

## Raw material for new genes

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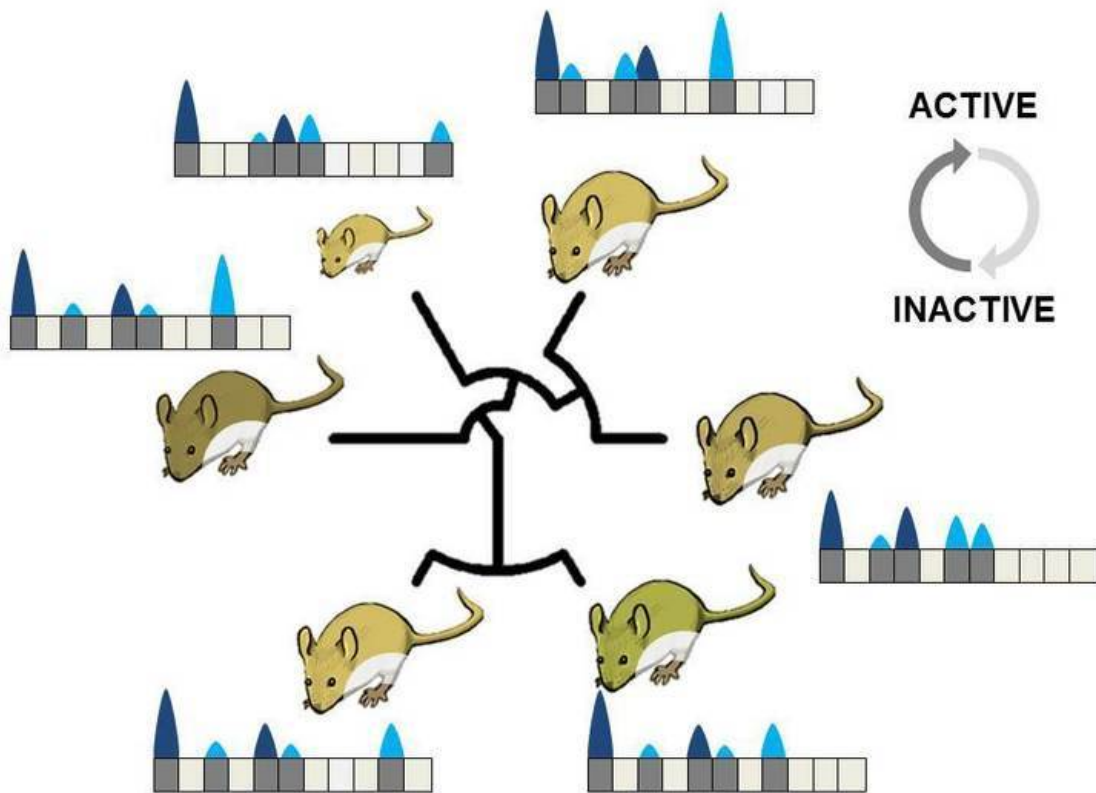


The "mini mouse" *Mus mattheyi* is one of ten mouse species that researchers have studied at the Max Planck Institute for Evolutionary Biology in their gene expression. Just like in other mammals, 95% of the genome is not translated into proteins. Credit: MPI for Evolutionary Biology

Every region of DNA codes for a gene. Well, not quite. Although an organism's genome contains some regions that are read and transcribed into RNA, many of those do not give rise to functional genes. Scientists at the Max Planck Institute for Evolutionary Biology in Plön have now studied the genome of the house mouse *Mus musculus* and its relatives and have found that new functional genes can evolve from such putatively useless DNA regions within a short time.

Mice are popular experimental animals for behavioural and genetic studies. But not all mice are the same. The house mouse, *Mus musculus*, which is often used in European laboratories, is one of 39 known species in its genus. The genus *Mus* arose around ten million years ago, whereas the house mouse has only been a distinct species for 500,000 years. New species often emerge as a result of changes to existing [genes](#). Three years ago, however, scientists at the Max Planck Institute in Plön discovered that many genes are created entirely from scratch and are not just modified copies of older genes.

In their recent study, the researchers analyzed the genome of the mouse, concentrating on regions without known genes. In some mouse species, many of these regions are read and transcribed into RNA, while in others they are not. The scientists analyzed RNA molecules from various tissues of ten mouse species of the genus *Mus* and compared them to molecules that occur in a "reference mouse", a laboratory mouse of the species *Mus musculus*, the genome of which is known to the researchers in detail.



Evolution changes the activity within the genome: A comparison of different mouse species shows regions of the genome where the DNA is transcribed (blue peaks). The dark blue peaks represent regions that contain genes. The light blue peaks show regions where the DNA is transcribed without genes being present. Credit: MPI for Evolutionary Biology

The researchers determined what proportion of the genome in each species and each tissue is transcribed into RNA. They found that each species synthesizes approximately the same amount of RNA. However, the genome regions that are read are not always the same. The genome can be thought of as an office and the regions that are read as workers. Accordingly, different companies have the same number of workers, but

their jobs would be differently distributed.

## **The potential of becoming a gene**

The results show that only very closely related species share a high percentage of RNA molecules. The researchers' analyses also showed that overall there are very few regions in the genome that are not transcribed into RNA molecules. "We used to interpret the additional molecules as faulty measurements or biological junk, as we have no idea why these regions are read. In fact, these transcripts could serve as candidates for new genes," Rafik Neme of the Max Planck Institute for Evolutionary Biology explains. DNA segments that are read but have no known function or gene designation are known as protogenes. The scientists assume that any DNA segment which can be transcribed into RNA has the potential to act as a gene. If a gene with an important function arises, it is permanently retained. If the entire genome is transcribed into RNA, nearly every segment is a protogene.

Most inactive regions of a given species are active in related [species](#). "This indicates that such regions can be activated or deactivated relatively easily," Neme says.

## **Unused RNA gets lost**

In the course of evolution, varying amounts of RNA arise in different tissues. The researchers suspect that RNA molecules tend to evolve rapidly within a short period rather than in the long term, because if they fail to perform important functions, they are lost again.

In conclusion, the genome can be very easily transcribed into RNA. Each part of the genome can be, and is, read. "The genome therefore consists almost entirely of genes and protogenes," Neme says. "Extensive

transcription into RNA enables protogenes to be tested continuously to determine whether they are suitable candidates for new genes."

"The molecular apparatus for reading and transcribing DNA automatically involves the creation of new genes. Any part of the [genome](#) containing no genes could therefore become important at some time in the course of evolution," Diethard Tautz, Director at the Max Planck Institute in Plön explains.

**More information:** Rafik Neme et al. Fast turnover of genome transcription across evolutionary time exposes entire non-coding DNA to gene emergence , *eLife* (2016). [DOI: 10.7554/eLife.09977](https://doi.org/10.7554/eLife.09977)

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