Title: Genomic analysis of Poxvirus, functional characterization of hypothetical proteins and identification of potential inhibitors

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Abstract

Poxviruses possess a highly intricate structure relative to other viruses and contain a substantial double-stranded DNA molecule. A distinctive feature of this virus is its morphogenesis, which involves two primary forms: the Mature Virion and the Envelope Virion structures, both of which are responsible for infecting new hosts and initiating systemic infection within the same host. Another feature of viruses within the Poxvirus family is that their genomic organization consists of a highly conserved central core region, which is encased by predominantly variable terminal regions containing inverted terminal sequences. Recent outbreaks caused by the Mpox virus, which belongs to the genus Orthopoxviridae, as well as frequent infections of other poxvirus species from different genera, underscore the urgent need for increased research on smallpox like viruses and related diseases in humans, as well as the development of novel therapeutic agents targeting poxvirus infections.

Researchers in the first article conducted a comprehensive comparative genomics analysis to identify the conserved and variable regions of MPXV. Their investigation showed that genes involved in replication, transcription, and virion assembly are still quite similar among isolates, making them a stable evolutionary core. On the other hand, auxiliary genes, multigene families, and loci with a lot of repeats are mostly found in variable regions. These areas exhibit increased mutation and rearrangement rates, possibly serving as crucial determinants in host adaptability, immunological evasion, and modifications of virulence traits(1).

The second study (2024) focused on the functional and structural examination of potential MPXV proteins by computational modeling. By predicting protein structures, inferring likely biological activities, and screening for potential small-molecule inhibitors, the authors discovered several previously uncharacterized targets with considerable therapeutic potential. Their findings underscore that even the uncharacterized hypothetical protein of MPXV, especially those elevated in infection to humans may be susceptible to pharmacological targeting and are relevant to antiviral research(2).

These two studies together give us more information about how MPXV works. The first explains how the virus keeps its genome intact while still allowing for adaptive flexibility. The second uses this knowledge to improve medication discovery. This integrated approach improves surveillance efforts, makes functional annotations more accurate, and helps with the strategic planning of new antiviral drugs and diagnostic tools.

Reference

1. Yu Z, Zou X, Deng Z, Zhao M, Gu C, Fu L, et al. Genome analysis of the mpox (formerly monkeypox) virus and characterization of core/variable regions. Genomics. 2024;116(1):110763.
2. Raen R, Islam MM, Islam R, Islam MR, Jarin T. Functional characterization and structural prediction of hypothetical proteins in monkeypox virus and identification of potential inhibitors. Mol Divers. 2025;29(2):1589-617.