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

Luis Diambra[1]

1 Universidad Nacional de La Plata

Potential competing interests: No potential competing interests to declare.

The manuscript presents a basic bioinformatic analysis of the network of interactions of genes involved in COVID-19, using Genecard and STRING databases. There they observe that some genes would be potential targets of microRNAs. Regarding this observation, the authors claim to have found epigenetic regulators: "The protein-protein interaction and miRNA-gene networks constructed in this study provide a fundamental framework for detecting protein-coding genes and epigenetic regulators." This gives the title to the paper. First of all, I do not agree with this claim given that the protein-protein network is public and was not constructed in this paper. The only new inference could be microRNAs. However, there is a serious argumentative flaw in this inference. The genes selected in Genecard have their expression affected by COVID-19. We know that miRNAs downregulate gene expression. Therefore, the simple selection and assembly of networks do not allow us to conclude anything sentence similar to the above. The study should focus on downregulated genes in COVID-19 patients. However, this study was already carried out and published [1]. In that paper, authors report a set of 29 miRNAs that are down-regulating genes involved in epigenetic mechanisms, including BPs linked to H3K4 methylation and regulation of histone methylation. Further, they suggest that gene expression changes could be due to SARS-CoV-2-encoded viral miRNAs.

1.- L Diambra, AM Alonso, S Sookoian, CJ Pirola (2022)
Single cell gene expression profiling of nasal ciliated cells reveals distinctive biological processes related to epigenetic mechanisms in patients with severe COVID-19. Computers in Biology and Medicine Volume 148, 105895. DOI:doi.org/10.1016/j.compbiomed.2022.105895