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Biological Impacts of MicroRNAs in Covid-19: Implications for Anti-Viral miRNA-Based Therapies

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Dear Editor,

Severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) is a novel sever pathogenic coronavirus (CoVs) causing coronavirus disease 2019 (COVID-19), which has become an international concern due to the outbreak and crucial health burden worldwide. SARS-CoV-2 belongs to Coronaviridae family, which are positive single-stranded RNA and contains the largest RNA genome in viruses (1). Interestingly, miRNAs are small non-coding regulator RNAs that involved in various biologic and pathologic processes such as inflammatory responses as well as viral infection. It has been shown that miR-9, miR-98, miR-223, and miR-214 expression in CoVs-infected host cells could be changed and subsequently leads to modification in cytokines production (2). miRNA-target prediction via bioinformatics analysis revealed that miR-5197-3p could interact with SARS-CoV-2 gRNA, which could not target any genes in the human genome (3). Therefore, miRNA-based therapy could be proposed for SARS-CoV-2 treatment through the viral genome suppression. In this line, a comparative viral genome analysis showed that six host miRNAs, including let-7a, miR-101, miR-126, miR-23b, miR-378, and miR-98 might be considered as anti-viral miRNAs which could suppress SARS-CoV-2 target genes including nonstructural protein (nsp), nucleocapsid and spike glycoprotein that (4). Based on our analysis through the VIRmiRNA database, the most of virus-derived miRNAs involved in IFNβ related pathway. COVID-19 treatment with IFNβ, especially in the early stage of the disease, has a beneficial effect in patients (5). PANTHER (protein annotation through evolutionary relationship) analysis indicated that SARS-CoV-2-derived putative miRNAs might inhibit transcription factors and regulators such as STAT1 (6). Suppression of STAT1 expression as a major anti-viral mediator in the IFN signaling pathway by SARS-CoV ORF6 protein suggests that IFN treatment could be more effectiveness in COVID-19 patients (7). Zhi Liu et al., performed computational approaches demonstrated that SARS-CoV-2-derived MR-147-3p via inhibition of transmembrane protease, serine 2 (TMPRSS2) enhances the viral spike (S) priming as the predicted target of miR-4661-3p which facilitates the virus entry into the gastrointestinal tract (8). In addition, gastrointestinal symptoms are associated with poor prognosis in COVID-19 patients. Although these results are preliminary and experimental attempts are inevitable for better pre-clinical and clinical assessment of COVID-19. In summary, it can be concluded that cost and time benefits in silico analysis of virus and/or host miRNAs as well as the target genes network would be a valuable point of view to figure out the underlying molecular mechanisms of COVID-19. Moreover, virus or host genome scanning may lead to discover the promising targets in order to control viral pathogenicity with anti-viral miRNA-based therapies.

Footnotes

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