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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.