Queensland Government

Australian Government
Department of Agriculture, Fisheries and Forestry

Background

Hendra virus (HeV) was first described in 1994 following the outbreak of a novel disease fatally affecting horses and humans in south-east Queensland. Sporadic outbreaks continue to be identified (in 1999, 2004, 2006, 2007, 2008, 2009 & 2010), with a total of 45+ known equine cases (75% CFR) and 7 known human cases (50% CFR) to date.

Bats (flying foxes) have been identified as the natural host of the virus.

The 'Henipavirus Research Adoption Forum' held by the Australian Biosecurity CRC in July 2007 brought together over 40 delegates from a range of research end-users. Facilitated discussion sessions reviewed both national and international henipavirus research to date, identified gaps in existing knowledge, and proposed future research priorities. There was a consensus by end-users that more information on the ecology of Hendra virus was needed before changes to policy and/or practice could occur. In identifying the most significant research gaps and the highest priorities for further research, there was broad agreement on the need to better understand the extent of HeV strain variation in bats in the Australian region, and associated variability in transmission efficiency and pathogenicity.

Previous attempts to recover Hendra virus/nucleotide sequence from bats in Australia have had limited success. However, our understanding of HeV infection dynamics in bats, in conjunction with improved sampling and diagnostic approaches to maximize test sensitivity, has significantly advanced in recent years, translating to an increased likelihood of successful detection in bats.

In this proposal, the key research question is 'What is the diversity of Hendra viruses occurring in Australia'.

Objectives

- sample populations of bats at multiple times and locations
- screen pooled urine/faecal samples by PCR using a 'generic' HeV primer set
- map the diversity of identified strains using phylogenetic analyses
- convey findings to end-users to inform risk management and diagnostic test improvements.

Results & Discussion

We have made multiple PCR detections of Hendra virus genome in flying fox urine samples collected under flying fox roosts. Results to June 2010 suggest positive findings are more likely in the months June – October, and may suggest infection or excretion is more likely at this time. Only one in three sampling events yield evidence of infection, suggesting that infection is intermittently present in flying fox colonies. All PCR-positive samples were forwarded to AAHL for virus isolation. Multiple isolates have been obtained over location and time. These are the first isolates from bats since the initial isolation in 1996 (Halpin *et al.*, 2000).

The project has been an outstanding success in detecting Hendra virus genome and virus isolation in urine collected under roosts of flying foxes.

Recommendations:

- That the diversity, frequency and occurrence of Hendra and related viruses in Australian flying fox populations be further investigated
- That future work elaborates the spatial and temporal pattern of infection in identified infected colonies.
- That possible nocturnal interactions between flying foxes and horses be examined.
- That research to elaborate the proximate triggers for spillover from bat populations be supported.