susceptibility to SBV infection, but differences in seroprevalence suggest different roles for sympatric ruminants in SBV epidemiology. The role of vector species in the transmission of SBV in alpine ecosystems should be analyzed.

Acknowledgments

We thank Mariano Domingo for assistance during necropsy studies of stillborn calves, Joan Planas for technical assistance during livestock sample collection, and the rangers and staff of the Freser-Setcases National Hunting Reserve for their collaboration.

This study was supported by the Departament d’Agricultura, Ràmaderia, Pesca, Alimentació i Medi Natural de la Generalitat de Catalunya, and funded by the research project CGL2009-11631 of the Spanish Ministerio de Ciencia e Innovación.

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DOI: http://dx.doi.org/10.3201/eid1006.130961

References


9. Novell Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012

To the Editor: The genus Henipavirus (family Paramyxoviridae) contains 3 established species (Hendra virus, Nipah virus, and Cedar virus) and 19 newly identified species, including 1 full-length sequenced virus, Bat Paramyxovirus EidhelicGH-M74a/GHA/2009 (1,2). The zoonotic pathogens Hendra virus and Nipah virus have been associated with lethal neurologic and respiratory diseases in humans, horses, and pigs (3–5). The known natural reservoirs of henipaviruses are fruit bats (1,3); these viruses have not been reported in other wild animals.

We report on a novel henipavirus-like virus, Mojiang paramyxovirus (MoJV), in rats (Rattus flavipectus) in China.

In June 2012, in Mojiang Hani Autonomous County, Yunnan Province, China, severe pneumonia without a known cause was diagnosed in 3 persons who had been working in an abandoned mine; all 3 patients died. Half a year later, we investigated the presence of novel zoonotic pathogens in natural hosts in this cave. For the investigation, we collected sample swabs from 20 bats (Rhinolophus ferrumequinum), 9 rats (R. flavipectus), and 5 musk shrews (Crocidura dracula) from the mine for virome analysis.

All samples were processed by using a virus particle–protected nucleic acid purification method, followed by sequence-independent PCR amplification of extracted RNA and DNA (6). The amplified viral nucleic acid libraries were then sequenced by using an Illumina Genome Analyzer II (Illumina Trading, Beijing, China) for a single read of 81 bp. All raw reads were then aligned to the nonredundant protein database of the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/RefSeq/) by using BLASTx (http://blast.ncbi.nlm.nih.gov).
nih.gov/Blast.cgi) after filtering reads as described (6). The taxonomy of the aligned reads was parsed by using the MEGAN4 MetaGenome Analyzer (7).

On the basis of the nonredundant protein alignment results, we identified 38 sequence reads that were classified as Henipavirus spp. However, the sequences shared low nucleotide and amino acid identities with known henipaviruses. The reads were then used for reads-based PCR to identify the partial genome of this virus. The remaining genomic sequences were determined by using genome walking. The 5′ and 3′ untranslated regions were obtained by nested PCR with combined specific primers and henipavirus-specific degenerate primers as described (8), and the exact sequences of the 5′ and 3′ genome termini were determined by rapid amplification of cDNA ends.

MojV shares similar features with known henipaviruses. The virus has a genome length of 18,404 nt (submitted to GenBank under accession no. KF278639), and has the characteristic henipavirus gene order: 3′-nucleocapsid (N) protein (539 aa); P/V/W/C proteins (phosphoprotein; 694 aa, 464 aa, 434 aa, 177 aa); matrix protein (340 aa); fusion protein (545 aa); attachment glycoprotein (625 aa); and large (L) protein (2,277 aa)-5′ (online Technical Appendix Figure, wwwnc.cdc.gov/EID/article/20/6/13-1022-Techapp1.pdf). The predicted conserved sequences between genes showed features characteristic of henipaviruses (online Technical Appendix Table). The central domain of the N protein contains 3 conserved motifs common in all paramyxoviruses: QXW [I/V] X K [A/C] XT, FX[T/I/L][R/K][Φ[G/A][L/I/V] XT, and FX3YPX2ΦSΦAMG, where Φ

**Figure.** Phylogenetic trees based on the nucleocapsid proteins (A) and large proteins (B) of Mojiang paramyxovirus (MojV) and other previously reported paramyxoviruses. Bold font indicates MojV and Henipavirus spp. Scale bars indicate nucleotide substitutions per site.
dicted MojV genes exhibited similari
Mononegavirales
mains within the L proteins of the order
conserved in the phosphoprotein gene
ation, the RNA editing site (AAAA
Noncollectable from the other 2 rats).
In the 3 MojV-pos
lymphoid tissues from 1 of the 3 MojV-pos
- separately re-evaluate the 34 anal swab
ing the L gene of MojV were designed to
related to Henipavirus spp. The
- specific nested primer sets target-
L gene of MojV were designed to sep-
ly host major mammalian paramyxoviruses.
and N of Henipavirus was and a
distant from other clusters. Thus, con-
sidering the same genome features
between MojV and other henipav-
ves, we confirmed that MojV could
be classified as a new species closely related to Henipavirus spp.
Specific nested primer sets target-
The nucleotide identities of pre-
Amino acid identity
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N (53.0%–57.0% identity), phospho-
protein (37.8%–43.0% identity), matrix (59.5%–63.4% identity), fusion
(47.5%–51.4% identity), attachment
glycoprotein (36.6%–41.8% identity), and L (55.9%–58.6% identity). Using
we used the phy-
logenetic trees based on N and L pro-
teins to describe the evolutionary rela-
relationships between MojV and members
of the family Paramyxoviridae (Figure). MojV clustered with the 4 mem-
ers of the genus Henipavirus and was
distant from other clusters. Thus, con-
sidering the similar genome features
between MojV and other henipav-
urses, we confirmed that MojV could
be classified as a new species closely related to Henipavirus spp.
Henipavirus spp. viruses might infect
more mammalian hosts than previously
thought and that bats may not be the
only hosts of henipaviruses.
This work was supported by a Na-
tional S&T Major Project (China Mega-
Project for Infectious Disease; grant no.
2011ZX10004-001) from the People’s
Republic of China, and by a Basic Re-
search and Operating Expenses grant (no.
2013IPB301) from the Institute of Patho-
biology, Chinese Academy of Medical
Sciences and Peking Union Medical College.

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DOI: http://dx.doi.org/10.3201/eid1902.11006

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Novel Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012

Technical Appendix

Figure. Genomic organization of Mojiang paramyxovirus. N, nucleocapsid protein; L, large protein; P/V/W/C, phosphoprotein; M, matrix protein; F, fusion protein; G, attachment glycoprotein.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Gene stop</th>
<th>Intergenic region</th>
<th>Gene start</th>
</tr>
</thead>
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<td>MojV, gene</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>/N</td>
<td>CTT</td>
<td></td>
<td>AGGATTCAGG</td>
</tr>
<tr>
<td>N/P</td>
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<td>CTT</td>
<td>AGGATCCAAG</td>
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<tr>
<td>P/M</td>
<td>TCATAAAAAA</td>
<td>CTT</td>
<td>AGGAGTCAAG</td>
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<tr>
<td>M/F</td>
<td>ATATAAAAAA</td>
<td>CTT</td>
<td>AGGTGTCAGG</td>
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<tr>
<td>F/G</td>
<td>TTAATAAAAA</td>
<td>CTT</td>
<td>AGGAGTCAGG</td>
</tr>
<tr>
<td>G/L</td>
<td>TTACAAAAAA</td>
<td>CTT</td>
<td>AGGATTCAGG</td>
</tr>
<tr>
<td>Consensus sequences for henipaviruses</td>
<td>TWAHRAAAAAA</td>
<td>CTT</td>
<td>AGGANMCARG</td>
</tr>
</tbody>
</table>

*N, nucleocapsid; P, phosphoprotein (P/V/W/C); M, matrix; F, fusion; G, glycoprotein; L, large protein.