

dio dishes are still hampered by ionized gas clouds and low resolution. Best are telescopes sensitive to the shortest radio waves—millimeter waves—but the dishes, detectors, and data processing technology for this part of the spectrum were developed only in the past few decades. “There is only a tiny window where we can see the event horizon,” says Heino Falcke, an astrophysicist at Radboud University in Nijmegen, the Netherlands, and chair of the EHT science council. “The Milky Way is like a milky glass.”

Early this decade, Doeleman and other EHT researchers began testing the idea with millimeter-sensitive dishes in Hawaii, California, and Arizona. Later, they extended the array to include the Large Millimeter Telescope in Mexico. Along the way, they got a good enough image of the black hole in M87 to see the base of its matter-spewing jets—data that are helping them understand how the jets are created (*Science*, 19 October 2012, p. 355). In 2015, they glimpsed the magnetic field around Sgr A*, which may help explain how black holes heat up the material around them (*Science*, 4 December 2015, p. 1242).

But to see the event horizon itself, the EHT had to grow even larger. Over the years, it has evolved from a loose, poorly funded group to a worldwide collaboration involving 30 institutions in 12 countries. Next month it will include far-flung additions, including the IRAM dish in Spain, the South Pole Telescope, and the Atacama Large Millimeter/submillimeter Array (ALMA), a large international observatory comprising 66 dishes in northern Chile. With its huge dish area, ALMA is the big catch because it will boost the EHT’s sensitivity by an order of magnitude. “That’s the key for us,” Doeleman says.

Adding new instruments isn’t simple. The technique for combining signals from distant dishes is known as very long baseline interferometry, and most millimeter-wave telescopes are not equipped to take part. EHT researchers had to visit each facility

to tinker with its hardware and install new digital signal processors and data recorders. In the case of ALMA, that took some persuading. “We had to go into the bowels of ALMA and rewire it,” Doeleman says. “It required political buy-in at all levels.”

The campaign next month will be a nervous time for the EHT team. All eight observatories need clear skies and no technical glitches to get the best possible observations. “The first time, things can go wrong,” Falcke says. Data volumes will be so large that they have to be recorded on hard drives and shipped back to the Haystack Observatory and the Max Planck

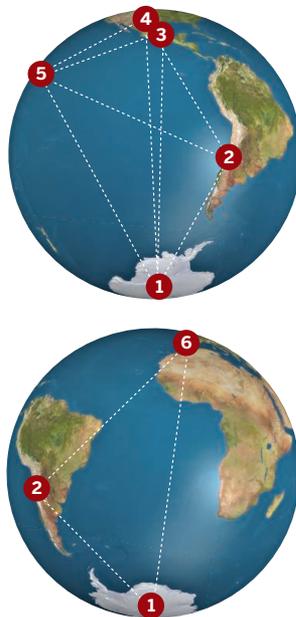
Institute for Radio Astronomy in Bonn, Germany, for processing. There, devices known as correlators, made from clusters of PCs but with the power of supercomputers, will spend months crunching through the data, combining the signals from separate dishes as if they came from a single dish as wide as Earth. Adding further delay, data from the South Pole Telescope won’t arrive until September or October, when planes can retrieve the hard drives after the Antarctic winter.

When the data finally all come together sometime next year, the team hopes to see a bright ring of light from photons orbiting close to the event horizon, with a dark disk in its center. The ring should be brighter on one side, where the rotation of the black hole gives photons a boost, although the images on this first attempt may not be as crisp as the team’s simulations. “It’ll probably be a crappy image, but scientifically it will be very interesting,” Falcke says.

Doeleman hopes to see structure in the matter swirling around the event horizon and watch, movielike, as gas falls into it and vanishes. Such observations might help explain why some black holes gorge on matter and shine brightly, whereas others—like Sgr A*—seem to be on a starvation diet. Falcke has a simpler wish. “The event horizon is the defining thing about a black hole,” he says. “I hope to see it; to literally see it.” ■

A shot in the dark

The Event Horizon Telescope now combines eight millimeter-wave radio observatories into a global telescope. The farther apart they are, the better the resolution.



1. South Pole Telescope 2. Atacama Large Millimeter/submillimeter Array and Atacama Pathfinder Experiment (Chile) 3. Large Millimeter Telescope (Mexico) 4. Submillimeter Telescope (Arizona) 5. James Clerk Maxwell Telescope and Submillimeter Array (Hawaii) 6. IRAM 30-meter (Spain)

GENOMICS

Sequencing all life captivates biologists

Project would read genomes of more than a million eukaryotes—just for starters

By Elizabeth Pennisi, in Washington, D.C.

“To sequence everything in the world—that is the reason we are here.” With those words last week, China’s genome pioneer Huanming Yang publicly kicked off what he hopes will become a massive international collaboration that will dwarf the Human Genome Project of the 1990s and provide a new basis for understanding and conserving the world’s life.

Yang, head of BGI in Shenzhen, China, arguably the world’s largest sequencing center, has teamed up with John Kress, an evolutionary biologist at the Smithsonian National Museum of Natural History in Washington, D.C., and two university colleagues, who have hatched what they are calling the Earth BioGenome Project (EBP). The audacious goal of the still-unfunded effort is to decipher the genomes of every species, starting with the 1.5 million named eukaryotes—the group of organisms that includes plants, animals, and microbes such as amoebas.

Last week, their call to action found a receptive audience here among the evolutionary biologists, conservationists, and others at a conference called BioGenomics2017. The EBP organizers drew parallels to the Human Genome Project, launched more than 30 years ago. That effort also began as an ambitious, controversial, and technically daunting proposal. Yet it eventually led to the first human genome, entirely new DNA technologies that are driving medical advances, and a \$20 billion industry.

The EBP would focus instead on the natural world. It “will enable us to understand what biodiversity means,” at a time when so much of it is vanishing, says Marie-Anne Van Sluys, a plant microbiologist at the University of São Paulo in São Paulo, Brazil. With genomics, “the focus has always been on humans, but the reality is that if the rest of the ecosystem collapses, we are not going to be very far behind,” adds Aristides Patrinos, a human genome pioneer and now chief



This greater bird of paradise in Indonesia and the plants around it may have their DNA deciphered.

scientist with Novim, a think tank based in Santa Barbara, California. The EBP could also help researchers “understand evolutionary processes on different timescales,” says Guojie Zhang, an evolutionary biologist at BGI and the University of Copenhagen. And by revealing genetic variation across all of life, it might aid conservation management and crop improvement.

As currently proposed, the EBP’s first step would be to sequence in great detail the DNA of a member of each eukaryotic family (about 9000 in all) to create genomes on par or better than the current reference human genome: complete enough that researchers know the order of genes on each chromosome. Next would come coarser sequencing of one species from each of the 150,000 to 200,000 genera—similar to scores of existing plant and animal genomes. Finally, scientists would seek rough genomes of the remaining known eukaryotic species. Those could be refined as needed, says EBP co-founder Gene Robinson, director of the Carl R. Woese Institute for Genomic Biology at the University of Illinois in Urbana.

The entire eukaryotic effort would likely cost about the same as it did to sequence that first human genome—about \$4.8 billion in today’s dollars, estimate Robinson, Kress, and the EBP’s other co-founder, Harris Lewin, an evolutionary genomicist at the University of California, Davis. The EBP’s eukaryotic work could be accomplished in a decade, its organizers suggest. Getting all the known microbes sequenced could take another decade.

“If the money, the infrastructure, and the samples materialize, we can do

it,” says Harvard University evolutionary biologist Scott Edwards. Such optimism reflects the ever-decreasing costs and improving technology of DNA sequencing—one meeting presenter from Complete Genomics, based in Mountain View, California, says his company plans to be able to roughly sequence whole eukaryotic genomes for about \$100 within a year. Giants in the genomics field, such as BGI, the Wellcome Trust Sanger Institute in the United Kingdom, and newer sequencing centers such as one that has launched at The Rockefeller University in New York City, have already agreed to sequence some species.

The EBP has a head start thanks to several research communities pursuing their own animal and plant sequencing projects and the Earth Microbiome Project, which has already begun tackling noneukaryotes. The eukaryotic projects include Genome 10K, which seeks to sequence 10,000 vertebrate genomes, one from each genus; i5K, an effort to deci-

A head start

The Earth BioGenome Project could coordinate the efforts below and others that are already sequencing broad swaths of the planet’s life.

PROJECT	YEAR STARTED	SEQUENCING GOAL	NUMBER SEQUENCED
G10K	2009	9478 vertebrate genera	100
i5K	2011	5000 arthropods	30
GIGA	2013	7000 marine invertebrates	60
GAGA	2016	All 300 ant genera	25
B10K	2016	All 10,500 bird species	300
AOCC	2013	101 African food crops	22

pher 5000 arthropods; and B10K, which expects to generate genomes for all 10,500 bird species (see chart, below). The EBP would help coordinate, compile, and perhaps fund these efforts. “The [EBP] concept is a community of communities,” Lewin says. That decentralized approach could lessen concerns that the EBP would be a “big science” project that would take away funding from individual investigators. “I like small-scale science,” Edwards says. However, “There’s a role to play” for a coordinating body.

At a preconference planning session for the EBP last week, the 20 attendees emphasized that the effort needs to give developing countries, particularly those with high biodiversity, a chance to help shape the project’s final form. Attendees also debated the best strategy for the project. In addition to one genome from each eukaryotic family, the EBP could comprehensively sequence all the organisms in particular locations. Van Sluys advocates that approach because it reveals more about how organisms, and their environment, influence one another. Pamela Soltis, a plant evolutionary biologist at the University of Florida in Gainesville, suggests that the EBP pick places already under intense study—such as the National Science Foundation–supported NEON sites scattered around the United States, where there will be extensive long-term monitoring of the environment.

The planning group also stressed the need to develop standards that ensure high-quality genome sequences yet don’t exclude work done before they were established. Getting DNA samples from the wild may ultimately be the biggest challenge—and the biggest cost, several people noted. Not all museum specimens yield DNA preserved well enough for high-quality genomes. Over the next several months, the EBP’s organizers will expand the planning committee and outline a white paper before formally approaching foundations and other funding agencies for support.

There is no shortage of enthusiasm, however. After Lewin outlined the EBP in the closing talk at BioGenomics2017, he was surrounded by researchers eager to know what they could do. “It’s good to try to bring together the tribes,” says Jose Lopez, a biologist from Nova Southeastern University in Fort Lauderdale, Florida, whose “tribe” has mounted GIGA, a project to sequence 7000 marine invertebrates. “It’s a big endeavor. We need lots of expertise and lots of people who can contribute.” ■



Sequencing all life captivates biologists

Elizabeth Pennisi (March 2, 2017)

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Editor's Summary

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