

First genome sequence of Amur leopard highlights the drawback of a meat only diet

November 1 2016

The first whole genome sequence of the Far Eastern Amur leopard is published in the open access journal *Genome Biology*, providing new insight into carnivory and how it impacts on genetic diversity and population size.

Mr. Yunsung Cho, lead author from Ulsan National Institute of Science and Technology, said: "Using the Amur leopard genome and comparing it to that of other mammalian genomes we found that carnivory seems to be a strong selection force for genes involved in dietary adaptation - something not as apparent in mammals that are omnivores or herbivores. For example, cows could eat meat without it having a major impact on their health, but leopards eating grass would quickly die as they have evolved to survive on meat."

Specialized diets result in physiological, biochemical and morphological adaptations and carnivory is considered to be an evolutionary instable diet. Current research shows that animals in the cat family, Felidae, have relatively low [genetic diversity](#) and small population sizes. This could be due to the inflexible nature of their strict diet and explains their vulnerability and critical conservation status.

Mr. Cho explained: "Carnivory related genetic adaptations such as extreme agility, muscle power and specialized diet make leopards such successful predators, but these lifestyle traits also make them genetically vulnerable."

An international team of researchers sequenced the Amur leopard genome using a muscle sample of a female from Korea. They then analyzed a further 18 [mammalian genomes](#) including eight carnivores (domestic cat, tiger, cheetah, lion, leopard, polar bear, killer whale and Tasmanian devil), five omnivores (human, mouse, dog, pig, and opossum) and five herbivores (giant panda, cow, horse, rabbit, and elephant). Comparing the genomes they found that carnivores share two genes that are not present in other genomes that play an important role in bone development and repair, which could drive selection for a diet specialized towards meat.

Professor Steve O'Brien, who has been researching rare endangered cat species for decades emphasizes that "Leopards are the most widespread species of the big cats, found in Africa to the Russian Far East, and thrive in a variety of environments. However, populations are fast declining, especially the Amur leopard, which is now critically endangered and perhaps the most endangered animal species on Earth."

This is the first de novo genome assembly and the second leopard genome to be sequenced following the [snow leopard](#) published in 2013. The researchers hope that this Amur leopard reference genome will serve as a useful tool for understanding Felidae evolution and aid conservation.

Dr. Soonok Kim, who initiated and led the project as the PI of National Institute of Biological Resources of Korea adds: "Cats are also a good model for studying health issues, such as human diabetes, and this new leopard genome reference is an environmental treasure that could help us understand these conditions further."

More information: Soonok Kim et al. Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly, *Genome Biology* (2016). [DOI: 10.1186/s13059-016-1071-4](https://doi.org/10.1186/s13059-016-1071-4)

Provided by BioMed Central

Citation: First genome sequence of Amur leopard highlights the drawback of a meat only diet (2016, November 1) retrieved 23 May 2024 from <https://phys.org/news/2016-11-genome-sequence-amur-leopard-highlights.html>

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