

## Nipah Virus Outbreak in India Amidst of COVID-19 Pandemic

While the [coronavirus disease 2019](#) (COVID-19) pandemic hit the world with devastating impact, the southern Indian state of Kerala was dealing with it in a firm manner, keeping case counts low enough that the healthcare system was never overwhelmed at any point, while supporting the needs of the economically deprived who had no means of regular income-generating work.

However, within this period there was a brief scare, related to the identification of a single case of encephalitis due to the [Nipah virus](#). This pathogen had caused an outbreak in 2018, and a single case also occurred in 2019.



A new study deals with the single case that occurred in 2021, at the end of August, with no discoverable [chain of transmission](#), apparently ending with the death of the index patient.

### Introduction

The Nipah virus (NiV) is a virus that causes acute severe encephalitis and [acute respiratory distress syndrome](#) with a high lethality rate. It was first detected in Malaysia, in an outbreak among pig farmers, in 1981, causing severe encephalitis. The transmission was then determined to be via direct contact with respiratory secretions or body fluids from animals like pigs or bats, that harbor infection with the virus.

Another potential route of transmission is via the consumption of fruits, or palm sap, contaminated with the saliva of the [bats](#).

Nipah is considered to be endemic in South-East Asia, with Singapore, Bangladesh and India all having reported outbreaks of the [virus](#) since then. In Bangladesh, the virus was considered to have spread to humans via bat saliva-contaminated palm sap or when they climbed trees contaminated with bat excreta.

In India, the first outbreak occurred in West Bengal, on the eastern coast, bordering Bangladesh, mainly involving an index patient hospitalized in Siliguri during January-February 2015, which spread to his visitors and [health workers](#). The next occurred in Kozhikode district, Kerala state, in May 2018,

in the town of Perambra, with 23 cases and a fatality rate of 89% (21 deaths). However, this was successfully contained.

Further testing by the Indian Council of Medical Research – National Institute of Virology (ICMR-NIV) showed that the bat species [Pteropus medius](#) contained anti-NiV nucleic acid and antibodies. At this time, about one in five bats from Thodupuzha 200 km from Kozhikode, contained NiV RNA. The lack of bat movement record-keeping in India severely hampers an assessment of the spread of the virus.

These bats appear to have a smaller home range than another fruit bat species, [P. vampyrus](#), found in Malaysia, but this may vary with food availability. It is essential to track bat movements and their interconnections to help understand to what extent this virus can spread to adjoining bat colonies.

In fact, during the 2018 outbreak, a quarter of bats were seropositive for [anti-NiV antibodies](#). The high seroprevalence could mean lower viral spread.

### **Study**

The only case that occurred this year, in August 2020, was in an adolescent male presenting with acute encephalitis, who rapidly worsened and died. With early detection by the local doctors, both state and national epidemiological interventions succeeded in limiting the [outbreak](#).

The patient tested positive for serum anti-NiV IgM, but virus isolation was unsuccessful. The researchers carried out [quantitative real-time RT-PCR](#) (qRT-PCR), enzyme-linked immunosorbent assay (ELISA) based antibody detection and whole genome sequencing, contact tracing and isolation, and bat testing in the region.

All potential contacts of the adolescent boy who developed meningo-encephalitis were traced, and isolated. The bats near the boy's home were sampled, with throat swabs, rectal swabs and blood samples, using real-time RT-PCR, as well as [ELISA testing](#) for anti-Nipah IgG bat immunoglobulin G (IgG) antibodies.

They also carried out a [plaque](#) reduction neutralization test (PRNT) In order to detect neutralizing antibodies.

The results showed the presence of Nipah RNA and [IgG antibodies](#) to the virus within the serum of the young male patient. Immediate measures were taken to set up a diagnostic site for NiV, to enable rapid contact testing once traced, and for bat testing.

The field laboratory screened 125 contacts in all, all of whom were asymptomatic, as well as suspected NiV cases not linked to the index case. No further cases were detected. However, 12 close contacts were found to be [COVID-19 positive](#) by qRT-PCR, with 10 Delta variants being detected.

[Phylogenetic analysis](#) showed that the NiV genomic sequences from the index case formed a distinct subtype from the Bangladesh genotype, subclustering with the Nipah I ("Indian") genotype sequences. They showed over 99% similarity to the NiV sequences from human samples (2018) and *P. medius* samples (2019). NiV RNA could not be detected in any of the bat samples in the present study.

The researchers also sampled bats belonging to *P. medius*, [Rousettus leschenaultia](#), and *Pipistrellus* species. About one in five bats of the *P. medius* species were found to be seropositive for anti-NiV IgM in the current outbreak, and one in three *R. leschenaultia* bats, but no bat was found to be positive for viral RNA.

When classified by site, Kodyathur, about one kilometer from the home of the index case, and Thamarassery, 18 kilometers away, were found to have 20% and 56% seropositivity among bats, respectively. The presence of [neutralizing antibodies](#) in *P. medius* samples was confirmed by PRNT, but *R. leschenaultii* samples were not found to contain neutralizing activity against NiV.

Two [juvenile bats](#) were also found to be seropositive for anti-NiV IgG antibodies, indicating an enzootic cycle had occurred quite recently.

### **Conclusion**

The results of the field investigation indicate a sporadic spill-over episode from *P. medius* into humans. These have a significant [seropositivity rate](#), indicating their potential reservoir status.

The transmission cycle appears to implicate pigs and bats, according to currently available data, with *P. medius* being the major reservoir species. This is the only bat from this genus found on the Indian subcontinent, and in [Kerala](#), it seems to support a stable population of the virus that circulates locally.

While successive outbreaks have occurred in regions separated by 200 kilometres, the paucity of records detailing the movement of [Pteropus bat species](#) has hampered an assessment of virus spread by this means.

The fact that all bat samples proved to be negative for viral RNA corroborates previous studies that have shown a low rate of test positivity among these bats. Since virus shedding is dependent on the [immune status](#) of the individual, pregnancy, increases in the viral burden, and stress, among other factors, this variability is to be expected. Adult bats may be reinfected as immunity wanes in about seven years.

Seasonal outbreaks have been reported so far, mostly associated with the breeding season and fruit harvesting season, but in Kerala, the three outbreaks have occurred in May, June and August respectively. Immunity may wane over time, along with the loss of [maternally-derived antibodies](#), which could influence the transmission among bats.

Local epizootic spread in bats are thought to have caused the [Bangladesh outbreaks](#). Sporadic outbreaks may be due to these factors, interacting with human-bat spill over transmission events.

There is also a possibility that other NiV-seropositive bat species may play a role in transmission to humans. In India, *R. leschenaultii* and *P. pipistrellus* are potential reservoirs of the virus, having tested positive by RT-PCR. Since these [fruit bats](#) share the same food sources, they may experience interspecies transmission.

In fact, in the current study, *R. leschenaultia* were found to be seropositive, but anti-NiV neutralizing antibodies were not detected, indicating that the serology could be affected by the presence of other cross-reacting Henipaviruses. This is borne out by [Vietnamese studies](#), indicating that the seropositivity may be due to cross-reacting antibodies elicited by non-neutralizing epitopes.

The sporadic occurrence of spill over transmission indicates the need for more stringent surveillance, with educational campaigns to raise the level of awareness in the vulnerable local population. This could limit the interactions between humans and bats and thus prevent spill over events at the human-bat interface. Continuing surveillance for acute encephalitis and [severe acute respiratory infections](#) will help detect NiV cases early and prevent further transmission.

**Source:**

<https://www.news-medical.net/news/20211215/Containing-a-Nipah-virus-outbreak-amidst-the-COVID-19-pandemic.aspx>