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# Molecular detection of a novel paramyxovirus in fruit bats from Indonesia

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## Abstract

**Background:** Fruit bats are known to harbor zoonotic paramyxoviruses including Nipah, Hendra, and Menangle viruses. The aim of this study was to detect the presence of paramyxovirus RNA in fruit bats from Indonesia.

**Methods:** RNA samples were obtained from the spleens of 110 fruit bats collected from four locations in Indonesia. All samples were screened by semi-nested broad spectrum reverse transcription PCR targeting the paramyxovirus polymerase (L) genes.

**Results:** Semi-nested reverse transcription PCR detected five previously unidentified paramyxoviruses from six fruit bats. Phylogenetic analysis showed that these virus sequences were related to henipavirus or rubulavirus.

**Conclusions:** This study indicates the presence of novel paramyxoviruses among fruit bat populations in Indonesia.

## Background

The genus *Henipavirus* in the subfamily *Paramyxovirinae*, family *Paramyxoviridae*, contains two highly pathogenic viruses, i.e., Hendra virus and Nipah virus. Hendra virus causes fatal pneumonia and encephalitis in horses and humans. The first case was identified in 1994 and Hendra virus disease still continues to arise sporadically in Australia [1,2]. Nipah virus also causes acute encephalitis and respiratory symptoms in animals and humans, with a high mortality rate. Outbreaks of Nipah virus have occurred in Malaysia, Singapore, Bangladesh, and India [1,2]. Henipaviruses have been isolated from fruit bats including *Pteropus vampyrus* [3], *Pteropus hypomelanus* [4], *Pteropus hylaei* [5], *Pteropus poliocephalus*, and *Pteropus alecto* [6], which are considered to be their natural reservoirs. Epidemiological studies demonstrate that Hendra and/or Nipah virus-seropositive fruit bats are widely distributed throughout Asian countries [7-11]. No human cases of henipavirus infection have been reported in Indonesia, although *Pteropus vampyrus* that are seropositive for both Nipah virus and Hendra virus are distributed nationwide [12,13]. These findings

indicate the presence of henipavirus or henipa-like viruses in Indonesian fruit bats, suggesting the need for further epidemiological investigations.

Menangle virus, belonging to the genus *Rubulavirus* of the *Paramyxoviridae* family, has been identified in pteropus bats from Australia [14]. Menangle virus is a zoonotic paramyxovirus that causes febrile illness with rash in humans [15]. Tioman virus, belonging to the genus *Rubulavirus*, has also been isolated from *Pteropus hypomelanus* on the island of Tioman, Malaysia [16]. Although Tioman virus showed antigenic cross-reactivity to Menangle virus, the pathogenicity of Tioman virus remains unclear. There have been no reports of rubulavirus infections in the Indonesian fruit bat population.

The current study used molecular sequencing and phylogenetic analysis to identify RNA sequence from potential paramyxoviruses in fruit bats from Indonesia.

## Results

A total of 110 fruit bats belonging to four different species were sampled from four locations in Indonesia (Figure 1). *Pteropus vampyrus* was captured in Panjalu District (n = 26) and Lima Puluh Kota District (n = 20). Other pteropus bats captured in Popayato District (n = 4) and Paguyaman District (n = 25) were considered to be closely related to *Pteropus hypomelanus*, based on the shared nucleotide sequence identity of their 16S rRNA (96%) and

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