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Molecular and biochemical detection of bacterial community with COVID-19 patients

A thesis

submitted to the College of Science, University of Diyala in
partial fulfillment of the requirements for the Master Degree in
Biology
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2022 A.C

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Chapter one

Introduction

Coronavirus disease 2019 also known as COVID-19, is a new public health emergency that poses a threat to humanity. Despite the fact that it began in China's Hubei province in late 2019, it has been spread to many countries in the world (Wang *et al.*, 2020a). This pandemic disease is caused by the novel coronavirus SARS-Cov-2 (Lake, 2020). Strong immune response during viral infections, as well as a SARS-CoV-2, may be required for COVID-19 to be resolved. In severe individuals, however, chronic immune activation can develop to a hemophagocytosis-like condition, with uncontrollable cytokine production, (Wan *et al.* ,2020). IL-18 is produced by macrophages in the early stages of viral infections, and it stimulates the production of IL-6 and IFN, both of which are important for viral host defense (Lagunas and Chávez ,2020).

Human microbiotas are communities of microorganisms living in symbiosis with humans (Yamamoto *et al.*, 2021). They play an important role in the host immune response to respiratory viral infections. Microbiota regulating the immune system and their metabolites affect human physiological health and diseases by participating in host digestion and nutrition, promoting metabolic function. Intestinal microecological disorders in individuals may be involved in the occurrence and development of COVID-19 in the host through interaction with ACE2 (Wang *et al.*, 2021).

The opportunistic pathogens in COVID-19 patients; e.g. human feces and respiratory tract microbiome could be changed significantly (Yamamoto *et al.* ,2021). Bacterial coinfection is a worrying problem as it complicates treatment in COVID-19 patients and may worsen the prognosis and increase the likelihood of fatality (Chen *et al.*, 2020). Antibiotics are required in the majority of severe COVID-19 patients (Martinez *et al.*, 2021). The World

Health Organization (WHO) proclaimed the global problem of antibiotic resistance, a worldwide hazard to public health , implying that this vital defense was decreasing. The ability of an organism to infect a host and produce disease is referred to as virulence. The virulence factors are molecules that help the bacterium invade the host at the cellular level (Sharma *et al.*, 2017).

Aim of study

This study aims to evaluate the correlation between viral infection and the diversity of bacterial community including immunological response measurement ,the steps of this study were:

- 1-Explore the association between the infection of COVID-19 with age and gender.
- 2-Assessment the concentration of interleukin-18 in COVID-19 patients.
- 3-Identify the microbial diversity from different sources (urine, stool, and sputum) samples who COVID-19 patients suspected of bacterial co /superinfection .
- 4-Investigate the antibiotic susceptibility profile and virulence factors that correlate with the most diverse clinical bacterial isolates that obtained from one of the three samples sources of COVID-19 patients .
- 5- genetic study the more opportunistic bacteria isolated from COVID – 19 patients .

Summary

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The severe acute respiratory syndrome coronavirus 2 (SARS-CoV2), which causes coronavirus disease 2019 (COVID-19) was first identified in December 2019 in Wuhan, China and is currently circulating worldwide. Current study was performed from October - 2021 to January -2022, included 310 specimens COVID -19 patients that hospitalized at Baqubah teaching hospital with control groups .

Both gender and age were considered, the samples included (25 urine, 25 stool, 100 blood, and 20 control for each, and 100 sputum). The correlation between age, gender, and IL-18 was estimated. The statistical analyses showed the patient's age was ranged from 15 to 25 years had a lower incidence COVID-19 ($P < 0.05$). While women were more likely to be infected by COVID-19 ($P < 0.05$). IL-18 levels were studied to evaluate the differences between the patients and control groups . For the quantitative determination of human interleukin 18 (IL-18), ELISA assay was used. In general, the concentration of IL-18 was significantly ($P \leq 0.001$) higher in all selected patients' sera compared to the control. However, the highest concentration of IL-18 levels was measured in the serum of elderly patients (70 - >80 years old) with 447 ± 191.1 (pg/ml) . Urine , stool (20 controls for each), and sputum samples were collected from 25 COVID -19 patients, then cultured on different culture media. Vitek 2 was used to identification the bacterial isolates.

Urine culture growth of COVID -19 patients displayed 15 (60%) growth which included, *E. coli* 8 (53%), *Pseudomonas aeruginosa* 2(13 %) *Klebsiella pneumoniae* 2(13%) *Staphylococcs aureus* 1(7%) ,*Staphylococcu epidermidis* 1(7%), *Proteus mirabilis* 1(7%).