Structure-Function Characteristics of SARS-CoV-2 Proteases and Their Potential Inhibitors from Microbial Sources

ABSTRACT

The COVID-19 pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), is considered the greatest challenge to the global health community of the century as it continues to expand. This has prompted immediate urgency to discover promising drug targets for the treatment of COVID-19. The SARS-CoV-2 viral proteases, 3-chymotrypsin-like protease (3CLpro) and papain-like cysteine protease (PLpro), have become the promising target to study due to their essential functions in spreading the virus by RNA transcription, translation, protein synthesis, processing and modification, virus replication, and infection of the host. As such, understanding of the structure and function of these two proteases is unavoidable as platforms for the development of inhibitors targeting this protein which further arrest the infection and spread of the virus. While the abundance of reports on the screening of natural compounds such as SARS-CoV-2 proteases inhibitors are available, the microorganisms-based compounds (peptides and non-peptides) remain less studied. Indeed, microorganisms-based compounds are also one of the potent antiviral candidates against COVID-19. Microbes, especially bacteria and fungi, are other resources to produce new drugs as well as nucleosides, nucleotides, and nucleic acids. Thus, we have compiled various reported literature in detail on the structures, functions of the SARS-CoV-2 proteases, and potential inhibitors from microbial sources as assistance to other researchers working with COVID-19. The compounds are also compared to HIV protease inhibitors which suggested the microorganisms-based compounds are advantageous as SARS-CoV2 proteases inhibitors. The information should serve as a platform for further development of COVID-19 drug design strategies.