

An Assessment of the Epidemiology, Transmission, Diagnosis, Prophylaxis, and Pandemic Potential of the Nipah Virus †

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Abstract: Nipah Virus (NiV) is an enveloped, negative-sense RNA virus that belongs to the Paramyxoviridae family. The first emergence was seen in Malaysia in 1998 and then subsequently caused numerous outbreaks in Southeast Asia. It is highly pathogenic to an extensive range of mammals and is considered to have pandemic capabilities because of its ability to transmit from animals and person to person. At first, it is thought that it is the Japanese B encephalitis virus (JEV) as it is associated with pigs and detection of specific IgM antibodies in patient sera. The reservoir of NiV is Bat (i.e., Pteropus species or Fruit bats). There are six genes present in the RNA genome of NiV, which encodes for Nucleocapsid (N), Fusion protein (F), Phosphoprotein (P), Matrix protein (M), Glycoprotein (G) & Polymerase protein (L). Transmission of NiV is primarily from Bats to animals or bats to humans or animals to humans, but human to human transmission is barely occurring, such as in the outbreaks seen in Bangladesh and India. The incubation period in animals is 4 - 21 days, and by raw date, palm ingestion is about 10 days. The NiV infection clinical symptoms range from asymptomatic to very severe, and most of the patients show symptomatic symptoms associated with CNS and respiratory diseases. Diagnosis of NiV can be done by various ways like Serological methods (ELISA, Virus Neutralization & Luminex) and Molecular methods (RT-PCR, Tissue Culture method, and Immunohistochemistry). At present, there are no vaccines available for NiV, but symptomatic treatment is given to the patient.

Keywords: Nipah Virus (NiV); Paramyxoviridae; JEV (Japanese B encephalitis virus); RT-PCR; ELISA.

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Conflicts of Interest

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