodological examples in traditional epidemiology and molecular epidemiology, as well as genetic epidemiology, to a worldwide audience.

The first keynote address was by Dr. Yi-Hsiang (Sean) Hsu (Hebrew SeniorLife Institute for Aging Research, Harvard University and Broad Institute of the Massachusetts Institute of Technology, Boston, MA, USA), who illustrated several analytical pipelines to identify targets from genome-wide association studies in a systematical manner. The discussed approaches by Dr. Hsu can identify causal variants, upstream

Abbreviations: CC, Catalyst Conference; FASEB, Federation of American Societies for Experimental Biology.

regulators, target genes, affected tissues and cell types, gene functions, and disease mechanisms with clinical relevance and implication. One example is that machine learning can be implemented to produce gene regulatory circuits. Dr. Hsu indicated that molecular epidemiology and multiomics technology, such as three-dimensional views of the genome, can help dissect the enhancer–promoter interactions to understand more thoroughly about the development of different complex diseases, such as obesity and heart failure.

The second keynote speaker was Dr. Xia Yang (Department of Integrative Biology and Physiology, University of California, Los Angeles, CA, USA) who presented methodologies and applications of multitissue multiomics systems biology of complex diseases. Dr. Yang discussed how genetic and environmental risk factors interact to perturb gene networks, which, in turn, contribute to the development of a wide spectrum of complex diseases. Dr. Yang explained that gene network modelling involves multitissue multiomics integration and is a powerful approach to identify tissue- or cell-specific mechanisms. Several examples on multitissue multiomics studies were given to provide high resolution, systems level molecular, cell-cell, and tissue-tissue interaction maps to pinpoint key regulators. Dr. Yang also provided examples that systems biology approaches can guide the selection of novel therapeutic agents to normalize disease networks.

In the afternoon session, Dr. Atsushi Goto (Department of Health Data Science, Graduate School of Data Science, Yokohama City University, Yokohama, Japan) explained to the audience about how the Mendelian randomization approach can be used to investigate the causal relation between phenotypes such as diabetes and cancer, particularly in a population-based prospective study context. Dr. Goto laid out the analytical workflow for conducting a Mendelian randomization study, such as the model assumptions that should be taken into account. Dr. Goto also illustrated the Japan Public Health Center-based Prospective (JPHC) Study (n = 140 420 aged 40 to 69 years), which adopted a prospective cohort study design that followed participants from 1990 to 2019. The Mendelian randomization approach can improve the evidence for causal effect from observational studies.

Dr. Brian Chen (University of California, San Diego, CA, USA and FOXO Technologies, Minneapolis, MN, USA) discussed how epigenetics can be used to estimate biological aging, as demonstrated through research on epigenetic clocks. He illustrated the importance of data sources, data preparation, and how machine learning has played a key role in the development of epigenetic clocks. Dr. Chen indicated that we could understand better the contributors to aging, both on a molecular and clinical level, using the epigenetic clocks. He showed that epigenetic clocks get "reset" upon induced pluripotency, have been shown to exist in multiple species from mice to whales, change in response to certain interventions, and have been associated with mortality and many other age-related traits.

Results from the survey of this CC delivered a positive overall impression of the conference: 100% of attendees indicated that the quality of research presented was satisfactory; more than 75% of attendees indicated that the content presented is likely to influence their own research. Some attendees shared the opinion that the topic of this CC can be expanded by including the areas of COVID-19, oncology, neuroscience, immunology/autoimmunity, and infectious disease. Finally, approximately 90% of respondents indicated that they plan to attend this meeting again in the future, either virtually or in person.

ACKNOWLEDGMENTS

Special thanks to all the speakers, the FASEB team (Dr. Hannah V. Carey, Ms. Andrea Bauerfeind, Ms. Ying Zhu, and their team members), and to all attendees for their genuine support throughout the organization and duration of the CC. K.K.C. is supported by grants from City University of Hong Kong (Hong Kong SAR, China) New Research Initiatives/Infrastructure Support from Central (APRC) and Hong Kong Innovation and Technology Fund (ITF) (Hong Kong SAR, China). B.H.C. is an employee of FOXO Technologies, Inc. (Minneapolis, MN, USA).

CONFLICT OF INTEREST

The other authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

All authors provided critical perspectives and comments and contributed equally to the writing and editing of the manuscript.