Advancing the Rapid Engineering of Vesicular Stomatitis Virus through Synthetic Virology

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Introduction

Vesicular Stomatitis Virus is a negative-sense RNA virus belonging and it has attracted significant attention in recent years due to its potential as a model organism for understanding viral pathogenesis, as well as its promising applications in gene therapy, oncolytic virotherapy, and vaccine development. Traditional methods for studying and engineering VSV have been limited by time-consuming and labor-intensive processes. However, the advent of synthetic virology, a multidisciplinary approach combining molecular biology, genetic engineering, and computational tools, has revolutionized the ability to rapidly manipulate VSV and other viruses for various research and therapeutic purposes. Synthetic virology allows for the precise engineering of viral genomes, enabling researchers to design and construct viral variants with tailored properties. This ability to control and modify viruses at a genomic level has accelerated the development of novel viral vectors, therapeutic strategies, and disease models. In this article, we explore how synthetic virology has advanced the rapid engineering of VSV, focusing on the methodologies, applications, and future prospects of this exciting field [1,2].

Description

Vesicular Stomatitis Virus is a negative-strand RNA virus that primarily infects livestock, causing vesicular lesions on the mouth, udder, and hooves of affected animals. Although VSV is not considered a major threat to human health, its genetic and biological similarities to other clinically significant viruses, such as rabies and Ebola, make it an attractive model for studying viral infections and developing novel antiviral strategies. VSV has several characteristics that make it a valuable tool in synthetic virology. First, its genome is relatively simple compared to other viruses, consisting of a singlestranded, negative-sense RNA molecule that encodes five structural proteins: nucleoprotein, phosphoprotein, matrix protein, glycoprotein and the RNAdependent RNA polymerase. The virus also exhibits robust replication in cultured cells and can be easily propagated in a laboratory setting, making it ideal for genetic manipulation. Moreover, VSV's relatively small genome and the presence of an uncomplicated replication mechanism make it a suitable candidate for genetic engineering. The ability to insert foreign genes into the VSV genome has been explored in numerous applications, including vaccine development and oncolytic virotherapy. Synthetic virology involves the design and creation of viral genomes using synthetic biology techniques, including gene synthesis, genome assembly, and genetic modification. The goal is to engineer viruses for specific purposes, such as understanding viral biology, creating viral vectors for gene delivery, or designing novel vaccines and therapeutics. The power of synthetic virology lies in its ability to design viral genomes with highly predictable outcomes, providing researchers with tools that were previously unavailable using traditional virology methods [3-5].

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Conclusion

In the past 20 years, there has been remarkable progress in the in vitro culture of human norovirus. From early attempts with B-cell lines to the development of sophisticated human intestinal organoid models, these advancements have significantly improved our ability to study norovirus pathogenesis, viral replication, and interactions with host cells. As a result, we now have a more accurate understanding of the virus's lifecycle, the receptors it uses to enter cells, and its relationship with the gut microbiome. Moreover, these developments have opened up new possibilities for drug and vaccine development, which are crucial for controlling norovirus infections and reducing their public health impact. While challenges remain, particularly in scaling up the replication of human norovirus in vitro, these advancements represent a crucial step forward in the fight against one of the world's most prevalent gastrointestinal pathogens. As research continues to evolve, the prospects for new therapies and vaccines against human norovirus are brighter than ever.

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Conflict of Interest

None.

References

- 1. Chua, Gilbert T., Joshua Sung Chih Wong, Ivan Lam and Polly Po Ki Ho, et al. ["Clinical characteristics and transmission of COVID-19 in children and youths during](https://jamanetwork.com/journals/jamanetworkopen/article-abstract/2779416) [3 waves of outbreaks in Hong Kong.](https://jamanetwork.com/journals/jamanetworkopen/article-abstract/2779416)" *JAMA Netw Open* 4 (2021): 218824-218824.
- 2. Feldman, Charles and Ronald Anderson. "[The role of co-infections and secondary](https://link.springer.com/article/10.1186/s41479-021-00083-w) [infections in patients with COVID-19](https://link.springer.com/article/10.1186/s41479-021-00083-w)." *Pneumonia* 13 (2021): 1-15.
- 3. Shen, Xu-Rui, Rong Geng, Qian Li and Ying Chen, et al. ["ACE2-independent](https://www.nature.com/articles/s41392-022-00919-x) [infection of T lymphocytes by SARS-CoV-2](https://www.nature.com/articles/s41392-022-00919-x)." *Signal Transduct Target Ther* 7 (2022): 83.
- 4. Billard, Marie-Noëlle and Louis J. Bont. "[Quantifying the RSV immunity debt](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(22)00544-8/fulltext) [following COVID-19: A public health matter.](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(22)00544-8/fulltext)" *Lancet Infect Dis* 23 (2023): 3-5.
- 5. Messacar, Kevin, Rachel E. Baker, Sang Woo Park and Hai Nguyen-Tran, et al. ["Preparing for uncertainty: Endemic paediatric viral illnesses after COVID-19](https://www.thelancet.com/article/S0140-6736(22)01277-6/fulltext) [pandemic disruption.](https://www.thelancet.com/article/S0140-6736(22)01277-6/fulltext)" *Lancet* 400 (2022): 1663-1665.

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