Screening of Potential Antiviral Compounds - Assessing Efficacies Against Dengue Virus TXST NEXT

Background

Epidemiology

Dengue viruses (DENV) are spread to people through the bite of Aedes species (Ae. Aegypti or *Ae*. infected albopictus) mosquito. Approximately, more than 3 billion people live in areas with high risk of dengue. It is the leading cause of illness in areas with risk vector borne disease (CDC, 2023).

Genome

DENV is a member of the Flavivirus genus of single-stranded positive-sense RNA viruses that causes severe generalized diseases in humans. There are four DENV serotypes (1, 2, 3 and 4), with type 2 and 3 being the most virulent forms (Vicente et al. 2016).

Structure

Mature DENV particles have a diameter of approximately 500nm. The surface is made up of a lipid bilayer which incorporate two transmembrane viral proteins to form a glycoprotein shell. The core contains the nucleocapsid formed by a viral RNA genome complex with capsid protein. The glycoprotein shell has 180 copies of envelope (E) and membrane protein (M or prM). The capsid (C) protein interacts with the viral RNA genome during assembly of the virus (Murugesan and Manoharan 2019).





Rationale

- The spread of the virus has increased due to travel and industrialization, and the only available approved vaccine is for use in children living in the area where dengue is endemic; hence the need for discovery of more potent vaccine candidates that is available for use even among adults.
- Due to the lack of vaccine and treatment candidates against dengue virus, the discovery of prophylactic and treatment options remains a top priority of USA Military Infectious Disease Research Program (MIDRP).

Hypothesis

Many recently discovered antiviral compounds have been via repurposing a compound with established functions. Based on this, we hypothesize that assessing and docking millions of established compounds with dengue virus protein (3U1I) will provide headway in the discovery of antiviral agents against dengue virus.

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Results

Zinc ID and Docking Scores of Top Five Active Compounds Docked Against DENV-3 (PDB:3U1I)

Zinc ID	docking score	Structure
ZINC000095356735	-9.695	$ \bigcirc 0 \qquad N - NH \\ \square 0 \qquad \qquad \square 0 \qquad \qquad \square 0 \qquad \square $
ZINC000084005152	-9.189	
ZINC000027064104	-9.169	HN S NH O F F
ZINC000244701329	-9.15	H_2N H_2N H H_2O H_2
ZINC000019236560	-8.528	



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Figure 3: ZINC000027064104 compound colored by atom types (C, blue; H, white; N, blue; O, red; S, yellow)





Future Studies

- Screening of all the compounds against DENV 2 and 3 to establish their antiviral effects, and their ability to serve as a counter measure approach against dengue virus infection.
- Determination of the mechanism of actions for the most potent compounds from screening against dengue virus infection and spread in human body.

References

lational Centre For Emerging and Zoonotic Infectious Diseases (NCEZID), Division of Vector-Borne Diseases (DVBD) rbinger, KH., Fröschl, G. et al. Serotype influences on dengue severity: a cross-sectional study on 485 confirmed dengue cases in Vitória, Brazil. BMC Infect Murugesan A, Manoharan M. Dengue Virus. Emerging and Reemerging Viral Pathogens. 2020:281–359. doi: 10.1016/B978-0-12-819400-3.00016-8. Epub 2019 Sep 20. PMCID: PMC7149978. Noble CG, Seh CC, Chao AT, Shi PY. Ligand-bound structures of the dengue virus protease reveal the active conformation. J Virol. 2012 Jan;86(1):438-46. doi:





Figure 5: ZINC000019236560 compound colored by atom types (C, green; H, white; N, blue; O, red; S, yellow)



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