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Viral integration into human genome, hopes for breakthroughs

Abstract

Many viral infections to humans may be deadly events especially tropical diseases, like HIV, Ebola or others. Pathogenic pathways and therapeutic decision-making should be explored. Viral integration into human genome is the key avenue for preventing and reducing human deaths via deadly viruses. Throughout these process, less casualty will be achieved by modern therapeutics. This Article discusses possible mechanisms and pathways for this virus-induced human deaths.

Keyworks: viral infection, HIV, genome-wide associate study, human genome, CD4 T cells, COVID-19

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Introduction

Viral infections to humans can cause a lot of medical diseases and human deaths.[1–5] Targeting or therapeutics for viral infections are difficult due to vast numbers, types and strains of viruses in nature and diversity for viral pathogeneses and pathways that are still unknown for us.[3–6] Facing with this challenge and dilemma, new discoveries in medical knowledge and techniques should be scaled-up. To conclude, any breakthroughs in medical theories about different viruses can bring up huge socioeconomic benefits and feedbacks.

Human genome pathways

Among vast types of viral infections and pathogenesis, system building and related pathways are especially important and benefiting. Human genomic studies and techniques are one of the most important avenues. Past hypothesis and knowledge should be renewed (Box 1).

BOX 1 Hypotheses and pathways for viral integrations into human cells and genomes

Genome-wide association study for different human cells
Immune response and function for different types of immune cells, growth factors, interleukins or antibodies
Investigation of viral DNA into different somatic cells of human origins or humanized animal cells
Technical promotion for greater speed of genome drafting and reducing costs of genome sequencing as much as possible
Cornerstone discoveries throughout these human genome studies
Therapeutic studies for curability of most deadly virus infections and induced deaths

Pathological analysis and knowledge

The most harmful viral pathogenesis might come from virus-integration of cell genomes.[7] However, this hypothesis was not finally proved by global scientists. Studying the HIV-integration (human immuno-deficient virus) of cell genomes of different animal or human cells/tissues is groundbreaking and as a good example for future studies. Associated evidence and association between viral infection and cancer development began very early (from 1930 to 1950).[8–10] This kind of research is biologically narrow-range of genomic studies. It is technologically not suit to clinical viral diagnosis and therapeutics decision-making. Limited information was encompassed throughout whole processes. More information is needed for expanding viral diagnosis, pathogenesis and therapeutic purposes. New avenues are proposed for viral-genomic interaction and associative studies.[11,12]

Technical progress

The genome-wide techniques for virus-penetration undergo dramatic progress. Drafting human genomes from 3 billion USD for one genome in 1990-2000 to next generation sequencing (NGS) in 2010 (approximately 4000 USD one genome).[13–15] This dramatic technical improvement helps us to testify early hypotheses with easiness and correctness. At present, genomic sequencing technique is with much less cost and in large-scale. New ideas are converged and mechanisms with different types of viruses split globally (Figure 1).[16–18]

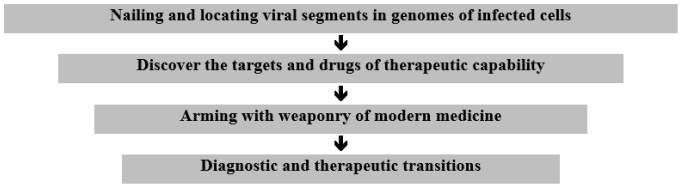

Figure 1 Progress of genomic-related drugs and therapies

New evaluative systems

New evaluative systems can be attempted. A lot of different viruses or human cell types can be experimentally evaluated. We enlist them in several pathways;

► In vitro or in vivo evaluate HIV virus in CD4 T lymphocytes[11]

- Explore different coronavirus in epithelial cells of respiratory tracts[12]
- HPV virus to keratinocytes[8]
- Many other viruses in human lymphocytes or cellular types of many key organs[12]
- Human genome technical studies and data[10]

Conclusion

Healthy environments for experimental revolution, sufficient funds, and publication supports can facilitate these genomic researches. It can provide more avenues for starting-up new exploration.

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Conflicts of interest

The authors declares that there are no conflicts of interest.

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