



by the wind, mostly around the equator. Around 14% of the surface is classified as 'hummocky' — hilly or mountainous — and 1.5% is 'labyrinth' terrain, with valleys carved by rain and erosion. There are surprisingly few impact craters, suggesting that the moon's surface is fairly young.

Titan is the only world in the Solar System aside from Earth with known bodies of liquid on its surface. However, these seas and lakes are filled with liquid methane rather than water, and they cover just 1.5% of the moon's surface.

"The most profound discovery of Cassini is that Titan is so diverse," says Ralph Lorenz, a planetary scientist at the Johns Hopkins University Applied Physics Laboratory in Laurel, Maryland. "It's almost like a completely different world."

By 2034, NASA plans to send a drone to Titan on the Dragonfly mission, which will fly across the surface and study it in multiple locations. But there are no current plans to send further orbiters to Saturn or its moons, so this map is likely to remain our best global view of Titan for the foreseeable future.

By Jonathan O'Callaghan

# LAB SEQUENCES GENOMES OF A CONTINENT'S BUTTERFLIES

Draft genomes of more than 800 varieties hint at the role of interbreeding in the animal's evolution.

By Ewen Callaway

**W**hen biologist Nick Grishin wanted to tackle big questions in evolution — why some branches of the tree of life are so diverse, for instance — his team set out to sequence the genomes of as many butterflies as it could: 845 species, to be precise.

In a study that some researchers are hailing as a landmark in genomics, Grishin's group at the University of Texas Southwestern Medical Center in Dallas sequenced and analysed the genome of what it called a "complete butterfly continent": every species of the creature in the United States and Canada. The study was posted on the bioRxiv server on 4 November<sup>1</sup>.

"I think it's bloody amazing, because the technology involved in sequencing 845 species is there," says James Mallet, an evolutionary biologist at Harvard University in Cambridge, Massachusetts. "It's a beautiful piece of work."

The data allowed Grishin's team to build an evolutionary tree detailing the relationships of all the butterflies, as well as to determine the pace at which new species formed. The

team suggests that fast-diversifying groups of butterflies are those that swap genes with close relatives through interbreeding — a phenomenon that could extend to other organisms.

Others, however, point out that most of these genomes will be of limited use to other researchers, because they are low-quality 'drafts' comprised of thousands of short DNA stretches, and not higher-quality sequences that have been assembled into longer stretches. Grishin says that the sheer number of genomes, even of low quality, allows his team to draw broad conclusions about evolution that could not be made from more limited data sets. He plans to make the genomes publicly available.

## Butterfly patterns

Grishin, whose research group studies the shape and evolution of proteins, started researching butterflies after reading a 2012 paper<sup>2</sup> on the diverse tropical genus *Heliconius*, whose species have elaborate wing patterns that mimic those of other butterflies. The study found that some genes that determine wing patterns seemed to have



A *Heliconius* butterfly.

TIM ZUROWSKI/SHUTTERSTOCK

## News in focus

been passed between three *Heliconius* species through interbreeding, instead of being inherited from the species' common ancestor, and suggested that such swaps explain the huge diversity of *Heliconius* butterflies.

Inspired by that work, Grishin wondered whether such a connection could be seen in other butterflies. "Some groups diversify very rapidly and there are many species in them, and others are kind of empty," he says. "So to understand why and how that happens, we would need to sequence them all."

At one time, sequencing hundreds of butterfly genomes would have been unaffordable, but costs have plummeted in recent years. Collecting samples for every species in the United States and Canada was still a challenge, however. Grishin's team worked with amateur butterfly enthusiasts as well as museum collections across the United States to gather data – a single leg from a dead specimen was enough to obtain a draft-quality genome.

Once they had sequenced the genomes of all 845 species, the researchers worked out the evolutionary relationships. Their butterfly family tree broadly agreed with existing ones based on anatomy and more limited genetic analyses, although the group did reclassify 40 species and suggested several new groupings at the genus level.

The tree also revealed that some butterfly groups have evolved faster than others. Two of the fastest-evolving ones, commonly known as the blues and the whites, have developed highly specialized interactions with other organisms that might explain their rapid evolution, say Grishin's team. The blues, or Polyommatinae, form symbiotic relationships

**“Some groups diversify very rapidly. To understand how that happens, we would need to sequence them all.”**

with ants, whereas whites, or Pierini, have developed adaptations to feed on mustard plants that are toxic to many other insects.

An analysis of genes shared by multiple species also showed that these diverse groups were likely to have acquired genes through interbreeding. Many of the genes that are swapped between species are thought to be involved in mate recognition and other factors that can cause species splits. Grishin says that by spreading such genes, interbreeding – rather than the gradual accrual of new mutations – could be helping to drive the evolution of butterfly species.

The link between interbreeding and

speciation is “an idea that is sort of coming to the fore”, says Mallet, who co-led a team that reported similar findings in *Heliconius* butterflies this month<sup>3</sup>.

### Missing data

In addition to the draft genomes, Grishin's team generated ‘reference’ genomes, in which genes are assembled into chromosome sequences, for 23 species.

High-quality genomes such as this are the targets of other large-scale projects to sequence the tree of life. In 2018, a consortium called the Earth BioGenome Project laid out plans to decode the genomes of the roughly 1.5 million known species of eukaryote – animals, plants, protozoans and fungi – at an estimated cost of US\$4.7 billion over 10 years.

Grishin is enthusiastic about these efforts, particularly for vertebrates. But he thinks there are too many unknown species of invertebrate to sequence them all in the near future. “I don't think they will succeed very quickly,” Grishin says. “Our efforts – where we just jump right in and do things right away without much fuss about it – may be helpful.”

1. Zhang, J., Cong, Q., Shen, J., Opler, P. A. & Grishin, N. V. Preprint at BioRxiv <https://doi.org/10.1101/829887> (2019).
2. Heliconius Genome Consortium. *Nature* **487**, 94–98 (2012).
3. Edelman, N. B. et al. *Science* **366**, 594–599 (2019).

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