Short Communication

Multi-reassortant G3P[3] group A rotavirus in a horseshoe bat in Zambia

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Group A rotavirus is a major cause of diarrhoea in humans, especially in young children. Bats also harbour group A rotaviruses, but the genetic backgrounds of bat rotavirus strains are usually distinct from those of human rotavirus strains. We identified a new strain of group A rotavirus in the intestinal contents of a horseshoe bat in Zambia. Whole genome sequencing revealed that the identified virus, named RVA/Bat-wt/ZMB/LUS12-14/2012/G3P[3], possessed the genotype constellation G3-P[3]-I3-R2-C2-M3-A9-N2-T3-E2-H3. Several genome segments of LUS12-14 were highly similar to those of group A rotaviruses identified from humans, cows and antelopes, indicating interspecies transmission of rotaviruses between bats and other mammals with possible multiple genomic reassortment events.

The GenBank/EMBL/DDBJ accession numbers for the viral sequences are LC158116–LC158126.

Three supplementary tables are available with the online Supplementary Material.

Group A rotavirus (RVA) is a major cause of diarrhoal illness of humans worldwide. The RVA genome comprises 11 segments of dsRNA. Each segment encodes one viral structural protein (VP1, VP2, VP3, VP4, VP6 or VP7) and one non-structural protein (NSP1, NSP2, NSP3 or NSP4), except for segment 11, which encodes both NSP5 and NSP6. A complete genotype classification system was proposed, defining the genotype constellation of RVAs as follows: Gx–P[x]–Ix–Rx–Cx–Mx–Ax–Nx–Tx–Ex–Hx, representing VP7–VP4–VP6–VP1–VP2–VP3–NSP1–NSP2–NSP3–NSP4–NSP5 (Matthijnssens et al., 2008). This classification system has facilitated the comparison of various RVA genotypes and increased our knowledge about the genetic diversity of RVA.

Domestic and feral animals as well as humans are susceptible to RVA infection. The three bat-borne RVAs are as follows: RVA/Bat-wt/KEN/KE4852/2007/G25P[6] from a straw-coloured fruit bat (Eidolon helvum) in Kenya (Esona et al., 2010) and RVA/Bat-tc/CHN/MSLH14/2012/G3P[3] and RVA/Bat-tc/CHN/MYAS33/2013/G3P[10] from a lesser horseshoe bat (Rhinolophus hipposideros) and a Stoliczka’s trident bat (Aselliscus stoliczkanus) in China, respectively (He et al., 2013; Xia et al., 2014). The nucleotide sequences of these bat RVAs are distant from those of other mammalian RVAs and are therefore considered bat-specific, and only the nucleotide sequences of the genes encoding VP4 and NSP4 of RVA/Bat-wt/KEN/KE4852/2007/G25P[6] are highly similar to those of other mammalian RVAs (Esona et al., 2010; He et al., 2013; Xia et al., 2014). Here, we identified and characterized a new RVA strain isolated from an insectivorous bat in Zambia.

We captured three horseshoe bats (Rhinolophus spp.) and 13 Schreibers’ long-fingered bats (Miniopterus schreibersii)
at Leopard’s Hill Cave in Lusaka, Zambia, with permission from the then Zambia Wildlife Authority (Act No. 12 of 1998), now the Department of National Parks and Wildlife, Ministry of Tourism and Arts. None of the bats showed signs of acute infection. They were euthanized by inhalation of diethyl ether, and spleen, lung, kidney and liver tissues and intestinal contents were collected through dissection. The species were identified according to the nucleotide sequence of the gene encoding mitochondrial cytochrome b, as described previously (Sasaki et al., 2012). For viral metagenomic analysis, intestinal contents from three horseshoe bats were pooled and enriched for viral sequences that were used to generate a library, which was sequenced using the Ion Torrent PGM System (Life Technologies), as described previously (Sasaki et al., 2015). Among 1,638,834 total sequence reads, BLASTn analysis assigned 452 reads to RVA at an E value cut-off of 10^{-4}. To screen for the gene encoding RVA VP7 in the 16 captured bats, we used the High Pure Viral RNA kit (Roche Diagnostics) for extracting nucleic acids from individual intestinal contents, which were then subjected to nested reverse transcription PCR (RT-PCR) using the primer sets described by Li et al. (2016). RVA nucleotide sequences encoding VP7 were detected in one Bushveld horseshoe bat (Rhinolophus simulator).

We next determined the nucleotide sequences of 11 genome segments of the detected RVA. The RNA sample was denatured at 98 °C for 2 min in the presence of 1 M betaine and 2.5% DMSO (Darissa et al., 2010), and was then subjected to conventional RT-PCR, using SuperScript IV Reverse Transcriptase (Life Technologies), Tks Gflex DNA Polymerase (Takara Bio) and specific primers for the sequence reads and universal primers for RVA (Fujii et al., 2012). The 11 genome segments of RVA were sequenced using RNA from the intestinal contents positive for the gene encoding VP7. We then attempted to confirm the 5′- and the 3′-terminal regions of each genome segment using the RACE approach with the SMARTer RACE cDNA Amplification kit (Takara Bio). The 5′-termini of VP4- and VP2-encoding segments and the 3′-termini of VP2- and NSP2-encoding segments were recovered using RACE analysis. Information on all primers used in this study is summarized in Tables S1–S3 (available in the online Supplementary Material). The sequences were deposited in the GenBank/EMBL/DDBJ database under accession numbers LC158116–LC158126. According to the RVA nomenclature proposed by the Rotavirus Classification Working Group (Matthijnssens et al., 2011a), we named the RVA strain as RVA/Bat-wt/ZMB/LUS12-14/2012/G3P[3] (LUS12-14). We used RotaC 2.0 (http://rotac.regatools.be) to assign LUS12-14 to the G3-P [3]-I3-R2-C2-M3-A9-N2-T3-E2-H3 genotype constellation (Maes et al., 2009). It has been reported that RVA was detected in some tissues of domestic and experimental animals (Ramig, 2007). To assess the infection of the bat by LUS12-14, we extracted RNA from the spleen, lung, kidney and liver tissues of the bat in which LUS12-14 was detected in the intestinal contents. VP4- and NSP2-encoding segments of LUS12-14 were exclusively detected in the spleen RNA by RT-PCR using specific primers (Table S2).

Table 1 shows the genotype assignment of LUS12-14, the nucleotide positions determined in this study and the nucleotide sequence identities between each segment of LUS12-14 and the strain with the most closely related genome segments. The genome sequences encoding VP7, VP4, VP3 and NSP2 of LUS12-14 shared >97% nucleotide identities with those of RVA/Human-tc/ITA/PA260-97/1997/G3P[3] (Table 1), which was isolated from a child with acute diarrhoea in Italy (De Grazia et al., 2007). We used the maximum likelihood component (500 bootstrap replicates) parameter of MEGAT6 software to deduce the phylogenies of VP7 and VP4 segments according to their nucleotide sequences (Kumar et al., 2016). LUS12-14 VP7 and VP4 clustered with related G3- and P[3]-genotype RVA strains, respectively (Fig. 1). The VP1 genome segment of LUS12-14 exhibited 97.8% nucleotide sequence identity with RVA/Antelope-wt/ZAF/RC-18-08/2008/G6P [14] isolated from a sable antelope with gastroenteritis in South Africa (Matthijnssens et al., 2009). The NSP4 and

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genotype of LUS12-14</th>
<th>Nucleotide position*</th>
<th>Strains with the most closely related segments</th>
<th>Nucleotide identity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>VP6</td>
<td>I3</td>
<td>21–1339</td>
<td>RVA/Rat-wt/CHN/RA108/2013/G3P[3]</td>
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<tr>
<td>VP2</td>
<td>C2</td>
<td>1–2717</td>
<td>RVA/Human-wt/GHA/GH018-08/2008/G8P[6]</td>
<td>96.1</td>
</tr>
<tr>
<td>NSP1</td>
<td>A9</td>
<td>26–1531</td>
<td>RVA/Rabbit-tc/CHN/N5/1992/G3P[14]</td>
<td>89.5</td>
</tr>
</tbody>
</table>

*The nucleotide positions correspond to those of the Wa strain; RVA/Human-tc/USA/Wa/1974/G1P[8], JX406747–JX406757.
NSP5 genome segments of LUS12-14 showed 98.0 % and 98.6 % nucleotide sequence identities with RVA/Cow-wt/ZAF/1604/2007/G8P[1] and RVA/Cow-wt/ZAF/1603/2007/G6P[5], respectively, from the genomes extracted from stool samples of calves with diarrhoea in South Africa (Jere et al., 2012).

The VP6, VP2, NSP1 and NSP3 genome segments of LUS12-14 showed relatively low (<97 %) nucleotide sequence identities with RVA sequences deposited in the GenBank/EMBL/DDBJ nucleotide database. Therefore, we deduced the phylogenies of these segments according to their nucleotide sequences. The LUS12-14 VP6 genome segment clustered with I3-genotype RVA strains and was closely related to RVA/Rat-wt/CHN/WC179/2013/G3P[45], the rat RVA strain detected in China (Li et al., 2016) (Fig. 2). The VP2 genome segment of LUS12-14 clustered with the human RVA C2 genotype (Fig. 2). The NSP1 genome segment of LUS12-14 clustered with the A9 genotype of bat RVAs, although it was more closely related to the rabbit strain RVA/Rabbit-tc/CHN/95/G3P[14] (Guo et al., 2012) (Fig. 2). The NSP3 genome segment of LUS12-14 clustered with the T3-genotype RVA strains and was most closely related to RVA/Human-tc/THA/T152/1998/G12P[9], the human RVA strain in Thailand (Pongsuwanna et al., 2002) (Fig. 2). Moreover, there was no close genetic relationship between LUS12-14 and other bat-derived RVAs.

![Phylogenetic analyses of the genes encoding VP7 and VP4.](image-url)

**Fig. 1.** Phylogenetic analyses of the genes encoding VP7 and VP4. The rotavirus strain LUS12-14 identified in this study, its related strains, and the representative reference strains were included in the analysis. LUS12-14 is shaded grey. Genotypes are shown to the right of the trees. The bootstrap values obtained after 500 replicates are indicated at major tree roots. The scale bars represent the numbers of nucleotide substitutions per site.
Fig. 2. Phylogenetic analyses of the genes encoding VP6, VP2, NSP1 and NSP3. The rotavirus strain LUS12-14 identified in this study, its related strains and the representative reference strains were included in the analysis. The analysis is described in the legend of Fig. 1.
Complete genome classification studies have revealed the emergence of reassortant RVAs carrying genome segments of RVAs from different mammalian species, suggesting interspecies transmission (Esona et al., 2010; Jere et al., 2012; Li et al., 2016; Matthijnssens et al., 2009, 2011b). Reassortment contributes to the high genetic diversity of RVA strains. In the present study, we identified and characterized a new RVA strain designated LUS12-14 in the faeces of an insectivorous bat in Zambia. In contrast to known bat-borne RVAs, the LUS12-14 genome comprises segments that are nearly identical or closely related to those of other mammalian RVA strains, suggesting that LUS12-14 represents a multi-reassortant RVA derived from other mammalian RVA strains that presumably emerged from recent interspecies transmission.

Among the related RVA strains, RVA/Human-tc/ITA/PA260-97/1997/G3P[3] may originate from canine and feline RVA strains (Matthijnssens et al., 2011b), and strains RVA/Cow-wt/ZAF/1604/2007/G8P[1] and RVA/Cow-wt/ZAF/1603/2007/G6P[5] may have been generated through reassortment events between bovine, giraffe and antelope RVAs (Jere et al., 2012). The identification of LUS12-14 suggests that bats are susceptible to infection by zoonotic RVAs and serve as a host involved in the evolution of RVA through cycles of interspecies transmission accompanied by genome reassortment events.

Although diarrhoea in humans caused by RVA is common in Zambia (Beres et al., 2016; Mpabalwani et al., 2016), little is known about the genotypes of endemic RVA strains of human and other mammals. We detected LUS12-14 in the spleen tissue and faeces of one insectivorous bat, suggesting that LUS12-14 originated from the bat. However, it is unclear whether other bats are infected with LUS12-14 and whether the virus-host relationship detected here is fortuitous. Further studies on LUS12-14 or other zoonotic RVA strains in bats are required to confirm that bats serve as a reservoir of zoonotic RVA strains. These studies also contribute to our understanding of the evolution of RVA in nature, including that in bats.

Acknowledgements

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References


