

真核生物ゲノムアセンブリにおける内在性二本鎖 DNA ウイルスの全体像の解明

Exploring the endogenous dsDNA viral landscape in eukaryotic assemblies

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研究成果概要

Genomic fragments originating from viruses are pervasive in eukaryotic genomes, with retroviral elements being the most extensively studied examples. In contrast, the contribution of double-stranded DNA (dsDNA) viruses to eukaryotic genome evolution has remained largely unexplored. We have developed a large-scale computational strategy to systematically detect dsDNA virus-derived regions across eukaryotic genomes. Applying this approach to more than 37,000 publicly available genome assemblies, we uncovered widespread viral signals embedded in thousands of eukaryotic lineages.

Our analysis reveals that dsDNA virus-associated sequences are present in a substantial fraction of eukaryotic genomes and can constitute a considerable portion of genomic content in some species. These regions link diverse eukaryotic hosts to a broad spectrum of viral lineages, including both known groups and deeply divergent viral branches that have not been previously recognized. The resulting host-virus association network greatly extends current knowledge of dsDNA virus diversity and host range.

Together, our findings highlight the extensive and previously underappreciated footprint of dsDNA viruses in eukaryotic genomes. This resource provides a foundation for future investigations into long-term virus-host interactions and their roles in shaping eukaryotic genome architecture and evolution.