



Letter to the Editor

Non culturable bacteria associated with COVID-19: More details are demanded

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Coronavirus disease 2019 (COVID-19) is a zoonotic infection caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with the extreme acute respiratory syndrome. Coronavirus is a zoonotic infection with a positive polarity RNA envelope that belongs to the Coronaviridae family. There are four recognized genera of coronavirus, however on January 10, 2020, a new coronavirus arose in Wuhan, China, causing a serious pulmonary outbreak. Severe acute respiratory syndrome coronavirus 2 appears to be the third highly deadly human coronavirus to develop in the recent two decades, following SARS coronavirus and Middle East respiratory syndrome (MERS) coronavirus [1].

Severe acute respiratory syndrome coronavirus 2 infection associated with a bacterial pathogen (combined viral and bacterial pneumonia) was described in COVID-19. Secondary bacterial pneumonia can develop after a viral respiratory illness has cleared up or during the healing period [2].

In fatal instances, bacterial infections are more prevalent than in recovered patients. If bacterial infections are the cause of death in COVID-19, this has significant implications for patient treatment [3].

The death rate for patients who acquired secondary infections was 56.7 %, compared to 10.6 % for all COVID-19 patients hospitalized. In 78 % of the cases, Gram-negative bacteria were found. The most common pathogen was *Klebsiella pneumoniae* (29 %), followed by *Acinetobacter baumannii* (21%). *Pseudomonas aeruginosa* (9.6%) and *Escherichia coli* (8.2%). methicillin-resistant *Staphylococcus aureus* was isolated only in 1.29%. High levels of carbapenem resistance were seen in *Acinetobacter baumannii* (92.6%) followed by *Klebsiella pneumoniae* (72.8%) [4].

According to recent research, bacterial coinfection occurred in 3.1–3.5% of COVID-19 patients at admission, with subsequent bacterial infections occurring in up to 15% of patients following hospitalization [5].

Atypical organisms linked to COVID-19 are organisms that are difficult to grow and do not show up on a gram stain. Because antibiotics must be able to enter intracellularly to reach their intended target, they are difficult to separate and treat due to their intracellular nature. Because atypical organisms lack cell walls, such as *Mycoplasma pneumoniae*, the most prevalent, beta-lactam antibiotics are not indicated. Antibiotic resistance, poor compliance, and an inability to take oral medicines are all factors that contribute to

treatment failure. Furthermore, some individuals may have obstructive lung lesions or a misdiagnosis.

Atypical pneumonia can be contracted from a variety of causes. *Mycoplasma pneumoniae*, which is associated with close living conditions such as at school and military barracks, legionella from stagnant water sources, *Chlamydophila pneumoniae*, *Coxiella burnetii*, and *Francisella tularensis* from various mammalian sources are among the most commonly identified atypical pathogens [6].

In conclusion: Secondary infections in COVID-19 patients have been linked to poor health outcomes. Non-culturable bacteria have been associated with death in COVID-19 patients, and they may require a specific antibiotic to preserve the patient's life. More research is needed to validate this issue, as there is currently little evidence available.

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