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Splicing regulatory elements in context of splice acceptor regulation in Influenza A

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Pre-mRNA splice site selection and regulation critically depends on RNA-binding proteins, particularly members of SR and hnRNP families, which recognize splicing regulatory elements (SREs) near splice sites in a position-dependent manner. Of the Influenza A virus (IAV) segmented genome, segment 7 and 8 use the host splicing machinery to generate transcript variants through alternative splicing. Differences in SRE capacity and thus, splicing efficiency across subtypes may affect viral replication, gene expression and pathogenicity. To investigate splicing regulation, in silico predictions of SREs near splice acceptors in segment 7 and 8 were performed using the HEXplorer tool. Splicing efficiency was assessed by qRT-PCR and Nanopore sequencing to detect minor variants. RNA affinity chromatography assays were used to identify subtype-specific RBPs near the splice sites in pre-pandemic, post-pandemic, and laboratory IAV strains.

Segment 8 exhibited clear subtype-specific differences: post-pandemic strains displayed an altered NS1/NS2 expression ratio. SRE profiles near the splice acceptor correlated with differential splicing. RNA affinity chromatography assays indicated altered SR protein recruitment across subtypes. Comparison with segment 7 revealed shared and distinct regulatory mechanisms. These findings emphasize strain-specific splicing regulation, suggesting adaptive control of gene expression that may inform future antiviral strategies targeting viral RNA processing.

Keywords

Bioinformatical analysis, Influenza A Virus, splicing, Locked nucleic acids, NXF1 Pathway, mRNA processing

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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