

GUT MICROBIOME FEATURES IN COVID-19: ANALYSIS OF A COHORT OF HOSPITALIZED PATIENTS

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Objectives: This study investigates whether the SARS-CoV-2 infection can be associated with alterations in the gut microbiome composition and if such variations could correlate with the severity of symptoms and disease outcomes.

Methods: We performed shotgun metagenomic sequencing of stool samples of 45 patients, aged between 30 and 95 years, hospitalized with COVID-19. Patients were grouped by clinical severity (i.e., non-critical or critical), type of hospitalization (non-intensive care or intensive therapy unit) and outcome (survival or deceased) to explore the impact of the gut microbiome changes on patients' health.

Results: COVID-19 severity is associated with alterations in the intestinal microbiome, reduced microbial biodiversity and increased *Escherichia* and *Bacteroides* genera. No statistical significance was found between the extent of dysbiosis and clinical severity. We found an enrichment of micro-eukaryotic species e.g. *Candida albicans*, *Candida tropicalis*, *Saccharomyces cerevisiae* and bacterial species previously associated with diseases as well as unhealthy cardiometabolic markers e.g. *Escherichia coli*, *Bacteroides fragilis*, *Clostridium bolteae*, *Clostridium innocuum*, *Clostridium symbiosum*, *Eggerthella lenta*, *Enterococcus faecium*, and *Flavonifractor plautii*.

Conclusion: Our findings suggest a trend of correlation between the degree of intestinal dysbiosis and the severity of the disease, likely depending on the depletion of some microorganisms with immunomodulatory effect. Furthermore, gut dysbiosis could explain the inflammatory outcome, which persists after viral negativization and might justify possible future complications.