Enantiomers of quinolones and their activeness for different targets to cure malaria: An advanced computational approach

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May 7, 2020

Abstract

In the case of chiral antimalarial drugs (chloroquine, primaquine, and quinacrine), it becomes very difficult to understand the mechanism of these chiral drugs because these drugs are prescribed in the racemic form in which one enantiomeric form cures malaria, while another does not, or cause side effects. Here, we have developed a computational method for the enantiomeric interaction of chiral antimalarial drugs with different targets for the first time. Using Marvin sketch and Discovery Studio Visualizer, all the pdb files of all the enantiomers were obtained, while the pdb files of targets (β-hematin, DHFR-TS, DHFR-TS quadruple mutant) were obtained from the protein data bank. All the enantiomers were docked with different targets to find the binding affinity using AutoDock Tools (ADT) 4.2). The enantiomeric forms causing side effects as well as the most biologically active enantiomeric forms and their target were resolved. Docking study showed that the most biologically active enantiomeric forms in the presented chiral antimalarial drugs are 'R' of chloroquine; 'S' of primaquine and 'R' of quinacrine'. The presented study helps not only in determining the target of these chiral drugs but also in discovering the most biologically active enantiomeric form of these drugs, which may be responsible for the better treatment of malaria. Besides, the presented study also opens the doors for the better treatment of other disease for which the chiral drugs taken in the present study are prescribed such as chloroquine and hydroxychloroquine for coronavirus (2019-nCoV). Keywords: Chiral quinolones, targets, computational study and (2019-nCoV).

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