CHINESE-AMERICAN LUNG ASSOCIATION

2020 CALA Happy Friday Seminar

July 31st , 2020

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Time: EST 10:30 am; PST: 7:30 am; Beijing time: 10:30 pm

Supraglottic Lung Microbiome Taxa and Pulmonary Abnormalities in an HIV Longitudinal Cohort

Jin Zhou PhD
Associate Professor
Epidemiology & Biostatistics Department
University of Arizona

Human immunodeficiency virus-1 infection (HIV) increases risk of non-infectious pulmonary complications. We hypothesize that an altered lung microbiome is associated with lung inflammation and evidence of lung disease. We examined the association between lung microbiome, lung function and pulmonary inflammation longitudinally in an HIV infected population before and after antiretroviral treatment (ART). We further characterized the dynamics of two distinct lung microbiome pneumotypes over time after starting ART. Thirty patients with a diagnosis of HIV and relatively advanced disease were followed in up to three visits for a maximum of three years after starting ART. At each visit, we performed pulmonary function test (PFT) and bronchoscopy with bronchoalveolar lavage (BAL) collection. The genus-level taxa were divided into two pneumotypes: supraglottic predominant (pneumotypeSPT) or background predominant (pneumotypeBPT) taxa. Weighted Spearman was used to identify genus-level taxa significantly correlated with lung function and inflammatory markers. Among eight genera that had significant positive correlations with inflammatory chemokine/cytokine levels in BAL (i.e., interleukin-8, inducible protein-10, monokine induced by IFN-γ, and interleukin-6), five were pneumotypeSPT. Subjects with higher SPT/BPT ratios had higher levels of inflammation. The presence of SPT taxa was associated with worse pulmonary function. Previously defined BPT and SPT microbial taxa had different effect on inflammation markers and lung function in an HIV positive population. The complex lung function-microbiome-inflammatory network suggests that lung microbiome may play a critical role in modulating lung function of HIV infected individuals.