

# Study of viral integration into human genome, is technique

## Abstract

Many viral infections to humans are deadly, like HIV, Ebola or others. The request of discovery and treatments of this pathogenesis is needs updating knowledge and techniques. This Editorial discusses one of these hypotheses.

**Keywords:** viral infection, HIV, genome-wide associate study, human genome, DNA sequencing

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## Introduction

Many viral infections to humans are deadly, like HIV, Ebola or others. The request of discovery and treatments of this pathogenesis is needs updating knowledge and techniques. The most harmful viral pathogenesis might be virus-penetration into human genomes of infected cells or tissues.<sup>1,2</sup> This hypothesis has been less systematically studied and finally proved. If it is true, new therapies will be quickly discovered. Studying the HIV-integrating to the genomes of different animal or human cells/tissues is a paramount task in current HIV-treatment study. This study is not overwhelmed now.

## Methods

Systemic genome-wide study for human genomes and virus-penetration is unavoidable avenue to in-depth study of HIV/AIDS or other deadly viruses. These researches ranges from biology to pathology. Diagnostic and therapeutic issues include about costs and techniques.<sup>3-5</sup>

## Discussion

Drafting human genomes is earliest very difficult. The cost was developed from human genome project -3 billion USD for one genome in 2000 (approximately one dollar for one base) to next generation sequencing (NGS) in 2010 (approximately 4000 USD one genome).<sup>3-5</sup> This dramatic technical improvement might prove my early hypotheses soon.

At present, genomic sequencing technique is a convention. A plenty of similar methods are emerging.<sup>6</sup> With the assistance of computational work, mathematics and new genomic editing study, viral-integration into human cells might be finally resolved.<sup>7</sup> The therapeutic breakthroughs are waiting ahead.

## Conclusion

Currently, genome wide associate study is becoming normal convention in most global labs. This kind of sequence exploration and scientific landscape can be finished within ten years. It is exciting to look at it.

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## Conflict of interests

The author declares that there are no conflicts of interest.

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