

A new 3-D koala genome will aid efforts to defend the threatened species

January 26 2021, by Parwinder Kaur

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Koalas are unique in the animal kingdom, living on a eucalyptus diet that would kill other creatures and [drinking so little](#) their name comes from the Dharug word *gula*, meaning "no water." Today, many koala populations across Australia are in decline, due to habitat destruction caused by agriculture, urbanization, droughts and bushfires intensified by climate change, and diseases such as chlamydia and koala retrovirus.

Genetic information can play a key role in the effort to conserve koalas and other species. A detailed map of the koala genome is vital to understanding their susceptibility to disease, their genetic diversity, and how they may respond to new environmental pressures.

We have [created](#) a new "chromosome-length" sequence of the [koala genome](#), which will allow researchers to study its three-dimensional structure and understand its evolution.

A unique creature under threat

The modern koala is the only living representative of the marsupial family *Phascolarctidae*, a family that once included several genera and species. During the Oligocene and Miocene epochs (from 34 to 5 million years ago), the ancestors of modern koalas lived in rainforests and [didn't eat only leaves](#).

During the Miocene, the Australian continent began drying out, leading to the decline of rainforests and the spread of open eucalyptus woodlands. Koalas evolved [several adaptations](#) that allowed them to live on a specialized eucalyptus diet. This specialization makes them picky eaters, so they're very prone to habitat loss.

Koalas are listed as a vulnerable species by the [International Union for Conservation of Nature](#). It was hunted heavily in the early 20th century for its fur, and large-scale cullings in Queensland resulted in public outcry, initiating a movement to protect the species. Sanctuaries were established, and koalas whose habitat was disappearing were relocated.

Koalas are particularly vulnerable to bushfires; they are slow moving and eucalypt trees are very flammable. They instinctively seeks refuge in higher branches, exposing them to intense heat and flames. Bushfires also fragment the animal's habitat, which restricts their movement and

leads to population decline and [loss of genetic diversity](#).

Piecing together the puzzle

The koala genome was [first sequenced in 2013](#). This was only the first step in understanding koala genetics—akin to finding all the pieces of the puzzle, but being unsure how to put them all together into the meaningful patterns of genes and chromosomes.

Our new chromosome-length assembly follows the work of others, especially the [Koala Genome Consortium](#) and the Koala Genome Project led by Australian geneticist [Rebecca Johnson](#). It is based on [a draft](#) by the Earlham Institute in the UK.

We used big-data sequencing methods such as Hi-C, [3-D-DNA](#) and [Juicebox Assembly Tools](#) courtesy of [DNA Zoo](#) labs to create our chromosome-length assembly.

We organized the genome into 8 chromosomes, a great improvement on the [draft](#) of 1,907 fragments we began with.

Vital for conservation

A high-quality genome sequence is [essential](#) if we want to bring genetic insights to conservation management initiatives. Some 200 Australian vertebrate species currently have species recovery plans, and 80% of those plans include genome-based actions. However, only 15% of those species have any genomic data available.

Our chromosome-length koala genome assembly enables a highly detailed 3-D view of the genome architecture for koala. It is easier to use than earlier genomes, and means conservation management initiatives

will have fast, cost-effective and reliable analysis options available.

This will give us insights into koalas' genetic susceptibility to diseases like koala retrovirus (KoRV) and chlamydia. It may also form a basis for innovative vaccines. What's more, it can be used in new conservation management strategies that aim to diversify the koala gene pool.

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Provided by The Conversation

Citation: A new 3-D koala genome will aid efforts to defend the threatened species (2021, January 26) retrieved 6 May 2024 from <https://sciencex.com/news/2021-01-d-koala-genome-aid-efforts.html>

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