Genome Sequence of a Novel Kunsagivirus (Picornaviridae: Kunsagivirus) from a Wild Baboon (Papio cynocephalus)

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ABSTRACT

The picornaviral genus Kunsagivirus has a single member, kunsagivirus A, which was discovered in migratory bird feces. We report here the discovery of a novel kunsagivirus in wild yellow baboon (Papio cynocephalus) blood. The genomic sequence of this virus indicates the probable need for the establishment of a second kunsagivirus species.

The Picornaviridae family of the order Picornavirales contains viruses with positive-sense single-stranded RNA genomes that produce nonenveloped virions. Picornaviruses infect birds, fish, and mammals belonging to a diverse array of species, including primates. Currently, the family consists of 54 species grouped into 31 officially recognized genera, including the recently formed genus Kunsagivirus. Kunsagivirus A (strain Roller/SZAL6-KuV/2011/HUN, GenBank accession number KC935379) is the only classified member of the only species included in the genus, Kunsagivirus A. This virus was discovered in a fecal sample collected in Hungary in July 2011 from an Afro-Palearctic long-distance migratory bird, the European roller (Coracias garrulus), using sequence-independent random reverse transcriptase PCR (RT-PCR) amplification of virion-associated nucleic acids, 5’-3’ rapid amplification of cDNA ends (RACE), and Sanger sequencing (1). However, as this virus was found in the feces of only a single bird, it is unclear whether Kunsagivirus A naturally infects roller birds or a food source.

Here, we report the genomic sequence of a novel virus detected in the blood of baboon M27, a wild adult male yellow baboon (Papio cynocephalus) sampled in Mikumi National Park in Tanzania in 1986 (2). In brief, RNA was isolated from blood plasma using the MinElute virus spin kit without carrier RNA (Qiagen, Valencia, CA), and random hexamers were used to prime cDNA synthesis (Life Technologies, Inc., Grand Island, NY), as previously described (3). Deep-sequencing libraries were prepared using the Nextera XT kit (Illumina, San Diego, CA) and sequenced on an Illumina MiSeq. Low-quality (Phred <30) and short reads (<100 bp) were removed with CLC Genomics Workbench 7.1 (CLC bio, Aarhus, Denmark), and the remaining reads were assembled de novo using the MEGAHIT assembler and compared against all viral sequences in the NCBI GenBank database as of 22 June 2016 (4). A single 7.4-kb-long contig was highly similar to the genome of Kunsagivirus A, with 50.8% pairwise identity across the coding sequence when aligned using ClustalW with an IUB cost matrix (gap extension cost, 6.66; gap open cost, 15). The novel virus, which

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we name Bakunsa virus (BKUV [sigil for baboon kunsagivirus]), probably represents a second species in the genus *Kunsagivirus*.

Our reconstruction of the coding-complete BKUV genome from a blood sample suggests that wild baboons in Africa are a natural host for kunsagiviruses. However, the absence of kunsagivirus sequences in other metagenomic studies of African monkeys (3, 5–11) indicates that these infections may be either acute or relatively rare if persistent. If kunsagivirus A truly infects birds, our discovery of a baboon kunsagivirus infers a broad host range for kunsagiviruses relative to members of other picornaviral genera. However, whether primates serve as the natural reservoir for some kunsagiviruses, or are an incidental “dead-end” host, remains an open question, and the natural course, incidence, and pathogenesis of kunsagivirus infections in baboons, or the potential of kunsagivirus cross-species transmission, remain unknown.

**Accession number(s).** The GenBank accession number of BKUV isolate baboon/M27-KuV/1986/TAN is KY670597.

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**REFERENCES**

1. Boros A, Kiss T, Kiss O, Pankovics P, Kapusinszky B, Delwart E, Reuter G. 2013. Genetic characterization of a novel picornavirus distantly related to the marine mammal-infecting aquamaviruses in a long-distance migrant bird species, European roller (*Coracias garrulus*). J Gen Virol 94: 2029–2035. https://doi.org/10.1099/vir.0.054676-0.

2. Rogers J, Kidd KK. 1993. Nuclear DNA polymorphisms in a wild population of yellow baboons (*Papio hamadryas cynocephalus*) from Mikumi National Park, Tanzania. Am J Phys Anthropol 90:477–486. https://doi.org/10.1002/aja.1330900407.

3. Lauck M, Sibley SD, Hyeroba D, Tumukunde A, Weny G, Chapman CA, Ting N, Switzer WM, Kuhn JH, Friedrich TC, O’Connor DH, Goldberg TL. 2013. Exceptional simian hemorrhagic fever virus diversity in a wild African primate community. J Virol 87:688–691. https://doi.org/10.1128/JVI.00433-12.

4. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol 215:403–410. https://doi.org/10.1016/S0022-2836(05)80360-2.

5. Bailey AL, Lauck M, Ghai RR, Nelson CW, Heimbruch K, Hughes AL, Goldberg TL, Kuhn JH, Jasinska AJ, Freimer NB, Apetrei C, O’Connor DH. 2016. Arteriviruses, pegiviruses, and lentiviruses are common among wild African monkeys. J Virol 90:6724–6737. https://doi.org/10.1128/JVI.00573-16.

6. Kapusinszky B, Mulvaney U, Jasinska AJ, Deng X, Freimer N, Delwart E. 2015. Local virus extinctions following a host population bottleneck. J Virol 89:8152–8161. https://doi.org/10.1128/JVI.00671-15.

7. Bailey AL, Lauck M, Sibley SD, Friedrich TC, Kuhn JH, Freimer NB, Jasinska AJ, Phillips-Conroy JE, Jolly CJ, Marx PA, Apetrei C, Rogers J, Goldberg TL, O’Connor DH. 2016. Zoonotic potential of simian arteriviruses. J Virol 90:630–635. https://doi.org/10.1128/JVI.01433-15.

8. Bailey AL, Lauck M, Sibley SD, Pecotte J, Rice K, Weny G, Tumukunde A, Hyeroba D, Greene J, Correll M, Gleicher M, Friedrich TC, Jhrling PB, Kuhn JH, Goldberg TL, Rogers J, O’Connor DH. 2014. Two novel simian arteriviruses in captive and wild baboons (*Papio spp.*). J Virol 88: 13231–13239. https://doi.org/10.1128/JVI.02203-14.
9. Bailey AL, Lauck M, Weiler A, Sibley SD, Dinis JM, Bergman Z, Nelson CW, Correll M, Gleicher M, Hyeroba D, Tumukunde A, Weny G, Chapman C, Kuhn JH, Hughes AL, Friedrich TC, Goldberg TL, O’Connor DH. 2014. High genetic diversity and adaptive potential of two simian hemorrhagic fever viruses in a wild primate population. PLoS One 9:e90714. https://doi.org/10.1371/journal.pone.0090714.

10. Bailey AL, Lauck M, Mohns M, Peterson EJ, Beheler K, Brunner KG, Crosno K, Mejia A, Mutschler J, Gehrke M, Greene J, Ericsen AJ, Weiler A, Lehrer-Brey G, Friedrich TC, Sibley SD, Kallas EG, Capuano S, Rogers J, Goldberg TL, Simmons HA, O’Connor DH. 2015. Durable sequence stability and bone marrow tropism in a macaque model of human pegivirus infection. Sci Transl Med 7:305ra144. https://doi.org/10.1126/scitranslmed.aab3467.

11. Sibley SD, Lauck M, Bailey AL, Hyeroba D, Tumukunde A, Weny G, Chapman CA, O’Connor DH, Goldberg TL, Friedrich TC. 2014. Discovery and characterization of distinct simian pegiviruses in three wild African Old World monkey species. PLoS One 9:e98569. https://doi.org/10.1371/journal.pone.0098569.