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Preface

"Integration of viral sequences into eukaryotic host genomes: legacy of ancient infections"

All living organisms were exposed to infection by numerous viruses during their evolution and apparently survived this arms race. If we define a virus as an infectious protein-based particle carrying nucleic acids, viruses may already have been around at the time that simple unicellular organisms appeared on earth. This suggests living organisms and their viruses may have a shared history of over three billion years.

Most of our genetic information is stored in chromosomal DNA in the cell nucleus. The genomic DNA has evolved by increasing its length and coding capacity via various mechanisms, including mutations, duplication, recombination and horizontal gene transfer. In addition, we know that viruses as invading genetic elements had a profound impact on genome evolution of living organisms. In vertebrates, DNA sequences closely related to that of retroviruses were discovered in their genomes in the late 1960s. It subsequently became evident that these endogenized sequences, named endogenous retroviruses, accounts for at least 8% of the current human genome and about 10% of the mouse genome. These calculations do not even include retrotransposons, such as LINE and SINE elements, which can be found scattered throughout our genome. Endogenous retroviruses are derived from the genomes of ancient retroviruses that infected the germ line, thereby stably integrating their genome into that of the host, such that these new sequences are inherited in a Mendelian fashion. In other words, endogenous retroviruses are remnants of ancient retroviral infections or "viral fossils".

For fifty years since the discovery of endogenous retroviruses, it was believed that only the reverse-transcribing RNA viruses can end up in the host cell genome because DNA integration forms an essential step in their replication cycle. However, in 2010, two groups independently discovered endogenous viral elements (EVEs) of non-retroviral RNA viruses, including bornavirus and filovirus, in the genome of several mammalian species. These breakthrough discoveries raised fundamental questions about the role of EVEs in host evolution. How do hosts incorporate non-reverse transcribing viral sequences into the own chromosomes? Have these non-retroviral EVEs influenced the diversity and evolution of the host genome? At present, products of several endogenized retroviruses have been shown to play important roles in cellular functions and mammalian biology, such as placenta formation and mRNA transmission between neuronal synapses. On the other hand, very little is currently known about the potential biological function of EVEs derived from non-retroviral viruses in host cells.

This special issue focuses on EVEs that can be found in the genomes of a wide range of host organisms, including mammals, insects and plants and discusses their features and potential functions. Details of the evolutionary analyses of EVEs in vertebrate species are described by M Horie and K Tomonaga for bornaviruses ((-)ssRNA viruses), Y Kobayashi, T Shimazu, K Murata, T Itou and Y Suzuki for adenoviruses (dsDNA viruses) and T Dennis, W Souza, S Marsile-Medun, J Singer, S Wilson and R Gifford for circoviruses (ssDNA viruses). P Pereira, J Abrantes, H Baldauf and P Esteves provide an interesting story on endogenization of a the betaretrovirus rabbit endogenous retrovirus-H in Lagomorph genera. K Kryukov, MT Ueda, T Imanishi and S Nakagawa describe the development of a system for detecting EVE-like sequences in eukaryotes using all available eukaryotic and viral genome assembly sequences. Furthermore, an intriguing story on a novel insect-infecting virus group and pervasive endogenization into insect genomes is presented by H Kondo, S Chiba, K Maruyama, IB Andika and N Suzuki. For plant-derived EVEs, Y Huiwen, X Wang, Y Xu and X Deng, and Q Xu contribute a detailed analysis of endogenous pararetroviruses (reverse-transcribing dsDNA viruses) in six Citrinae genomes. Moreover, JL Carrasco, J Sanchez-Navarro and S Elena report that the 30K-superfamily of plant viral movement proteins in the *Arabidopsis thaliana* genome are expressed at different stages of plant development. This special issue presents new aspects on a wide variety of EVEs in various host organisms and we strongly believe that more discoveries can be expected from this fascinating research field in the near future.

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