1 Executive Summary

The 2010 Annual Meeting of the B Cell and T Cell Epitope Discovery Programs was held November 16 and 17 at the Bethesda Marriott in Bethesda, Maryland. The meeting provided an opportunity for the contractors of the Immune Epitope Database and Analysis Resource (IEDB) and the B Cell and T Cell Epitope Discovery programs to present their project status and plans and to discuss common interests.

The two-day meeting started with a presentation of the status of the IEDB. The IEDB team has focused on adding epitope data from literature and Epitope Discovery groups, increasing its user base and usability, enhancing the Analysis Resource, and improving data consistency and quality. The infectious disease, allergy, and autoimmune peptidic epitope references are now in maintenance mode, and non-peptidic references are being curated in collaboration with Chemical Entities of Biological Interest (ChEBI) database. The coverage of alleles for the MHC Class I and II epitope prediction tools has greatly expanded, and the accuracy of Class II predictions has significantly improved. The addition of a protein tree has facilitated searching for epitopes. Efforts are currently underway to simplify direct submission of data by developing a wizard interface in the Data Submission Tool.

The IEDB presentation was followed by eleven 60 minute presentations by the B Cell and T Cell Epitope Discovery contractor teams.

David Lewinsohn (Oregon health and Science University) first described their recent efforts in using Mycobacterium tuberculosis (Mtb)-specific T cells to define immunodominant CD8 antigens and epitopes from Mtb with three distinct and complementary approaches. William Kwok (Benaroya Research Institute at Virginia Mason) then presented their study to follow the dynamic and phenotypic changes of the CD4+ T cell mediated immune response in human subjects during the course of natural influenza infection or before and after vaccination. His group also used MHC class II tetramers to identify and characterize the Yellow Fever Virus (YFV)-specific CD4+ T cell responses of YFV vaccine recipients. The morning session concluded with Benjamin Doranz (Integral Molecular, Inc.) discussing their studies to generate high-resolution epitope maps for human antibodies against the immunodominant envelope proteins of Dengue, Hepatitis C, and Chikungunya Viruses.

After the lunch break, Bjoern Peters (La Jolla Institute for Allergy and Immunology) described progress to date of systematically mapping B cell epitopes in a set of 12 vaccinia virus antigens of specific immunological relevance using three complementary epitope mapping techniques (linear peptide mapping, X-ray crystallography, and viral mutagenesis). Jacqueline Sharon (Boston University) next reported on their work characterizing antibody epitopes of Francisella tularnensis, especially its LPS component. James Robinson (Tulane University) described his team's effort in identifying novel B cell epitopes on Lassa virus (LASV) proteins and elucidating mechanisms of antibody-mediated protection or pathogenesis in humans infected with LASV. The day finished with James Crowe (Vanderbilt University Medical Center) presented the progress his interdisciplinary team has made in indentifying antibody epitopes to vaccinia andH5 influenza viruses.

The second day started with a presentation by Alessandro Sette (La Jolla Institute for Allergy and Immunology) on their work to discover and validate cytotoxic and helper T cell epitopes presented by HLA class I and class II MHC molecules, respectively, that are derived from the four dengue virus (DENV) serotypes known to cause disease in humans. Daniel Altmann (Imperial College, London, UK) next spoke on Burkholderia pseudomallei (Bp), a Gram negative bacterium that causes melioidosis, and their work annotating and validating its T cell epitopes. Søren Buus (University of Copenhagen) discussed his team's work to identify T cell epitopes in Yellow Fever virus using an integrated approach involving cellular immunology, immunochemistry, and bioinformatics. The meeting concluded with Alessandro Sette presenting recent work on identifying HLA class II T cell epitopes of Mycobacterium tuberculosis.

The presentation title and presenters, in the order they presented, are listed below.

1.1 Presentation Titles

The Immune Epitope Database and Analysis Resource
AlessandroSette and Bjoern Peters
La Jolla Institute for Allergy and Immunology

Human classical and non-classical CD8 Mtb antigens and epitopes
David Lewinsohn
Oregon Health & Science University, Portland, OR

CD4+ T cell responses to 2009 H1N1 Influenza A virus and Yellow Fever Virus
William Kwok
Benaroya Research Institute at Virginia Mason

Mapping of the Antibody Epitopes and Functional Regions of Dengue, Hepatitis C, and Chikungunya Virus Envelope Proteins
Benjamin Doranz
Integral Molecular, Inc.

Discovering targets of antibody responses in vaccinia virus and their mechanism of protection
Bjoern Peters
La Jolla Institute for Allergy and Immunology

Protective and Pathogenic B-Cell Epitopes in Tularemia
Jacqueline Sharon
Boston University

Roles of protective or pathogenic B cell epitopes in human Lassa fever
James E. Robinson
Tulane University

Human antibodies to poxviruses and avian influenza virus

James E. Crowe, Jr.
Vanderbilt University Medical Center

The Identification of Class I and Class II T cell epitopes from Dengue virus
Alessandro Sette
La Jolla Institute for Allergy and Immunology

T cell epitopes from Burkholderia pseudomallei
Daniel Altmann
Imperial College, London, UK

Complete Analysis of T Cell Epitopes in Yellow Fever Virus
Søren Buus
University of Copenhagen

The Identification of HLA class II T cell epitopes from Mycobacterium Tuberculosis
Alessandro Sette
La Jolla Institute for Allergy and Immunology