

Molecular detection and characterization of human gyroviruses identified in the ferret fecal virome

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Abstract The recently described novel gyroviruses may infect chickens and/or humans; however, their pathogenic potential is unknown. In our metagenomic investigation, we detected many of the novel gyroviruses in the fecal viromes of ferrets with lymph node and organ enlargement. The complete genomic sequences of selected gyrovirus strains showed 90.7–99.4 % similarity to homologous reference gyrovirus strains. This study did not demonstrate an association between gyrovirus shedding from ferrets and the observed background disease; however, it provides evidence for genetic diversity among gyroviruses and raises the possibility that pet ferrets may transmit gyroviruses to heterologous hosts, e.g., humans.

Several new members of the genus *Gyrovirus* (family *Circoviridae*) have been described during the past three years. Chicken anaemia virus (CAV) causes anaemia, bone marrow atrophy and severe immunosuppression in poultry and represents the prototype species within the genus. Newly described members include human gyrovirus (HGyV), avian gyrovirus 2 (AGV2), GyV3, GyV4, GyV5 and GyV6 [1–5]. It is of interest that some of these new gyrovirus types have been identified in human skin (HGyV), blood (HGyV) and stool (all gyroviruses) specimens, although an etiologic role of these viruses in human disease has not been demonstrated [1–7]. Furthermore, in addition to CAV, AGV2, HGyV and GyV4 have also been detected in chicken serum, meat and skin [1–3].

In this study, 23 diarrheic stool specimens were collected from 20 pet ferrets (*Mustela putorius furo*) housed in a shelter. The animals had a background disease characterized by lymph node and spleen enlargement. The majority of samples (21 samples of 18 ferrets) were subjected to viral metagenomics. In brief, the genomic RNA was extracted using a Viral RNA Mini Kit (QIAGEN) according to the manufacturer's instructions. The RNA sample was denatured at 97 °C for 5 min in the presence of 10 μM random hexamer tailed by a common PCR primer sequence [8]. A reverse transcription reaction mixture containing 400 μM dNTPs, 1X AMV RT buffer and 1 U AMV reverse transcriptase (Promega) was added and then incubated at 42 °C for 45 min. Five microliters of cDNA was amplified in a final reaction volume of 50 μl including 500 μM PCR primers, 200 μM dNTP mixture, 1.5 mM MgCl₂, 1X Taq DNA polymerase buffer and 0.5 U Taq DNA polymerase (Thermo Scientific). The reaction conditions consisted of a denaturation step at 95 °C for 3 min, 40 cycles of amplification (95 °C for 30 s, 48 °C for 30 s,

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72 °C for 2 min) and a final extension step at 72 °C for 8 min.

Enzymatic fragmentation was carried out from 100 ng of the amplified cDNA using the reagents of the NEB-Next® Fast DNA Fragmentation & Library Prep Set for Ion Torrent™ kit (New England Biolabs) according to the manufacturer's instructions. Adaptor ligation was performed using reagents from the same kit, whereas barcoded adaptors were retrieved from the Ion Xpress™ Barcode Adapters (Life Technologies). The barcoded library DNA samples were column extracted using a Gel/PCR DNA Fragments Extraction Kit (Geneaid) and then run on a 2 % precast gel (Life Technologies). Products between 300 and 350 bp were used directly without further purification in the PCR mixture of the NEBNextR Fast DNA Fragmentation & Library Prep Set for Ion Torrent™ kit (NEB). Library DNA was subsequently amplified (initial denaturation at 98 °C for 30 s, followed by 12 amplification cycles of 98 °C for 10 s, 58 °C for 30 s and 72 °C for 30 s, and termination at 72 °C for 5 min). The amplified library DNA was purified using a Gel/PCR DNA Fragments Extraction Kit (Geneaid) and was quantified fluorimetrically on a Qubit® 2.0 fluorometer using the Qubit® dsDNA BR Assay Kit (Life Technologies). Approximately equimolar aliquots of the individually barcoded products were mixed in a single tube, and this library mixture was used in subsequent emulsion PCR according to the manufacturer's protocol using an Ion PGM Template Kit on an OneTouch v2 instrument. Enrichment of the templated beads (on an Ion One Touch ES machine) and further steps of pre-sequencing set-up were performed according to the 200 bp sequencing protocol of the manufacturer (Life Technologies). The sequencing protocol recommended for the Ion PGM™ Sequencing Kit on a 316 chip was strictly followed. Raw sequence data were mapped onto reference sequences from the GenBank database using CLC Bio software (<http://www.clcbio.com/>). Sequence alignments and distance matrixes using the *p*-distance algorithm were prepared in MEGA 6 using the MUSCLE program [9].

Viral metagenomics generated an average of 67,737 sequence reads (range, 36,337–87,870) from each barcoded cDNA library. The metagenomic assemblage identified coronaviruses and a great diversity of gyroviruses (including HGyV, AGV2, GyV3, GyV4 and CAV; Table 1) in 50 % (9/18) and 44 % (8/18) of the animals, respectively. Although detection of chicken-origin gyroviruses (such as CAV and AGV2) in the fecal specimens was not surprising, the identification of putative human gyroviruses in the ferret fecal virome was somewhat unexpected; therefore, we systematically screened by PCR all available ferret stool samples for different gyroviruses, including those that were previously found exclusively in humans, in chickens, or both.

The PCR primers targeted the VP1 gene of HGyV/AGV2, GyV3, GyV4 and CAV, and the VP2 genomic region of HGyV/AGV2 and GyV3 [3, 4]. When the results of targeted PCR and metagenomic analysis were merged, the stool samples of 14 animals were found to contain traces of gyrovirus genomic DNA. The main type was HGyV (identified in 13 of 14 animals). Eleven animals shed a mixture of gyroviruses; CAV was a commonly seen strain in specimens containing multiple gyroviruses (11/11), whereas GyV3 was amplified by PCR from two, and GyV4 and AGV2 from one ferret each. Interestingly, genomic DNA of another GyV3 and three GyV4 strains was identified by viral metagenomics in specimens that were negative by gene-specific PCR. Sequence variation in the primer-binding region provided a possible explanation for PCR failures in some instances and suggested limited sensitivity of published GyV3- and GyV4-specific PCR primers [3, 4].

Subsequently, PCR primers were designed for the amplification of representative full-length gyrovirus genomes. PCR assays with back-to-back primers were performed in a reaction volume of 20 µl containing 250 µM dNTP mix, 250 nM each primer, 1X Phusion Green HF Buffer and 0.3 U Phusion DNA polymerase (Thermo Scientific). Amplification conditions were as follows: denaturation at 98 °C for 30 s, 40 cycles of 98 °C for 10 s, 53 or 59 °C for 30 s (for GyV4 and HGyV/AGV2, respectively) and 72 °C for 90 s, and a final extension at 72 °C for 10 min. Sequencing of the amplified genomes was performed using the 'primer-walking' approach and Sanger sequencing using an ABI PRISM® 3100-Avant Genetic Analyzer and BigDye Terminator v3.1 Cycle Sequencing Kit (Life Technologies). Primers used for amplification and sequencing are presented in Table 2. The full-length genomes of five ferret-origin gyrovirus strains (three HGyV, one AGV2, one GyV4) were determined, and three representative genome sequences were deposited in the GenBank database (accession numbers: KJ452213 for AGV2 G17, KJ452214 for HGyV G13 and KJ452215 for GyV4 G14). Short fragments (~15–25 nucleotides in length) in the non-coding region could be sequenced only by a modified sequencing protocol due to the high GC content of the predicted hairpin structure just downstream the VP1, although back-to-back and other primers designed to amplify smaller products (559 bp for HGyV and AGV2 and 599 bp for Gyv4) spanning the putative hairpin structure worked well in our hands. Sequencing issues concerning these non-coding fragments even after cloning has been reported by other research groups [5]. In the present study, PCR assays and sequencing reactions in the presence of different concentrations of DMSO, betaine and Q-solution (QIAGEN) were tested, but early termination of the sequencing reaction was always observed (Fig. 1, panel

Table 1 Results of metagenomic and gyrovirus PCR analyses of ferret fecal samples

Sample name	Metagenomic analysis				PCR			
	HGyV/ AGV2	GyV3	GyV4	CAV	HGyV/AGV2	GyV3	GyV4	CAV
G1	+	-	+	-	+ (FR823283, 100 %)	-	-	+ (FJ360724, 100 %)
G2	N.D.				+ (FR823283, 100 %)	-	-	+ (FJ360724, 100 %)
G3	+	-	+	+	+ (FR823283, 100 %)	-	-	+ (no sequence)
G4	-	-	-	-	-	-	-	-
G5	-	-	-	-	-	-	-	-
G6	N.D.				-	-	-	-
G7	-	-	-	-	+ (FR823283, 100 %)	-	-	-
G8	-	-	-	-	-	-	-	-
G8A	-	-	-	-	+ (FR823283, 100 %)	-	-	+ (no sequence)
G9	-	-	-	-	+ (FR823283, 100 %)	+ (JQ308210, 99.0 %)	-	+ (FJ360724, 100 %)
G10	-	-	-	-	-	-	-	-
G10A	-	-	-	-	-	-	-	-
G11	-	-	-	-	+ (FR823283, 100 %)	+ (JQ308210, 99.0 %)	-	+ (no sequence)
G12	-	-	-	-	-	-	-	-
G13	+	-	-	-	W (FR823283, 99.4 %)	-	+ (JX310702, 94.6 %)	+ (FJ360724, 100 %)
G14	+	-	W (JX310702, 90.7 %)	-	W (FR823283, 99.4 %)	-	-	+ (FJ360724, 100 %)
G15	-	-	-	-	+ (FR823283, 100 %)	-	-	+ (FJ360725, 100 %)
G16	-	-	-	-	-	-	-	-
G17	+	-	-	-	W (JQ690763, 95.9 %, HM590588, 94.2 %)	-	-	-
G18	+	-	-	-	+ (FR823283, 100 %)	-	-	+ (FJ360724, 100 %)
G19	+	+	-	-	W (FR823283, 99.4 %)	-	-	+ (FJ360724, 100 %)
G20	+	-	-	-	+ (FR823283, 100 %)	-	-	-
G20A	-	-	-	-	-	-	-	-
Positive samples	8/21 (38.1 %)	1/21 (4.8 %)	3/21 (14.3 %)	1/21 (4.8 %)	14/23 (60.9 %)	2/23 (8.7 %)	1/23 (4.3 %)	11/23 (55 %)
Positive animals	8/18 (44.4 %)	1/18 (5.6 %)	3/18 (16.7 %)	1/18 (5.6 %)	14/20 (70 %)	2/20 (10 %)	1/20 (5 %)	11/20 (47.8 %)

Two samples were taken at different dates from ferrets labelled as G8, G10 and G20. Accession numbers of the references and nt similarities of those to our sequences are indicated in parentheses

HGyV, human gyrovirus; AGV2, avian gyrovirus 2; GyV3 and GyV4, gyrovirus 3 and 4; CAV, chicken anaemia virus. "HGyV/AGV2" indicates that HGyV and/or AGV2 sequences were detected in the sample. N.D., not done. W, whole genome sequence

A). A modified PCR using 7-deaza-dGTP (New England Biolabs) in a reaction volume of 20 µl contained 250 nM primers specific for the GC-rich region (Table 1), 25 µM dATP, dCTP, dTTP and 7-deaza-dGTP (New England Biolabs), 1X DreamTaq Green Buffer and 0.5 U DreamTaq

DNA Polymerase (Thermo Scientific). The cycling profile was as follows: denaturation at 95 °C for 3 min, 40 cycles of 95 °C for 30 s, 54 °C for 30 s and 72 °C for 1 min, and a final extension step at 72 °C for 10 min. As in the previous attempts, these sequences were also terminated

Table 2 Primer sequences designed for the amplification and sequencing of gyrovirus sequences from ferret fecal samples

Primer name Position	5'-3' primer sequence	Function
human gyrovirus/avian gyrovirus 2		
GGyV1-F1 203-231	AGTAAACTGAGACTCATACCGGTACAGGG	back-to-back PCR, sequencing
GGyV1-R1 202-172	TACATATCGTTGGTTACCACGCCTTGTG	back-to-back PCR, sequencing, modified PCR of GC-rich region
GGyV1-F2 1009-1031 (1012-1034)	ACGATGGCACTGGAGACACAGAC	back-to-back PCR, sequencing
GGyV1-R2 1008-986 (1011- 989)	CCTCTGTGGTAGAAGCCAAAGCG	back-to-back PCR, sequencing
GGyV1-F3 1098-1124 (1101-1127)	GCGTTAAGAGGAGGATCTTCAACCCAC	back-to-back PCR, sequencing
GGyV1-R3 1097-1074 (1100-1077)	GGCGATCAAAGGATCTTCTACGCG	back-to-back PCR, sequencing
GGyV1-F4 1494-1519 (1497-1522)	GAGCACCTGGCAGATTTTACAATGCC	back-to-back PCR, sequencing
GGyV1-R4 1493-1472 (1496-1475)	TAGGGTGCATCACCAGGAGAGC	back-to-back PCR, sequencing
GGyV1-F/1 685-710	GAGATCCAAATTGGTATCGGGTCAAC	sequencing
GGyV1-F/2 1683-1706 (1686-1709)	TAGAGGGCTTCCCAGTTAAAGGTG	sequencing
GGyV1-F/3 1946-1968 (1949-1971)	GGTGACCCTGGTCATTTCCCTAG	sequencing
GGyV1-F/4 2039-2060 (2042-2063)	CGACGGTGGTTAACACTTGTGC	sequencing, modified PCR of GC-rich region
GGyV1-R/1 539-518	AAGTTGCCCTCTTGCCCTAAGC	sequencing
GGyV1-R/2 662-639	GGAGACGAACTTGTGGATGCTCG	sequencing
gyrovirus 4		
GGyV4-F (974- 992)	TCAGATTCAGACGGAGACC	back-to-back primers
GGyV4-R (973- 954)	CCATTCCACAAAAGTCCC	back-to-back primers
GGyV4-F/1 1446-1469	TGCAAATGGAAGTAGGCCGACAG	sequencing
GGyV4-F/2 277-299	ATGGCAGGGTACTTATTGCCGTG	sequencing
GGyV4-F/3 1835-1862	TCGGTACATTGTTTCTCGCGGAATTTAG	sequencing, modified PCR of GC-rich region
GGyV4-R/1 538-517	ACTAAAGCGATGGTCAGGGCTG	sequencing
GGyV4-R/2 405-384	AGCAAAAATTCAGTCCCGAG	sequencing, modified PCR of GC-rich region
GGyV4-R/3 1256-1232	TCAGCCTGTCCAGACTGATATACGG	sequencing

Primer positions without parentheses refer to human gyrovirus, and values in parentheses indicate primer positions in avian gyrovirus 2

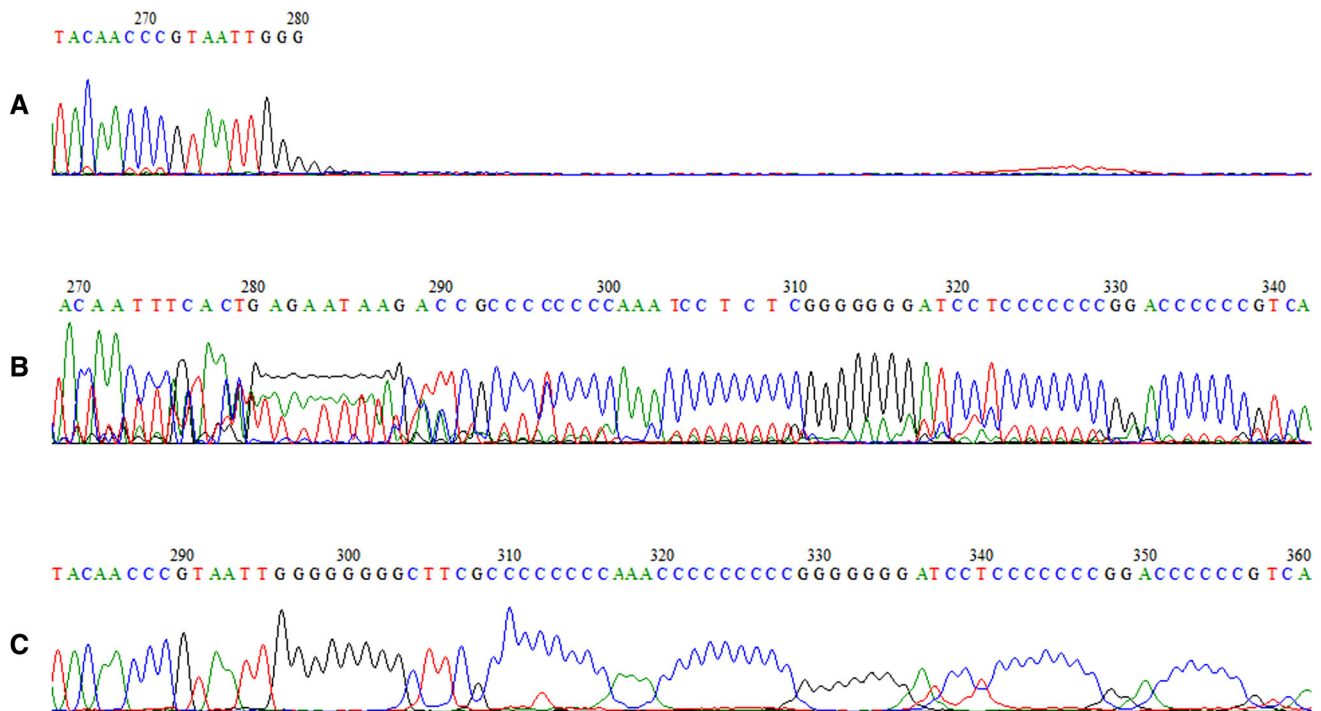


Fig. 1 Sequencing of the GC-rich non-coding region of the human gyrovirus strain G13. Panel A: early termination after amplification and Sanger sequencing. Panel B: sequences determined using PCR

with 7-deaza-dGTP in the reaction mixtures. Panel C: sequences after the utilization of 7-deaza-dGTP in both PCR and sequencing reaction mixtures

before reaching the GC-rich region or yielded ambiguous sequencing results (Fig. 1, panel B). High-quality sequences for the hairpin region were only obtained when 2.5–5 μ M 7-deaza-dGTP was included in both the PCR and sequencing reaction mixtures (Fig. 1, panel C). As a result, alternating reiterations of homo-G-polymer and homo-C-polymer regions, 61 nt (HGyV/AGV2) and 42 nt (GyV4) in length, were revealed in the missing genomic region.

The three HGyV genomes were 2375 nt long; the genome sequences were identical to each other and were closely related (94.5 %) to the AGV2 G17 strain, which has a genome length of 2378 nt. The complete genomic sequence of Hungarian HGyV G13 was 61 nt longer than that of the reference HGyV (accession number: FR823283), which lacked the GC-rich region identified in our HGyV and AGV2 genomes as well as in the AGV2 genomes deposited in the GenBank database (accession numbers: JQ690763, HM590588). The complete genomes of HGyV G13 and AGV2 G17 showed 99.4 % and 94.2–95.9 % similarity along the overlapping regions of the whole genomes of homologous reference strains HGyV and AGV2, respectively. Although the genome of the G17 strain had a codon insertion affecting the potential VP2 and VP3 proteins, the overall genome size and structure of the non-coding region were comparable with those of the G13 and the AGV2 reference genome sequences.

The full-length genome of the Hungarian GyV4 strain, G14, was 2028 nt long, i.e., six bases shorter than the only GyV4 reference genome sequence available in GenBank (accession number: JX310702). These two genome sequences showed 90.7 % nt similarity to each other. The nt and amino acid similarities along the VP1 and VP2 regions showed an inverse pattern (86.7 % and 94 % nt and 92.6 % and 88.9 % aa similarity, respectively) to the reference sequence. This lower sequence similarity between GyV4 strains suggests a greater diversity within this group of gyroviruses than seen among HGyV and AGV2 strains, which are believed to be minor sequence variants of the same virus [3].

PCR results obtained using diagnostic primers were systematically confirmed by sequencing of the amplicons. Briefly, the short HGyV sequences (251–429 nt long) amplified using the diagnostic primers [3, 4] shared 100 % identity among themselves. A 392-nt-long stretch [3, 4] in two GyV3 strains shared 98 % nt sequence identity with each other and 99 % to the reference sequence (accession number: JQ308210). The only GyV4 sequence (239 nt long) amplified using diagnostic primers [3] showed 93.3 % and 94.6 % nt similarity to our G14 strain and the reference GyV4 strain, respectively. CAV strains showed 99–100 % similarity to each other and 100 % similarity to the reference strains found in GenBank. No traces of GyV5

and GyV6 were observed in the metagenomic analyses; thus, the study was not extended to the examination of these novel gyroviruses. Unfortunately, determination of whole genomic sequences of additional gyroviruses was not possible because of the small amount of stool samples and/or poor amplification results.

The identification of genetically related, practically indistinguishable, gyroviruses in the fecal viromes of humans and ferrets is an interesting finding [2–7]. Ferrets in the Hungarian shelter were fed regularly with chicken meat. This could be an explanation for why a well-known chicken pathogen, CAV, and a newly described member of the genus, AGV2, were detected in the feces of these animals. Similarly, food-associated acquisition and passive transfer through the gut could explain the detection of gyroviruses in the feces of humans and cats as reported in other studies [3–5, 10]. However, gyroviruses were also detected in human blood, and thus the possibility that certain gyroviruses are capable of infecting a mammalian host cannot be ruled out [6, 7].

It is worth noting that ferret coronaviruses have also been detected in fecal specimens by high-throughput sequencing. Coronaviruses are a common cause of diarrhoea in a variety of animal species and may induce systemic disease [11]. Novel gyroviruses have already been detected in diseased humans and chickens [1, 3–5], and it seems plausible that, like CAV [1], these novel members of the genus may also induce immune suppression in a different host species, such as ferrets. However, this assumption awaits supporting epidemiological and experimental data.

In summary, the finding that genetically identical gyroviruses can be detected in humans and ferrets warrants close monitoring of these newly described viruses. The causative role and the host range of different gyroviruses must be explored to help better understand the findings of this study.

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Conflict of interest The authors declare that they have no conflict of interest.

References

- Rijsewijk FA, Dos Santos HF, Teixeira TF, Cibulski SP, Varela AP, Dezen D, Franco AC, Roehle PM (2011) Discovery of a genome of a distant relative of chicken anemia virus reveals a new member of the genus *Gyrovirus*. *Arch Virol* 156(6):1097–1100
- Sauvage V, Cheval J, Foulongne V, Gouilh MA, Pariente K, Manuguerra JC, Richardson J, Dereure O, Lecuit M, Burguiere A, Caro V, Eloit M (2011) Identification of the first human gyrovirus, a virus related to chicken anemia virus. *J Virol* 85(15):7948–7950
- Chu DK, Poon LL, Chiu SS, Chan KH, Ng EM, Bauer I, Cheung TK, Ng IH, Guan Y, Wang D, Peiris JS (2012) Characterization of a novel gyrovirus in human stool and chicken meat. *J Clin Virol* 55(3):209–213
- Phan TG, Li L, O’Ryan MG, Cortes H, Mamani N, Bonkougou IJ, Wang C, Leutenegger CM, Delwart E (2012) A third gyrovirus species in human faeces. *J Gen Virol* 93(6):1356–1361
- Gia Phan T, Phung Vo N, Sdiri-Loulizi K, Aouni M, Pothier P, Ambert-Balay K, Deng X, Delwart E (2013) Divergent gyroviruses in the feces of Tunisian children. *Virology* 446(1–2):346–348
- Maggi F, Macera L, Focosi D, Vatteroni ML, Boggi U, Antonelli G, Eliot M, Pistello M (2012) Human gyrovirus DNA in human blood, Italy. *Emerg Infect Dis* 18(6):956–959
- Biagini P, Bédarida S, Touinssi M, Galicher V, de Micco P (2013) Human gyrovirus in healthy blood donors, France. *Emerg Infect Dis* 19(6):1014–1015
- Djikeng A, Halpin R, Kuzmickas R, Depasse J, Feldblyum J, Sengamalay N, Afonso C, Zhang X, Anderson NG, Ghedin E, Spiro DJ (2008) Viral genome sequencing by random priming methods. *BMC Genom* 9:5
- Tamura K, Stecher G, Peterson D, Filipinski A, Kumar S (2013) MEGA6: molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol* 30:2725–2729
- Zhang X, Liu Y, Ji J, Chen F, Sun B, Xue C, Ma J, Bi Y, Xie Q (2014) Identification of a chicken anemia virus variant-related gyrovirus in stray cats in China, 2012. *BioMed Res Int* 2014:313252
- Provacia LB, Smits SL, Martina BE, Raj VS, Doel PV, Amerongen GV, Moorman-Roest H, Osterhaus AD, Haagmans BL (2011) Enteric coronavirus in ferrets, the Netherlands. *Emerg Infect Dis* 17(8):1570–1571