

cal symptom of Zika—2 days after donating blood. The scientists looked for, but did not find, genetic signatures that would point to a mutation that might be fueling the virus's rapid spread or the serious complications.

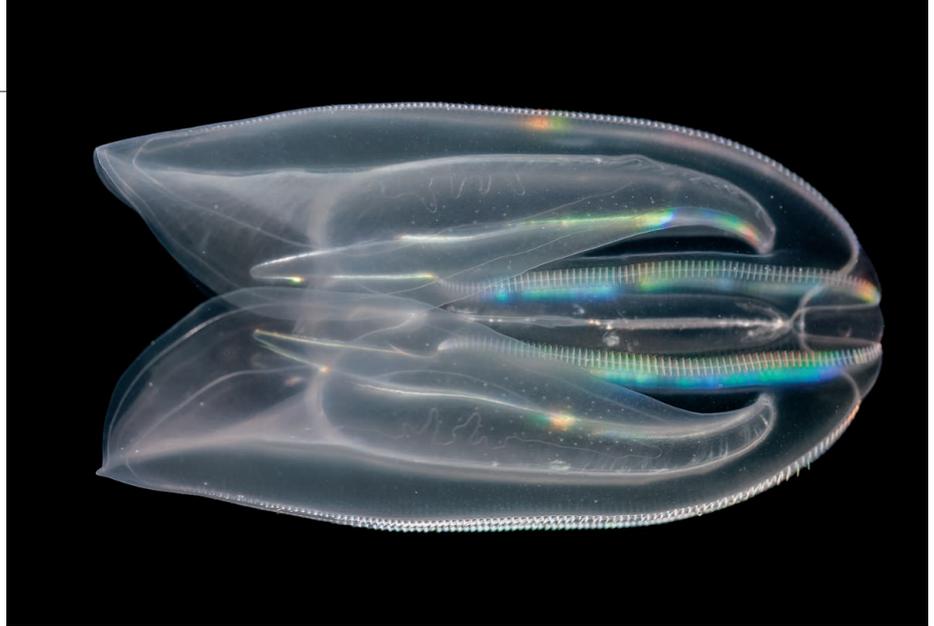
To try to retrace the virus's route, the scientists compared the genomes of the Brazilian samples to those from patients in nine other countries, six from the current outbreak in the Americas and one each from French Polynesia, the Cook Islands, and Thailand. The sequences from the Americas were the most closely related; the sequence from a patient in Thailand in 2013 was the most distant. That's consistent with the leading theory that the virus entered Brazil only once, from someone infected in the 2013 Zika epidemic in French Polynesia, and spread to the rest of the Americas from there, says Oliver Pybus, an evolutionary biologist at the University of Oxford in the United Kingdom, and a co-author on the paper.

It could have arrived, the authors say, during the Confederations Cup soccer tournament in late June 2013. That event brought the Tahitian national team to a stadium in Recife, near the epicenter of the Brazilian epidemic. (Tahiti lost to Uruguay, 8–0.) But that was several months before cases of Zika were reported in Tahiti, and Pybus thinks it's more fruitful to look at broader travel patterns rather than discrete events.

"If we can map flows of people and animals," researchers might be able to find patterns that could help forecast outbreaks, Pybus says. "No amount of looking at individual events is ever going to do that for us." He and his co-authors calculated that during 2013, air travel from Zika-endemic areas to Brazil increased by almost 50%, from roughly 3500 passengers arriving per month to nearly 5000.

Although researchers tend to focus on the well-studied outbreak in French Polynesia, other Zika-endemic countries have much larger populations and send more travelers to Brazil, Pybus notes. More than 1000 airline passengers arrived from the Philippines per month in 2013; Indonesia and Thailand sent similar numbers. It's plausible, he says, that travelers brought the virus directly from Southeast Asia to Brazil, and not from French Polynesia. Scott Weaver from the University of Texas Medical Branch in Galveston agrees. "The Philippines is a very likely source, it just hasn't been sampled," he says.

Scientists need more virus genomes from those countries to sort out the route Zika took to Brazil, Pybus says. "We have a bit of a black hole when it comes to understanding Zika transmission in Southeast Asia." The Tahitian team playing in Recife "is a great story," Pybus says, "but who knows if it's true." ■



Comb jellies such as *Mnemiopsis leidyi* have a through-gut, challenging when this evolutionary innovation arose.

## EVOLUTION

# Comb jelly 'anus' guts ideas on origin of through-gut

Videos of captive marine creatures unexpectedly show jellies defecate from pores, not via their mouth

By Amy Maxmen

**N**o butts about it, the butthole is one of the finest innovations in the past 540 million years of animal evolution. The first animals that arose seem to have literally had potty mouths: Their modern-day descendants, such as sea sponges, sea anemones, and jellyfish, all lack an anus and must eat and excrete through the same hole. Once an independent exit evolved, however, animals diversified into the majority of species alive today, ranging from earthworms to humans.

One apparent advantage of a second hole is that animals can eat while digesting a meal, whereas creatures with one hole must finish and defecate before eating again. Other possible benefits, say evolutionary biologists, include not polluting an animal's dining area and allowing an animal to evolve a longer body because it does not have to pump waste back up toward the head.

However, several unprecedented videos of gelatinous sea creatures called comb jel-

lies, or ctenophores, now threaten to upend the standard view of the evolution of the so-called through-gut. On 15 March, at the Ctenopoloosa meeting in St. Augustine, Florida, evolutionary biologist William Browne of the University of Miami in Florida debuted films of comb jellies pooping—and it wasn't through their mouths.

Browne's videos elicited gasps from the audience because comb jellies, whose lineage evolved long before other animals with through-guts, had been thought to eat and excrete through a single hole leading to a saclike gut. In 1880, the German zoologist Carl Chun suggested a pair of tiny pores opposite the comb jelly mouth might secrete some substance, but he also confirmed that the animals defecate through their mouths. In 1997, biologists again observed indigestible matter exiting the comb jelly mouth—not the mysterious pores.

Browne, however, used a sophisticated video setup to continuously monitor two species that he keeps in captivity, *Mnemiopsis leidyi* and *Pleurobrachia bachei*. The movies he played at Ctenop-

**"Looks like I've been wrong for 30 years. ... If people don't see this video, they won't believe it."**

**George Matsumoto**, Monterey Bay Aquarium Research Institute

oozoa capture the creatures as they ingest tiny crustaceans and zebrafish genetically engineered to glow red with fluorescent protein. Because comb jellies are translucent, the prey can be seen as it circulates through a network of canals lacing the jellies' bodies. Fast-forward, and 2 to 3 hours later, indigestible particles exit through the pores on the rear end. Browne also presented a close-up image of the pores, highlighting a ring of muscles surrounding each one. "This is a sphincterlike hole," he told the audience.

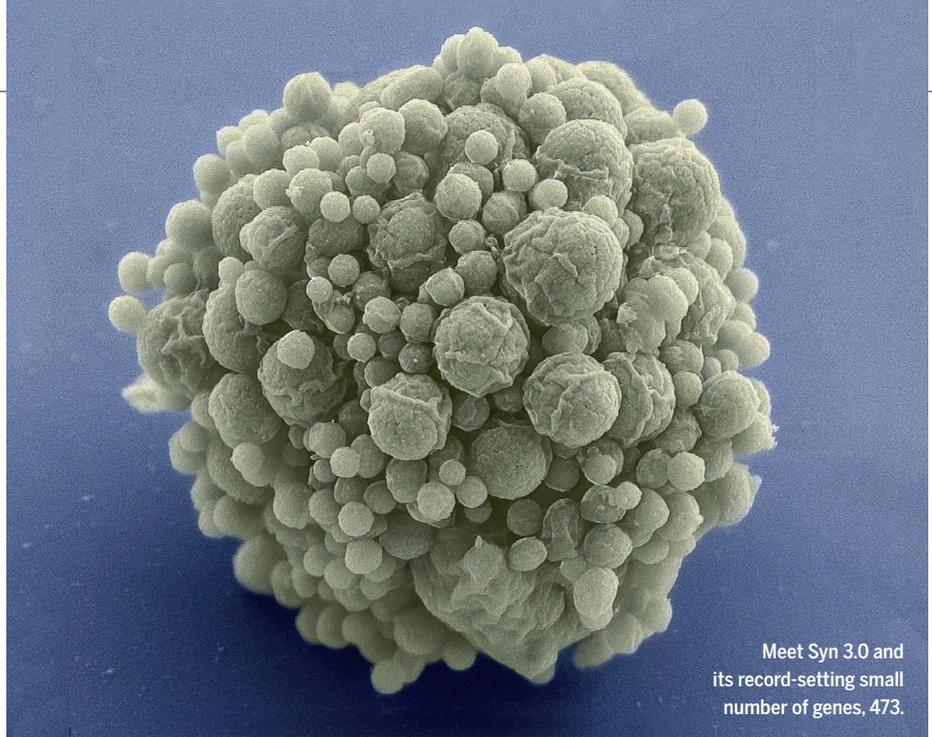
"Looks like I've been wrong for 30 years," said George Matsumoto, a marine biologist at Monterey Bay Aquarium Research Institute in Moss Landing, California, after he saw Browne's talk. "If people don't see this video, they won't believe it," he added. Matsumoto said he, as well as the biologists before him, likely missed the bowel movements because they did not observe their animals long enough after a meal. Jellies seen to expel waste from their mouths might have been, in effect, vomiting because they were fed too much, or the wrong thing.

According to recent DNA analyses, comb jellies evolved earlier than other animals considered to have one hole, including sea anemones, jellyfish, and possibly sea sponges. (Some studies suggest sponges arose first.) Consequently, Browne's as-yet unpublished findings disrupt the step-wise progression of digestive anatomy from one to two holes early in animal evolution.

One possibility is that the comb jellies evolved through-guts and anuslike pores on their own, independent of all other animals, over hundreds of millions of years. Alternatively, a through-gut and exit hole may have evolved once in an ancient animal ancestor, and subsequently became lost in anemones, jellyfish, and sponges. Perhaps if you're an anemone or a sponge stuck to a rock, suggests Matsumoto, it's better to push waste back into the current rather than below.

Browne is currently exploring the latter theory by seeing whether comb jellies activate the same genes when developing their pores that other animals do when growing an anus. If he finds that the genes are different, the evolution of our most unspeakable body part will no longer be considered the singular event zoologists long supposed. "We have all these traditional notions of a ladderlike view of evolution, and it keeps getting shaken," says Kevin Kocot, an evolutionary biologist at the University of Alabama, Tuscaloosa. ■

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Meet Syn 3.0 and its record-setting small number of genes, 473.

## SYNTHETIC BIOLOGY

# Synthetic microbe has fewest genes, but many mysteries

One-third of 473 genes in microbe have unknown functions

By Robert F. Service

**W**hen it comes to genome size, a rare Japanese flower, called *Paris japonica*, is the current heavyweight champ, with 50 times more DNA than humans. At the other end of the scale, there's now a new lightweight record-holder growing in petri dishes in California. This week in *Science*, researchers led by genome sequencing pioneer Craig Venter report engineering a bacterium to have the smallest genome—and the fewest genes—of any freely living organism, smaller than the flower's by a factor of 282,000. Known as Syn 3.0, the new organism has a genome whittled down to the bare essentials needed to survive and reproduce, just 473 genes. "It's a tour de force," says George Church, a synthetic biologist at Harvard University.

The microbe's streamlined genetic structure excites evolutionary biologists and biotechnologists, who anticipate adding genes back to it one by one to study their effects. "It's an important step to creating a living cell where the genome is fully defined," says synthetic biologist Chris Voigt of the Massachusetts Institute of Technology in Cambridge. But Voigt and others note that this complete definition remains

a ways off, because the function of 149 of Syn 3.0's genes—roughly one-third—remains unknown. Investigators' first task is to probe the roles of those genes, which promise new insights into the basic biology of life.

As Syn 3.0's name suggests, it's not the first synthetic life made by Venter, who heads the J. Craig Venter Institute (JCVI) and is a founder of Synthetic Genomics, a biotech company, both in San Diego, California. In 2010, Venter's team reported that they had synthesized the sole chromosome of *Mycoplasma mycoides*—a bacterium with a relatively small genome—and transplanted it into a separate mycoplasma called *M. capricolum*, from which they had previously extracted the DNA. After several false starts, they showed that the synthetic microbe booted up and synthesized proteins normally made by *M. mycoides* rather than *M. capricolum* (*Science*, 21 May 2010, p. 958). Still, other than adding a bit of watermark DNA, the researchers left the genetic material in their initial synthetic organism, Syn 1.0, unchanged from the parent.

In their current work, Venter, along with project leader Clyde Hutchison at JCVI, set out to determine the minimal set of genes needed for life by stripping nonessential



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Editor's Summary

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