

Title: Modified oxymatrine as novel therapeutic inhibitors against Monkeypox and Marburg virus through computational drug design approaches

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Abstract: Global impact of viral diseases specially Monkeypox (mpox) and Marburg virus, emphasizing the urgent need for effective drug interventions. Oxymatrine is an alkaloid which has been selected and modified using various functional groups to enhance its efficacy. The modifications were evaluated using various computational analysis such as pass prediction, molecular docking, ADMET, and molecular dynamic simulation. Mpox and Marburg virus were chosen as target diseases based on their maximum pass prediction spectrum against viral disease. After that, molecular docking, dynamic simulation, DFT, calculation and ADMET prediction were determined. The main objective of this study was to enhance the efficacy of oxymatrine derivatives through functional group modifications and computational analyses to develop effective drug candidates against mpox and Marburg viruses. The calculated binding affinities indicated strong interactions against both mpox virus and Marburg virus. After that, the molecular dynamic simulation was conducted at 100 ns, which confirmed the stability of the binding interactions between the modified oxymatrine derivatives and target proteins. Then, the modified oxymatrine derivatives conducted theoretical ADMET profiling, which demonstrated their potential for effective drug development. Moreover, HOMO-LUMO calculation was performed to understand the chemical reactivity and physicochemical properties of compounds. This computational analysis indicated that modified oxymatrine derivatives for the treatment of mpox and Marburg virus suggested effective drug candidates based on their binding affinity, drug-like properties, stability and chemical reactivity. However, further experimental validation is necessary to confirm their clinical value and efficacy as therapeutic candidates.

Keywords: Oxymatrine derivatives, Monkeypox (mpox) virus, Marburg virus, Computational drug design, Molecular docking

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