

Reference genomes provide first insights into genetic roots of mustelid physiological and behavioral diversity

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Mustelids are the most ecologically and taxonomically diverse family within the order Carnivora. From the tayra in the neotropics to the wolverine in the subarctic, they inhabit a variety of ecological niches and developed corresponding species-specific traits related to their diet, reproductive strategy and morphology. An international team of scientists led by the Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW) conducted a comparative analysis of whole genomes of several mustelids to obtain insights into the molecular basis of these adaptations.

The team found that multiple sources of genomic variation contributed to [candidate genes](#), including those that change the number, position, orientation or size of [genes](#) in a [species' genome](#). The latter forms of genomic variation are frequently neglected in genome studies of wildlife species, and the authors argue that this needs to change. The results are published in the scientific journal *Molecular Ecology*.

The Mustelidae are the most ecologically and taxonomically diverse family within the mammalian order Carnivora and includes the badgers, ferrets, weasels and otters. Even closely related mustelids often inhabit different ecosystems where they face very different challenges. Consequently, they evolved a large variety of species-specific behavioral, morphological and physiological adaptations related to diet and reproduction. As recent developments in sequencing technologies

and [analytical methods](#) permit the construction of draft genomes for many [wild species](#), mustelids provide wildlife geneticists with the opportunity to unravel the roots of this diversity by identifying regions in the genome associated with ecologically relevant traits.

"We focused on the subfamily Guloninae, within which several species occupy a variety of ecological niches, ranging from the omnivorous tayra (*Eira barbara*) in the neotropics to the carnivorous wolverine (*Gulo gulo*) in the resource-scarce subarctic," says Lorena Derežanin, a Ph.D. student at the Department of Evolutionary Genetics of the Leibniz-IZW and first author of the paper.

"This is the first study comparing the genomes of ecologically disparate species within this diverse subfamily and sheds light on how these species evolved," says Klaus-Peter Koepfli, a senior research scientist at George Mason University in the US and a co-author on the study.

The research team produced the first reference genome of the tayra and compared it to the available genomes for the wolverine and the sable (*Martes zibellina*), two other members of the Guloninae that are ecologically quite different. They found that not only do the "single nucleotide variants," essentially single "letter" changes in the genetic code, contribute to species differences in genes associated with ecologically relevant traits, but that large scale changes known as structural variants were also important, affecting parts of specific genes or multiple genes.

"Our results are important, as they demonstrate that many types of processes responsible for genomic variation need to be considered, including those that can rapidly change the number and function of genes in a genome," says Derežanin.

"If we use the metaphor of a book to represent the DNA sequences in a

genome, then the kind of changes we are talking about are akin to deleting, moving, or duplicating large chunks of text, on a scale of paragraphs, pages or even whole chapters," adds Daniel Förster, a scientist at the Leibniz-IZW and senior author of the paper.

The research team identified modifications in many genes that could be associated with the species' different ecologies. For example, in the genome of the tayra, the only Guloninae species that breeds throughout the year, they found many modifications of pregnancy-related genes. In the wolverine, a circumpolar carnivore that must cope with seasonal food scarcity, many modified genes were associated with diet and body condition.

"In a sense, starving for longer periods is part of the wolverine lifestyle, and we identified candidate genes that allow them to cope with this," says Jörns Fickel, head of the Leibniz-IZW Department of Evolutionary Genetics. "Generating further genomes for species from this diverse mammalian family will be a strong foundation to help us understand how genomes evolve in response to different environmental challenges."

More information: Lorena Derežanin et al, Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae, *Molecular Ecology* (2022). [DOI: 10.1111/mec.16443](https://doi.org/10.1111/mec.16443)

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