



Guangzhou RNA club

Probing the role of RNA structural heterogeneity in viral RNAs

Zoom meeting link:

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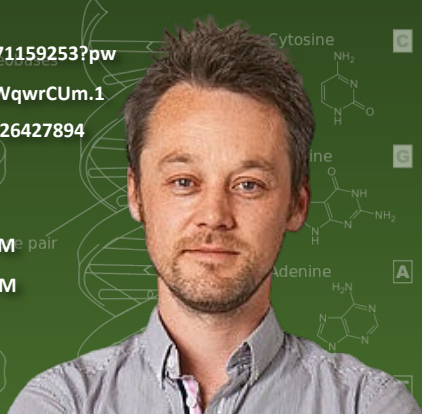
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Time (China): 2024-11-6 20:00 PM

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Abstract:

RNA is a dynamic molecule capable of adopting multiple structures that can interconvert to fulfill its functional roles. The emerging understanding of RNA structural heterogeneity highlights the significance of these conformational changes in regulating processes within viral life cycles. Traditional in-solution chemical probing has been invaluable in studying RNA structure within cells but is limited by its ensemble nature, which averages structural information across all conformations. To overcome this limitation, we developed and applied two complementary strategies. FARS-seq combines physical separation of RNA conformations with high-throughput functional profiling, revealing key motifs in the HIV-1 5' untranslated region (UTR) that impact dimerization and Pr55Gag binding. Meanwhile, Nano-DMS-MaP leverages long-read sequencing to provide isoform-resolved structural insights, identifying distinct structural differences between unspliced and spliced HIV-1 RNAs at the packaging site. These differences likely account for the selective packaging of unspliced RNAs into viral particles. Together, FARS-seq and Nano-DMS-MaP offer new approaches to elucidate the role of RNA structural heterogeneity in viral genome regulation.

HOST & PANELISTS



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Guangzhou RNA club

探讨RNA结构异质性在病毒RNA中的作用

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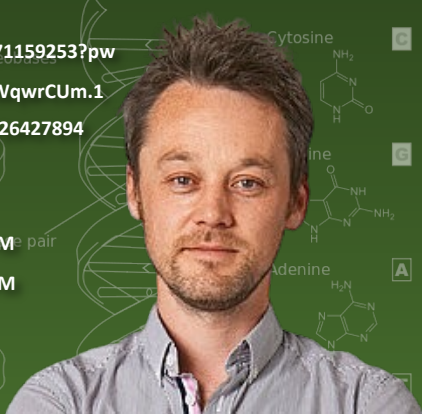
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CNRS分子与细胞生物学研究所

摘要:

RNA是一种动态分子，能够采用多种相互转换的结构来实现其功能作用。对RNA结构异质性的新认识强调了这些构象变化在病毒生命周期内调节过程中的重要性。传统的溶液内化学探针在研究细胞内RNA结构方面具有不可估量的价值，但受其集合性质的限制，它平均了所有构象的结构信息。为了克服这一限制，我们开发并应用了两种互补策略。FARS-seq将RNA构象的物理分离与高通量功能分析相结合，揭示了 HIV-1 5' 非翻译区 (UTR) 中影响二聚化和Pr55Gag结合的关键基序。与此同时，Nano-DMS-MaP 利用长读测序技术提供同种异构体解析的结构见解，识别未剪接和剪接的HIV-1 RNAs 在包装部位的明显结构差异。这些差异可能解释了为什么会有选择性地未剪接的RNA包装成病毒颗粒。FARS-seq和Nano-DMS-MaP共同为阐明RNA结构异质性在病毒基因组调控中的作用提供了新的途径。

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