Ontological representation and analysis of the molecular interactions related to COVID-19-associated Acute Kidney Injury

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Abstract

COVID-19 is related to multiple organ injuries, and its effects on the kidneys is well demonstrated in the literature. This study aims to expand and ontologically present knowledge available regarding the relationship between COVID-19 and Acute Kidney Injury (AKI). To achieve our goal, we conducted literature mining and utilized data available from the Anatomical structures, Cell Types, Biomarkers (ASCT+B) to determine kidney biomarkers involved in the process. We utilized BioGRID data to determine SARS-CoV-2 and host protein/gene interactions implicated in COVID-19 associated AKI. By using the above two resources, we found 17 biomarkers (out of 146) interacting with 14 SARS-CoV-2 viral proteins, yielding a total of 36 interactions. In addition to ACE2 being the most significant SARS-CoV-2 receptor and its implications being well studied, multiple other interactors are discovered and are presented in our paper. We utilized Reactome for pathway analysis and the Coronavirus Infectious Disease Ontology (CIDO) as a platform to represent our findings ontologically. Our CIDO-based ontological representation will provide a systematic and computer-interpretable logic knowledge representation of the molecular interactions related to COVID-19-associated AKI mechanisms, leading to the uncovering of many scientific insights. The recently added protein-protein interactions (PPIs) will further expand on the already existing knowledge regarding COVID-19 associated AKI PPIs. Our work provides host/virus interaction information, allowing for discovering potential targets and developing pharmacological therapies to treat AKI in COVID-19 patients.

Keywords

COVID-19, Acute Kidney Injury, Ontology, CIDO, ASCT+B, Protein-protein interaction BioGRID, Reactome

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