Co-infections in patients with COVID: A case series

Dear Editor,

Respiratory viruses may be associated with varying rates of microbial co-infections. There is previous evidence to show lack of bacterial co-infections following Middle East respiratory syndrome and only a small incidence with the severe acute respiratory syndrome-associated coronavirus-1.[1] We are reporting three patients of severe acute respiratory illness (fever and bilateral pneumonitis) with laboratory-confirmed (RT-PCR) COVID, who developed microbial co-infections. All had received protocolized pharmacological therapy including

remdesivir/oral hydroxychloroquine, subcutaneous low molecular weight heparin, intravenous dexamethasone, prophylactic antibiotics as well as vitamin C and oral zinc supplementation in the ICU. All three patients had presented with raised total leucocytic count (TLC: 19,600; 23,600; and 23,400/mm^3, respectively) in contrast to the expected immunosuppression and decreased TLC associated with COVID. The microbial organisms detected in the patients upon blood culture included *Enterococcus faecium* (sensitive to vancomycin, teicoplanin, and linezolid); *Staphylococcus xylosus* (resistant to erythromycin, ceftriaxone, ciprofloxacin, and tetracycline; sensitive to teicoplanin, vancomycin, linezolid, and cotrimoxazole) and non-albicans candida without any bacterial growth, respectively. An adequate response was seen with vancomycin in a patient with *E. faecium*, and with teicoplanin to S. *xylosus* as evidenced by an improvement in clinical condition, fall in TLC, and negative repeat blood cultures. The patient with candidemia, however, succumbed to COVID-induced acute respiratory distress syndrome within next couple of days.

A systematic review showed a 14% incidence of laboratory-confirmed bacterial co-infection among the patients with COVID admitted to ICU.[1] Thus, our findings help to emphasize that co-infections in patients with COVID are a clinical problem. The bacterial organisms detected by us are not commonly encountered otherwise. *E. faecium* was reported as the least common of co-infections in COVID with an incidence of 1/3834 patients.[1] Within the *Enterococcus* species, only 10% of infections are constituted by *E. faecium*.[2] It is more likely to be seen in immunosuppressed, elderly, critically ill, those on mechanical ventilation or long-term antibiotic therapy, for causing infections and multi-systemic manifestations.[2,3] S. *xylosus*-induced sepsis also presents an uncommon occurrence. The organism is usually incriminated in infections among animals, with very few case reports amongst humans. It is a normal commensal on the skin and mucosa and becomes a cause of infections either as part of nosocomial pathology or in immunosuppressed individuals.[4] Lastly, invasive candidemia reported in the third case by us is also known to have a predisposition for immunosuppressed patients. Thus, it is possible that the microbial co-infections in COVID are preferential of flora that thrives in immunocompromised patients. It is interesting to note that all of these patients with co-infections during COVID illness presented with raised TLC, even though the neutrophil–lymphocyte ratio was high and suggestive of COVID. There are previous data to show that raised TLC in COVID is associated with a poor prognosis.[5]

Thus, surveillance for microbial co-infections, even uncommon ones, is required in patients with COVID and the role of raised TLC remains pertinent for the same.

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Conflicts of interest
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