

3.16 Obstructive Sleep Apnea Post-COVID-19, The Role of the Upper Airway Microbiome

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Background: Post-COVID fatigue has become a recognised and common phenomenon. Acute SARS-CoV-2 infection causes dysbiosis to the respiratory microbiome. Obstructive Sleep Apnea (OSA) shares many risk factors for severe COVID-19 and may account for symptoms of Post-COVID fatigue. Disruption of the upper airway microbiome following SARS-CoV-2 infection may contribute to the development of OSA Post-COVID-19.

Methods: Patients with Post-COVID fatigue were recruited from the Post-COVID clinic, and controls from the Sleep Clinic. All patients had a WatchPAT sleep study and nasal lavage. 16s rRNA gene sequencing was performed on nasal lavage samples. **Results:** Individuals with Post-COVID fatigue had significantly altered upper airway microbiome, with reduced diversity and altered bacterial composition compared to those who had never had COVID. Patients with Post-COVID fatigue were enriched with *Anaerococcus*, *Moraxella*, *Streptococcus*, and *Staphylococcus*. Furthermore, those with Post-COVID fatigue and evidence of OSA were also enriched with *Anaerococcus*, *Streptococcus*, *Staphylococcus* and additionally *Veillonella*.

Conclusion: SARS-CoV-2 infection causes persistent dysbiosis of the upper airway microbiome. Those with Post-COVID fatigue and Post-COVID OSA have a distinct microbial signature in their upper airways.

Conflict of Interest: The authors declare that they have no conflict of interest.