EDITORIAL COMMENT

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# Nipah Upsurge: The Wave of Deadly Virus

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Nipah virus (NiV) infection is an upcoming zoonotic infection that causes medically significant disease in both animals and humans. The natural primary hosts of the virus are fruit bats (flying foxes) of the Pteropodidae Family and genus Pteropus.[1,2]

Nipah virus (NiV) is a member of the family Paramyxoviridae, genus Henipavirus.It was initially identified during an outbreak of encephalitis and respiratory illness that took place in Kampung Sungai Nipah, Malaysia in 1998 where pigs were the intermediate hosts and the name Nipah originated from this place of breakout. It was back in 2004 in Bangladesh, when humans became infected with this viral disease as a result of consuming date palm sap already contaminated by infected fruit bats. In a hospital setting in India, human-to-human transmission has also been documented.[1]

NiV infection in humans presents with a wide range of clinical symptoms, from asymptomatic infection to life threatening acute respiratory syndrome and even fatal encephalitis. The most common signs are fever, headache, myalgia, vomiting, dizziness, tachypnea, altered sensorium, convulsions, involuntary movements, reduced level of consciousness and prominent brain-stem dysfunction. It is also capable of infecting pigs, cats, dogs, goats, horses and other domestic animals.

The genome of the causative agent consists of six genes that yield nucleoprotein, phosphoprotein, matrix, fusion, glycoprotein and large RNA polymerase and contains around 18250 nucleotides due to an extended open reading frame of the P gene.[3] The G and F proteins of NiV are required in mediating the viral entry into the cell as well as for inducing neutralizing antibodies.[4] The P protein is the only essential gene product for replication of the genome and the additional often serve as virulence factors.[5,6]

Infections caused by NiV in humans and animals can be confirmed by isolating the causative organism, nucleic acid amplification and serological tests like ELISA. This infection can also be detected by molecular level diagnostic tests like Real Time-Polymerase Chain Reaction (RT-PCR), Taqman test and Duplex nested RT-PCR.[3]

Currently, there is no vaccine to prevent this disease in either humans or animals. Intensive supportive care is the mainstay of treatment in human cases. The key fundamental to keep a check on the outbreak and controlling it and reducing the morbidity/mortality rate is early recognition of the breakout and establishing preventive strategies on a preliminary basis. There is an essential requisite to have collaboration between healthcare research institutes and international coordination among human-animal virologists and ecologists to thoroughly understand and decipher this viral epidemic. Concurrently there is also a requirement of instructing and guiding the public regarding the good standards of personal and food hygiene.

World Health Organisation has convened a Task Force to formulate a strategic time based plan for the development of diagnostic and therapeutic procedures and vaccines for Nipah. The Center for Epidemic Preparedness and Innovation has declared that it will financially support the development of vaccines for humans against Nipah. However, until additional measures become available, health education followed by scrutiny and surveillance along with the outbreak response prevail to be the most efficacious public health tools to tackle and battle this disease.[7]

## REFERENCES

1. http://www.who.int/csr/disease/nipah/en/
2. https://www.cdc.gov/vhf/nipah/index.html
3. Kulkarni DD, Tosh C, Venkatesh G, Senthil Kumar D. Nipah virus infection: current scenario. Indian Journal of Virology. 2013;24(3):398-408.
4. Tamin A, Harcourt BH, Ksiazek TG, Rollin PE, Bellini WJ, Rota PA. Functional properties of the fusion and attachment glycoproteins of Nipah virus. Virology. 2002;296(1):190–200.
5. Devaux P, Cattaneo R. Measles virus phosphoprotein gene products: Conformational

flexibility of the P/V protein amino-terminal domain and C protein infectivity factor function. J Virol. 2004;78(21):11632–40.
6. Devaux P, Hodge G, McChesney MB, Cattaneo R. Attenuation of V- or C defective measles viruses: infection control by the inflammatory and interferon responses of rhesus monkeys. J Virol. 2008;82(11):5359–67.
7. Chatterjee P. Nipah virus outbreak in India. Lancet 2018;391(10136):2200

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