Associations between SARS-CoV-2 and bacteria in the hospital environment

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Video Byte

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Abstract

SARS-CoV-2 is the notorious virus responsible for the COVID-19 pandemic. Like other viruses, it coexists with a multitude of other microorganisms that could influence our susceptibility to infection. Thus, identifying associations between bacteria and SARS-CoV-2 could lend critical insight for the development of strategies for COVID-19 prevention and treatment. To meet this need, researchers recently characterized the microbial communities associated with COVID-19 patients, health care providers, and indoor surfaces in the hospital environment using 16S rRNA sequencing. They found SARS-CoV-2 RNA on 16% of the surfaces in COVID-19 patient rooms, with the highest prevalence in floor samples and lower prevalence on bed rails. SARS-CoV-2-positive samples had higher bacterial diversity than SARS-CoV-2-negative samples. Interestingly, bacteria in the genus *Rothia* were commonly found in the samples containing SARS-CoV-2, suggesting the existence of an association between these microorganisms. *Rothia* species are common members of the human oral microbiome but can also invade the gastrointestinal tract and are associated with cardiovascular disease. These findings suggest that *Rothia* could be used as an indicator of individuals with increased risk of COVID-19 complications and may facilitate the development of effective methods to reduce SARS-CoV-2 virulence.