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SARS-CoV-2 shedding in saliva and dynamic changes in white blood cell counts

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Background: The most recent coronavirus (COVID-19) epidemic soon turned into a pandemic and presented a threat to the entire world. However, there is no reliable data on possible connections between SARS-CoV-2 shedding in bodily fluids, particularly saliva, and white blood cell (WBC) count. The possible relationship between changes in blood cell counts and viral shedding in saliva in a cohort of COVID-19 patients was examined in the current investigation.

Methods: In this early clinical study, 24 age-matched COVID-19 patients without comorbidities were observed for a total of 5 days to see whether changes in the amount of viral shedding in saliva would correlate with temporal changes in WBC count. Half of the patients were men, and the other half were women. By performing SARS-CoV-2 rapid antigen testing on patient saliva samples using the SARS-CoV-2 quick Antigen Test Kit (Roche, Basel, Switzerland), viral shedding in saliva was subjectively assessed. These patients were divided into two groups: those who coughed up sputum and those who did not. On days 1, 3, and 5, each patient's WBC counts, including leukocyte (LYM), neutrophil (NEU) counts were reported.

Results: According to the study's findings, both groups of people who had sputum had significantly higher levels of WBC, LYM, and NEU on the fifth day compared to the first day. However, there were no appreciable changes in the levels of lactate dehydrogenase (LDH), neutrophil-to-lymphocyte ratio (NLR), or C-reactive protein (CRP).

Discussions: This study demonstrates that measuring changes in the number of blood LYMs and laboratory values like CRP and LDH as biomarkers (it shown in the ROC curve) are reliable indicators of the quantity of viral shedding in both sputum-producing and non-sputum-producing individuals. The findings of our study indicate that the measured parameters show the degree of viral shedding in sputum-producing individuals.

MicroRNAs as biomarkers for discriminating high D-dimer from normal D-dimer COVID-19 patients

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MicroRNAs (miRNAs) as remarkable regulators of immune pathways that are implicated in inflammation and antiviral immune responses are considered potential therapeutic targets in Coronavirus disease (COVID-19). Indeed, thrombosis and coagulation abnormalities including a significant increase in D-dimer and fibrinogen, caused by high blood clots in COVID-19 patients could be associated with miRNAs expression. The current attempt was made to elucidate the behavior of peripheral blood mononuclear cells (PBMCs) miRNAs as biomarkers to discriminate COVID-19 patients with normal and abnormal coagulation indices. A bioinformatics approach was used to predict miRNAs involved in the D-dimer pathway (miR-19a-3p, miR-223-3p, miR-143-5p, miR-494-3p, and miR-301a-5p).

The expression pattern and the diagnostic potency of selected miRNAs were determined by the Real-Time PCR method and the receiver-operating characteristic (ROC) curve test, respectively. The association between D-dimers and inflammatory factors with the miRNA expression levels was evaluated using Spearman correlation. ROC curve analysis in the selected groups suggested that miR-223-3p and miR-494-3p can be considered as remarkable biomarkers for discriminating COVID-19 patients with abnormal coagulation indices from normal COVID-19 patients. A significant positive correlation was distinguished between miR-494-3p and D-dimer, and Fibrinogen levels. Also, the miR-223-3p level expressed in COVID-19 cases with normal coagulation indices was significantly lower than that in healthy controls. Therefore, the expression level of the predicted miRNAs, paired with the ROC curve results, suggests that these factors may serve as potential biomarkers for discriminating the two studied groups and also could be considered as therapeutic targets for preventing coagulation in COVID-19 patients.

Zoonotic importance of bovine herpes virus in man and animal

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The zoonotic importance of Bovine Herpes Virus (BoHV) in both people and animals is a subject of major interest and worry. According to reports, BoHV infection has a serious financial impact on the cattle business globally, harming both animal health and output. BoHV infection typically affects cattle, which can develop a variety of clinical symptoms including respiratory illness, reproductive problems, and generalized illness. The virus has substantial financial ramifications for the livestock industry because it can result in abortion, stillbirth, neonatal mortality, and decreased fertility. Furthermore, BoHV is known to cause latent infection, with the potential for reactivation and recurrent virus shedding, further complicating disease control methods. The zoonotic potential of BoHV is gaining attention. The fact that BoHV can spread from animals to people has been documented in numerous research, underscoring the virus' importance as a possible risk to the public's health.

Humans, particularly those who deal closely with infected animals, such as farmers, veterinarians, and abattoir employees, are at risk of contracting BoHV. BoHV infection in people might present as a minor respiratory disease, conjunctivitis, or even more serious side effects including encephalitis and meningitis. Understanding BoHV's zoonotic significance is critical for developing effective management and prevention strategies. It is possible to lower infection rates and financial losses in the cattle business by implementing stringent biosecurity measures and routine testing in livestock populations. Additionally, it is essential to increase awareness among those who are at a high risk of exposure, such as farmers and animal health experts, in order to lessen the spread of BoHV from animals to humans. In conclusion, the importance of the zoonotic transmission of the bovine herpesvirus to both humans and animals cannot be overstated. To effectively address BoHV infections in both animal and human populations, it is critical to prioritize research, surveillance, and prevention activities.