

Mapping the Molecular Determinants of Influenza Virus RNA Synthesis Initiation and Termination

Sunday, September 13, 2026 6:06 PM (1 minute)

Influenza A viruses contain a segmented genome of eight negative-sense, single-stranded RNAs (vRNAs), each packaged with a viral RNA polymerase and nucleoprotein into viral ribonucleoprotein complexes (vRNPs). These vRNPs undergo both transcription and replication, producing (I) capped, polyadenylated mRNAs and (II) uncapped, full-length vRNAs via a complementary RNA (cRNA) intermediate. Transcription is primed by host-derived capped RNAs and terminates by polyadenylation at a polyuridine stretch upstream of the 5' terminus. In contrast, replication is triggered by interaction of the vRNP with a second polymerase and the host factor ANP32, initiating RNA synthesis de novo and replicating the RNA end to end.

However, important mechanistic details governing initiation and termination remain poorly understood. To address these gaps, we combine an in vitro reconstitution system with long-read Nanopore sequencing to directly profile terminal RNA sequences. This approach promises to reveal fundamental mechanisms underlying initiation and termination of influenza virus RNA synthesis.

Keywords

Professional status of the speaker

Graduate student

Junior scientist status

Yes, I am a junior scientist.

Registration ID

INF26-100

Authors: WITTE, Leander (University of Oxford); Prof. FODOR, Ervin (University of Oxford)

Co-author: Dr QADIR, Amina (University of Oxford)

Presenter: WITTE, Leander (University of Oxford)

Session Classification: Poster slam

Track Classification: Virus Replication