Genetic diversity-based design of Nipah virus Fusion protein vaccines candidate sequences in Malaysia, Bangladesh, and India.

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Introduction

Nipah virus (NiV) is a highly pathogenic zoonotic paramyxovirus causing encephalitis and severe respiratory disease in Southeast Asia with high mortality. Current treatment measures for NiV infection are insufficient, and there is no approved vaccine against NiV for either animals or humans. NiV has an envelope with filamentous nucleocasids containing a genome of six major structural proteins (N-P-M-F-G-L). Nipah virus has continued to re-emerge in India, Bangladesh, and Malaysia, and person-to-person transmission appeared in the outbreak. Although several NiV vaccine studies have been reported, no vaccines or treatments are currently licensed for human use. In this study, we evaluate NiV vaccine antigen design options, including the fusion glycoprotein.

Method

All the NiV Fusion protein sequences available in December 2022 in National Center for Biotechnology Information (NCBI) GenBank database(http://www.ncbi.nlm.nih.gov/genbank/) were included in the analysis. The sequence dataset included **70** glycoproteins that deleted sequences from unknown sources or too short in length. The sequences were aligned and assembled

using the CLC Main Workbench software, version 6.9 (CLC Bio, Aarhus, Denmark).

Result

This study aims to compare genetic sequences of NiV fusion protein strains in Malaysia and Bangladesh and investigate the maximum likelihood of phylogenetics. The KV NiV-F consensus sequence showed higher similarity to and clustering with the Bangladeshi viruses. The KV NiV-F consensus sequence was 93.3%-93.9% homologous with the reference NiV F sequences.

Conclusion

Our NiV F representative sequences suggest this human vaccine could be utilized as an efficient emergency vaccine to disrupt the potential spreading of Nipah disease in an outbreak setting.