

## BAT-BORNE ZONOTIC VIRUSES RISK OF EMERGENCE IN EUROPE: HENDRA VIRUS, MENANGLE VIRUS AND NIPAH VIRUS

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### Abstract

*The livestock's surveillance of bat-borne zoonoses, as the Paramyxovirus infections with Hendra virus, Menangle virus and Nipah virus, it's a new concern of national veterinary authorities all over the world. The high volume of commercial trade and the human travel between European countries and the countries where bat-borne zoonoses are endemic make a risk of virus introduction into the European continent. In this paper, we review the factors associated with bat-borne zoonoses risk of emergence in European free-countries in relation to the introduction of the Paramyxoviruses Hendra, Menangle and Nipah. Hendra virus proved to be pathogen for horses and humans, while Menangle and Nipah viruses for swine and humans. Until now, Hendra and Menangle viruses' transmission to the humans have been only after a close contact with infected animals. Transmission of Nipahvirus can be done by contact with human patients and infected animals (human-human transmission was proved). In the light of this data the Hendra, Menangle and Nipah viruses have a limited potential of introduction if the national authorities apply an efficient border control of all live animals imported from endemic areas and evaluate all suspect cases of human diseases. The natural reservoir of all three viruses are fruit-bat species (genus Pteropus), and the bat migration may be another route of viruses introduction into Europe. The routes of Pteropus bats migration from the endemic territories to European countries have not been investigated, and are slight indications of major migration pathways into Europe. Also, fruit-bat species classified as host reservoir for specific zoonotic Paramyxovirus could transmit the virus to another bat species (e.g. Rousettus aegyptiacus may overlap with some migratory European bat species). In conclusion, the risk of emergence of Hendra, Menangle and Nipah viruses into the European countries seems to be low, but the risk cannot be excluded until the complete investigation of the route of migration for all fruit-bat species with history of infection.*

**Key words:** epidemiology, infection, transmission, risk factors, surveillance.

### INTRODUCTION

The bat-borne zoonosis and the livestock's surveillance in this respect must be the new concern of the national veterinary authorities. It is already known that bats are reservoir hosts of several emerging viruses (Calisher et al., 2006), some of them have been already reported in Europe and other possess high potential for introduction into the EU (Simons et al., 2014). The bats host a broad spectrum of viruses belonging to family Arenaviridae (Tacaribe virus), family Bunyaviridae (genus *Bunyavirus*, Catu virus, Guama virus, Nepuyo virus); genus *Hantavirus*, Hantaan virus; genus *Phlebovirus*, Rift Valley fever virus, Toscana virus; unassigned genus, KaengKhoi virus, Bangui virus), family Coronaviridae (SARS

coronavirus, MERS coronavirus), family Flaviviridae (genus *Flavivirus*, Bukalasa bat virus, Carey Island virus, Central European encephalitis virus, Dakar bat virus, Entebbe bat virus, Japanese encephalitis virus, Jugra virus, Kyasanur Forest disease virus, Montana myotis leucoencephalitis virus, Phnom-Penh bat virus, Rio Bravo virus, St. Louis encephalitis virus, Saboya virus, Sokuluk virus, Tamana bat virus, Uganda S virus, Yokose virus), family Filoviridae (genus *Ebolavirus*, Bundibugyo ebolavirus, Reston ebolavirus, Sudan ebolavirus, Taï Forest ebolavirus, Zaire ebolavirus; genus *Marburgvirus*, Marburg marburgvirus), family Herpesviridae (Agua Preta virus, cytomegalovirus of *Myotis lucifugus*, Parixa virus), family Orthomyxoviridae (genus *Influenzavirus A*,

influenza A virus), family *Paramyxoviridae* (genus *Henipavirus*, Hendra virus, Nipah virus; genus *Rubulavirus*, Mapuera virus, Menangle virus, Tioman virus; undetermined genus, parainfluenzavirus of *Rousettus leschenaultia*), family *Picornaviridae* (Juruaca virus), family *Reoviridae* (genus *Orthoreovirus*, Nelson Bay virus, Pulau virus, Broome virus; genus *Orbivirus*, Ife virus, Japanaut virus, Fomede virus), family *Rhabdoviridae* (genus *Lyssavirus*, Aravan virus, Australian bat lyssavirus, Duvenhage virus, European bat lyssavirus 1, European bat lyssavirus 2, Irkut virus, Khujand virus, Lagos bat virus, Rabies virus; unclassified genus, Gossas virus, Kern Canyon virus, Mount Elgon bat virus, Oita 296 virus), family *Togaviridae* (genus *Alphavirus*, Chikungunya virus, Sindbis virus, Venezuelan equine encephalitis virus), Issyk-kul (Keterah virus), Mojui dos Campos virus, Yogue virus, Kasokero virus (Halpinet et al., 2000; Badrane and Tordo, 2001; Chua et al., 2001; Childs, 2004; Li et al., 2005; Leroy et al., 2005; Calisher et al., 2006; Kurth et al., 2012; Luby, 2013; Memish et al., 2013; Ithete et al., 2013; Simons et al., 2014).

Despite the large number of human pathogenic viruses which were isolated from bats, is quite possible that several undiscovered viruses are still hosted in bats, many of them in a silent way. Moreover, it has been established that bat-borne zoonotic viruses are significantly more than rodent-borne zoonotic viruses (Luis et al., 2013).

On the list of emerging zoonoses are some bat-borne paramyxoviruses: Hendra virus, Menangle virus and Nipah virus. These viruses have been identified in various bat species (fruit bats of the genus *Pteropus*) in Africa, Australia, South America or Asia. Also, three paramyxoviruses have been identified in insectivorous bats in Europe, but they are not phylogenetic related with *Pteropus*-paramyxoviruses (Kurth et al., 2012). Although to date has not been reported *Pteropus* – paramyxoviruses in free-ranging European bats, the inter-species spillover of viruses should be considered. The high volume of goods traded and the human travel frequency between European countries and countries where bat-borne zoonoses are endemic, rise a risk of virus introduction into the European continent.

In this paper, we review the factors associated with bat-borne zoonoses and their risk of emergence in European free-countries in relation to the introduction of the Paramyxoviruses Hendra, Menangle and Nipah.

## MATERIALS AND METHODS

In this study we correlated the results of 31 scientific papers that present epidemiological features of paramyxovirus infections with Hendra, Menangle and Nipah viruses.

The method of analyses consist in the evaluation of the introduction routes of Hendra, Menangle and Nipah viruses to the EU by human travel, by trade, by bat migration, by accidental transport of bats and by the expansion of bats areal following ecological and climate changes.

## RESULTS AND DISCUSSIONS

Hendra virus have been shown to be pathogenic for horses and humans, while Menangle and Nipah viruses are pathogenic for pigs and humans (Wong et al., 2007).

### *Human travel*

Transmission of Nipahvirus can be done by contact with human patients and infected animals (human-human transmission was proved) (Homaira et al., 2007), while the human cases of Hendra and Menangle viruses infection were associated only with animal contact (Philbey et al., 1998; Field H., 2009; Young et al., 2011). Therefore, the travellers (tourism, business, or migrations) could be the main route for transmission of Nipah virus into the EU. Bangladesh, India, Malaysia and Singapore had registered Nipah virus infections outbreaks in humans (Homaira et al., 2007; Harit et al., 2006; Clayton et al., 2012; Paton et al., 1999).

In our opinion, national authorities should apply efficient border control and should evaluate all suspect cases of human diseases related to people coming from high risk area, where active outbreaks of Nipah virus infections were reported. The recommendation is supported by MERS-CoV cases of human infections, another bat-borne disease, when the

European outbreaks were related with human travel. (ECDC, 2015).

### **Trade**

The paramyxoviruses could be introduced in Europe with vegetable food products or live-animals and animal products and sub-products imported. Until present, only for Nipah virus was proved transmission by palm sap drinking, and for this reason it was assumed that all unprotected fruit grown in the endemic regions could be contaminated with saliva or urine of *Pteropus* bats (Rahman et al., 2008). Because only horses and pigs were involved in human transmission of this paramyxoviruses, in the live-animals trade should be restricted at least these species when active outbreaks were reported. If the national authorities applies an efficient border control of all live animals imported from endemic areas then Hendra, Menangle and Nipah viruses will have limited potential of introduction.

### **Bat migration**

The natural reservoir of Hendra, Menangle and Nipah virus are fruit-bat species (genus *Pteropus*), and the bat migration may be another way of introduction of viruses into Europe. The median travel distance of the migratory bats is 860 km (Tsoar et al., 2011) and in some circumstances bat species from endemic areas can be in contact with European bat species (e.g. *Rousettusaegyptiacus* may overlap with some migratory European bat species). However, the routes of *Pteropus* bats migration from the endemic territories to European countries have not been investigated, and are slight indication of major migration pathways into Europe (Fleming and Eby, 2003; Hutterer et al., 2005).

### **Accidental transport of bats**

*Pteropus* bats are often involved in aircraft strikes (Parsons, 2009), and transcontinental flights could bring in Europe infected dead bats. Also, bats could be transported in bilge waters of transoceanic ships. In both cases, the European airports and ports should take measures to collect and destroy the bat carcass remains.

### **Areal expansion of bats by ecological and climate changes**

The adaptation of some bat species in response to climate changes has been reported (Lundy et al., 2010).

Deforestation, fragmentation, and urbanization of *Pteropus* bats habitat conducted to Hendra and Menangleviruses' emergence (Philbey et al., 1998; Daszak et al., 2001).

## **CONCLUSIONS**

The risk of emergence of Hendra, Menangle and Nipah viruses into the European countries seems to be low, but cannot be ignored. The risk associated with each route of virus introduction cannot be assessed for entire Europe into unitary manner. The volume of human travel and trade are quite different from one country to another. Until today, the routes of migration for all fruit-bat species with history of infection have not been entirely investigated. Ecological changes can create different opportunities for expansion of bats habitat.

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