

巨大ウイルスの遺伝子獲得にはウイルス間の遺伝子転移が大きく寄与している

Gene Transfer Among Viruses Substantially Contributes to Gene Gain of Giant Viruses

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研究成果概要

The phylum *Nucleocytoviricota* comprises a diverse group of double-stranded DNA viruses that display a wide range of gene repertoires. Although these gene repertoires determine the characteristics of individual viruses, the evolutionary processes that have shaped the gene repertoires of extant viruses since their common ancestor are poorly characterized. In this study, we aimed to address this gap in knowledge by using amalgamated likelihood estimation, a probabilistic tree reconciliation method that infers evolutionary scenarios by distinguishing origination, gene duplications, virus-to-virus horizontal gene transfer (vHGT), and gene losses. We analyzed over 4,700 gene families from 195 genomes spanning all known viral orders. The evolutionary reconstruction suggests a history of extensive gene gains and losses during the evolution of these viruses, notably with vHGT contributing to gene gains at a comparable level to duplications and originations. The vHGT frequently occurred between phylogenetically closely related viruses, as well as between distantly related viruses with an overlapping host range. We observed a pattern of massive gene duplications that followed vHGTs for gene families that was potentially related to host range control and virus–host arms race. These results suggest that vHGT represents a previously overlooked, yet important, evolutionary force that integrates the evolutionary paths of multiple viruses and affects shaping of *Nucleocytoviricota* virus gene repertoires.

発表論文(謝辞あり)

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