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Subtype agnostic genome reconstruction of the human metapneumovirus using long reads

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Conventional workflows for viral genome reconstruction commonly rely on reference-based reconstruction methods. To generate an accurate consensus sequence, these workflows require a reference genome closely related to the target viral strain.

Recent evolutionary processes of the human metapneumovirus (hMPV) include long segmental duplications (DUPs) of over 100 nucleotides in the attachment (G) protein locus. These DUPs introduce sequence complexity that complicates the genome reconstruction, particularly when the sequencing reads are shorter than the duplicated segments. The lengths of DUPs observed in recently emerging hMPV subtypes fall into a “twilight zone” of what can be algorithmically detected from short-read next-generation sequencing data, which typically has an average read length of 150 nucleotides. As a result, recent DUPs in the hMPV genome may remain undetected or inaccurately reconstructed.

We propose a novel computational workflow based on long-read sequencing technologies. Long reads can span entire duplicated segments, facilitating more accurate detection of structural variants such as DUPs. In the case of hMPV, improved DUP detection can lead to more reliable reference strain selection, thereby enhancing the accuracy of genome reconstruction and subsequent taxonomic classification. This project lays the groundwork to establish a robust, routine, and future-proof genomic surveillance during seasonal hMPV epidemics.

Keywords

hMPV, long reads, segmental duplication, virus evolution

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Professional Status of the Speaker

Graduate Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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