Antiprotons Captured at CERN

An American–West German group has stored hundreds of antiprotons in a Penning trap; a precision measurement of the antiproton's inertial mass is next on the agenda

RESEARCHERS from the University of Washington, the University of Mainz in West Germany, and the Fermi National Accelerator Laboratory have for the first time captured antiprotons from a high-energy accelerator and stored them for several minutes in an electromagnetic ion trap. With projected improvements in the trapping process, the achievement opens the way to a precision measurement of the inertial mass of the antiproton. A fundamental theorem of physics requires the antiproton to have exactly the same rest mass and lifetime as the proton. Other studies of the properties and possible uses of antiprotons may also be possible.

Antiprotons are fairly routinely produced in proton accelerators when the high-speed protons strike a metal target. But, when generated in usefully large numbers, the antiprotons have energies in the billion-electron-volt range. These antiprotons have far too much energy to be captured in an electromagnetic ion trap. A special Penning trap, for example, can hold ions in a potential energy well generated by static magnetic and electric fields and can capture particles with energies of a few kiloelectron volts (keV), a million times lower.

The European Laboratory for Particle Physics (CERN) near Geneva has a unique complex of machines culminating in the Low-Energy Antiproton Ring (LEAR), which can slow down, collect, and concentrate antiprotons into a beam with energies as low as 5 million electron volts (MeV). For this reason, Gerald Gabrielse, Xiang Fei, Kristian Helmerson, Steve Rolston, Robert Tjoelker, and Thomas Trainor of the University of Washington, Hartmut Kalinowsky and Johannes Haas of the University of Mainz, and William Kells of Fermilab traveled to CERN for their experiment.

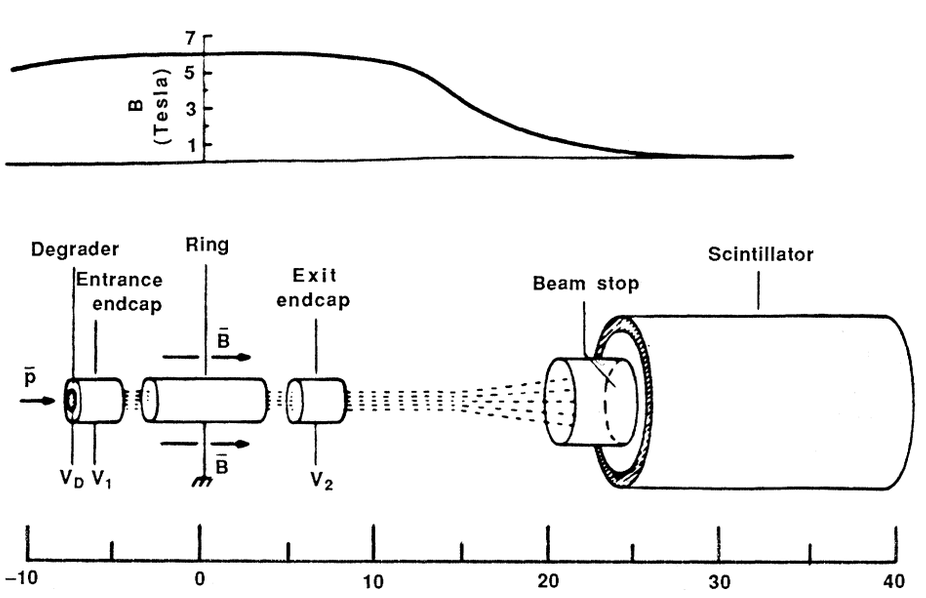
First on the agenda was to slow down the antiprotons emerging from LEAR in the form of a pulse containing about 10^8 particles with an energy of 21.3 MeV. To achieve this, the researchers inserted a thick disk of beryllium in the path of the antiprotons just before they entered the Penning trap. Because of the high energy of the antiprotons, the probability of annihilation events involving protons in the beryllium nuclei was small, but a few antiprotons could lose energy by way of collisions with the electrons in the material. About 1 antiproton in 10^4 was slowed to an energy of 3 keV or less and could be captured in the trap.

The trap itself had two main components. The first was a 6-tesla superconducting magnet that generated a field parallel to the path of the antiprotons. The strong magnetic field prevented the particles from escaping in the radial direction as they spiraled around the magnetic field lines. The second component was an assembly of three cylindrical electrodes. The center or ring electrode was always grounded, whereas a negative potential up to 3000 volts could be switched onto the endcap electrodes in only 15 nanoseconds. With no voltage on any electrode, the antiprotons would pass through the trap in a little more than 150 nanoseconds.

To prevent this, the researchers initially put the −3000 volts on the exit endcap, so that antiprotons with energies of 3 keV or less would be reflected back toward the entrance endcap. By the time the particles arrived there, the voltage was switched to the entrance endcap, thereby reflecting them once again. By repeating this sequence, the researchers were able to hold antiprotons in the trap for several minutes. To detect how many antiprotons were captured, the researchers removed the voltage on the exit endcap, which released the particles from the trap to a beam dump, where they annihilated. A scintillator counted the pi mesons that result from the annihilations.

After the maximum attempted trapping time of 10 minutes, only five antiprotons remained in the trap out of the several hundred initially captured. The principal reason for loss of antiprotons was the residual pressure in the evacuated trapping apparatus. Collisions with the nuclei of gas molecules result in proton-antiproton annihilation events, resulting in a decay in the number of trapped particles with time.

While it all sounds easy enough, Gabrielse told *Science* that the actual experiment was



Antiproton trap: *Schematic diagram of the magnetic field profile, the trap electrodes, and the scintillator that detects antiprotons released from the trap. Antiprotons from LEAR enter from the left, lose energy in the beryllium degrader, and oscillate from one end of the trap to the other before being released and detected.*

much more dramatic. For starters, the group was allowed only 1 day to collect data before a lengthy LEAR shutdown at CERN. Then, the high-voltage cables broke just a few hours before data taking was to begin, necessitating an all-night rush repair job. Finally, a critical device needed to feed a pulse of antiprotons into LEAR (a kicker magnet) failed, and the CERN accelerator operators had to make an untried backup kicker work on the first attempt.

In a future experiment, Gabrielse and his co-workers propose to determine the antiproton mass from the frequency of the circular motion of the antiprotons around the magnetic field lines in the trap (cyclotron resonance frequency). They hope to improve the accuracy of the present best measurement by a factor of 10^4, thereby making it one of the three most stringent limits on any possible violation of the CPT (charge conjugation–parity–time-reversal) theorem of physics.

To measure the mass this accurately, it will be necessary to further slow the axial motion in the trap from the kiloelectron volt energies of the present experiment to a maximum of about 5×10^{-4} eV, the thermal energy associated with the ambient temperature of 4.2 K. The investigators propose to achieve this so-called axial cooling by filling the trap with a buffer "gas" of low-energy or cold electrons. Collisions between the hot antiprotons and the cold electrons slow down the antiprotons as in any mixture of hot and cold gas particles.

For the best measurement, there should be just a single antiproton cooled to 4.2 K. But it will also be necessary to increase the trapping time to at least 1 day and preferably several weeks. The main way to accomplish this is to improve the vacuum. The group plans to cool an improved trapping apparatus to 4.2 K by immersing it in liquid helium, thereby turning it into a massive cryopump capable of an ultrahigh vacuum.

Trapped antiprotons may be useful for many kinds of studies because, once the particles are accumulated, the trap could be moved to a nearby laboratory where it acts as an antiproton source. A group from the Los Alamos National Laboratory has its own plans to measure the gravitational constant of an antiproton. There also has been some speculation that large numbers of antiprotons might be useful as an energy source for space and military applications, although the leap from hundreds of antiprotons to macroscopic quantities is staggering to contemplate. ■ **ARTHUR L. ROBINSON**

ADDITIONAL READING

G. Gabrielse *et al.*, "First capture of antiprotons in a Penning trap: A keV source," in preparation.

Briefing:

Viroids May Be Escaped Introns

Viroids are the smallest known infectious agents, which so far have been shown to occur only in plants. They are made up of single-stranded RNA circles having between 270 and 380 nucleotides. To date they have not been shown capable of coding for any proteins of their own, and appear to be totally dependent on their hosts' metabolic machinery for replication. In short, they are something of a biological enigma, not least of which is the question of their origin.

As it has become possible in recent years to compare nucleic acid sequences across a broad range of structures, this latter question may now be solved. Gail Dinter-Gottlieb of Drexel University, Philadelphia, reports that viroids share many detailed structural similarities with a certain class of intervening sequences, known as group I introns, and concludes that viroids may be "escaped introns." If correct, this would confirm independent speculations along these lines made in 1979 by Francis Crick of the Salk Institute and Theodor Diener of the Plant Protection Institute, Beltsville, Maryland.

Group I introns are found in mitochondrial messenger and ribosomal RNA genes, chloroplast transfer RNA genes, and nuclear ribosomal RNA genes. They are characterized by the possession of a series of more or less conserved sequences (called boxes, in the diagram), which impose certain secondary and tertiary structure constraints. But they are most notorious in that at least some of them are able to self-splice, that is to excise themselves and ligate the parent strands in the absence of enzymes, releasing a small, circular RNA.

The close similarity in size between, for instance, the potato spindle tuber viroid (PSTV), which has 359 nucleotides in its circle, and the excised ribosomal RNA intron from *Tetrahymena thermophila*, which comprises 399 bases, is striking. But, as Dinter-Gottlieb shows in her survey, the resemblances go far beyond gross anatomy.

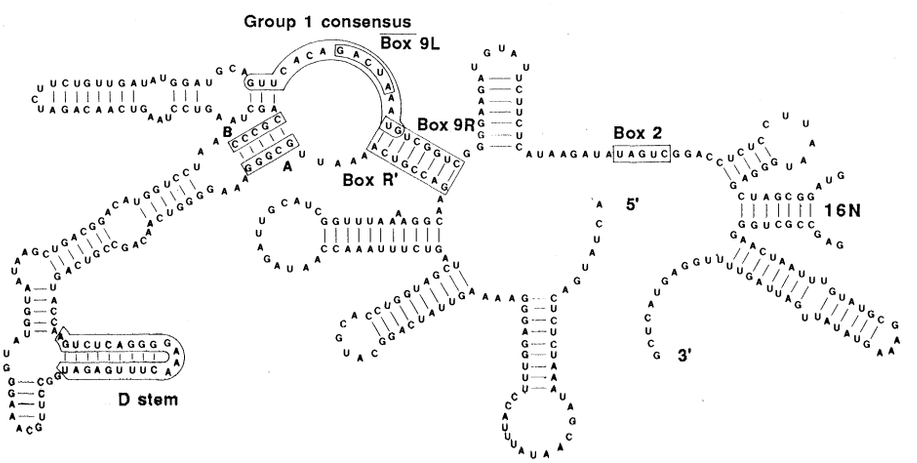
For instance, a sequence of 16 bases that characterizes all group I introns, and is known as the group I consensus sequence, is also to be found in viroids. So, too, are many elements of the conserved sequences, or boxes, that govern the three-dimensional structure of introns. Significantly, the order with which these conserved regions are arranged in viroids is the same as in introns, prompting the speculation that the secondary and tertiary configurations are similar. However, as calculations predict and experience shows, viroids in a completely protein-free state assume a distinctive rod shape. In order to be disposed like a group I intron, a viroid molecule would have to be stabilized by proteins, which may not be unlikely as PSTV was recently found in a ribonucleoprotein complex in vivo.

The structural intimacy between these two interesting classes of circular RNA's is finally secured by the fact that parts of the central conserved region that is so characteristic of viroids also appears in group I introns.

An evolutionary relationship between the two species therefore seems virtually certain. But, as Dinter-Gottlieb says, "the question still remains as to whether viroids evolved from introns or whether both evolved from a common ancestor molecule." ■

ROGER LEWIN

G. Dinter-Gottlieb, "Viroids and virusoids are related to group I introns," *Proc. Natl. Acad. Sci. U.S.A.*, **83**, 6250 (1986).



A group I intron. *Conserved regions (boxes) impose a characteristic secondary and tertiary structure, which is closely matched by viroids.*