

Review of: "In Silico Investigation of Potential COVID-19-Associated MicroRNA Signatures"

Alejandra Garcia-Gasca¹

¹ Research Center for Food and Development A.C.

Potential competing interests: No potential competing interests to declare.

This is an interesting article in which the authors used an in silico integrative approach (from database searching and enrichment analysis, to miRNA target prediction) to identify, first a gene/protein-protein network interaction in the COVID-19 context, and then a miRNA-target gene(s) network, identifying eight highly interacting miRNAs with target genes related with SARS-CoV-2 infection and COVID-19 (here called COVID-19-related genes).

It was somehow expected that the interaction network of COVID-19-related genes/proteins would consist of inflammatory and immune proteins, thus the results seem right. Differential expression analysis also seems correct, although the authors could point out that this analysis may require experimental validation. Finally, the miRNA target gene network identified eight miRNAs targeting 22 (not 24) of the top immune/inflammatory genes; the authors conclude that these eight identified miRNAs could represent a signature to improve COVID-19 diagnosis. In this regard (in my opinion), improving diagnosis would not be as relevant as improving treatments; diagnosis methods (both PCR- and antigen-based) are widely used and available, however, miRNA-based therapies could eventually become more significant, therefore I suggest discussing this possibility.