Viral Diseases and Natural Products: Prospects in COVID-19 Treatment (Part IV)

According to literature, COVID-19 pandemic, which emerged at the end of 2019, caused by coronavirus SARS-CoV-2, has become the most deadly disease in recent history, particularly its current mutant variant (Delta strain). Till August 06, 2021, more than 200 million people were infected, accounting for a total of 4.26 million cases of death [1]. Many drugs have been used to treat this infection, and also some vaccines (AstraZeneca, Pfizer, Novavax and Moderna etc.) are in use now in order to prevent it, but no complete cure for this disease has been found yet. Drug development from active ingredients obtained from natural sources might be a good strategy for COVID-19 management after completion of research and clinical trials. We have published three volumes of these special issues on natural products against viral diseases, especially COVID-19, in Current Pharmaceutical Design [2-4]. However, more articles have been received, thus are incorporated in this current part IV. This issue comprises a total of five papers dealing with natural products and viral diseases.

Shahriar et al. [5] have discussed the taxonomy, structure of SARS-CoV-2, history, transmission, epidemiology, pathology, clinical features and impacts of COVID-19. A summary of possible drug targets, attempted physical and chemical measures, as well as vaccine candidates, has also been provided. How this coronavirus is different from other coronaviruses, the obstacles in managing this disease and the possibility of a second wave have also been reviewed. In this way, a comprehensive overview of information regarding COVID-19 has been presented [5]. On the other hand, Wijayasinghe et al. [6] have critically evaluated the findings of the natural product-based anti-coronaviral research that has been published during the last two decades, and attempted to provide a comprehensive description of their utility as potential broad-spectrum anti-coronaviral drugs, thereby providing leads that may guide/facilitate anti-SARS-CoV-2 drug development studies.

Kaur et al. [7] have presented a review, based on the publically available literature, of the knowledge regarding epidemiology, virology, diagnosis, clinical features, pharmacological and therapeutic ways to treat the novel coronavirus. This can be helpful in offering novel insights and potential therapeutics for fighting this disease. The rapid development of new drug molecules is the need of the hour to fight COVID-19. Rehman et al. [8] adopted a computational approach to identify lead molecules from nature. Ligands from the natural compounds library available at Selleck Inc (L1400) have been screened for their ability to bind and inhibit the main protease (3CLpro) of SARS-CoV-2. Kaempferol, Quercetin, and Rutin were bound at the substrate-binding pocket of 3CLpro with high affinity and made to interact with the active site residues through hydrogen bonding and hydrophobic interactions. The binding affinity of Rutin was found to be much higher than Chloroquine and Hydroxychloroquine, and the reference drug Remdesivir. The results suggested that natural compounds, such as flavonoids, have the potential to be developed as novel inhibitors of SARS-CoV-2 with a comparable/higher potency as that of Remdesivir. However, their clinical usage in COVID-19 patients is a subject of further investigations and clinical trials [8].

The seven known human strains of CoV were analyzed for the host and viral factors responsible for human outbreaks by Ahmad et al. [9]. The molecular factors responsible for host-susceptibility, virulence and pathogenesis were reviewed to predict emergence and re-emergence of additional human CoV strains. CoV spike protein was evaluated as a potential viral receptor for host switching and the target for pharmaceutical design. The high propensity of mutations and “molecular adaptations” in coronaviruses create the hot spots and exhibit a high potential for “host switching” leading to the emergence of more virulent strains of human CoVs. The public/global health agencies, medical communities and research scientists should be prepared for the emergence and re-emergence of new human CoV strain(s) leading to potential disease outbreaks. The inhibitors binding with conserved druggable regions of spike proteins from multiple strains CoV may have utility as broad-spectrum antiviral drugs to combat the future emergence of CoVs [9].

Hopefully, this special issue will help researchers to develop therapeutic drugs for COVID-19. We are thankful to all authors who submitted their articles in this Special Issue, and reviewers, who secured their time in providing valued feedback to improve the submitted manuscripts. Last but not least, GEs are also thankful to the editor-in-chief (Prof. Alessandro Antonelli, Italy) and the management staff (Kazim et al.) of Current Pharmaceutical Design for their cooperation throughout the processing of the manuscripts.

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