Biology

A cellular light show

The cells in L. Stephen Frawley's laboratory sparkle with pinpoints of light. These brief flashes take place inside a cell when an enzyme called luciferase encounters the compound known as luciferin. What's important about this light show is that the production of luciferase by the cell has been tied to the activity of another gene in the cell. The twinkling of each cell thus provides Frawley and his colleagues at the Medical University of South Carolina in Charleston with a way to see when a particular gene becomes active.

Frawley's group lights up a cell by using a fine needle to inject into it a large number of luciferase plasmids, circular loops of DNA that contain the gene encoding the enzyme. In addition to the luciferase gene, these plasmids include the same DNA sequence that serves as a switch for the gene for prolactin, a hormone secreted by the pituitary cells with which the researchers work. As result, when a cell turns on its prolactin gene, it also flips on the gene that encodes luciferase. Once they add luciferin to these cells, investigators can follow the activity of the prolactin gene by using a sensitive light-gathering camera to record every glimmer.

Jeremy M. Tavare of the University of Bristol in England and his colleagues reported in the August 1995 CURRENT BIOLOGY that injected luciferase plasmids enabled them to monitor gene activity in single living cells taken from a hamster cell line. Yet cell lines, collections of cells maintained indefinitely in test tubes, often differ from cells freshly obtained from an organism. Pituitary cell lines, for example, don't respond to the same cues for prolactin production that fresh cells do. Consequently, Frawley and his group have studied pituitary cells taken directly from rats.

The activity of the prolactin gene in a normal cell varies significantly over time, Frawley's group reports in the May MOLECULAR ENDOCRINOLOGY. With their system, the investigators are comparing how closely the secretion of prolactin corresponds to the activity of its gene. More important, says Frawley, his group's results establish that microinjection of luciferase plasmids can help investigators follow the activity of almost any gene in a single, normal cell for hours or even days. "One can monitor, dynamically, what goes on in normal cells. The only limit is your imagination," says Frawley.

The gene that keeps plants off Geritol

When plants in poor soil get low on iron, a protein in the roots of many species helps them take in oxidized iron compounds that are normally unusable.

David Eide of the University of Minnesota School of Medicine in Duluth and his colleagues report that they have now found the gene that encodes this iron-transporting protein.

They hope to use the gene, *iron-regulated transporter 1* (*IRT1*), to create plants that take up lots of iron and thus serve as a source of iron-rich food. *IRT1* may also promote the uptake of cadmium. If so, researchers could engineer plants that help remove this pollutant from contaminated soil.

Eide and his colleagues inserted DNA fragments from *Arabidopsis thaliana*, a weed that manages well in poor soil, into yeast cells, they report in the May 28 PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES. Each fragment contained a single gene. They then grew the yeast in an iron-poor medium, where it would normally die. However, some yeast survived—those that absorbed iron more efficiently because they had received an *IRT1* gene, the team concludes.

IRT1 resembles genes involved in zinc transport in other types of yeast. Nematodes, rice, and people have similar-looking genes of unknown function. Eide suspects that *IRT1* may be part of a new family of genes that encode metal-transporting proteins.

Paleontology

Richard Monastersky reports from Washington, D.C., at the Sixth North American Paleontological Convention

Ancient whales: Thirsty at sea

Water, water, everywhere but what's a whale to drink? That's the question J.G.M. Thewissen posed while studying the earliest chapter in the story of cetaceans.

Although modern whales can ingest seawater, they evolved from four-legged land mammals that needed freshwater to survive. Indeed, the first whales must have lived in freshwater—their fossils are found in deposits from ancient rivers and lakes in Pakistan. Thewissen, a paleontologist at Northeastern Ohio Universities College of Medicine in Rootstown, and his colleagues wondered when whales developed the ability to drink saltwater.

To answer the question, they turned their attention to teeth. As mammals grow, oxygen atoms in the tooth enamel record information about the type of water the animal drinks. Oxygen typically comes in two isotopes, and saltwater contains a significantly higher ratio of heavy oxygen than freshwater does.

The researchers measured the isotopic ratio of oxygen in four ancient whale fossils. The three oldest species showed isotopic signatures similar to those of modern river dolphins, which drink freshwater. The fourth fossil whale, called *Indocetus*, had a greater proportion of heavy oxygen, like modern whales.

Indocetus lived around 48 million years ago, only 4 million years after the earliest known whales. Within that geologically short period, whales must have evolved the specialized kidneys that enable them to drink saltwater, the researchers conclude in the May 30 NATURE.

"The exciting thing is that this tells you when whales became independent from freshwater," says Thewissen. The earliest whales could not have strayed far from coastlines because they had to return to a river to drink, as manatees do today. One of the fossil whales, *Ambulocetus,* apparently led such a lifestyle: Its bones come from saltwater deposits, but its teeth show a freshwater isotopic signature.

Once whales could survive on seawater, though, they could migrate across oceans and spread around the world, says Thewissen. The fossil record supports this theory. Whales had reached several other continents by the time of *Indocetus*.

Telling time 400 million years ago

By refining a common geologic technique, two Texas scientists have developed a kind of magnetic stopwatch for measuring time far back in Earth's history.

The technique hinges on a rock's "magnetic susceptibility"—its propensity for becoming magnetized when placed in a magnetic field. Rocks rich in iron have a high susceptibility.

Paleontologist Rex E. Crick and geophysicist Brooks B. Ellwood of the University of Texas at Arlington measured the magnetic susceptibility of marine rocks, which contain iron-rich sediments shed by the continents as well as the iron-poor shells of ocean creatures. By measuring variations in the rocks' susceptibility, they could track changes in the amount of sediment eroding from the continents, which reflect fluctuations in rainfall and temperature. Scientists believe that cyclical wiggles and wobbles in Earth's orbit drive these climate changes.

Crick and Ellwood improved on existing techniques by developing an instrument and protocol that together make possible highly sensitive measurements of susceptibility, they say. By matching the rise and fall of susceptibility to Earth's orbital cycles of known duration, they can deduce how long it took individual sedimentary layers to form. This technique gives them a way to time the appearance and disappearance of the fossils in each layer with a resolution of 10,000 or 20,000 years, a veritable blink in geologic time.

With this tool, they can study rates of evolution hundreds of millions of years ago as well as match events around the world. This ability will help resolve questions of how quickly extinctions spread, Crick and Ellwood say.