

Joseph Petrosino

Dr. Joseph Petrosino was hired as a tenure track faculty member at the Baylor College of Medicine (BCM) in 2006 with a National Institute of Allergies and Infectious Diseases-funded Career Development Award Project from the Western Regional Center of Excellence for Biodefense and Emerging Infectious Disease. As a result of his comparative genomics studies of *Francisella tularensis*, a pathogenic bacterium with the potential to pose a severe threat to public health and safety, the field has moved closer to the goal of creating new rationally-designed attenuated vaccines for this Category A select agent. In 2007, Dr. Petrosino and his colleagues procured funding from the NIH Common Fund Human Microbiome Project (HMP). As a large-scale sequencing center Principal Investigator for the HMP, Dr. Petrosino lead consortium efforts for standardized clinical sample preparation, sequencing, and analysis. This allowed microbial communities from diverse body sites and niches to be compared with minimal technical bias. As a result of the success of his efforts and to extend the efforts of the HMP, BCM announced the opening of the Alkek Center for Metagenomics and Microbiome Research (CMMR) in January 2011, with Dr. Petrosino serving as the Director for the Center. Currently, the CMMR is pursuing over 50 metagenomics projects in humans and model systems that target the improvement of human health through detection and modulation of the microbes that reside on and in us.

Current Positions:

Assistant Professor – Baylor College of Medicine, Department of Molecular Virology and Microbiology, Human Genome Sequencing Center, Department of Ophthalmology

Member – Cell and Molecular Biology, Translational Biology and Molecular Medicine programs, Baylor College of Medicine Diabetes and Endocrinology Research Center, and the Texas Medical Center Digestive Diseases Center.

Lecture topic

The Human Microbiome: An Underappreciated Organ Important for Human Health

The microbes that colonize the human body (the microbiome) outnumber human cells by 10:1. The genes encoded by these bacteria outnumber the genes in the human genome by 100:1. We in the Alkek Center for Metagenomics and Microbiome Research (CMMR) are using metagenomic and systems biology approaches to better understand how the human microbiome contributes to our daily health. Among the questions being addressed are: is there a “core” set of organisms or genes that characterize the organisms that colonize everyone? How unique are the collections of organisms in each individual? How does our microbiome change over the course of our lives? How do diet, race, and gender impact the microbiome? How do human genetics shape the microbiome? And, conversely, how does the microbiome impact our daily health? Further, we are not limiting these studies to bacterial communities, but to viruses and microbial eukaryotes as well.