CAMILLE M. MOORE, PH.D. NATIONAL JEWISH HEALTH

INVESTIGATOR BIOGRAPHY

Dr. Moore is an assistant professor in the Division of Biostatistics and Bioinformatics at National Jewish Health. Dr. Moore earned her Ph.D. in Biostatistics at the University of Colorado Denver.

SELECT HONORS

Dr. Moore has been the recipient of the Strother Walker Award for Outstanding PhD Biostatistics Student from the University of Colorado Denver, the Marvin Porter Award for Outstanding MS Biostatistics Student from the University of Colorado Denver, and several travel grants from the Colorado School of Public Health, Department of Biostatistics.

MEDICAL FOCUS

Poor asthma control is associated with increased morbidity, mortality and healthcare utilization. However, patients with refractory asthma exhibit significant clinical and inflammatory variability, making treatment decisions difficult. The development and progression of refractory asthma is incompletely understood but involves a complex interplay of genetic and environmental factors and a variety of pathogenic mechanisms. These factors may change over the disease course. The advent of advanced, high-throughput “next-generation” RNA sequencing (RNA-Seq), has the potential to aid in the diagnosis, prognosis, and treatment of refractory asthma and other complex diseases. While several studies have identified subtypes of severe/refractory asthma, a major problem is that most analyses have been confined to cross-sectional data, which measure asthma-related factors at a single time point and assumes these factors remain stable over time. This is a significant limitation given that asthma, by definition, is a variable disease with potential fluctuations in symptoms and treatment response over time and with the seasons. It is essential that future research integrate molecular-based longitudinal studies to fully understand the pathogenesis of refractory asthma and the stability of biomarkers over time.

RESEARCH PROPOSAL

Dr. Moore’s goal is to understand the underlying mechanisms of refractory asthma and how gene expression changes within subjects over the disease course. Her group is now in the early phases of conducting a longitudinal cohort study of refractory asthma, which will include RNA sequencing of bronchial and nasal brushings at several time points. However, no well-developed statistical methods currently exist for appropriately analyzing data from correlated RNA-Seq studies. To address this barrier, Dr. Moore is developing specialized statistical methods for the analysis of longitudinal RNA-Seq data, in order to increase the ability to detect important changes in gene expression over time and under different treatment and environmental conditions. These analyses will deepen our understanding of how chronic diseases evolve in subjects over time, will help identify biomarkers associated with refractory asthma phenotypes, disease progression and treatment response, and can yield important diagnostic information to guide treatment of refractory asthma with targeted therapies.