and their characteristic earthquakes should be the USGS's own backyard, the San Francisco Bay area. The San Andreas fault cuts right up the San Francisco Peninsula, but it also splays northward into a pair of fault systems of which the Calavaras is a part. These dissect the heavily populated East Bay region. Although the opposing sides of some of these faults appear to be harmlessly slipping by each other, the record of earthquake activity in the 19th century suggests otherwise.

According to historical records, the Bay area was far more active in the 19th century than it has been of late. In 1981 William Ellsworth and his colleagues at the USGS in Menlo Park pointed out that in the 50 years after the San Francisco earthquake of 1906 (magnitude 8) there were far fewer earthquakes larger than magnitude 5 than in the 50 years preceding that great earthquake (*2*).

Recalling the suggestion that great earthquakes are preceded by increased seismic activity and followed by relative quiesence, the USGS group added further weight to an earlier contention that a new stage in that cycle had begun in the Bay area in 1955 when the frequency of earthquakes larger than magnitude 5 seemed to increase. The 1979 Coyote Lake (magnitude 5.9) and Livermore (magnitude 5.8) earthquakes fit that increasing trend, as does the Morgan Hill event. It is the largest since 1911 and, says Ellsworth, is typical of the earthquakes of magnitude 6 to 7 that struck the area about once a decade on average in the 19th century. (An earthquake of magnitude 7 is 32 times more energetic than an event of magnitude 6.)

The Morgan Hill earthquake may have strengthened confidence in the forecasting of earthquakes, but the latest event to be "captured" by geophysical instrumentation provided no encouragement that their timing can be precisely predicted. This earthquake gave no detectable warning, despite a dense seismometer network and geodetic surveys only 1 week and 1 day before the main shock. It was another reminder that even the tiniest of foreshocks cannot be depended on to appear and that present routine geodetic surveys are possibly 100 times too insensitive to catch any premonitory slippage of a moderate earthquake.

—**Richard A. Kerr**

Additional Reading

1. W. H. Bakun, *Bull. Seismol. Soc. Am.* **70**, 1181 (1980).
2. W. L. Ellsworth, A. G. Lindh, W. H. Prescott, D. G. Herd, in *Earthquake Prediction*, D. W. Simpson and P. G. Richards, Eds. (American Geophysical Union, Washington, D.C., 1981), pp. 126–140.

First mRNA Splicing Intermediate

Seven years ago researchers in several laboratories discovered that many genes in nucleated organisms are interrupted by noncoding regions, called introns. Attempts to discover how introns are precisely excised from messenger RNA (mRNA) precursors have, to many people's surprise and frustration, borne little fruit. A major hindrance in these efforts has been the equally surprising failure to develop rapidly an efficient and reproducible in vitro splicing system, which is essential for experimental dissection of the components and intermediates involved. This barrier has been removed within the last year, and the new first insights into the mRNA splicing system are beginning to be reported.

Phillip Sharp and his colleagues at Massachusetts Institute of Technology (MIT) have just published in *Cell* a description of a "lariat-type" configuration for an excised intervening sequence in their splicing system (*1*). Michael Green, in collaboration with Tom Maniatis at Harvard, discussed a similar observation at this year's Cold Spring Harbor meeting on RNA processing. Until now there has been no unambiguous observation of an excised intron from a mRNA precursor. That the excised intron should be in the form of a lariat is particularly intriguing since such RNA structures are highly unusual.

Precursor RNA molecules have fallen into three classes as far as their splicing attributes are concerned. The first contains transfer RNA's (tRNA), which are tightly configured into striking secondary structures. The precision of intron excision appears to be determined not by sequences within the intron but by the structure of the tRNA itself. In ribosomal RNA (rRNA) and mitochondrial mRNA's splicing appears to depend in part on the presence of four short conserved sequences within the intron. Introns in the third group, nuclear mRNA, are always bounded by the nucleotides GT and AG plus short "consensus sequences," which presumably play a role in recognition of splice sites. Although there has been steady progress in working out the splicing mechanisms for tRNA and rRNA, mRNA processing has remained enigmatic, apart from the almost certain involvement of an additional small RNA species known as U1, part of which is very similar in sequence to one of the consensus sequences.

Using the in vitro splicing system developed in their laboratory last year, Sharp and his colleagues Paula Grabowski and Richard Padgett monitored the dynamics of intron excision from an experimental precursor. The universal failure to isolate excised introns has lead to the belief that normally they are rapidly degraded. As luck would have it, degradation activity in the in vitro system appears to be missing, allowing a glimpse of this elusive species.

While they were analyzing the products of the splicing reaction on various types of gels, the MIT researchers noticed slower than expected migration of several putative intermediates, including the intron itself. Following various manipulations and leaning heavily on the recent observations by Mary Edmonds and John Wallace, of the University of Pittsburgh (*2*), on branched structures in poly(A) molecules, Sharp and his co-workers realized they too might be dealing with a branched RNA molecule. They finally concluded that the branch was part of a lariat configuration. Although the *Cell* paper speculates on the possible addition of a small RNA molecule to the intron as part of the splicing process, Sharp and his colleagues now dismiss this idea and look to the intron itself to form the loop.

The MIT and Harvard results seem to exclude the still current idea that mRNA introns might be excised by attrition—a nuclease nibbling through the sequence. They also indicate that a sequence within the intron might be important in the splicing process, which is interesting in view of the observation that a large proportion of the intron can be removed without preventing splicing.—**Roger Lewin**

References

1. P. J. Grabowski, R. A. Padgett, P. Sharp, *Cell* **37**, 415 (1984).
2. J. C. Wallace and M. Edmonds, *Proc. Natl. Acad. Sci. U.S.A.* **80**, 960 (1983).