UCLA Mattel Children's Hospital
Children's Discovery & Innovation Institute

UCLA Department of Pediatrics

2018-2019 William F. Friedman Endowed Fellow

Sean Fitzwater, M.D., M.H.S.
Pediatric Fellow
Pediatric Infectious Disease

Project Title: Whole genome sequencing of Staphylococcus aureus isolates to describe transmission in the NICU and determine genetic factors associated with transmission and invasion

Sean Fitzwater is a second year fellow in the division of Pediatric Gastroenterology. He served as an epidemiologist at Johns Hopkins for the International Vaccine Access Center, where he worked as a scientific advisor for a media group which worked to advocate vaccine introduction to low income countries, acted as a coordinator for a multi-site bacterial meningitis surveillance program in India, and provided analytical expertise to groups performing research early childhood illness in India. Their work catalyzed the introduction of the *Haemophilus influenzae* B conjugate vaccine into the Indian national immunization program. As a master's student, he assisted with developing laboratory capacity in Lima, Peru, and performed epidemiological work studying tuberculosis and novel diagnosis techniques. His work helped developed rapid culture-based resistance methods that are currently in use in Peru. As a new graduate from university, he managed the research laboratory of Dr. Eva Harries at UC Berkeley, which has provided him with intimate knowledge of the organization, financing, and coordination needed to run projects and a laboratory. His experience managing research labs, performing laboratory and epidemiological research and working in diverse settings demonstrates his commitment and qualification to a career in research.

Staphylococcus aureus (Staph) is a bacterium that causes serious infections. The Staph lives on the skin and in the nose of many people and can be easily spread to premature babies. Newborn and premature can easily get Staph into their bodies become sick. Outbreaks in intensive care units are common. This study's will better understand how the bacteria spread in the hospital, and what genetic changes help the bacteria spread and cause illness. This will be done by reading the genome from the Staph that has been grown from babies at UCLA. We will see look for closely related bacteria in different babies to find when outbreaks happen and see whether the Staph came from inside or outside the hospital. We will to see what genetic changes make the Staph more likely to make babies sick and what changes help it spread between babies. We will used this to help control Staph spread between babies and better understand how Staph infections work.