

Molecular Anatomy of an Influenza Virion

Content

Influenza virions are complex and vary in their shape and composition. As a result, no single method can describe them in detail. We therefore applied a multidisciplinary approach, generating a highly detailed model of an average influenza virion that provided a basis for assessing natural variation.

By combining cryo-electron tomography, proteomics, lipidomics and molecular modelling, we reconciled measurements of virion morphology with the identity, quantity and structures of virion components. Our pseudoatomic model revealed a crowded membrane with a distinctive lipid composition and an interior densely packed with both viral and host proteins.

We next used our model to assess the effects of natural virion variation. First, we considered the range of influenza virion morphologies. We found that elongated 'bacilliform' virions have an equivalent surface area to spherical virions, but that transition from one to the other would constrain the viral genome complex and force it to become disordered. Consistent with this, we could not observe a '7+1' arrangement of genome segments in spherical virions. Second, we examined how influenza virions vary between hosts. We showed that the incorporation of some proteins, notably tetraspanins, varies drastically between hosts but that this variation does not compromise infectivity. Third, we examined changes over time. We found that as an infection progresses influenza virions package exponentially more of the immunosuppressive protein NS1.

Thus, by comparison to a detailed model of an average virion we showed that the same influenza virus produces different virions from different hosts, and at different times during an infection.

Choose primary session

Visualising Flu

Choose secondary Session

Viral Replication

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