Researchers use Web 2.0 apps to share vaccine study

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In a manuscript published today in *Immunity*, scientists at the Benaroya Research Institute at Virginia Mason (BRI) and the Baylor Institute for Immunology Research (BIIR) report the results of a comparative study of the molecular immune responses to influenza and pneumococcal vaccines. In addition, cutting-edge web technology was used to improve dissemination of data in order to accelerate the pace of scientific discovery.

The article features interactive figures (iFigures!; http://www.interactivefigures.com) that can be customized and allow for dynamic investigation of the primary data from a web portal that was developed as part of this study and could serve as a model for future scientific publishing and data sharing.

The study, which was led by Karolina Palucka, MD, PhD (BIIR), Damien Chaussabel, PhD (BRI) and Jacques Banchereau, PhD (BIIR), utilized a systems immunology approach and high-throughput profiling techniques to analyze the molecular and cellular responses following vaccination. They found that the influenza vaccine led to gene activity induced by interferon, while the pneumococcal vaccine led to an increase of myeloid- and inflammation-related gene activity, suggesting that the two vaccines elicit immune protection via distinct immune response pathways.

"This union of cutting-edge human immunology and state-of-the-art data mining capabilities really moves our research to the next level by

streamlining the discovery process and identifying novel approaches to combating diseases," noted Dr. Palucka. "By understanding the immune pathways by which these vaccines work, we can better guide the development of effective vaccines for other infectious diseases."

Systems biology approaches like the one presented in this publication generate enormous amounts of data with measurements of tens of thousands of parameters. Often, much of the data sees little investigation. In order to extend the value of data generated in this study, the authors developed web applications to allow exploration of the data by the broader scientific community. The article links directly to iFigures! in the web portal, which allows dynamic investigation of the presented figures and underlying data. Readers can interact with and customize the article's figures by adding variables or adjusting parameters. They are able to fine-tune their view of the data based on their own research interests and expertise and investigate additional hypotheses with the full dataset.

"Our goal was to make accessing these very complex datasets simple and enjoyable for investigators who have unique knowledge of immunology or medicine, but who may not have a lot of bioinformatics or statistics experience," explained Dr. Chaussabel. "They will be able to look up their favorite molecules and gain insights that only they, with their unique knowledge about these molecules, could obtain."

In addition, the system includes tools to enhance and encourage the sharing of new findings and insights. Novel analyses can be gathered, organized and shared through the web portal's email and social networking applications.

"The ease with which findings can be shared puts the enormous amount of data collected by these types of systems biology studies just a few clicks away from thousands of immunology experts," said Gerald

Nepom, MD, PhD, Director, BRI. "This publication and web portal liberate the data, which can be reanalyzed in new ways by scientists anywhere in the world to help accelerate discoveries."

Provided by Immune Tolerance Network