Open and closed forms of assembled henipavirus nucleoprotein suggest structural basis of genome access

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Henipaviruses, such as Nipah virus, can cause deadly illness and constitute WHO blueprint priorities due to their pandemic potential. Their genomes are packaged within a nucleocapsid consisting of viral nucleoproteins (N). Currently, it is unclear how the encapsidated genome is released from N to allow the viral polymerase to read its sequence. Here, we present the high-resolution cryo-EM structure of a helical N-RNA filament from Langya henipavirus (LayV), allowing us to identify vertical interactions crucial for assembly. We show that assembly efficiency is sequence-dependent and prefers 5'-genomic sequences. Further, we solve the structure of an RNA-free assembly of LayV-N. Structural comparison of the RNA-bound and RNA-free LayV-N shows a conformational opening and closing, even within the assembled state. Our data suggest that N within nucleocapsids may undergo local conformational changes, switching between closed and open states, to temporarily allow access to the encapsidated RNA without nucleocapsid disruption.