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Research Title:

Itaconate-dependent genomic and metabolomic signatures within the lung during Klebsiella pneumoniae infection

Gram negative bacteria are the most common pathogens that cause nosocomial pneumonia in critically ill patients. Klebsiella pneumoniae (KP) in particular has grown in prominence worldwide with increasing prevalence of antibiotic resistance, hypervirulent strains, and invasive clinical syndromes. Immune mechanisms of host defense responsible for clearance of KP infection from the lung are largely unknown. We are interested in understanding the role of an anti-inflammatory metabolite, itaconate, in host defense within the lung during Klebsiella pneumoniae infection. All computational data has been collected across time points and tissues in our infection model but needs to be extracted and analyzed. The candidate will be expected to perform analyses using Gene Set Enrichment Analysis (GSEA), CLC Genomics, and R packages for analysis of data sets. These analyses will be included within a manuscript for publication.