

Molecular Mechanisms of Deletion-containing Viral Genome Formation and Immune System Interaction in Influenza Viruses

Inhalt

Highly pathogenic avian influenza viruses (HPAIVs) occasionally cross the species barrier and often induce excessive host inflammation in humans. Deletion-containing viral genomes (DVGs) arise through internal deletions during error-prone Influenza A virus (IAV) replication and can have immune stimulatory potential. We hypothesize that virus-specific DVG landscapes contribute to HPAIV pathogenicity and could further serve as prognostic markers for pandemic risk assessment. By characterizing DVG signatures across seasonal and highly pathogenic IAV strains, this study identified a range of HPAIV-specific small viral RNAs (mvRNAs) derived from several genome segments. Results from PRR-immunoprecipitations demonstrated that selected HPAIV-derived mvRNAs act as potent PKR-specific immune activators, potentially driving virus-induced host inflammation. Furthermore, distinct RNA secondary structures and selective DVG packaging suggest that specific structural motifs govern both their encapsidation and immune recognition. This project aims to unravel the molecular determinants of DVG formation, characterizing DVG-specific RNA structural elements and dissecting the role of the viral polymerase complex in DVG biogenesis. It further investigates DVG-driven immune activation, and finally, the therapeutic potential of engineered DVGs and mvRNAs as antiviral and immunomodulatory tools.

Keywords

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PhD student

Junior scientist status

Yes, I am a junior scientist.

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