

Investigating the Influence of Various Receptor Organizations on Filamentous Influenza A Motility Under the Presence of Antibodies

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This study examines the multifaceted interactions of the glycan-binding surface proteins of the Influenza A virus (IAV), illuminating the fundamental factors shaping its motility and consequential infectivity. It explores the interactions between IAV's viral surface proteins, neuraminidase (NA), and hemagglutinin (HA), and how they influence virus motility. HA binds to sialic acid (SA) on the cell surface. These bonds form and break off randomly, leading to viral motility. NA cleaves SA along its path. This creates self-avoiding, random walks on the cell surface. This motility gives IAV an advantage in crossing the mucus barrier and infecting non-ciliated cells.

Through a Monte Carlo simulation, this study renders filamentous IAVs with various HA/NA organizations and simulates their motion in the presence of HA/NA-targeting antibodies. The findings reveal that virions with NA polarization exhibit the strongest persistent directional motion and disabled HA/NA result in significantly weaker directional motion, implying the potential treatment of IAV through HA/NA inhibitors. Overall, this research provides insight into the fundamental factors governing IAV motility and creates a strong foundation for more advanced models.

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