Abstractions

FIRST AUTHOR

In 1999, the Galileo spacecraft sent back its first images of Jupiter's outer rings. These confirmed that two of Jupiter's moons, Amalthea and Thebe, are the sources of the dust that makes up the planet's two outermost, gossamer rings. But the images also showed a barely visible, unexplained extension of dust beyond the most distant of the two moons, which has been dubbed the Thebe extension. On page 72, astronomers Douglas Hamilton from the University of Maryland in College Park and Harald Krüger at the Max Planck Institute for Solar System Research in Katlenburg-Lindau, Germany perform planetary-dust forensics to show that Jupiter's shadow is responsible for creating the gossamer extension.

What motivated you to explain the Thebe extension?

I wrote a graduate thesis on the ring systems of Jupiter and Saturn. The 1999 Galileo images of the Thebe extension puzzled the ring community and piqued my interest. In 2003, Galileo became the first spacecraft to fly through a planetary ring, and it gathered new data from Jupiter's outer ring, including dust grain size and speed, and even orbital orientation, allowing us to solve the puzzle.

Why did you suspect that Jupiter's shadow might be the culprit?

The main clue is that the ring material extends both inward and outward from the source satellite, Thebe. Simple circular orbits just can't do this. So I went searching for forces capable of producing elliptical orbits. Electromagnetic forces from Jupiter's spinning magnetic field, enhanced by grain charges varying in Jupiter's shadow, worked. The new Galileo dust data — interpreted by my co-author's indispensable efforts — verified parts of our theory.

Are these dust dynamics applicable to other planetary ring systems?

Yes. Although Saturn's main rings are composed mainly of large chunks of ice, some of the fainter rings are dust. Uranus and Neptune also have dusty systems. The shadow effect is strongest at Jupiter because it is nearest to the Sun and experiences the most sunlight of all ringed planets.

What else is left to know about planetary rings?

We can't fully answer some basic questions about rings. For example, we want to know if Saturn's rings formed at the same time as the planet or more recently. Studying rings in our Solar System lays the foundation for understanding ringed extrasolar planets when they are eventually detected. ■

MAKING THE PAPER

Evan Eichler

Genome match maps new regions of human genetic structural variation.

Much genetic variation between individuals may lie in regions of the genome containing areas of structural diversity. A new study reveals more than 1,700 such regions, nearly half of which had not been previously sequenced. Changes in these regions between individuals are likely to hold the keys to information about many diseases as well as to the evolutionary processes that shaped human history.

Previous studies had documented changes in structural features of the genome — inversions, deletions and duplications affecting from a few thousand to a few million base pairs. "We knew there was lots of structural variation out there," says Evan Eichler, a human geneticist at the Howard Hughes Medical Institute, University of Washington in Seattle and the lead author of the study. "But we didn't have any sequence-based resolution or any systematic approach to really capture that variation."

Yet, knowing the type of variation that existed in these regions and precisely where in the genome these regions are located was likely to be important. Regions of structural variation are thought to be unstable and rapidly evolving, some of them containing genes likely to have emerged relatively recently. Humans and chimpanzees are 98.9% identical in sequence, with some 35 million base-pair differences between them. Structurally variable regions of the human genome account for more than three times that amount of base-pair differences between humans and chimpanzees, says Eichler.

To find one type of these prone-to-change regions, Eichler and Jeffrey Kidd, a doctoral student in his lab and first author on the paper on page 56, devised a method to find what Eichler calls "one-armed bandits". They created libraries of over a million overlapping pieces of DNA spanning the genomes of eight individuals from diverse geographic ancestry. Kidd then pulled out fragments that at one end matched a reference sequence of the human genome, to precisely map their locations, but at the other end, or "arm", had no match in terms of length and/or orientation. He looked at these regions in more detail, sometimes at the sequence level, in the genomes of the eight individuals.

"Wherever he found these discordant fragments, he found missing parts of the human genome that were in some individuals and not in others," says Eichler. By piecing together the sequence of nucleotides within these regions, the group produced the first high-resolution sequence map of structural variation.

The results show the need for complementary approaches to human genomic sequencing, says Eichler. Most sequencing technologies are designed to detect only small variations, such as single-nucleotide substitutions. In these systems, DNA from one individual is examined and the resulting sequence aligned to that of a reference genome — with no means to retrieve regions of variability that don't line up. "If we just sequence multiple humans without being comprehensive, we're not going to capture these complex regions thoroughly enough," Eichler says.

Eichler's group is now trying to find associations between regions of structural variation and conditions such as autism, epilepsy and diabetes. In addition, the team is interested in comparing the function of genes found within these regions in humans and other primates to find evolutionary clues as to how humanness arose. ■

FROM THE BLOGOSPHERE

A recent article in the *Journal of the American Medical Association* (J. Ross *et al. J. Am. Med. Assoc.* **299,** 1800–1812; 2008) stimulated discussions of ghost-writing and guest authorship in several NPG blogs (see Nautilus, http://tinyurl.com/46yt62).

The article by Ross *et al.* documented a drug-industry practice of paying unidentified authors to write a paper, and adding as authors the names of academics who were not substantially involved in the research. The practice conceals the pharmaceutical industry's role, it says, and potentially misleads doctors and other readers.

Integrity in medical research is paramount, according to the Spoonful of medicine blog, and yet it is common for principal investigators to comment on drafts by postdocs rather than actually writing a paper. The blog goes on to compare and contrast paid-for authorship (or non-authorship) with standard practice in academic laboratories.

Nature Network presents a discussion of the long history of honorary authorship and whether medical writers should receive an acknowledgement or credit as authors. ■

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