

Pattern in Mass Extinctions

For six years John Sepkoski of the University of Chicago has been engaged in the tedious job of compiling records of when families of marine organisms vanished from the fossil record. Recently, with David Raup, also at Chicago, he drew up graphs presenting the data. A curious pattern emerged, one that the scientists could neither explain nor ignore. Roughly every 26 million years for the last 250 million years, the numbers of extinctions jumped above the background of extinctions that occur in the normal course of life. Mass extinctions, they conclude, are not random events, as has been widely believed. Instead, it appears, at regular intervals something perturbs the biological system, not destroying it but resetting it so powerfully that the ensuing changes forever twist the course of evolution.

In 1977 two scientists suggested that 32 million years elapse between mass extinctions, but the idea was not pursued. The periodicity in mass extinctions was very unexpected," Sepkoski says. "We expected that it probably would be random, because it has usually been assumed that each mass extinction was caused by a unique plexus of stress." Instead they found that a 26-million-year cycle seems to be "a very robust feature of the data."

The hypothesis, if correct, means that there is some force outside terrestrial biology that periodically upsets the system. Some organisms survive whatever blow afflicts the planet, but which ones do depends not on qualities developed to ensure survival, but on chance and good fortune, such as living in middle or high latitudes where extinction is less common than in the tropics, says David Jablonski of the University of Arizona in Tucson. While organisms can prepare for catastrophes that may occur on shorter time scales, they cannot prepare for an event that occurs only once in 26 million years.

One puzzling aspect of the 26-million-year period is that no natural process is known to follow a cycle of that length. Raup and Sepkoski generally favor a solar or galactic forcing agent for the pattern, but still are searching for a specific cause. "We're kind of stumped," Sepkoski says. "We can speculate, but so far we haven't found anything in the astronomical or solar literature that has fixed cycles in that range." The only thing that comes close, he says, is the passage of the solar system through the arms of the Milky Way galaxy. But that event occurs in periods between 50 million and 100 million years—too long to explain the mass extinction peaks.

At a meeting last month on the dynamics of mass extinction, Eugene Shoemaker of the United States Geological Survey in Flagstaff, Ariz., reported that every 50 mil-

lion years the earth may withstand a significant impact with one of the rocky bodies vaulting through space. A strong 50-million or 52-million-year period could mean that the peaks are an amalgam of periodic and random events, so that the average position of the random events would fall midway between impacts, Sepkoski told SCIENCE NEWS. But when Raup and Sepkoski ran their computer simulations using a 52-million-year cycle with some random events included, the results were not conclusive. "We feel that a 52-million-year cycle is less plausible than a 26-million-year cycle, but it's a possibility," Sepkoski says.

The causes of mass extinctions have been pondered for several centuries, but in the last few years new life has been infused into the topic. This vigor stems mainly from the hypothesis that one of the extinction peaks occurred 65 million years ago when an asteroid struck the earth, bringing huge numbers of organism families to an abrupt end (SN: 1/12/80, p. 22; 11/14/81, p. 314). Regardless of whether the impact idea is right, "it's thrown the entire

forum of mass extinction debate into a much more testable framework," Jablonski says. Likewise, the Raup/Sepkoski hypothesis, with its firm statistical underpinning, can be tested and debated by paleontologists trying to patch together the record of ancient life. One reason for the widespread interest in the 26-million-year cycle is that it is based on Sepkoski's new data set, which refines the time between sampling periods in the geologic record to a few million years. This still is coarse in relation to the time scale of extinction, making it difficult to discern whether a mass extinction happened suddenly or over a period of up to a million years or more. Nonetheless, it is far better than has been available so far.

One way to test the hypothesis, Jablonski says, is to refine the fossil time scale further still, and to look more closely at ecological and geographical patterns of extinction. He says the cyclic nature of extinctions is "a very seductive idea. The biological world blithely goes on and all of a sudden from outside, some terrible catastrophe comes in and resets the evolutionary clock. Then biology picks itself up and continues to evolve and the survivors, whatever they may be, continue to evolve and re-radiate and get clobbered again in a periodic sort of pattern."

—C. Simon

Unconstrained harvest of brain genes

The nerve cells that make up the intricate, powerful, diverse communication network of the brain are ruled by their genes, as are all cells. In an ambitious merger of the most recent techniques for genetic and brain research, scientists are beginning to identify the thousands of genes active only in brain cells and are using them to discover "in an unconstrained way" perhaps unexpected rules of brain activity.

In the first analyses of genes from a grab bag of those active in the brain, the investigators have discovered two novel proteins, one of which may be the signal chemical in a major, previously unrecognized system of brain connections. The work also provides evidence for a new twist to gene function, Floyd E. Bloom of the Salk Institute in San Diego, Calif., reported last week at the meeting in Boston, "Molecular Biology Now and Tomorrow, Thirty Years of DNA."

The collection of genes active specifically in the brain was compiled by comparing gene activity in the rat brain, liver and kidney. When a gene is active, enzymes transcribe it into a molecule called messenger RNA, which carries information from the gene to the rest of the cell. The scientists estimate that 30,000 different types of messenger RNA molecules are produced by brain cells and that more than half, and perhaps as many as 90 percent, of these different messages reflect

genes active only in the brain.

So far more than 200 different brain messenger RNA molecules have been examined. The researchers have concentrated their analyses on those detectable only in brain cells. In each case they determine the sequence of nucleotides, the subunits of the gene or messenger RNA that encode information for making protein. By applying the genetic code, the scientists deduce the amino acid sequence of the protein it encodes. Then they chemically synthesize parts of the protein and make antibody that binds to these parts for use in locating the protein both to regions within the brain and to areas within individual cells.

The first messenger RNA so analyzed was located in large nerve cells throughout the brain. Its distribution within the cells suggests a role in synthesis or transport of material in the receiving branches (the dendrites) of nerve cells.

Another of the first group of brain-specific genes to be analyzed appears likely to be a signal chemical. Bloom and Robert J. Milner (also at the Salk Institute) and J. Gregor Sutcliffe and Thomas M. Shinnick of Scripps Clinic in La Jolla, Calif., report that this messenger RNA encodes a chain of more than 300 amino acids that is probably processed in brain cells to form shorter chains, called peptides. The scientists synthesized the three peptides anticipated, and made a set of 8 to 10 an-