Detection of polyoma and corona viruses in bats of Canada

Vikram Misra,1 Timothy Dumonceaux,2 Jack Dubois,3 Craig Willis,4 Susan Nadin-Davis,5 Alberto Severini,2 Alex Wandeler,5 Robbin Lindsay2 and Harvey Artsob2

Correspondence
Vikram Misra
vikram.misra@usask.ca

1Department of Veterinary Microbiology, Western College of Veterinary Medicine, 52 Campus Road, University of Saskatchewan, Saskatoon, SK S7N 5B4, Canada
2National Microbiology Laboratory, Canadian Science Centre for Human and Animal Disease, 1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
3Manitoba Conservation, Wildlife and Ecosystem Protection Branch, Box 24, 200 Saulteaux Crescent, Winnipeg, MB R3J 3W3, Canada
4Department of Biology and Centre for Forest Interdisciplinary Research, University of Winnipeg, 515 Portage Avenue, Winnipeg, MB R3B 2E9, Canada
5Centre of Expertise for Rabies, Ottawa Laboratory-Fallowfield, Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON K2H 8P9, Canada

Several instances of emerging diseases in humans appear to be caused by the spillover of viruses endemic to bats, either directly or through other animal intermediaries. The objective of this study was to detect, identify and characterize viruses in bats in the province of Manitoba and other regions of Canada. Bats were sampled from three sources: live-trapped *Myotis lucifugus* from Manitoba, rabies-negative *Eptesicus fuscus, M. lucifugus, M. yumanensis, M. septentrionalis, M. californicus, M. evotis, Lasionycteris (L.) noctivagans and Lasiurus (Las.) cinereus*, provided by the Centre of Expertise for Rabies of the Canadian Food Inspection Agency (CFIA), and *L. noctivagans, Las. cinereus and Las. borealis* collected from a wind farm in Manitoba. We attempted to isolate viruses from fresh tissue samples taken from trapped bats in cultured cells of bat, primate, rodent, porcine, ovine and avian origin. We also screened bat tissues by PCR using primers designed to amplify nucleic acids from members of certain families of viruses. We detected RNA of a group 1 coronavirus from *M. lucifugus* (3 of 31 animals) and DNA from an as-yet undescribed polyomavirus from female *M. lucifugus* (4 of 31 animals) and *M. californicus* (pooled tissues from two females).

INTRODUCTION

In a recent article, Jones et al. (2008) examined over 330 events of emerging infectious disease in humans over a 60 year period from 1940 to 2004. They concluded that most of the events were zoonotic and that over 70% of these could be attributed to wildlife. Other studies (Taylor et al., 2001; Woolhouse & Gowtage-Sequeria, 2005) provide similar estimates. Several of the zoonotic viruses that have emerged in various regions of the world in the last two decades are enzootic in bats and are transmitted, albeit infrequently, to humans and domestic animals (reviewed by Calisher et al., 2006; Dobson, 2005; Wong et al., 2007). Economic or sociological conditions that lead to an increase in bat–human contact appear to predispose these cross-species transmissions. In some of the emergent viruses, such as Hendra and Nipah viruses, there is evidence of direct transmission of bat viruses to horses and swine and from them to humans. Nipah virus has also been transmitted directly from bats to humans (Luby et al., 2006) and between humans (Gurley et al., 2007). For other viruses such as severe acute respiratory syndrome (SARS) (Lau et al., 2005), Marburg (Towner et al., 2007) and Ebola (Leroy et al., 2005), viruses similar to those causing disease in people have been isolated from or detected in bats. Melaka, a virus similar to Tioman virus previously isolated from bats (Chua et al., 2007), was recovered from an...
individual with severe respiratory disease. In addition, bat lyssaviruses in the UK (Nathwani et al., 2003) and Australia (Hanna et al., 2000; Samaratunga et al., 1998), both of which are considered to be free of terrestrial rabies, have caused fatal disease in people.

Increased human development in wilderness areas of Canada and encroachment into bat habitats could lead to similar inter-species transmission of potentially zoonotic viruses that may be present in bats, particularly via species which can roost in human-made structures. Additionally, widespread mortality of the so-called 'migratory tree bats', that has now been documented at industrial-scale wind energy facilities throughout North America (Arnett et al., 2008; Baerwald et al., 2008; Betts, 1998) has created the potential for direct virus transmission between formerly cryptic forest bat species and domestic pets or livestock and indirect transmission to wildlife species which scavenge bat carcasses at wind turbines (e.g. foxes, skunks and crows; Klug & Barclay, 2008). Identification of such viruses and characterization of their biology and epizootiology would be invaluable in anticipating and possibly preventing transmission to humans or, if it occurred, in controlling its spread and impact.

At least 17 species of bats have been detected in Canada. These include little brown bat (*Myotis lucifugus*), Yuma myotis (*M. yumanensis*), long-legged myotis (*M. volans*), fringed myotis (*M. thysanodes*), northern myotis (*M. septentrionalis*), eastern small-footed myotis (*M. leibii*), Keen's myotis (*M. keenii*), long-eared myotis (*M. evotis*), western small-footed myotis (*M. ciliolabrum*), California myotis (*M. californicus*), big brown bat (*Eptesicus fuscus*), silver-haired bat [*Lasionycteris* (*L.* noctivagans], hoary bat [*Lasiurus* (*Las.*) cinereus], red bat (*Las. borealis*), tri-coloured bat (formerly the eastern pipistrelle, *Perimyotis subflavus*), spotted bat (*Euderma maculatum*) and Townsend’s big-eared bat (*Corynorhinus townsendii*). Of these species, the little brown bat, silver-haired bat, hoary bat, northern myotis, big brown bat and eastern red bat have been observed in the province of Manitoba (details in Bilecki, 2003). During winter in Manitoba, the little and big brown bats and northern myotis bats hibernate, while the three other local species, the ‘migratory tree bats’ (silver-haired bat, hoary bat and eastern red bat), migrate south. The little brown and northern myotis bats hibernate in caves in the extensive limestone karst in the inter-lake and northern regions of Manitoba. Big brown bat hibernacula have not as-yet been identified. The little brown bats congregate at the caves in mid-August to late September, presumably to mate. Later in the year, they move to the caves where they habitually hibernate during winter. The bats leave the caves in mid-May to early June and females form maternity colonies in tree hollows and other structures, including buildings. Little brown bats, in particular, are common inhabitants of buildings throughout their range and are, therefore, the species most likely to be encountered by humans in Manitoba. In contrast, two of the three migratory tree bats (hoary and eastern red bats) have rarely been encountered by people historically, because they roost exclusively in the foliage of trees (Willis & Brigham, 2005). The third migratory species (the silver-haired bat) is also considered a tree-roosting species (Betts, 1998) but has been more often encountered by people when roosting in deadfall or woodpiles.

If bats indeed harbour viruses that have the potential to cause severe disease in humans and other domestic animals, and if climatic and socio-economic changes are likely to lead to conditions that facilitate contact between bats and domestic animals, it might be useful to identify viruses that infect bats. Such surveys have been conducted elsewhere in the world with the identification of several previously unknown bat viruses. Because of the devastating effect of SARS on the economy of several countries, most of these studies have specifically targeted coronaviruses (Carrington et al., 2008; Chu et al., 2006, Dominguez et al., 2007; Gloza-Rausch et al., 2008; Lau et al., 2005; Poon et al., 2005). Our objective in this study was to carry out a preliminary screen of bats in Canada for the presence of viruses of several families. We attempted to isolate viruses from fresh tissue samples taken from trapped bats in cultured cells of bat, primate, rodent, porcine, ovine and avian origin. We also screened nucleic acids purified from these samples by PCR using low-specificity primers designed to amplify nucleic acids from all members of certain families of viruses. We detected RNA related to that of Rocky Mountain bat coronavirus (RMBCV) from little brown bats and DNA of a previously undescribed polyomavirus from female little brown bats and California myotis.

**METHODS**

**Bats.** Bats for the study were obtained from three sources.

(i) Little brown bats were trapped using a harp trap set up at a cave in northern Manitoba during a September 2007 mating swarm. Some hibernating bats were also collected from hibernacula in two other caves in May 2008. Bats were euthanized on site by an overdose of inhaled isoflurane (Aerrane) and placed on ice for transport to the National Microbiology Laboratory (NML) in Winnipeg. Bats were processed for virus isolation within 48 h of collection. A Wildlife Scientific Permit (WB 06638) to trap the bats was obtained from the Wildlife and Ecosystem Protection Branch of Manitoba Conservation. The bats were treated in accordance with procedures approved by the Animal Care Committee of the Canadian Science Centre for Human and Animal Health (H-07-001 Rev.1). All individuals handling bats had been immunized against rabies and, according to recent tests, had antibody levels considered protective.

(ii) The Centre of Expertise for Rabies at the Canadian Food Inspection Agency (CFIA) provided bats diagnosed as negative for rabies. These bats had been submitted to the CFIA laboratories in Lethbridge, Alberta and Ottawa, Ontario, and frozen at −20 °C after diagnosis. This group of bats included little and big brown bats, silver-haired bats, hoary bats, Yuma myotis and California myotis.

(iii) Dead bats were collected for a survey of bat mortality at a Manitoba wind farm. These included silver-haired, hoary and red bats.
Sampling tissues. All bats were processed in biosafety level 3 facilities at either the NML or the CFIA Fallowfield laboratory in Ottawa. Carcasses were sprayed with 70% ethanol and placed on absorbent paper for 5 min before dissection. One kidney and spleen, and portions of liver, lung, small intestine and brain were removed from each bat. All tissues from each live-trapped bat were pooled. For bats obtained from CFIA and the wind farms, tissues from up to four bats of the same species were pooled. BA [Medium 199 (Gibco), 50 mM Tris/HCl, pH 7.6, 1% BSA and penicillin–streptomycin (Gibco)] was added to tissues from individual animals (2 ml) and pooled tissues (4 ml) and the tissues were homogenized either in a Polytron homogenizer or by shaking with a sterile ball bearing in a Retsch M300 oscillating homogenizer. The samples were then centrifuged at 16,000 g for 5 min and the supernatant was transferred to a fresh tube.

Inoculation of cultured cells. Lamb and pig kidney cells, baby hamster kidney cells (BHK-21), chicken fibroblasts and quail fibroblasts (QT-35) were obtained from Marta Sabara (CFIA) and mouse fibroblasts (NIH-3T3), African green monkey (Vero) cells and bat tracheal (BT) cells were obtained from James Strong (Public Health Agency of Canada, NML). All cells were grown in medium normally used to propagate the cells.

Extraction of nucleic acids. Total nucleic acids were extracted from 140 μl tissue homogenate using the QiAamp viral RNA mini kit (Qiagen) following the manufacturer’s instructions [this kit purifies viral DNA as well as RNA (Allan Grolla, personal communication)]. An additional washing step with buffer AW1 (Qiagen) was included. Before extraction, all samples were seeded with bacteriophage MS2 RNA as an internal control. Nucleic acid samples for PCR for DNA viruses and for the two-step real-time PCR for West Nile virus were analysed by BLAST to determine if they resembled known viral sequences. Bacteriophage MS2 RNA, seeded into raw samples as a control for RNA extraction, was detected using quantitative RT-PCR (Dreier et al., 2005) by the virology facility at the NML.

Broad spectrum PCR for polyomavirus detected a conserved portion of the VP1 and VP3 genes (Johne et al., 2005). The remainder of the genome of polyomaviruses from three bats was obtained by ‘long-range’ PCR using primers facing outwards from the initial product of the VP1 gene. The larger PCR product was cloned into pCRTOPO using a PCR cloning kit (Invitrogen). The sequence of the fragment was determined using primers bracketing the cloning site of pCRTOPO and additional primers were designed as sequencing progressed. Sequences were aligned into contigs using DNASTAR and represented complete sequences of both DNA strands. Open reading frames (ORFs) were deduced using MacVector 7. Deduced amino acid sequences of the Myotis polyomavirus genes for Large T-antigen, Small t-antigen, VP1 and VP2,3 were compared with those of other polyomaviruses using the PHYLIP 3.63 package. The complete nucleotide sequence of the Myotis polyomavirus and deduced amino acid sequences of the deduced proteins were submitted to GenBank and assigned the accession number FJ188392.

RESULTS

We attempted to detect viruses in Canadian bats by using two complementary strategies: to isolate virus in a variety of cultured cells and to screen samples by PCR using primers designed to amplify nucleic acids from members of selected families and genera of viruses and from individual viruses. The target viral families and genera were selected either because of a precedent for members spilling over into humans or because the tests were available in our laboratory, thus allowing us to undertake a broad generalized screening. In positive control reactions, the primers detected nucleic acids from representative target viruses.

Live-trapped M. lucifugus

We examined 31 live-trapped M. lucifugus (Table 1). Twenty-one bats were collected from a mating swarm in September 2007. Of these, thirteen were female and seven were male (one unknown). An additional five bats were collected from each of two cave hibernacula in May 2008. All of these bats were male. Various tissues from individual bats were pooled and attempts were made to isolate virus using cultured cells. However, we observed no virus particles by electron microscopy, even after repeated attempts to detect virus in tissue culture supernatants and concentrated material. We did, however, detect virus infection by PCR analysis of nucleic acids purified from tissue homogenates of seven of the 31 live-trapped M. lucifugus examined (Table 1). We determined the nucleotide sequence of the PCR products, which confirmed that four of the viruses were polyomavirus while three were coronavirus. All four bats from which we detected polyomavirus were females.

Bats from the Centre for Expertise in Rabies and bats collected from a wind energy facility

The Centre for Expertise in Rabies provided 84 bat carcasses representing four genera and six species
These bats were submitted to the Centre for Rabies Testing and were found to be negative for rabies virus. The carcasses, which had been stored frozen at \(-20\) °C, were thawed overnight at room temperature before dissection. We detected polyomavirus in a pool from two female *M. californicus* bats submitted to the Centre from British Columbia. We also obtained 15 bat carcasses representing the three migrating species (*Las. cinereus*, *L. noctivagans* and *Las. borealis*) from a wind plant near Winnipeg. The carcasses were collected in autumn 2007 and frozen at \(-20\) °C until the tissues were analysed by PCR. An additional *Las. cinerus* bat was submitted by a local veterinarian. No viruses were detected in these animals (total of 100).

### Myotis polyomavirus

Polyomavirus DNA was detected using primers designed from a conserved portion of the VP1 gene of polyomaviruses. Using primers designed from the nucleotide sequence of the VP1 fragment, we amplified the remainder of the viral genome from three bats. The sequence of the entire genome was determined and putative ORFs for major polyomavirus proteins (VP1, VP2 and 3, Large T antigen and Small t-antigen) were deduced. The derived amino acid sequences for these proteins were compared with those of all other known polyomaviruses. Only VP1 sequences were available for the goose polyomavirus. Fig. 1 depicts phylogenetic trees of the polyomavirus viral proteins based on a parsimony analysis of the amino acid sequences of the proteins. While there were some variations in the groupings when the sequences of the different proteins were compared, all four proteins of the *Myotis* bat virus were closely related to those of the mouse pneumotropic (Kilham) and squirrel monkey viruses.

### Myotis coronavirus

We amplified a 500 bp segment of RNA from a coronavirus in three *M. lucifugus* bats using primers designed to amplify a portion of the coronavirus RNA polymerase gene. Bat no. 14 was trapped in September 2007, while bats 24 and 30 were collected in May 2008; the three bats were from different caves (Table 1). The sequence of the amplified portion of the coronavirus gene most closely resembled those of the RMBCV sequence detected in *M. occultus* (Dominguez et al., 2007) and *E. fuscus* in Colorado (Dominguez et al., 2007). A comparison of the sequences (Fig. 2) using CLUSTAL_X showed that the sequences of viruses from *M. lucifugus* bats 14 and 24 were very similar. All three sequences were closely related to sequences amplified from *M. occultus* but had several differences from those amplified from *E. fuscus* (Dominguez et al., 2007).

When the 500 bp segment from the Myotis coronavirus was compared with corresponding sequences from coronaviruses detected in bats in North America, Europe and South-East Asia (Fig. 3), the sequences of the *Myotis* coronavirus most closely resembled sequences from Group 1 coronaviruses, including viruses from the other North American bats and Asian bats *Rhinolophus sinicus*, *Myotis ricketti* and *Miniopterus australis* (Woo et al., 2006). In our analysis, the sequences of coronaviruses detected in European bats (Gloza-Rausch et al., 2008) formed a distinct clade within the group 1 coronaviruses.

### DISCUSSION

The objective of the project was to screen bats in the province of Manitoba and other regions of Canada for viruses. Most of

Table 1. Virus nucleic acids detected in live-trapped *M. lucifugus*

<table>
<thead>
<tr>
<th>Bat no.</th>
<th>Sex*</th>
<th>Cave†</th>
<th>Virus detected‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>2</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>3</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>4</td>
<td>U</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>5</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>6</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>7</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>8</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>9</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>10</td>
<td>F</td>
<td>St G</td>
<td>Polyoma</td>
</tr>
<tr>
<td>11</td>
<td>F</td>
<td>St G</td>
<td>Polyoma</td>
</tr>
<tr>
<td>12</td>
<td>F</td>
<td>St G</td>
<td>Polyoma</td>
</tr>
<tr>
<td>13</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>14</td>
<td>M</td>
<td>St G</td>
<td>Corona</td>
</tr>
<tr>
<td>15</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>16</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>17</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>18</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>19</td>
<td>F</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>20</td>
<td>M</td>
<td>St G</td>
<td>NVD</td>
</tr>
<tr>
<td>21</td>
<td>F</td>
<td>St G</td>
<td>Polyoma</td>
</tr>
<tr>
<td>22</td>
<td>M</td>
<td>Dale’s</td>
<td>NVD</td>
</tr>
<tr>
<td>23</td>
<td>M</td>
<td>Dale’s</td>
<td>NVD</td>
</tr>
<tr>
<td>24</td>
<td>M</td>
<td>Dale’s</td>
<td>Corona</td>
</tr>
<tr>
<td>25</td>
<td>M</td>
<td>Dale’s</td>
<td>NVD</td>
</tr>
<tr>
<td>26</td>
<td>M</td>
<td>Dale’s</td>
<td>NVD</td>
</tr>
<tr>
<td>27</td>
<td>M</td>
<td>Abyss</td>
<td>NVD</td>
</tr>
<tr>
<td>28</td>
<td>M</td>
<td>Abyss</td>
<td>NVD</td>
</tr>
<tr>
<td>29</td>
<td>M</td>
<td>Abyss</td>
<td>NVD</td>
</tr>
<tr>
<td>30</td>
<td>M</td>
<td>Abyss</td>
<td>Corona</td>
</tr>
<tr>
<td>31</td>
<td>M</td>
<td>Abyss</td>
<td>NVD</td>
</tr>
</tbody>
</table>

*F, Female; M, male; U, unknown.

†Bats were collected at three caves: St George (St G), Dale’s and Abyss. Bats from St George cave were trapped during a mating swarm in September 2007. Bats from Dale’s and Abyss caves were collected in May 2008.

‡Polyoma or corona viruses were detected by PCR in tissue lysates of seven of 31 animals.

(Supplementary Table S2, available in JGV Online). These bats were submitted to the Centre for Rabies Testing and were found to be negative for rabies virus. The carcasses, which had been stored frozen at \(-20\) °C, were thawed overnight at room temperature before dissection. We detected polyomavirus in a pool from two female *M. californicus* bats submitted to the Centre from British Columbia. We also obtained 15 bat carcasses representing the three migrating species (*Las. cinereus*, *L. noctivagans* and *Las. borealis*) from a wind plant near Winnipeg. The carcasses were collected in autumn 2007 and frozen at \(-20\) °C until the tissues were analysed by PCR. An additional *Las. cinerus* bat was submitted by a local veterinarian. No viruses were detected in these animals (total of 100).
the viruses were detected in live-trapped *M. lucifugus*. Seven of the 31 animals (over 22%) examined yielded virus. With the exception of two *M. californicus*, no viruses were detected in any of the bats obtained from the rabies laboratory or the wind plant. These 100 bats represented eleven species. Our failure to detect viruses in these animals likely reflects the condition of the animals. All were thawed after being frozen for several months and it appeared that considerable time had elapsed between the death of these animals, many by trauma, and freezing. Bats from the wind plant may have been exposed to the elements for as long as 24 h before being found by searchers and collected. In contrast, the live-trapped bats were sampled within a day of euthanasia and maintained on ice during that period.
Using a strategy that exploited the circular nature of polyomavirus genomes (Johne et al., 2006), we recovered the entire genome of the virus detected in two Myotis species. Analysis of the complete sequence of the viral genomes recovered from three animals revealed an as-yet undescribed polyomavirus. We suggest that the virus should be called Myotis polyomavirus (MyPyV). The genome of MyPyV appeared to have the same arrangement of genes as other polyomaviruses, with potential ORFs for the capsid proteins VP1, VP2 and VP3. ORFs with potential splice sites, the non-structural proteins Small t and Large T antigens were also present. The genome contained other small ORFs, including one for a potential ‘agno’ protein. However, we could not detect significant similarity between the deduced amino acid sequence of these ORFs and peptides identified for the better-characterized polyomaviruses.

Some mammalian polyomaviruses cause tumours when susceptible rodents are infected experimentally and the newly discovered Merkel polyomavirus is associated with the aggressive Merkel cell skin cancer in humans (Feng et al., 2008). In addition, both the mouse polyomavirus and pneumotropic virus can cause disease when inoculated into newborn mice. However, the mammalian polyomaviruses are not generally associated with acute disease in natural non-immunocompromised hosts. While the naturally occurring mouse virus does retain its ability to cause fatal disease in newborn mice, infection under natural conditions in feral mice does not result in disease (Carroll et al., 2007), possibly because of the simultaneous transmission of virus and maternal immunity to newborn pups. In contrast with the mammalian viruses, at least two of the avian viruses cause acute, frequently fatal inflammatory disease in some species of psittacine birds and geese (Johne & Müller, 2007). The cycle of infection of most polyomaviruses in natural hosts has not been determined. However, the avian polyomavirus appears to have a unique form of reverse vertical transmission in the European pied flycatcher, where blowfly larvae transmit the virus to nestlings, which then infect the parents through the faecal–oral route (Potti et al., 2007).

Like other mammalian polyomaviruses in natural hosts, MyPyV appears not to cause disease in adult M. lucifugus. We detected the virus in apparently healthy bats in a mating swarm. While the number of bats we examined was too low to reach a definitive conclusion, it is interesting that we only detected the virus in females of two Myotis species. Myotis females rear pups in maternity roosts with little input into offspring care by males. It is tempting to
speculate that a natural cycle of infection involving ectoparasites, similar to that of the avian polyomavirus in the European pied flycatcher (Potti et al., 2007), might result in the infection of pups in crowded maternity roosts with subsequent infection of the females.

We detected RNA of a group 1 coronavirus in several of the M. lucifugus examined. Our analysis of the virus depends entirely on the nucleotide sequence of a 500 bp segment of the gene for the viral RNA polymerase. The information was sufficient to determine that we had detected a virus very closely related to RMBCV described by Dominguez et al. (2007). The M. lucifugus virus was most closely related (possibly a variant) to virus detected in M. occultus, but it was distinct from RMBCV from E. fuscus.

Since the discovery of SARS-like coronavirus in bats, several studies screening bats for coronaviruses have led to the discovery of many coronaviruses in bats of Asia, Europe and North America. These viruses appear to have a benign relationship with their Chiroptera hosts and display the diversity and constant population growth dynamics that are characteristic of long virus–host associations (Vijaykrishna et al., 2007). This led some to speculate (Vijaykrishna et al., 2007) that bats may be reservoir hosts for all coronaviruses and that rare spillover and adaptation in other species may have led to the development of coronaviruses of humans, domestic animals and other species.

Climatic and socio-economic changes in the coming years may lead to more frequent contact between bats and humans and domestic animals, increasing the chance of spillover of bat viruses and the emergence of new infectious diseases. While we failed to detect virus in bats killed at a wind energy facility, our sample size from this site was small. We suggest that this aspect of our survey should be repeated with larger numbers of bats, as wind plants are a potentially new source of transmission from cryptic, forest bat species which have historically had extremely low rates of contact with domestic animals or humans. Knowledge of viruses that parasitize bats and ecological factors that govern maintenance in bats may help us to reduce the chance of spillover infection or to ameliorate its effects should it occur. For instance, a catalogue of viruses parasitizing bats and molecular information on their gene products would make it easier to detect a virus in the early stages of an epidemic. It would also speed up the identification of reservoir species. Our preliminary study is a small step in that direction.

ACKNOWLEDGEMENTS

This project was funded by the Public Health Agency of Canada. The Sustainable Development Innovation Fund of Manitoba Conservation provided funding for survey work at the wind plant. The authors are indebted to Ms Antonia DeBernardo of PHAC for technical assistance. The authors are also indebted to Manitoba Conservation, Dale Brown of the Speleological Society of Manitoba and Joel Jameson, Trace Parkinson and Amanda Matheson for assistance with collecting bats in the field.

REFERENCES


