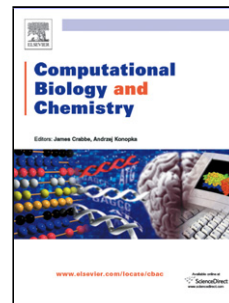


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Tetracyclines as a potential antiviral therapy against Crimean Congo Hemorrhagic Fever Virus: docking and molecular dynamic studies

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Abstract

Crimean-Congo Hemorrhagic Fever Virus (CCHFV) is one of the deadliest human diseases with mortality rate near 50%. Special attention should be paid to this virus since there is no approved treatment for it. On the other hand, the recent outbreak of Ebola virus which is a member of hemorrhagic fever viruses shows this group of viruses can be extremely dangerous. Previous studies have indicated that nucleoprotein of CCHFV, a pivotal protein in virus replication, is an appropriate target for antiviral drug development. The aim of this study is finding inhibitor(s) of this protein. Herein, a virtual screening procedure employing docking followed by molecular dynamic was used to identify small molecule inhibitors of the nucleoprotein from FDA-approved drugs. Regarding CCHFV, using in-silico method is a safe way to achieve its inhibitor(s) since this virus is categorized as a World Health Organization (WHO) biosafety level 4 pathogen and therefore investigation in general laboratories is restricted. In conclusion, considering docking and molecular dynamic results alongside with bioavailability of FDA-approved drugs, doxycycline and minocycline are proposed as potential inhibitors of CCHFV nucleoprotein. There is hope, this study encourage other research groups for in-vitro and in-vivo studies about the efficacy of those two medicines in CCHFV treatment.

Key words: Crimean Congo virus; Docking; Molecular dynamic; Doxycycline; Minocycline; FDA-approved drugs

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