

**La Jolla Institute for Allergy and Immunology Team Receives \$18 Million Consortium Grant**  
*Grant from National Institutes of Health for dengue and tuberculosis research*

LA JOLLA, CA (December X, 2015) – The La Jolla Institute for Allergy and Immunology (LJI) is pleased to announce that an international team led by LJI investigator Alessandro Sette, Ph.D., is one of four recipients of a Human Immune Profiling Consortium (HIPC) grant in 2015. With this prestigious grant, the LJI team will characterize the immune response to dengue virus (DENV) and *Mycobacterium tuberculosis* (TB), both of which represent major global health challenges.

“Advances in technology and data analysis have given us sophisticated tools to study the activity of the human immune system across diverse populations in unprecedented depth,” said Mitchell Kronenberg, Ph.D., President and Chief Scientific Officer. “The HIPC grant award is a testament to the caliber of our scientists and validates our sustained efforts to facilitate vaccine development. But most importantly, it provides us with the opportunity to unleash the full force of our collective scientific expertise and technological capabilities to trace what are the elements that make up an effective immune response.”

The HIPC award presented to LJI will support both research and the collection, shipping, and processing of thousands of samples from a network of clinical sites around the world (Sri Lanka, Nicaragua, Peru, and Sweden). Employing samples from such a geographically and ethnically diverse populations will ensure that conclusions drawn from this research are broadly applicable.

The consortium will apply unbiased methods to identify groups of genes expressed in T cells, and key white blood cell type, associated with protection from or susceptibility to the two diseases. These group of genes that determines function are sometimes referred to as gene signatures. This open-ended approach relies heavily on RNA sequencing, a cutting-edge technique to identify genes whose expression is enhanced or diminished by a particular condition. RNA sequencing studies will be overseen by Pandurangan Vijayanand, Ph.D., an expert in immunological genomics, and the vast amounts of data generated will be interpreted by a bioinformatics team led by Bjoern Peters, Ph.D. The research will also benefit from the expertise of lead scientists Daniela Weiskopf, Ph.D. and Cecilia Lindestam Arlehamn, Ph.D., who have each made several important contributions to the understanding of T cells in DENV and *M. tuberculosis* infection, respectively.

“By comparing and contrasting the gene expression signatures associated with disease and protection from disease, we will better understand what kind of immune responses vaccines should induce in order to be protective,” said Bjoern Peters, Ph.D., an associate professor in the Division of Vaccine Discovery, who is spearheading the tuberculosis project in addition to performing the bioinformatics analysis for both pathogens.

As T cells contribute to immunity and pathology in dengue and TB, this profiling effort is likely to identify new factors that affect the risk of developing severe disease from these pathogens, which could lead to

new indicators of effective vaccines. Development of vaccines for both diseases is urgent. Dengue prevalence is increasing as its mosquito vectors spread over greater areas and antibiotic-resistant TB strains are becoming more common. No vaccine against DENV has yet been approved, and the available TB vaccine provides only variable protection against pulmonary disease in adults.

In addition to direct implications for vaccine development, HIPC-supported research at LJI also addresses the fundamental question of whether infection with and vaccination against DENV or TB induce qualitative or quantitative changes in T cell populations. In other words, whether pathogen-specific T cells are an expanded population of previously existing cells, or if this expansion also involves a change that generates new T cell properties. The planned studies can help resolve this issue because of their scale and their use of whole-genome approaches, capturing all differences between healthy controls, previously infected, actively infected, and vaccinated populations. Further, comparing patterns across the two diseases will allow conclusions about T cell responses to viral pathogens in general, which would have fundamental impact on the understanding of human immunology.

The HIPC program was established by the National Institutes of Allergy and Infectious Disease to support the study of human immunology using modern analytic tools and computational methods. The overall goal is to provide a comprehensive understanding of the human immune system and its regulation, providing a foundation for the future study of immune-mediated diseases. Information gathered in the course of HIPC research is openly shared with the research community via the ImmPort database.

#### **ABOUT LA JOLLA INSTITUTE**

La Jolla Institute for Allergy and Immunology is dedicated to understanding the intricacies and power of the immune system so that we may apply that knowledge to promote human health and prevent a wide range of diseases. Since its founding in 1988 as an independent, nonprofit research organization, the Institute has made numerous advances leading towards its goal: life without disease®.

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