

# Marmoset sequence sheds new light on primate biology and evolution

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Common marmoset. (*Callithrix jacchus*) Credit: Carmem A. Busko/Wikipedia/CC BY 2.5

A team of scientists from around the world led by Baylor College of

Medicine and Washington University in St. Louis has completed the genome sequence of the common marmoset – the first sequence of a New World Monkey – providing new information about the marmoset's unique rapid reproductive system, physiology and growth, shedding new light on primate biology and evolution.

The team published the work today in the journal *Nature Genetics*.

"We study primate genomes to get a better understanding of the biology of the species that are most closely related to humans," said Dr. Jeffrey Rogers, associate professor in the Human Genome Sequencing Center at Baylor and a lead author on the report. "The previous sequences of the great apes and macaques, which are very closely related to humans on the primate evolutionary tree, have provided remarkable new information about the evolutionary origins of the human genome and the processes involved."

With the sequence of the [marmoset](#), the team revealed for the first time the genome of a non-human primate in the New World monkeys, which represents a separate branch in the primate evolutionary tree that is more distant from humans than those whose genomes have been studied in detail before. The sequence allows researchers to broaden their ability to study the [human genome](#) and its history as revealed by comparison with other primates.

The sequencing was conducted jointly by Baylor and Washington University and led by Dr. Kim Worley, professor in the Human Genome Sequencing Center, and Rogers at Baylor, and Drs. Richard K. Wilson, director, and Wesley Warren of The Genome Institute at Washington University, in collaboration with Dr. Suzette Tardif of The University of Texas Health Science Center in San Antonio and the Southwest National Primate Research Center.

"Each new non-human primate genome adds to a deeper understanding of human biology," said Dr. Richard Gibbs, director of the Human Genome Sequencing Center at Baylor and a principal investigator of the study.

## **Twinning**

The study revealed unique genetic characteristics observed in the marmoset, including several genes that are likely responsible for their ability to consistently reproduce multiple births.

"Unlike humans, marmosets consistently give birth to twins without the association of any medical issues," said Worley. "So why is it OK in marmosets but not in humans where it is considered high risk and associated with more complications?"

It turns out the marmoset gene *WFIKKN1* exhibits changes associated with twinning in marmosets.

"From our analysis it appears that the gene may act as some kind of critical switch between multiples and singleton pregnancies, though it is not the only gene involved," said Rogers, who added the finding could apply to studies of multiple pregnancies in humans.

The team was also looked for genetic changes associated with a unique trait found in marmosets and their close relatives, but not described in any other mammal. The dizygotic (or fraternal) twins in marmosets exchange blood stem cells called hematopoietic stem cells in utero, which leads to chimerism, a single organism composed of genetically distinct cells.

"This is very unusual. The twins are full siblings, but if you draw a blood sample from one animal, between 10 and 50 percent of the cells will

carry the sibling's DNA," said Rogers. "Normally, fraternal twins do not share the same DNA in this way, and in other animals, this chimerism can cause medical problems but not in marmosets. It is very unique."

"The translational implications of this work to pregnancy and reproductive medicine are significant. We have shown that there are several genes in the marmoset which likely enable ([twinning](#)). However, it is not just a question of why they have such a high rate of twinning, but how do they manage to rear and raise these twins so successfully," said Dr. Kjersti Aagaard, associate professor of obstetrics and gynecology – maternal fetal medicine at Baylor and a co-author on the study. "Given the relatively high rate of complications of twins we see, ranging from preterm birth to unique complications such as Twin Twin Transfusion Syndrome (seen only amongst identical or monochorionic twins), it is crucial to understand the underlying adaptive biology of the marmoset which enables them to avoid these complications."

## **Alloparenting**

Marmosets have a unique social system in which the dominant male and female serve as the primary breeders for a family, while their relatives also care for the offspring. They pick them up, carry them for long periods, and basically provide all the support allowing the breeders to reproduce again quickly. Interestingly the relatives who provide the care are reproductively suppressed, said Worley.

"This species is clearly adapted to rapid reproduction and to the potential for rapid population expansion," said Rogers. "Their ecological system connects with that as they are able to thrive in disturbed areas of forests. So one possibility is that they have evolved a feeding and dietary regimen that allows them to live in these type of conditions where they can reproduce quickly. This would be advantageous as any adults that move into a newly disturbed area would establish their offspring as the

early initial residents of the newly available area."

## Small body size

Marmosets also have a very small body size. The [genome sequence](#) showed this may be the result of positive selection in five growth hormone/insulin-like growth factor axis genes (GH-IGF) with potential roles in producing small body size.

Additionally, the team identified a cluster of genes that affect metabolic rates and body temperatures, adaptations associated with challenges of small body size.

## MicroRNAs

The study also provides new information about microRNAs, small non-coding RNA molecules that function to regulate gene expression.

"There has not been much research conducted on microRNAs in nonhuman primates, so we found this particularly important," said Worley.

A team led by Dr. Preethi Gunaratne, an associate professor of biology and biochemistry at the University of Houston and of pathology and a member of the Human Genome Sequencing Center at Baylor, and Dr. R. Alan Harris, an assistant professor of molecular and human genetics at Baylor, found marmosets exhibit a significant number of differences in microRNAs and their gene targets compared with humans, with two large clusters potentially involved in reproduction.

The sequence lays the foundation for further biomedical research using marmosets, said Rogers. "Researchers may have been more reluctant to

study the marmoset due to lack of basic information, but this genome sequence opens new avenues for future research relevant to various aspects of human health and disease."

Dr. Suzette Tardiff, professor of cellular and structural biology at the Barshop Institute for Longevity and Aging Studies at The University of Texas Health Science Center at San Antonio, a core scientist at the Southwest National Primate Research Center and an expert in marmoset biology and co-author on the paper, provided critical information regarding the biology of marmosets, and helped obtain samples for the sequence.

**More information:** The common marmoset genome provides insight into primate biology and evolution, [DOI: 10.1038/ng.3042](https://doi.org/10.1038/ng.3042)

Provided by Baylor College of Medicine

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