CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
R1120

Project Title:
Recruitment of First-Time, Tenure-Track Faculty Members

Award Mechanism:
Recruitment of First-Time, Tenure-Track Faculty Members

Principal Investigator:
Jiang, Ning

Entity:
The University of Texas at Austin

Lay Summary:

Dr. Ning Jiang received her Ph.D. degree from Georgia Institute of Technology before completing a postdoctoral training at Stanford University. Her research interests are focused on using a systems approach, combining high-throughput sequencing and microfluidics single cell analysis, to profile the T cell repertoire in tumor infiltrating lymphocytes.

As a graduate student under the supervision of Dr. Cheng Zhu at Georgia Institute of Technology, Dr. Jiang studied T cell antigen discrimination using a force-based adhesion assay with single molecule sensitivity. She found a signaling positive feedback loop involved in initial TCR and co-receptor binding to peptide-MHC. This co-receptor, CD8, has been known for its ability to modulate TCR binding to antigen. However, it was not clear how the low affinity MHC-CD8 interaction affects the TCR-peptide-MHC interaction that is of much higher affinity. This puzzle is explained by her finding that the TCR-pMHC interaction initiates a signaling cascade that activates CD8 to a higher binding state.

Having gained extensive experience in biophysics and T cell biology, Dr. Jiang developed a strong interest to apply systems biology approaches to immunity. Although detailed molecular mechanisms have been studied intensively in many areas of immunology, the immune repertoire – the makeup of hundreds of millions of B and T cells – had not yet been comprehensively characterized. With this question in mind, she joined Dr. Stephen Quake's lab in May 2007 to develop a high-throughput sequencing based method to profile the immune receptor repertoire supported by a postdoctoral fellowship from the Arthritis Foundation. She demonstrated the feasibility of using high-throughput sequencing to study the immune repertoire and provided evidence of convergent evolution in VDJ combinatorial usage as well as in specific sequences. Recently, she extended this study to investigate antibody repertoire ontogeny and discovered a stereotyped VDJ usage in adult B cell repertoire that was overlooked by many previous studies. At the same time, Dr. Jiang collaborated with Dr. Mark Davis at Stanford to examine gene expression profile of single sorted rare antigen specific human T cells by using the microfluidic chip based technology. This technology provides detailed analysis of activation status and functional capability of the immune repertoire with single cell resolution.

At the University of Texas at Austin, Dr. Jiang's lab will integrate high-throughput sequencing with single cell analysis to profile the tumor-infiltrating lymphocytes, to

establish a new set of "metrics" for cancer progression prediction and immune monitoring, and to provide new biomarkers for development of new therapies.