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Nipah virus Disease: Unusual and Obstinate Disease

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Abstract: *The aim of this work was to study the Nipah virus (NiV) infection, a newly emerging zoonosis that causes severe disease in both animals and humans. Human population have been plagued by diseases of various types and origins. Zoonotic disease which have the capability of been transmitted from specie to another or to other animals. According to WHO, Nipah virus infection was first recognized in a large outbreak of 265 suspected cases in peninsular Malaysia during September 1998 to April 1999. These pathogens typically survive in a reservoir host. The lists of possible reservoir hosts capable of transmitting disease to humans are apes, insects, rodents, and bats. The diseases are then passed to humans who come in contact with an infected animal through bites or scratches, an infected animal's environment, or animal secretions such as saliva, faeces, or mucus. Nipah virus is an enveloped, negative-sense, single-stranded RNA virus in the family Paramyxoviridae, genus Henipavirus. The name of the virus and disease was from the village of "Sungai Nipah" in Malaysia where the first human cases lived. Nipah virus invade its host by is by inducing syncytial cell formation which spread rapidly through the vascular tissue of the infected host. Incubation time is usually short between 2 and 10 days. The Nipah virus primarily attacks the respiratory system, which is supported by the finding of high concentrations of viral antigens are found in the respiratory tract and lung epithelium.*

Keywords: *Nipah virus, Zoonotic disease, Animal, Host, Outbreak.*

Introduction

Right through the history of the world, human population have been plagued by diseases of various types and origins. Zoonotic disease having the capability to jump from specie to specie or animals to humans or vice versa are particularly troublesome and deadly (Chadha *et al,* 2006). Zoonotic diseases are unique in that they are mainly caused by pathogens such as fungi, bacteria, parasites, or viruses. These pathogens typically survive in a reservoir host, which have immunity to the pathogen. The list of possible reservoir hosts capable of transmitting disease to humans is expansive; however the most common are apes, insects, rodents, and bats (WHO, 2018). The diseases are then passed to humans who come in contact with an infected animal through bites or scratches, an infected animal's environment, or animal secretions such as saliva, feces, or mucus. Often these diseases have a higher virulence

because of the lack of any immunity within the human population and the ease of transmission. Some more infamous Zoonotic diseases are West Nile, Rabies, Ebola, and Dengue fever. As of recent, more and more Zoonotic diseases are emerging because of an increase in human and wildlife interaction. An increase in farming and or deforestation has resulted in humans and wildlife into the same habitat. A prime example of this is the emergence of the Nipah virus (NiV) (WHO, 2009)

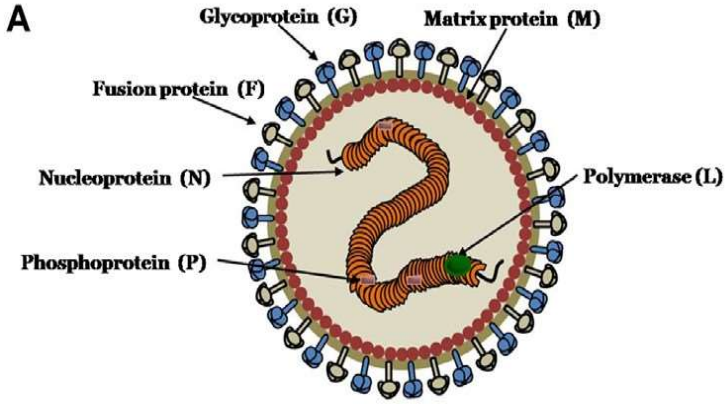
NiV was first identified during an outbreak of disease that took place in Kampung Sungai Nipah, Malaysia in 1998. On this occasion, pigs were the intermediate hosts. However, in subsequent NiV outbreaks, there were no intermediate hosts. In Bangladesh in 2004, humans became infected with NiV as a result of consuming date palm sap that had been contaminated by infected fruit bats. Human-to-human transmission has also been documented, including in a hospital setting in some parts of as neighbours of affected countries India.

NiV infection in humans has a range of clinical presentations, from asymptomatic infection to acute respiratory syndrome and fatal encephalitis. NiV is also capable of causing disease in pigs and other domestic animals. There is no vaccine for either humans or animals. The primary treatment for human cases is intensive supportive care (Eaton, 2001).

The Etiological Agent and its Morphology

Nipah virus is an enveloped, negative-sense, single-stranded RNA virus in the family Paramyxoviridae, genus *Henipavirus.* The name of the virus and disease was from the village of "Sungai Nipah" in Malaysia where the first human cases lived. Nipah virus is in the newly created Henipavirus genus with the closely related Hendra virus and Cedar virus. The Henipavirus family is pleomorphic, meaning their shape is varied, and traditionally 40 to 600 nm in diameter. The core of a virion contains a linear ribonucleprotein (RNP) comprising of negative sense single stranded RNA. Also present in the RNP are three critically important proteins, Nucelocapsid proteins (N) are tighly bound to the various nucleotides of the RNA strand. N protein is the most abundant protein present and necessary for capsid structure. Phosphoproteins (P) and large polymerase proteins (L) (Bonaparte *et al*, 2005)

The three key proteins and other two P, N, F, G, M, and L, are shown in their natural position and labeled. In the center of the virion is the negative sense single stranded RNA, covered by orange N proteins. The P proteins are pink, the F proteins are grey spikes, G proteins are blue spikes, M proteins are red circles, and L proteins are green as clearly shown on the structure mentioned bellow.



(Sun *et al*. 2018)

Mode of Transmission

Mode of transmission differs from country to country. Through analysis of urine and saliva collected from a suspected reservoir host from the original outbreak in Malaysia, a country of origin of the virus, the reservoir host has been identified as the *Pteropus* fruit bat (Chadha *et al,* 2006)

NiV infection has been found in 5 of 14 fruit bat species, with the highest being *Pteropus hypomelanus* with a 31% infection rate. Despite having a relatively high infection rate, the species of *Pteropus* fruit bats are not susceptible to the virus. The virus is primarily transmitted via body secretions or partially eaten fruit. Pigs have been found to be particularly susceptible to NiV as well as highly contagious to each other. Pigs have been identified as an intermediate and an amplifying host.

Humans have been found to be infected by three different pathways, *Pteropus* fruit bat to human, pig to human, and or human to human. Most recent transmission of NiV has been a result of human to human transmission through close contact through respiratory secretions or urine. However, the reservoir and intermediate hosts are *Pteropus* fruit bats and pigs, respectively. Because of the heavy prevalence of virus transmission via respiratory secretions it is assumed the main site of replication occurs in the tonsils of an infected host. (Coetzer *et al*, 2004).

Because of the variation in the effect and fatality rate of the Nipah virus outbreak in Bangladesh and India, a slightly altered transmission path is suggested. It is suggested a more direct path was taken from the reservoir host, *Pteropus* fruit bats, directly to humans. The large consumption of date palm sap by humans is looked to be where the virus was picked up (Sazzad *et al,2013*). *Pteropus* fruit bats feed heavily on date palm trees, licking the sap which contaminated the sap. Improper cooking of the sap resulted in humans ingesting the infected sap. A second mode of transmission is through contact with infected *Ptreopus* fruit bat feces, urine, or saliva, although human to human transmission had not been suggested in the Malaysia/Singapore outbreak.

Pathology of Nipah Virus

Nipah virus invade its host by is by inducing syncytial cell formation, these large multinucleated cells then spread rapidly through the vascular tissue of the infected host. Incubation time in pigs varies but is usually short between 2 and 10 days. The Nipah virus primarily attacks the respiratory system, which is supported by the finding of high concentrations of viral antigens are found in the respiratory tract and lung epithelium (Bossart, 2008).

Global outbreaks of Nipah virus

According to WHO, Nipah virus infection was first recognized in a large outbreak of 265 suspected cases in peninsular Malaysia during September 1998 to April 1999. Most patients had contact with sick pigs or had been in close physical contact with Nipah virus infected patients and then presented primarily with encephalitis. The outbreak was initially thought to be due to Japanese encephalitis, but it was later identified as Nipah virus encephalitis (Brown *et al*, 2008). This outbreak caused widespread panic and fear in Malaysia leading to considerable social disruptions and tremendous economic loss because of the mass culling of over one million pigs. In addition, eleven abattoir workers in Singapore developed a febrile illness caused by Nipah virus during March 1999 following close contact with imported pigs from Malaysia (Chua *et al*, 1999). The presentation of Nipah virus infection has been variable, ranging from the high mortality observed in the original Malaysian outbreak to an outbreak of low mortality disease among abattoir workers in Singapore, which presented as neurological illness and atypical pneumonia. No new outbreaks have been reported from these countries since May 1999.

Second most affected country is Bangladesh. The first identification of Nipah virus as a cause of an outbreak of encephalitis was reported in 2001 in Meherpur district of Bangladesh. Since then, outbreaks of Nipah virus encephalitis have been reported almost every year in selected districts of Bangladesh. The Nipah outbreaks have been identified in Naogoan (2003), Rajbari and Faridpur (2004), Tangail (2005), Thakurgaon, Kushtia and Naogaon (2007), Manikgonj and Rajbari (2008), Rangpur and Rajbari (2009), Faridpur, Rajbari and Madaripur (2010) and Lalmohirhat, Dinajpur, Rangpur and Comilla (2011) and Joypurhat, Rajshahi, Rajbari and Natore (2012). Repeated outbreaks of Nipah virus encephalitis were established in some districts. Sporadic cases of Nipah virus encephalitis have been reported, mostly from the west and north-western regions of Bangladesh almost every year, with high mortality and constituting a public health threat. Up to March 31, 2012, a total of 209 human cases of NiV infection in Bangladesh were reported; 161 (77%) of them died.

Recent outbreak of Nipah virus

According to WHO, on 19 May 2018, a Nipah virus disease (NiV) outbreak was reported from Kozhikode district of Kerala, India. This is the first NiV outbreak in South India. There have been 17 deaths and 18 confirmed cases as of 1 June 2018. The two affected districts are Kozhikode and Mallapuram. A multi-disciplinary team led by the Indian Government's National Centre for Disease Control (NCDC) was in Kerala in response to the outbreak. WHO is providing technical support to the Government of India as needed (Coetzer *et al*, 2004).

Symptoms of Nipah virus

In animals, typical clinical symptoms are observed in pigs where respiratory symptoms dominate. Nipah virus disease in pigs is also known as porcine respiratory and neurologic syndrome as well as barking pig syndrome based on clinical observation.

Symptoms of NiV infection in humans are similar to that of influenza such as fever and muscle pain. In some cases, inflammation of the brain occurs leading to disorientation or coma. Encephalitis may present as acute or late onset. The latter may be difficult to diagnose since exposure may have taken place several months earlier. Further, those who may have recovered from an acute episode may also have a relapse.

Detection and Treatment

There has yet to be a standard protocol in detecting Nipah viral infections but the most common process used currently is virus isolation from tissue samples. In all species NiV can be detected and isolated from the kidneys, cerebrospinal fluid, and the liver. Polymerase chain reaction, enzyme-linked immunosorbent, and immunofluorescence assays are also viable detection strategies (Torres-Velez, *et al*. 2008)

Prevention and Control

• Strict biosecurity of swine installations with the aim of avoiding contact with fruit bats and their secretions is essential, including: fruit tree set-back, using screens at open-air access and appropriate disposal of roof run-off

• An active surveillance program with rapid detection and immediate culling of seropositive swine is critical in preventing spread of disease and infection of humans

• Effective quarantines and control of animal movements must also be implemented early in an outbreak

• All materials and equipment from affected farms should be cleaned and disinfected before transport

• Control of any access to swine by wild or domestic animals must be enacted

Medical prophylaxis

• No vaccines yet exist but recent experiments in cats seem promising

(WHO, 2012;2018)

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