ID der Kurzfassung : **160**

Nascent transcript sequencing reveals cap-snatching specificity of influenza A virus

Inhalt

Influenza A virus mRNAs are synthesised in the nucleus by the viral RNA-dependent RNA polymerase (FluPol). To initiate viral transcription, FluPol binds host RNA polymerase II (RNAPII). The endonuclease subunit of FluPol then cleaves nascent transcript, producing a short capped RNA fragment, which primes viral mRNA synthesis. Previous studies suggested this cap-snatching process is largely dependent on transcript level, though others reported gene-specificity. However, these studies were based on sequencing Flu mRNAs and thus limited by small 12 nt primers, which are hard to uniquely map to the human genome.

Here, we present a complimentary approach of identifying the downstream portion of the host cap-snatched transcripts using polymerase intact nascent transcript (POINT) technology. We use native immunoprecipitation of RNAPII elongation complexes to isolate associated nascent RNAs and prepare 5′-end specific libraries, with reads long enough for unique mapping.

This approach allowed us to identify cap-snatching events directly from the 5′ ends of RNAPII-associated transcripts. We report a previously overlooked preference for variant spliceosomal U1 snRNAs and avoidance of the more abundant U1 snRNAs. These findings suggest that in addition to transcript abundance, other factors are regulating influenza A virus co-transcriptional cap-snatching and potentially support a model in which FluPol exhibits a higher degree of substrate specificity than previously appreciated.

Keywords

Registration ID

INF26-105

Professional status of the speaker

Postdoc

Junior scientist status

No, I am not a junior scientist.

Track Klassifizierung: Virus host cell interaction

Typ des Beitrags: Poster presentation