

Complete genome sequenced of elephant endotheliotropic herpesvirus 4

June 17 2016

The complete genome of Elephant Endotheliotropic Herpesvirus 4, known as EEHV4(Baylor), has been sequenced by researchers at Baylor College of Medicine and the Johns Hopkins School of Medicine, revealing unique characteristics of this particular species of Elephant Endotheliotropic Herpesvirus – which causes a deadly disease that affects Asian elephants in both managed care and free-range environments.

The findings appear in the current edition of *mSphere* from the American Society of Microbiology.

"The deadly form of the disease is predominantly associated with EEHV1, but milder disease has been caused by EEHV5 or EEHV4, of which less is known," said Dr. Paul Ling associate professor of molecular virology and microbiology at Baylor. "Here, we have determined the complete genomic DNA sequence, completed by the Human Genome Sequencing Center at Baylor, of a species of EEHV4 obtained from a trunk wash sample collected from a surviving Asian elephant calf after suffering from EEHV4."

This particular calf is part of a monitored herd at the Houston Zoo that is benefiting from a research collaboration among the Zoo, Baylor, Johns Hopkins and The National Zoo in Washington D.C., studying EEHV. The team developed a rapid diagnostic test allowing for regular blood and trunk-wash screenings.

Because of these screenings, researchers found that some elephants in the herd underwent sequential mild infections of different species of EEHV including EEHV4.

"It is likely that herds eventually become infected with multiple EEHV species and subtypes, so understanding the molecular makeup and learning more about the genetic relationships among the different species will provide information that could lead to controlling the disease," said Ling.

Researchers have already sequenced EEHV1A, EEHV1B and EEHV5. Within EEHV4(Baylor) they found 25 novel or missing genes - some present in EEHV4(Baylor) but not the others, as well as genes that were present within the others but that were missing from EEHV4(Baylor).

Another feature identified was the presence of 26 paralogous (originating from the same gene) members of a highly diverged family of transmembrane proteins. A more detailed description of these finding can be found in the accompanying manuscript, also currently published in *mSphere*.

Researchers were also able to identify the existence of two distinct subtypes of this virus species known as EEHV4A and EEHV4B.

"There are still questions surrounding EEHV pathogenicity where more research is needed," said Dr. Gary S. Hayward with the Johns Hopkins School of Medicine. "Once the differences in pathogenesis of the many [species](#) and their respective subtypes are better understood, detailed comparisons of the sequences and gene contents of all genome types will hopefully provide important and useful information for future diagnosis, evaluation and potential vaccine or antiviral approaches to diagnosing, treating and controlling EEHV-associated disease."

This is the second complete EEHV genome sequenced by this group, the other being EEHV1A (Kimba) in 2013.

Others who took part in this research include: Simon Y. Long, Sarah Y. Heaggans, with The Johns Hopkins School of Medicine; Angela Fuery, Rong-Sheng Peng, with Baylor College of Medicine; Xiang Qin, Kim C. Worley, Shannon Dugan,

More information: Paul D. Ling et al. Complete Genome Sequence of Elephant Endotheliotropic Herpesvirus 4, the First Example of a GC-Rich Branch Proboscivirus, *mSphere* (2016). [DOI: 10.1128/mSphere.00081-15](https://doi.org/10.1128/mSphere.00081-15)

Paul D. Ling et al. Comparison of the Gene Coding Contents and Other Unusual Features of the GC-Rich and AT-Rich Branch Probosciviruses, *mSphere* (2016). [DOI: 10.1128/mSphere.00091-16](https://doi.org/10.1128/mSphere.00091-16)

Provided by Baylor College of Medicine

Citation: Complete genome sequenced of elephant endotheliotropic herpesvirus 4 (2016, June 17) retrieved 18 July 2024 from

<https://phys.org/news/2016-06-genome-sequenced-elephant-endotheliotropic-herpesvirus.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.