X-RAY ASTRONOMY

Loss of ASTRO-E X-ray Satellite Hurts Japan's Space Science ...

TOKYO—Astronomers and astrophysicists are mourning the loss last week of a Japanese-American x-ray satellite that promised to give them their closest look yet at the region surrounding black holes and other objects that emit high-energy x-rays. A rocket failed to lift the $105 million ASTRO-E spacecraft into a sustainable orbit. The loss pinches particularly hard into Japan's space science efforts, which rely heavily on a small number of carefully targeted satellites.

"It leaves a big gap in our research program," says Tsuneyoshi Kamae, an astrophysicist at the University of Tokyo who helped develop one of ASTRO-E's three major instruments. Scientists say it could take at least 3 or 4 years to build and fly a replacement mission, if a suitable rocket can be found.

Launched on 10 February from the Kagoshima Space Center of Japan's Institute for Space and Astronautical Science (ISAS), ASTRO-E was to be the third major space telescope launched in a span of less than 7 months to study cosmic x-rays. It was meant to complement NASA's Chandra X-ray Observatory and the European XMM-Newton Observatory (see story below). Both those satellites, which are already in orbit, are focusing on low- and medium-energy x-rays; ASTRO-E would have concentrated on the high-energy end of the spectrum. "One corner of the triangle is now missing," says x-ray astronomer Joachim Trümper of the Max Planck Institute for Extraterrestrial Physics in Garching, Germany. "It's a very big loss for x-ray astronomy."

It is especially bad news for Japan's astronomers, who have applied their modest budgets to carefully targeted niches. "Even though Japan's [space program] is small, we've been able to join the world's front ranks in x-ray astrophysics," says Kazuo Makishima, an astrophysicist at the University of Tokyo.

ASTRO-E would have been the fifth Japanese x-ray mission. Its predecessor, ASCA, launched in 1993, has made several groundbreaking discoveries, including the detection of iron in the x-ray emissions from accretion disks, the swirls of gas and dust around black holes. Distortions of the normal fingerprint of iron bore telltale evidence of the enormous gravitational pull of the black hole, something expected but never before observed.

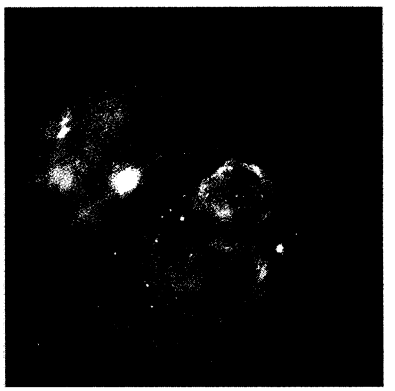
Not enough. Problems with Japan's M5 rocket after lift-off doomed the ASTRO-E satellite.

ASTRO-E's prime instrument, the x-ray spectrometer (XRS), developed by ISAS and NASA, is extremely sensitive, designed to measure the energy of individual x-ray photons hitting the detector. This would have allowed astrophysicists "to determine properties of accretion disks very close to black holes," says Richard Kelley, principal investigator for the XRS at NASA's Goddard Space Flight Center in Greenbelt, Maryland, who says that his team doesn't have any plans to relaunch a similar payload.

A second instrument, the hard x-ray detector (HXD), developed by ISAS and a group of astrophysicists at the University of Tokyo, was expected to set the direction for Japan's space x-ray efforts for the next decade. By focusing on very high energy x-rays, it would have ventured into relatively unexplored territory. These higher energies "are the least explored regions in astrophysics, and yet they contain some of the most violent astrophysical phenomena," says Tokyo's Kamae.

A group at Nagoya University is already at work on a next-generation very high energy x-ray instrument to be launched about 2007. But with ASCA nearing the end of its life, the loss of HXD leaves a gap in Japan's observational program. Makishima says that a dozen faculty members and 30 graduate students must now salvage what they can from 8 years spent planning and building HXD. "The most important thing will be to find some way to put this instrument in orbit," he says. In the meantime,

... While European Observatory Sends Back First X-ray Images



This view of supernova remnants in the Large Magellanic Clouds comes from Europe's new orbiting x-ray observatory, whose first pictures were released last week. Launched on 10 December, the X-ray Multi-Mirror Mission (XMM)–Newton—named after the father of spectroscopy—joins NASA's Chandra X-ray Observatory, which was sent into space last summer. Japan's ill-fated ASTRO-E was to have been the third in a planned trio of x-ray observatories (see accompanying story).

XMM-Newton will be able to detect much fainter emissions than Chandra can, although with less detail. The European observatory is "absolutely superior in doing certain types of observations, like taking spectra of faint, isolated neutron stars," says Martin Weisskopf of NASA's Marshall Space Flight Center in Huntsville, Alabama, a Chandra project scientist. "Chandra and Newton complement each other very well." In spite of the loss of ASTRO-E, "we are up for a prosperous new era in x-ray astronomy," predicts project scientist Fred Jansen of the European Space Research and Technology Centre in Noordwijk, the Netherlands.

–GOVERT SCHILLING

CREDITS: (TOP TO BOTTOM) ISAS; ESA

they will continue using ASCA and seek observing time on the U.S. and European x-ray observatories.

The failure of the M5 rocket, in its third launch after two successes, puts a cloud over future ISAS missions. The M5 is intended to be ISAS's primary launch vehicle for the next decade. Its next scheduled mission is not until the summer of 2002, giving some breathing room to fix whatever went wrong.

ISAS officials are focusing on the first stage of the rocket, in particular the possibility of damage to the graphite rocket nozzle. Onboard cameras transmitted images of sparks coming from the rocket nozzle just before altitude control problems developed about 40 seconds after lift-off. The rocket did not achieve the desired trajectory by the time the first stage separated, and the second and third stages failed to lift the satellite into orbit, causing it to burn up in the atmosphere.

–DENNIS NORMILE

With reporting by Govert Schilling in the Netherlands.

GENOMICS

Mouse Sequencers Take Up the Shotgun

MARCO ISLAND, FLORIDA—In a dramatic departure, the genome community will be using a controversial sequencing strategy—one that many scientists have publicly trounced—to tackle its next big target: the mouse. Discussions at a meeting* held here last week made clear that a good part of the mouse will be sequenced using the whole-genome shotgun method pioneered by J. Craig Venter of Celera Genomics in Rockville, Maryland. But it will be used in combination with the more incremental strategy used by the Human Genome Project, the publicly funded consortium sequencing the human genome and the genomes of other organisms. "Both approaches have something to offer for getting large, complex genomes sorted out," says Robert Waterston, who heads Washington University's sequencing center in St. Louis.

Less than 2 years ago, the sequencing community sharply criticized the shotgun approach when Venter announced that he planned to tackle the human genome this way (*Science*, 22 May 1998, p. 1185). In the shotgun approach, the entire genome is cut into tiny pieces and then sequenced and reassembled all at once. Many genome scientists thought Venter would never be able to put his millions of pieces of DNA back together in the right order—a process akin to assembling a jigsaw puzzle consisting almost entirely of blue sky. "Over 100,000 serious gaps" would remain, predicted Maynard Olson, a sequencing authority at the University of Washington, Seattle, in 1998.

But a collaboration between Celera and academic partners to sequence the 160-million-base genome of the fruit fly *Drosophila melanogaster* (*Science*, 5 February 1999, p. 767) is showing that a hybrid strategy—combining whole-genome shotgun data with sequence generated the more traditional way, one bit at a time—can work. Because the chromosomal locations of those bits, which are represented in bacterial artificial chromosomes (BACs), are known, they can help sequencers assemble data from the whole-genome shotgun approach more accurately. "*Drosophila* taught us a compelling lesson. The hybrid approach has a lot of validity," says Eric Green, a geneticist at the National Human Genome Research Institute (NHGRI) in Bethesda, Maryland. Venter seems to agree: He announced last month that Celera is relying on public data to speed its human genome effort.

Even so, the decision to sequence the 3-billion-base mouse genome this way is not being made lightly, and many details "are still being thrashed out," says Green. For Green and others, the mouse genome is pivotal because it can help them decipher the human genome. The mouse will be only the second mammal sequenced in its entirety, after the human, making possible all sorts of comparative analyses. Humans and mice share many of the same genes; indeed, many mouse aficionados assert that the best way to figure out how human genes work is to study them in the mouse.

Understandably, the consortium of 10 labs tackling the mouse wants to be sure to do it right. To sequence a genome to the desired standard of accuracy—99.99%—each small stretch must be represented perhaps five to 10 times in the various pieces of sequenced DNA, whatever method is used to produce them. As recently as last October, when the 10 labs received $21 million from NHGRI to begin on the mouse, no one had seriously considered tackling the mouse genome with anything but the tried-and-true approach (*Science*, 8 October 1999, p. 210). But that changed at the first meeting of the mouse network, when Richard Gibbs of Baylor College of Medicine in Houston proposed doing some "shotgunning" of the mouse. Not only might the shotgun approach be faster, suggested Gibbs, but it would ensure that the laborious front-end work needed to characterize the BACs wouldn't delay the project.

Most of the group was receptive, recalls Bruce Roe, who will sequence some of the mouse genome at the University of Oklahoma, Norman. But some were worried that a combined approach might diminish a key

MOUSE GENOME GRANTS

Principal investigator	Institution	Millions
Kucherlapati, Raju S.	Albert Einstein College of Medicine, Bronx, NY	$6.127
Nierman, William C.	Genomic Research, Rockville, Maryland	$1.60 (1 yr)
Gibbs, Richard A.	Baylor College of Medicine, Houston, Texas	$22.344
Roe, Bruce A.	University of Oklahoma, Norman	$12.192
Lander, Eric S.	Whitehead Institute for Biomedical Research	$21.507
Weiss, Robert B.	University of Utah, Salt Lake City	$6.067
McCombie, W. Richard	Cold Spring Harbor Laboratory, New York	$6.874
Smith, Douglas R.	Genome Therapeutics Corp., Waltham, Massachusetts	$12.874
McPherson, John D.	Washington University School of Medicine, St. Louis, Missouri	$24.642
Green, Eric	National Human Genome Research Institute, Bethesda, Maryland	$16.060

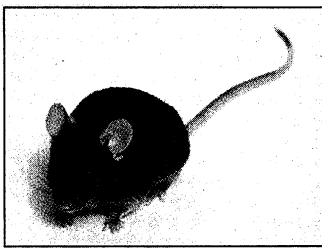


PHOTO CREDIT: THE JACKSON LABORATORY

* "Advances in Genome Biology and Technology I" was held 5 to 8 February.