

Deviated expression pattern of noncoding RNAs (microRNA and long noncoding circular RNA) in patients in the convalescent phase of post-COVID-19 disease

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Background: Approximately 10-30% of people infected with SARS-CoV-2 suffer from so-called long-COVID syndrome. Long-COVID has been recognised as a new multiorgan disease affecting organs including lung, brain and heart. The role of microRNAs (miRNAs) and circular RNAs (circRNAs) in long-COVID has not yet been examined. Here we investigated the expression of selected miRNAs and one circRNA (CDR1as) known to be involved in inflammatory diseases.

Results: We included 12 healthy (seronegativity to SARS-CoV-2 antigen) and 5 post-COVID volunteers. While the circulating level of all ncRNAs was near zero in healthy controls, a significant upregulation of circRNA CDR1as ($p=0.019$) was observed (see Figure).

Conclusion: This pilot study revealed SARS-CoV-2 associated miRNAs and a novel circRNA as possible biomarker in prediction of long-COVID.

