Researcher From MD Anderson Leads Molecular Data Mission For Improved Cancer Prognosis

Posted by: Eduarda Abreu June 24, 2014

A new study led by Han Liang, Ph.D., assistant professor in Biomedics and Computational Biology at the **University of Texas MD Anderson Cancer Center**, hopes to answer the question of how a patient will fare with his or her cancer treatment program by examining not only molecular information, but also clinical variables, such as age and tumor stage, using data from The Cancer Genome Atlas (TCGA). In short, they aim at translating biological data into clinical use.

Supported by the National Cancer Institute and National Human Genome Research Institute within the National Institutes of Health, TCGA is a research program that looks at genomic changes in more than 20 different types of cancer.

Liang believes that in the future such comprehensive –molecular profiling" could help identify patients who may be resistant to certain therapies, or else guide doctors in adjusting treatment strategies to each patient s unique genetic makeup.

The overall goal, Liang explained, was to address how and to what extent TCGA molecular data could impact cancer treatment.

This multi-institutional study of TCGA data included 953 samples from four cancer types: lung, ovarian, brain and kidney. Findings of this study asserting that, while still in the early stages of its development, molecular profiling may hold promise for cancer patient prognosis, are detailed in the article –Assessing the Clinical Utility of Cancer Genomic and Proteomic Data Across Tumor Types," which was published in June on the Nature Biotechnology journal online.

–We hope that molecular profiling of tumors will one day advance the clinical management of cancer, but the benefits of integrating molecular and clinical data have not been studied in depth," said Liang. –The true value of our study is to serve as a starting point for building future prognostic and therapeutic strategies based on molecular profiling."

Focusing attention on the four mentioned cancers, researchers evaluated the potential for predicting patient survival by studying molecular data from multiple tumor incidences, both alone and in combination with clinical variables. He was then able to develop an open-access platform that allows researchers to build and evaluate cancer survival prediction models based on the data.

–By analyzing data from multiple cancer types, we were able to evaluate prognostic models and identify gene alterations that led to tumor formation," he explained. –This would have not been obtained by looking at tumor data from just one cancer type."

Combining molecular data and clinical variables helped the team observe an improved prediction of cancer prognosis in kidney, ovarian, and lung cancers three of the four studied cancers. Liang does state, however, that further studying needs to be done. Using large data sets to measure cancer survivability, which is very unpredictable, is in its very early stages. However, the researcher believes that this is a good start.

–In contrast to previous studies driven by a single cancer or data type, we could evaluate patient survival prediction from different molecular data and describe the potential prognostic and/or therapeutic relevance across multiple cancers. This raised several important issues related to the potential clinical use of such large-scale molecular data," Liang said.

Other MD Anderson researchers involved in this study include Gordon Mills, M.D., Ph.D., chair of Systems Biology; Lauren Byers, M.D., assistant professor in Thoracic Head & Neck Medical Oncology, and John Weinstein, M.D., Ph.D., chair of Bioinformatics and Computational Biology. Other institutions joined the

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study, including **Baylor College of Medicine**, Dana-Farber Cancer Institute in Boston, the University of California, Santa Cruz, Oregon Health & Science University in Portland, Massachusetts General Hospital in Boston, and The **University of Texas at Austin**.

The study was funded by grants from the National Institutes of Health (NIH), the National Cancer Institute-MD Anderson Cancer Center Uterine SPORE career development award, and from the Estate of George S. Hogan, and the Lorraine Dell Program in Bioinformatics for Personalization of Cancer Medicine funded by the Michael & Susan Dell Foundation.

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