**Metatransciptomic multivariate analysis of bronchoalveolar lavage fluid amongst patients with COVID-19**.

**Abstract:**

In order to better understand how COVID-19 impacts the microbial community dynamics / functional profile from a hologenome standpoint, we conducted a multivariate comparison of publicly available human bronchoalveolar lavage fluid (BALF) metatranscriptomes samples amongst COVID-19 (*n*=48), community acquired pneumonia(*n*=25), and uninfected patients(*n*=32), hypothesizing that the COVID-19 cohort would contain unique information from which it could be possible to evaluate the impact of the human microbiome in COVID-19 disease onset and progression. After read filtering and batch effect sample removal, the remaining SARS-CoV-2 viral and microbial reads taxonomically classified (Kraken2), functionally characterized (SeqScreen), and analyzed for multivariable associations with linear models (MaAsLin2) associated with disease case and outcome (deceased *n*=20, survived *n*=19), while controlling for differences in publication and study design. Results demonstrated unique taxonomic and functional changes to the hologenome associated with COVID19 disease and outcome associated the COVID-19 cohort, with notable functional profiles within microbial communities through which analysis of predicted proteins and gene ontology terms could be used to predict disease and outcome severity amongst COVID-19 profiles, therein contributing knowledge about how the relationship between the human microbiome and the host susceptibility to and severity of COVID-19, and helped to generate important hypotheses that warrant further investigation.