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Editorial

Viral Integration into Human Genome, Potential Approaches

Da-Yong Lu[1]* and Ting-Ren Lu[2]

[1]*School of Life Sciences, Shanghai University, PR China*
[2]*College of Science, Shanghai University, PR China*

***Corresponding Author:** Da-Yong Lu, School of Life Sciences, Shanghai University, PR China.

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Abstract

Many viral infections to humans may be deadly events like HIV, Ebola or others. Pathogenic pathways should be explored. This Editorial discusses possible mechanisms for human deaths.

Keyworks: *Viral Infection; HIV; Genome-Wide Associate Study; Human Genome; CD4 T Cells; COVID-19*

Introduction

Many viral infections to humans may be fatal in the clinic. The request of diagnostic and therapeutic clues for this pathogenesis should be explored.

Past hypothesis

The most harmful viral pathogenesis might come from virus-integration of cell genomes [1,2]. However, this hypothesis was not finally proved. Studying the HIV-integration (human immunodeficient virus) of cell genomes of different animal or human cells/tissues is groundbreaking.

Methods

The genome-wide techniques for virus-penetration undergo dramatic progress [3-5]. Drafting human genomes is earliest very difficult. The cost was reduced from 3 billion USD for one genome in 1990-2000 to next generation sequencing (NGS) in 2010 (approximately 4000 USD one genome) [3-5]. This dramatic technical improvement might be useful to testify early hypotheses. At present, genomic sequencing technique is with much less cost and in large-scale. New ideas are converged globally [6-8].

New evaluative systems

New evaluative systems can be attempts:

- *In vitro* or *in vivo* evaluate HIV virus in CD4 T lymphocytes.
- Explore different coronavirus in epithelial cells of respiratory tracts.
- Many other viruses in human lymphocytes or cellular types of many key organs.

Conclusion

By these genomic approaches, curative treatments for deadly virus infection can be developed [2].

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