



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

 Connor R. Buechler,<sup>a,b</sup>  Adam L. Bailey,<sup>a,b</sup>  Michael Lauck,<sup>a,b</sup> Anna Heffron,<sup>a,b</sup>  Joshua C. Johnson,<sup>d</sup> Cristine Campos Lawson,<sup>d</sup> Jeffrey Rogers,<sup>c</sup>  Jens H. Kuhn,<sup>d</sup>  David H. O'Connor<sup>a,b</sup>

Department of Pathology and Laboratory Medicine, University of Wisconsin-Madison, Madison, Wisconsin, USA<sup>a</sup>; Wisconsin National Primate Research Center, Madison, Wisconsin, USA<sup>b</sup>; Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, USA<sup>c</sup>; Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, Maryland, USA<sup>d</sup>

**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-Palaearctic long-distance migratory bird, the European roller (*Coracias garulus*), 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 <Q30) 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

Received 3 March 2017 Accepted 15 March 2017 Published 4 May 2017

**Citation** Buechler CR, Bailey AL, Lauck M, Heffron A, Johnson JC, Campos Lawson C, Rogers J, Kuhn JH, O'Connor DH. 2017. Genome sequence of a novel kunsagivirus (*Picornaviridae*: *Kunsagivirus*) from a wild baboon (*Papio cynocephalus*). *Genome Announc* 5:e00261-17. <https://doi.org/10.1128/genomeA.00261-17>.

**Copyright** © 2017 Buechler et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to David H. O'Connor, [dhoconno@wisc.edu](mailto:dhoconno@wisc.edu).

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](https://www.ncbi.nlm.nih.gov/nuccore/KY670597).

## ACKNOWLEDGMENTS

We thank the University of Wisconsin, Department of Pathology and Laboratory Medicine and the WNPRC for funding and the use of its facilities and services. We thank the Tanzanian National Parks Authority (TANAPA) for permission to work at Mikumi National Park.

The content of this publication does not necessarily reflect the views or policies of the U.S. Department of Health and Human Services or of the institutions and companies affiliated with the authors. The funders of this research had no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

This work was funded by NIH grant TW009237 as part of the joint NIH-NSF Ecology of Infectious Diseases program and the UK Economic and Social Research Council, the Wisconsin Partnership Program through the Wisconsin Center for Infectious Diseases, and the NIH (grants R01 AI077376 and R01 AI084787). This publication was made possible in part by a grant (P51 RR000167) from the Office of Research Infrastructure Programs (ORIP), a component of the National Institutes of Health (NIH), to the Wisconsin National Primate Research Center (WNPRC), University of Wisconsin-Madison. This research was conducted in part at a facility constructed with support from Research Facilities Improvement Program grant numbers RR15459-01 and RR020141-01. This work was also funded in part through Battelle Memorial Institute's prime contract with the U.S. National Institute of Allergy and Infectious Diseases (NIAID) under contract HHSN2722007000161. J.C.J. performed this work as an employee of Battelle Memorial Institute. The subcontractors to Battelle Memorial Institute who performed this work are C.C.L., an employee of Concentric Methods, Inc., and J.H.K., an employee of Tunnell Government Services, Inc.

## REFERENCES

- 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>.
- 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/ajpa.1330900407>.
- 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.02433-12>.
- 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](https://doi.org/10.1016/S0022-2836(05)80360-2).
- 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>.
- 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>.
- 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>.
- Bailey AL, Lauck M, Sibley SD, Pecotte J, Rice K, Weny G, Tumukunde A, Hyeroba D, Greene J, Correll M, Gleicher M, Friedrich TC, Jahrling 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, Ericson 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>.