Brandon DeKosky, J Vaccines Vaccin 2017, 8:4 (Suppl)
DOI: 10.4172/2157-7560-C1-060

Comprehensive analyses of B cell receptor repertoires in response to vaccination and infection

Brandon DeKosky
The University of Kansas, USA

High-throughput immune repertoire sequencing has emerged as a critical step in the understanding of adaptive responses following infection, vaccination or in autoimmunity. However determination of native antibody variable heavy:light pairs (VH:VL) remains a major challenge and no technologies exist to adequately interrogate the $>10^6$ B cells in typical specimens. We developed a low-cost single-cell technology for sequencing complete antibody variable region repertoires from $>5x10^6$ B cells per experiment. Massive VH:VL repertoire analyses of human donors enabled rapid antibody discovery while also providing novel immunological insights regarding the immune response in healthy individuals. Most recently, we developed a facile technology for analysis of functional antibody binding. In this workflow, libraries of natively paired variable region heavy and light (VH:VL) amplicons are produced en masse and expressed in a yeast display platform optimized for human Fab surface expression. The yeast library is then functionally interrogated for binding to antigen probes using flow cytometry, leading to the efficient isolation of HIV-1 broadly neutralizing antibodies (bNAbs) from the B cell repertoire of an HIV-1 slow progressor and high-affinity neutralizing antibodies targeting Ebola virus (EBOV) glycoprotein from a vaccinated donor. Additional studies related to Zika virus and HIV vaccine responses will also be discussed. As DNA sequencing and technologies continue to progress, low-cost high-throughput single-cell antibody sequencing approaches will enable rapid antibody discovery and provide new insights into humoral immune responses associated with vaccine development, autoimmunity, and protection against infectious diseases.

Biography

Dr. Brandon DeKosky is an assistant professor of Chemical Engineering and Pharmaceutical Chemistry and affiliated with the Kansas Vaccine Institute at the University of Kansas, and his research emphasis is in high-throughput analyses of antibody immune responses. As a Ph.D. student at the University of Texas at Austin, Dr. DeKosky developed the very first technology for high-throughput sequencing complete antibody variable regions from single B cells, helping to resolve a major 20-year problem in immunology and biotechnology. As a postdoc at the U.S. National Institute of Allergy and Infectious Diseases, Dr. DeKosky applied high-throughput antibody sequencing and functional repertoire characterization to accelerate public health vaccine development. The DeKosky lab at KU now leverages high-throughput technologies to understand the critical features of adaptive immune protection and to develop novel strategies to combat human diseases.

dekosky@ku.edu

Notes: