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.

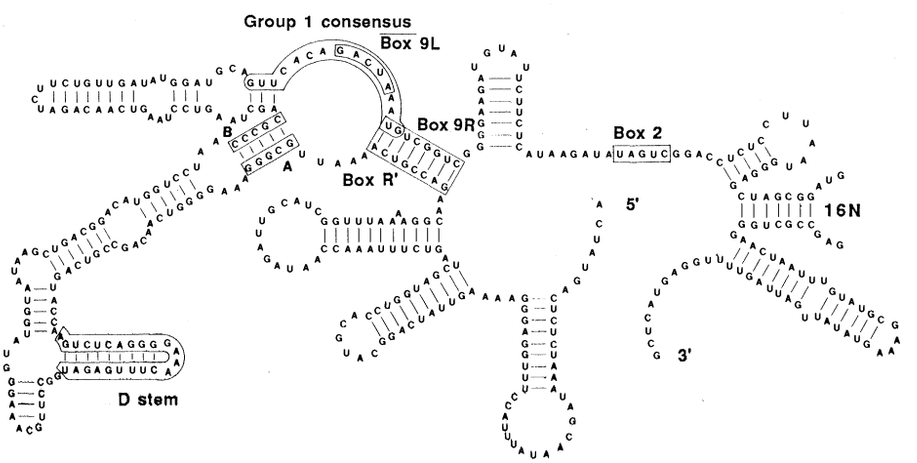
For instance, a sequence of 16 bases that characterizes all group I introns, and is known as the group I consensus sequence, is also to be found in viroids. So, too, are many elements of the conserved sequences, or boxes, that govern the three-dimensional structure of introns. Significantly, the order 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.*