Targeting Intrinsically Disordered Regions (IDRs) in Viral Proteins via Molecular Recognition Features (MoRF) Analysis

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In order to replicate, viral proteins hijack the host machinery. They interact with numerous viral proteins using molecular recognition features (MoRFs- induced folding upon binding) located inside intrinsically disordered regions (IDRs) during the infection cycle [1, 2]. IDRs are widely distributed in viral genomes and are often found to be associated with the pathogenicity and oncogenicity caused by the viruses [3]. This study looked into the IDRs/MoRFs found in the emerging viral diseases Human parainfluenza 4A virus (HPIV-4A) and Chandipura virus (CHPV). A rare infection, HPIV-4A, produces a milder respiratory disease. CHPV, on the other hand, is linked to encephalitic illness. In previous studies, Measles morbillivirus virus (MeV) and Vesicular stomatitis virus (VSV) were chosen as representative family viruses of HPIV-4A and CHPV, respectively, because they are densely ornamented with IDRs [4, 5]. Since phosphoprotein is highly disordered and needed for replication and transcription, it could be a promising drug target [6]. The IDRs/MoRFs found in phosphoprotein were targeted using conserved domain analysis and molecular docking. The compounds used in this docking study were then divided into three categories: phytochemicals, repurposed drugs, and antiviral drugs. To summarise, when compared to anti-viral drugs, repurposed drugs (derived from plants) and phytochemicals are the most effective inhibitors of MeV phosphoprotein. Antiviral approaches have so far been used to target viral structural proteins such as polymerase and protease [7]. Unfortunately, pharmacological inhibition of these structural proteins is sometimes surprisingly ineffective due to drug resistance. Inhibiting conserved MoRFs is a novel alternative to this strategy.

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