Research Highlights

Embryology

Deciphering the Complexity of Cellular, Developmental, and Genetic Biology

A Cellular Sidekick

A tiny sphere, lodged in the nucleus of many cells in plants and animals, houses a dizzying array of proteins and ribonucleic acids (RNAs). It may be involved in assembling and modifying the RNAs used during splicing—a step in the process by which information is copied from the DNA that makes up the genetic code onto RNA. But *exactly* what goes on in this sphere has eluded scientists for over 100 years. Variations of this so-called Cajal body, named by Joe Gall in 1999 after its discoverer, have been found in mammals, amphibians, insects, plants, and yeast. And Gall's lab is at the forefront of unraveling its mysteries.

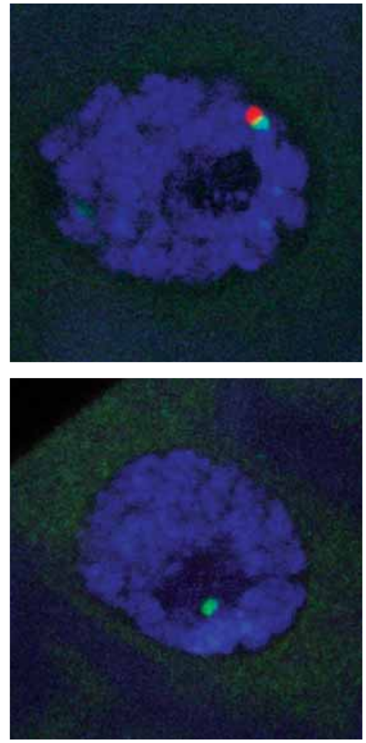
Cajal bodies in a cell's nucleus vary in number from one or a few up to 100 and can range free in the nucleus or be attached at specific locations on chromosomes. Some are associated with histone genes—histones are proteins that make up chromosomes and the structure around which DNA winds. A protein called coilin is also an important molecular player in the Cajal body. When it is made fluorescent, the protein coilin is the major marker for finding these elusive spheres.

Gall, with former Carnegie postdoctoral fellow Ji-Long Liu and colleagues, recently made some important discoveries in the fruit fly. Although coilin was not at the time known for *Drosophila*, the researchers used another marker associated with Cajal bodies in vertebrates. They were surprised to find the material in a different organelle near the Cajal body at the histone gene location. They named the new feature the histone locus body. The two bodies are often close to each other, suggesting that the Cajal body and the histone locus body carry out related functions. They also discovered, surprisingly, that *Drosophila* coilin sometimes resides in the histone locus body. This further supports a connection between the two structures, but also shows that coilin cannot be relied on to find Cajal bodies exclusively.

In a more recent study, Gall, Liu, graduate student Zehra Nizami, and visiting scientist Svetlana Deryusheva were able to identify the *coil* gene and determine the distribution of its coilin protein in *Drosophila*. They looked at a variety of tissue types and analyzed two *coil* mutants that could not produce the protein. They found that without the protein, the Cajal body was missing. But unexpectedly, the fruit flies seemed to be normal, which raises new questions about the tiny sphere. It may make RNA production more efficient or help store its components when they are in excess, but neither function may be absolutely essential.

The Mark of Zorro

Embryology's Jeff Han and colleagues are working to solve a mystery of human genetics—with the help of Zorro. To be precise, they have enlisted Zorro3, a transposon found in some yeast cells. A transposon is a sequence of DNA that jumps around the genome and is responsible for genetic change. Zorro3 is a type of transposon known as



These images show the Cajal body (red) and the histone locus body (green) in a normal fruit fly cell (top) and a mutant cell (bottom) that cannot produce the coilin protein. Without coilin, Cajal bodies are absent, but the histone locus bodies appear in both types of cells.

Image courtesy Molecular Biology of the Cell

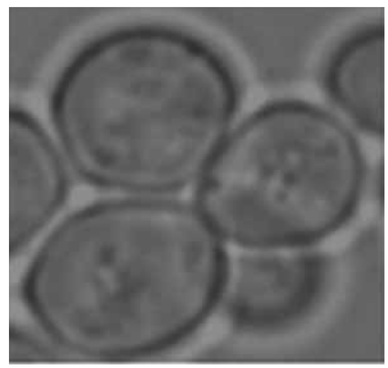
Embryology's Joe Gall (left) and predoctoral fellow Zehra Nizami pose in the lab. Ji-Long Liu identified the elusive *coil* gene in the fruit fly *Drosophila*. He found that without it, the coilin protein cannot be produced, and Cajal bodies are absent.

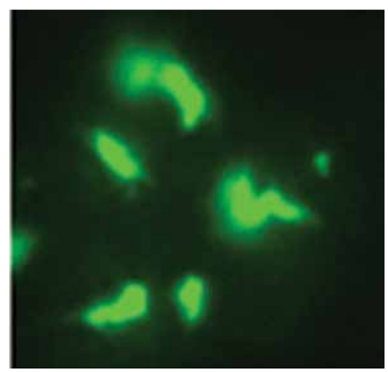
a LINE, or "long interspersed nuclear element." LINEs are spectacularly abundant in the human genome. About 75% of human genes contain at least one LINE insertion, and LINEs have been linked to health issues, particularly sterility. But despite their abundance, LINEs are poorly understood. How do they replicate themselves? Do they benefit their hosts, or are they just hugely successful genomic parasites?

Research on LINEs has been hampered by the lack of a good model organism for studying them. One possibility is ordinary baker's yeast (*Saccharomyces cerevisiae*), a laboratory staple that has long been a proving ground for new technologies in molecular biology. Its chromosomes are easily manipulated, with its relatively manageable genome. Unfortunately, *S. cerevisiae* happens to lack LINEs.

Han and his colleagues found a way around the problem. A distantly related yeast, *Candida albicans*, does host a LINE—namely, Zorro3. All the researchers had to do was snip Zorro3 from one yeast species and insert it into the genome of the other. It turns out, however, that *C. albicans* is a genetic oddball, using a slightly different genetic code from the universal code shared by nearly all other

Embryology, *Continued*





(Above) Research scientist Chun Dong was lead author on the *Genetics* paper reporting the transplant of Zorro3 to baker's yeast.

(Right) A modified version of the LINE-1 transposon Zorro3 was inserted into the genome of yeast cells (top). The green bodies (bottom) represent expressed Zorro3 proteins and can be used to track transposon particles in the experimental cells. The newly developed yeast model will be a powerful tool for studying LINE-1 transposons, which are extremely abundant in humans.

Images courtesy Jeffrey Han

organisms. As a result, the researchers had to reengineer Zorro3 to convert its code to the conventional code used by *S. cerevisiae*. There was another hitch as well. Because *S. cerevisiae* lacks LINEs, the researchers could not be sure that the new host cells contained factors Zorro3 needed to replicate itself. Han's team reasoned that because several closely related species host LINEs, perhaps an evolutionary ancestor of *S. cerevisiae* also hosted LINEs. If so, the associated machinery might still be present in the cells.

Their hunch turned out to be correct. The experimental Zorro3 elements transferred to *S. cerevisiae* performed admirably, even showing characteristics similar to human LINEs. With this new model system in hand, researchers can now begin to crack the secrets of these widespread but mysterious genetic elements. □

Geophysical Laboratory

Probing Planetary Interiors, Origins, and Extreme States of Matter

Getting to the Core

No one can sample the Earth's deep mantle or core, so how do scientists know what's there? Seismic surveys tell them about the elasticity and density of deep rocks and materials, while meteorites shed light on their chemical composition. However, a lot remains unknown. Now, the Geophysical Laboratory's newest staff member, Anat Shahar, is pioneering a field that blends isotope geochemistry with high-pressure experiments to examine planetary cores and the Solar System's formation.

Rocks and meteorites consist of isotopes—atoms made up of the same number of protons but different numbers of neutrons—which contain chemical fingerprints of long-gone eras. The lighter isotopes, with fewer neutrons, partially separate from heavier isotopes in a process called fractionation. The different ratios of these isotopes can reveal the physical and chemical changes these materials have undergone.

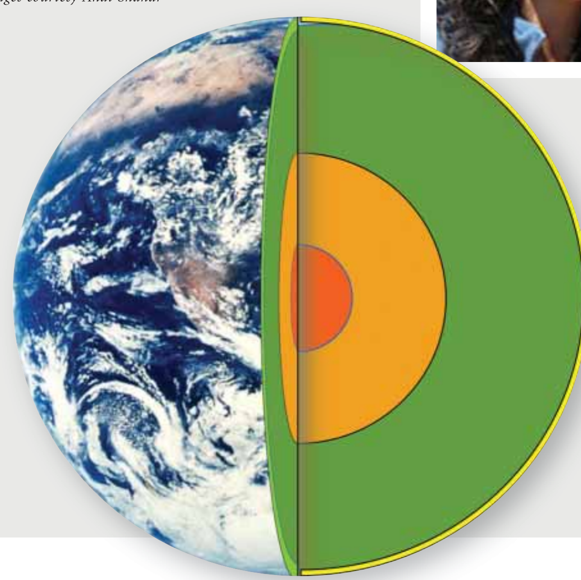
Comparing seismic measurements and information on materials, researchers know that Earth's outer core is not pure iron and nickel; something lighter is there. One candidate is silicon, the most abundant element in the crust. Shahar and her colleagues have found a way to test the silicon hypothesis. They developed lab techniques to define how isotopes of silicon and iron separate between metals characteristic of the core and silicate of the mantle under Earth-forming high pressures and temperatures. These results are compared with isotopes found in rocks on Earth and the most primitive meteorites called chondrites. Chondrites contain tiny grains of dust from the period when the Solar System began to coalesce.

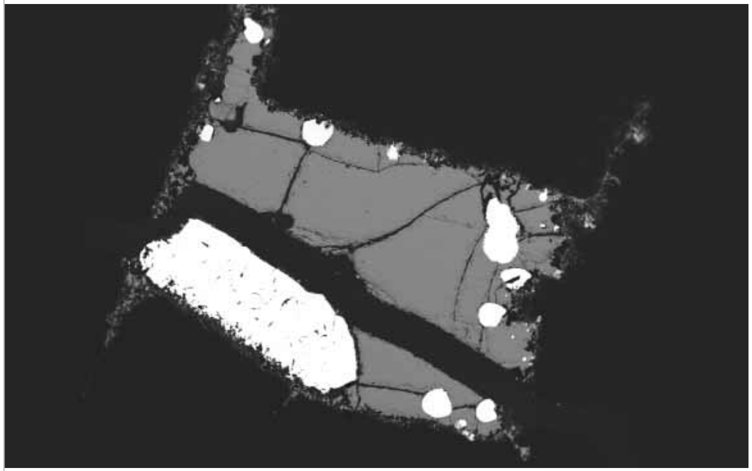
Shahar and team developed their new techniques based on a method called three-isotope exchange—where an isotope is spiked on one of two reactants. They are the first to use it under high temperatures and pressures to

(Right) The Geophysical Laboratory's newest staff scientist is Anat Shahar.

(Below) This cutaway of the Earth shows the top crust (yellow), mantle (green), outer core (light orange), and inner core (dark orange).

Images courtesy Anat Shahar





This image shows the results of an experiment from the piston cylinder apparatus that represents what goes on inside a planet. The brighter spots are metal with silicon dissolved in it to represent the core. The grayish part is silicate melt, which represents the mantle. The experiment was done at high pressure and temperature and then quenched to ambient conditions. The result freezes what was happening at those conditions.

Image courtesy Anat Shahar

investigate silicate and iron melt interactions. If some silicon sank to the core during the Earth's formation, the amount might be deduced from the differences in silicon-30 and silicon-28 between Earth rocks and meteorites. The scientists tested the hypothesis by examining separation values in the lab for proxy materials. They looked at silicon separation between silicate (mantle material) and iron-rich metals representative of the core under pressures of 9,900 times sea-level pressure and temperatures of 3270°F, and determined reference values. When combined with previous measurements of Earth rocks and meteorites, they found that the core could contain as much as 6% silicon by weight. They also demonstrated a powerful new research tool.

Tracing the Sources of Oddball Meteorites

When a meteorite found in Antarctica turned out to be unusually rich in oligoclase, a feldspar mineral, researchers explained it as a partial melt from a parent body that, unlike young Earth, never melted globally and failed to separate a metal core. But which body? Nothing comparable could be found in museum collections. And when the meteorite Almahata Sitta was spotted in space on a collision course with Earth, it prompted a worldwide astronomical alert. But after it was finally collected in the Nubian Desert and studied, researchers were not sure just what it was. It was too porous, too carbon rich, too heterogeneous in its magnesium/iron ratio to fit precisely into existing classification schemes.

In cases like these, puzzled meteorite researchers turn to oxygen isotope analyses. For both meteorites, Geophysical Laboratory geochemist Douglas Rumble was called on to analyze milligram samples for $^{17}O/^{16}O$ and $^{18}O/^{16}O$ isotope ratios. Rumble compared the meteorites' ratios with those of three potential sources: Moon, Mars, and a family of meteorites known as brachinites. These planetary bodies, heated by the decay of radioactive elements, equilibrated their oxygen isotopes through melting, mixing, and crystallization. On a graph their isotope ratios define parallel linear trends, termed mass-fractionation lines, with slopes of 0.52. A meteorite's ratios will usually fall on one of these mass-fractionation lines, identifying its source.

The ratios of the Antarctic meteorite matched the brachinite analyses, despite a distinct mineralogy that resembles that of Andean volcanoes instead of the mantle-like mineralogy of known brachinites. The meteorite likely derived from the brachinite parent body

(Above) Smoky trails in the sky above Sudan were captured by a cell phone camera after the Almahata Sitta exploded before impact.

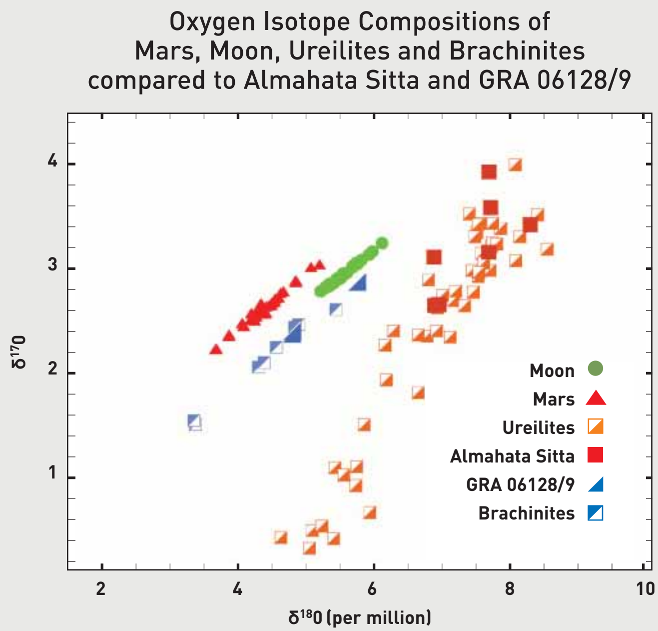
Image courtesy Mohamed Elhassan Abdelatif Mahir, Muawia H. Shaddad, and Peter Jenniskens

(Right) The Geophysical Laboratory's Douglas Rumble performed oxygen isotope analyses on the meteorite samples.

by a partial melting process that enriched it in feldspar.

Almahata Sitta shares the compositional range of a class of meteorites called ureilites, which scatter widely on the isotope plot with an overall slope of approximately 1.0. This trend unambiguously distinguishes ureilites from all other planetary bodies. Unlike Earth, Moon, or Mars, the ureilite parent body scarcely melted at all and so failed to equilibrate on a mass-fractionation line.

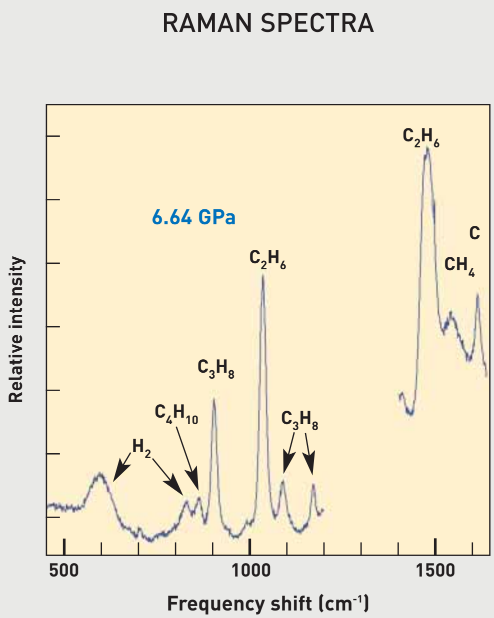
Rumble's work on these meteorites illustrates how subtle differences among the isotope ratios reveal the extraordinary variety of distant planetary bodies during their formation, and emphasizes the uniqueness of our own hospitable planet.

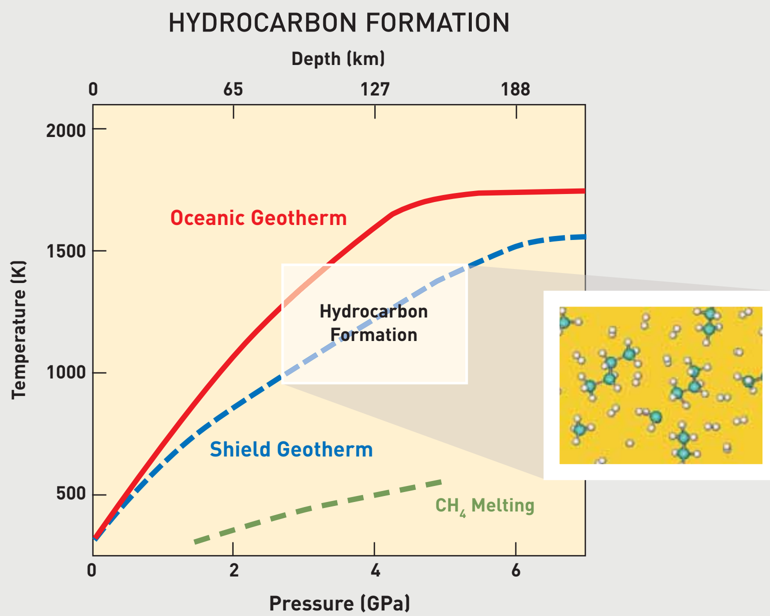


(A plot of $^{17}O/^{16}O$ and $^{18}O/^{16}O$ isotope ratios reveals a meteorite's source. Ratios of the Moon, Mars, and a family of meteorites known as brachinites define parallel linear trends, termed mass-fractionation lines, with slopes of 0.52. Despite its distinct mineralogy, the Antarctic meteorite GRA 06128/9 matched the brachinite analyses, and likely derived from the brachinite parent body by a partial melting process that enriched it in feldspar. Almahata Sitta shares the compositional range of a class of meteorites called ureilites. Unlike other source bodies, the ureilite body never equilibrated on a mass-fractionation line, so the points scatter widely on the plot.

Images courtesy Douglas Rumble

Geophysical Laboratory, *Continued*





Could deep carbon provide a source of hydrocarbons? Experiments by GL scientists have shown that under mantle pressures and temperatures, methane can disassociate and recombine to form heavier hydrocarbons. The image above left shows Raman spectra of the reaction products quenched after heating. The image above right depicts pressure–temperature range corresponding to hydrocarbon formation in laser-heating experiments compared with the model oceanic and shield geotherms and the methane melting line. The inset is an artisitc representation of dissociation products. Hydrocarbons forming in the upper mantle could be transported along deep faults to shallower depths in the Earth's crust. *Images courtesy Alexander Goncharov*

New Frontiers for Energy, Carbon Research

Carnegie has a long tradition of fostering transformational discoveries in fields spanning different disciplines. This year the Geophysical Laboratory capitalized on its legacy of research on materials under extreme pressures and temperatures to embark on two new interdisciplinary research ventures.

The U.S. Department of Energy selected the lab to host one of 46 Energy Frontier Research Centers, providing a five-year, $15 million award for the Energy Frontier Research in Extreme Environments Center (EFree). EFree will be directed by Ho-kwang (Dave) Mao and GL director Russell Hemley.

EFree brings together an unprecedented alliance of 35 key scientists from Carnegie, national labs, and universities for this research. The creation of EFree will allow GL

To mimic the high-pressure conditions of the deep Earth, scientists squeeze samples in a diamond anvil cell between two single-crystal diamonds, such as these diamonds fabricated at the Geophysical Laboratory by chemical vapor deposition. *Image courtesy Yufei Meng*

scientists to expand their fundamental studies of materials under extreme conditions while at the same time focusing research on scientific problems relevant to major energy challenges facing the world. EFree researchers will use high pressures and temperatures to create novel materials, including new classes of superconductors, superhard materials, high-energy density and hydrogen storage materials, and new ferroelectrics and magnetic systems—all of which have important applications for new energy technologies.

The Alfred P. Sloan Foundation has awarded Carnegie a $4 million grant over three years to initiate the Deep Carbon Observatory—an international, decade-long project to investigate the nature of carbon in Earth's deep interior. With GL's Robert Hazen as principal investigator, the observatory will coordinate the efforts of hundreds of researchers from more than two dozen countries.

The observatory's multidisciplinary research will focus on Earth's poorly understood deep carbon cycle and the possible influence this cycle may have on critical societal concerns related to energy, environment, and climate. Among the basic unanswered questions to be addressed by observatory scientists are the quantity and nature of carbon stored within the deep Earth and the fluxes between reservoirs, as well as the question of deep, abiotic hydrocarbons—those not derived from living cells—and the extent of deep microbial ecosystems, which by some estimates rival the total surface biomass.

Taken together, these two ambitious research initiatives will launch materials and Earth science in new directions, and put Carnegie at the center of two exciting new multidisciplinary fields. □

The DOE-funded EFree Center held its first workshop on September 11. More than 40 scientists attended. The partners discussed resources at their facilities and future collaborations. *Image courtesy Susana Mysen*

Global Ecology

Linking Ecosystem Processes with Large-scale Impacts

Can California Wine Take the Heat?

California wine accounts for over 90% of U.S. wine production and is the country's most valuable fruit crop. But wine production, like much of agriculture, is threatened by global climate change. Not only are rising temperatures likely to reduce grape harvests, but the quality of wine grapes is famously sensitive to climate. On the other hand, grape cultivation is a highly managed agricultural practice, often operating at a high profit margin, so grape growers may have more resources for adapting to climate change than other types of farmers. So what are the prospects for California wine in the face of global warming?

Kimberly Nicholas Cahill was a graduate student in Chris Field's lab and is now at the University of California-Davis. She combined research on the chemistry of Pinot Noir grapes with extensive interviews with winegrowers in the North Coast wine country to assess both the vulnerability of wine quality to climate change and the potential for winegrowers to adapt to change.

In her field study, Cahill found that, depending on the season, warm temperatures could either increase or decrease the concentration of the phenolic compounds that affect wine quality. Unfortunately, climate models project that California will suffer greater warming during the summer, while the grapes are ripening. Excess heat at that time hurts wine quality.

To adapt to impending climate change, winegrowers have both long- and short-term strategies available. To deal with rising heat in the short term, they can cool plants through irrigation or shading. Longer-term strategies

[Above] Vineyards have been part of the California for more than two centuries, but climate change in the upcoming century threatens both the quantity and quality of California wine.

[Right] Kimberly Nicholas Cahill was a graduate student in Chris Field's lab.

Image courtesy Chris Field

include growing new, heat-resistant varieties of grapes, or even relocating vineyards to cooler areas. The strategies all have their limitations, however. New, unfamiliar grape varieties may not be accepted by consumers. Relocating a vineyard is not only expensive, but also impractical for premium wines closely linked with the *goût de terroir*—taste of the earth—of their areas of cultivation.

Wine vineyards have been part of the California landscape for more than two centuries. How will they fare in the coming century? Overall, Cahill sees a fairly high capacity for adaptation, but adaptation can only do so much. To keep the wine flowing, we need to cut back on the carbon dioxide emissions that are driving climate change.

A Tropical Revolution

The Greg Asner lab's Spectranomics Project came out of the starting gate at lightning speed this year. It is the first-ever aerial biodiversity mapping system, and it promises to revolutionize monitoring, conservation, and management of critical tropical forests. Despite the logistical, environmental, and bureaucratic challenges of working at 60 remote sites in eight rain forest nations, the group collected more than 3,000 canopy plant species its first year. Its project goal is 10,000 species. Until now, there has been no database linking taxonomic, chemical, and spectral properties of canopy plants. The new system will allow aerially obtained spectral signatures to be compared with the database and thereby to map various species' characteristics—critical information for understanding how human use and climate change affect biodiversity.

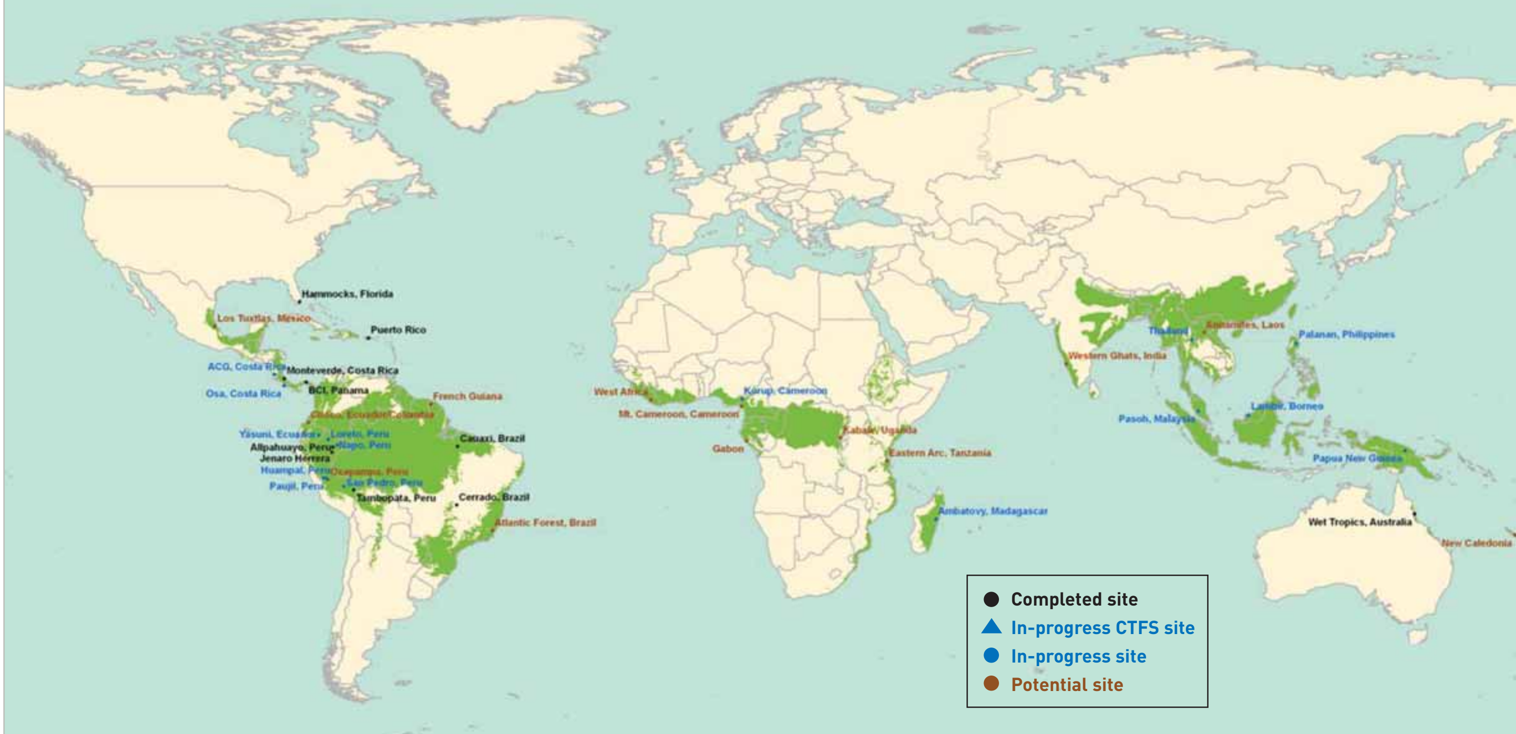
Analyzing wavelengths of reflected light—spectra—from plants yields species-specific chemical signatures. The team uses the fixed-wing Carnegie Airborne Observatory

Collecting samples from the treetops requires a variety of innovative approaches, including shooting them down. This shooter gets instructions from Smithsonian collaborator Joe Wright.

Image courtesy Asner lab

Global Ecology, *Continued*

SPECTRANOMICS COLLECTION SITES



The Asner team has a global network of botanical sites along three major axes of species variation. Current and planned research areas spotlight biodiversity hotspots in the Pacific islands, Australasia, Amazonia, Africa/Madagascar, Indonesia, and Central America. Sites are indicated on the map. *Image courtesy Asner lab*

(CAO) to inventory rain forest vegetation over nearly 40,000 acres per day. But it has lacked a library for interpreting new signatures and linking sensor data to species spectra. In phase one of the project, it is developing the database for this spectral comparison.

Many processes, scores of people, and collaborating organizations are involved worldwide. The group has developed an array of new protocols and specialized equipment. It obtains permits from foreign governments, surveys and identifies species, collects on-ground leaf spectra and samples, and then prepares and archives the specimens for shipment and high-volume analysis at Global Ecology.

In addition to its globe-trotting surveys, the team is

Once the team collects samples, it catalogs and processes them on-site.
Image courtesy Asner lab

developing computer algorithms to extract taxonomic information from the spectra. It has also created a Web portal so that anyone will be able to view, search, and organize species data by geography, chemistry, botany, and spectra.

Asner has already embarked on phase two of the project—developing a sensor called the Airborne Taxonomic Mapping System (AToMS). It will be one of the most advanced remote sensing systems ever built, far exceeding the capabilities of both the original CAO and current space-based sensors. It will fly on fixed-wing aircraft. Carnegie and the Smithsonian Tropical Research Institute (STRI) have agreed that, for operations in the New World tropics, AToMS will be based at the STRI hangar in Panama, providing complete access to the Caribbean and to Central and South America. For more see http://spectranomics.ciw.edu/. □

Observatories

Investigating the Birth, Structure, and Fate of the Universe

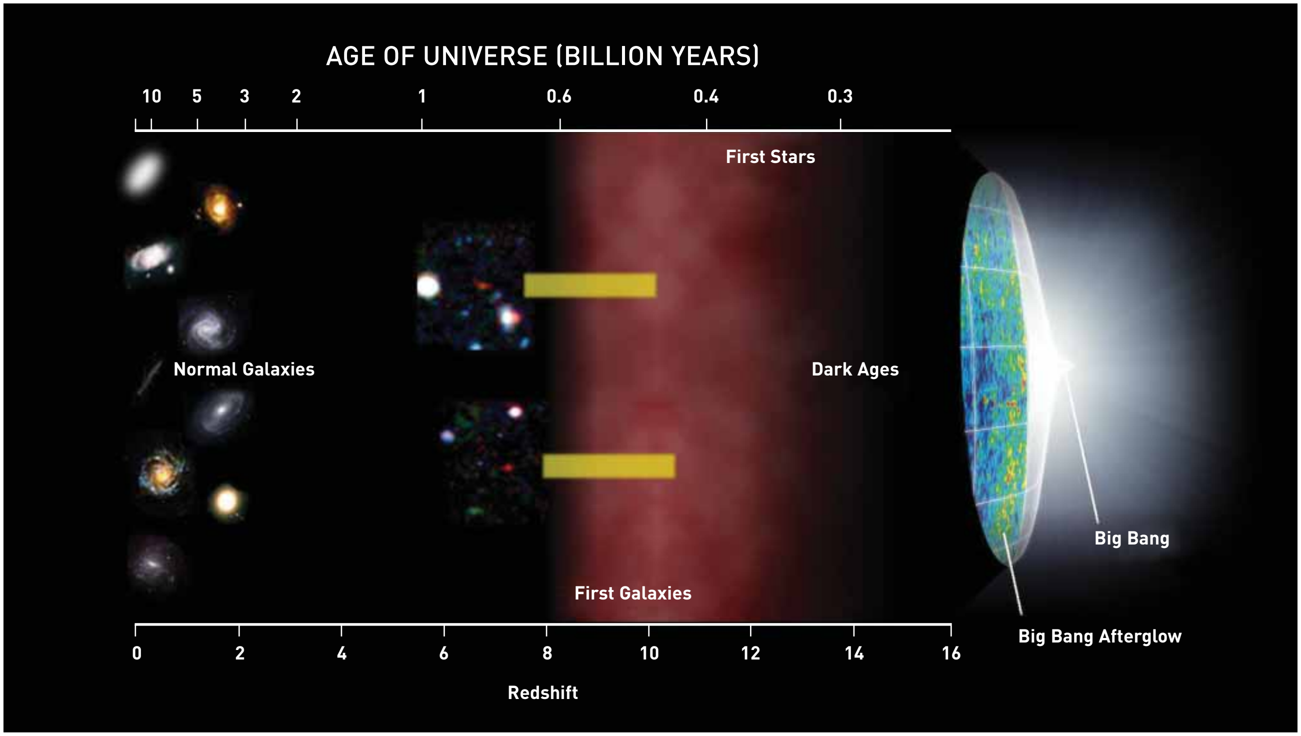
Turn On the Lights—the Party's Starting

The Big Bang created a hot, murky universe 13.7 billion years ago. About 300,000 years later, temperatures cooled, electrons and protons joined to form hydrogen, and the universe cleared. Some 200 million to 1 billion years after the Big Bang, neutral hydrogen began to form quasars, stars, and the first galaxies. The resulting intense energy reionized the gases, again making the universe partially opaque. Astronomers call this era the reionization epoch. Technology allows astronomers to observe to about 1 billion years post–Big Bang after the end of the reionizaton epoch.

Using new instrumentation and techniques, Alan Dressler, Patrick McCarthy, and colleagues Crystal Martin (U.C. Santa Barbara) and Marcin Sawicki (Saint Mary's University) are exploring this epoch. They are testing the theory that hot, young stars in the first galaxies provided the energetic light that reionized the gaseous intergalactic medium. This study will provide important information about the first galaxies and their effect on the gas that started the evolution from a simple universe to a staggeringly complex one.

Scientists look for signatures of hydrogen from this era called Lyman-alpha emission, which is light from hydrogen transitioning from its first excited state to its lowest state. In 2008 Dressler, McCarthy, and team reported on three Lyman-alpha sources from a billion years after the Big Bang using new multislit spectroscopy combined with a narrowband filter of the Inamori Magellan Areal Camera and Spectrograph (IMACS) on the Baade telescope at Carnegie's Las Campanas Observatory in Chile. They used a "venetian blind" mask to search the sky, and the spectrograph to disperse light over a narrow band of the infrared spectrum. This combination increased the contrast of very faint sources, allowing them to probe an order of magnitude more deeply than ever before.

The first three Lyman-alpha sources confirmed that the relatively bright sources could not have supplied enough energy for reionization. More importantly, it demonstrated that narrowband spectroscopy can discover extraordinarily faint sources. Ian Thompson and Greg Burley thus built a much more sensitive CCD camera that enabled the IMACS team to improve image quality significantly. During the course of a new search begun in April 2008, the team found more than a hundred Lyman-alpha candidates. They eliminated about half as interloping foreground objects, leaving 30 to 50 likely emitters. The large number of objects, some five to 10 times fainter than the original three, could provide the energetic photons needed to ionize the intergalactic gas. The data imply that such faint galaxies began ionization a half a billion years earlier than predicted. But detailed studies await exploration by facilities such as the Giant Magellan Telescope.

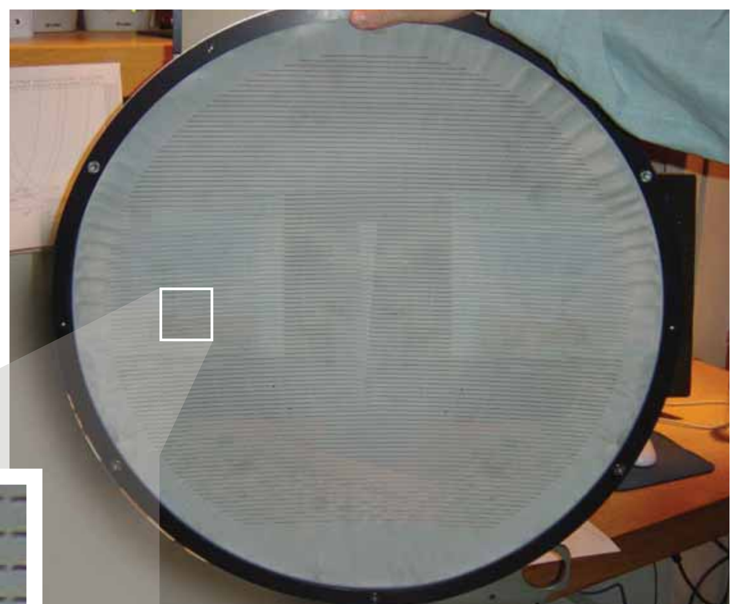


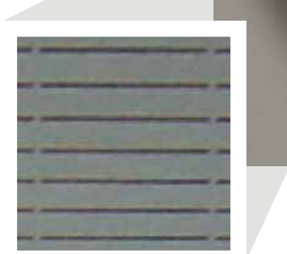
(Above) This diagram shows a simplified evolution of the universe.

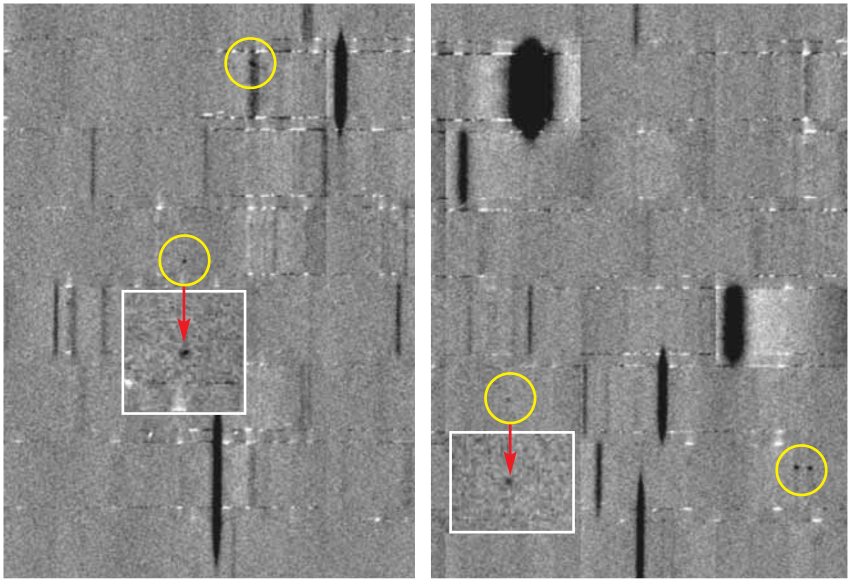
Image courtesy Ivo Labbé

(Right) This "venetian blind" mask is used for multislit spectroscopy, which the team combined with a narrowband filter of the Inamori Magellan Areal Camera and Spectrograph on the Baade telescope. The mask has about 100 parallel slits and looks like a venetian blind. The multiple slits allow light from different objects in the field of view to pass into the spectrograph. This instrumentation allows the astronomers to search the sky for very faint sources and probe an order of magnitude more deeply than before.

Image courtesy Alan Dressler







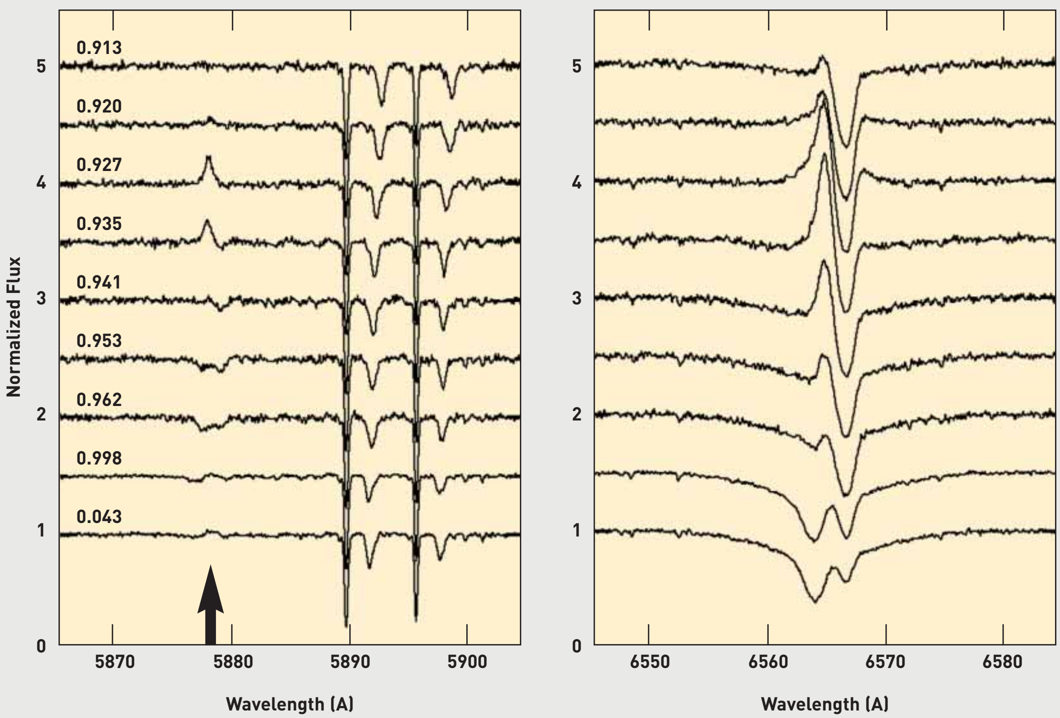
The red arrows on these images from the new instrumentation indicate two of the Lyman-alpha candidates. The objects in the circles show foreground emission objects.
Image courtesy Alan Dressler

Fleeting Glimpses of Glowing Helium

Twice a day, more or less, the tenuous outer atmospheres of giant, pulsating RR Lyrae stars are propelled outward by shock waves generated in their interiors. The outer layers cool as they expand and then fall back, to be met by the next shock. And so it goes. All the oldest stars in our galaxy become RR Lyrae stars late in their lives, pulsating rhythmically for about one percent of their lifetimes (some 100 million years) before going to the white-dwarf graveyard. Understanding the behavior of these stars is important because they are used as "standard candles" to measure distances in the universe. Previously, only hydrogen emission had been observed during these shock events. George Preston, director emeritus of the Observatories, discovered that they fleetingly emit the light of helium as well, a finding that challenges existing pulsation models.

Changes in the temperature and density of RR Lyrae stars are ascertained minute by minute by measuring the brightness and motion of the surface layers as shocks pass through them. Four years ago George Preston began to look at shocks in 10 stars, using a spectrometer at the du Pont telescope. Last March, while observing the shock phenomenon in one of the stars, he noticed a small excess of light in the yellow region of the spectrum and quickly realized that it was being produced by glowing helium, the second lightest and second most abundant element. Then, to his astonishment, the emission peak was replaced after 15 minutes by exceedingly weak absorption dips produced by helium in the infalling and outrushing gas. Preston then examined hundreds of spectra obtained during previous expeditions to Las Campanas and found dozens of examples of helium lines in the 10 stars he had been observing. He had missed the phenomenon year after year because it is so short-lived, and because he wasn't looking for it. Others had missed it as well.

Before this research, only hydrogen emission lines had been observed during these shock events. Helium is important because much higher temperatures (stronger shocks) are required to excite it. This discovery means that existing models for the pulsation behavior of these stars will have to be revised. The work also raises the hope that one day helium emission can be used to estimate helium abundances in these stars, a crucial parameter in the calculations that are undertaken to model star behavior over time. □



(Above left, top to bottom) Spectra of the RR Lyrae star RV Octantis were obtained at 7-minute intervals during a shock event in 2007. Helium emission is located in the third and fourth spectra above the vertical arrow. Proceeding down, the emission is quickly replaced by exceedingly weak absorption dips, which persist for an hour or so. (Above right) Emission at the H-alpha hydrogen line (at 6562.8 Angstrom) is much stronger than the helium emission because hydrogen is more abundant and is more easily excited in the shock. Unlike in the case of helium, a strong dip produced by infalling gas overlies the H-alpha hydrogen emission in all of the spectra—data that are grist for the theorist's mill.

(Below) Observatories Director Emeritus George Preston stands in front of the du Pont telescope at Carnegie's Las Campanas Observatory.
Image courtesy George Preston

Plant Biology

Characterizing the Genes of Plant Growth and Development

An Arms Race in Yellowstone

In Yellowstone National Park, predator and prey have engaged in an ancient duel for eons. Grizzly versus moose on the riverbank? Wolf versus elk in the snow-filled woods? In fact, this conflict is much older: virus versus bacteria in the bubbling hot springs.

The colorful microbial mats such as those in Yellowstone's famous hot springs are among the oldest ecosystems on Earth. Bacteria, archaea, and viruses create these complex layered communities, which thrive in extreme environments, such as hot springs and hypersaline lagoons. Studying them not only gives clues to the early evolution of life on Earth, but also, because the microbes evolve so rapidly, can give researchers glimpses of evolution in action.

Plant Biology's Devaki Bhaya and colleagues have uncovered an evolutionary "arms race" between photosynthetic cyanobacteria (formerly called blue-green algae) and the viruses that prey on them. The saga is revealed in the heat-loving cyanobacterium named *Synechococcus*, which contains arrays of CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats) and an associated group of genes that work together as a potent antiviral defense system.

The researchers used an approach known as metagenomics, in which genetic material from environmental samples is sequenced without the need for laborious culturing of individual microbial strains. They found that the CRISPR arrays in *Synechococcus* include a large number of unique sequences, some of which were similar to certain viral genes. Analyzing these sequences within both the cyanobacterial and viral populations suggests that the genetic content of both is changing rapidly. These results can

Members of Bhaya's team are making measurements and collecting samples from the Octopus Spring at Yellowstone National Park. The microbial mats in the hot spring are the site of an evolutionary "arms race" between cyanobacteria and viruses.

Plant Biology's Devaki Bhaya at Yellowstone National Park, winter 2008.

Images courtesy Devaki Bhaya

be viewed as a snapshot of the ongoing arms race between the attacking viruses and the defending cyanobacteria. As the virus populations mutate and evolve new genetic sequences to evade detection by the cyanobacterial defense system, the cyanobacteria need to acquire these sequences to help keep the viral attackers at bay. Intriguingly, the genes associated with CRISPR arrays encode proteins that have some similarity to those used to "silence" genes in plant and animal genomes.

Now that Bhaya's group has identified this rapid co-evolution of predator and prey in the natural environment, they plan to dig deeper to put together a comprehensive picture of an evolutionary contest that has raged for billions of years.

Confidence in Your Genes?

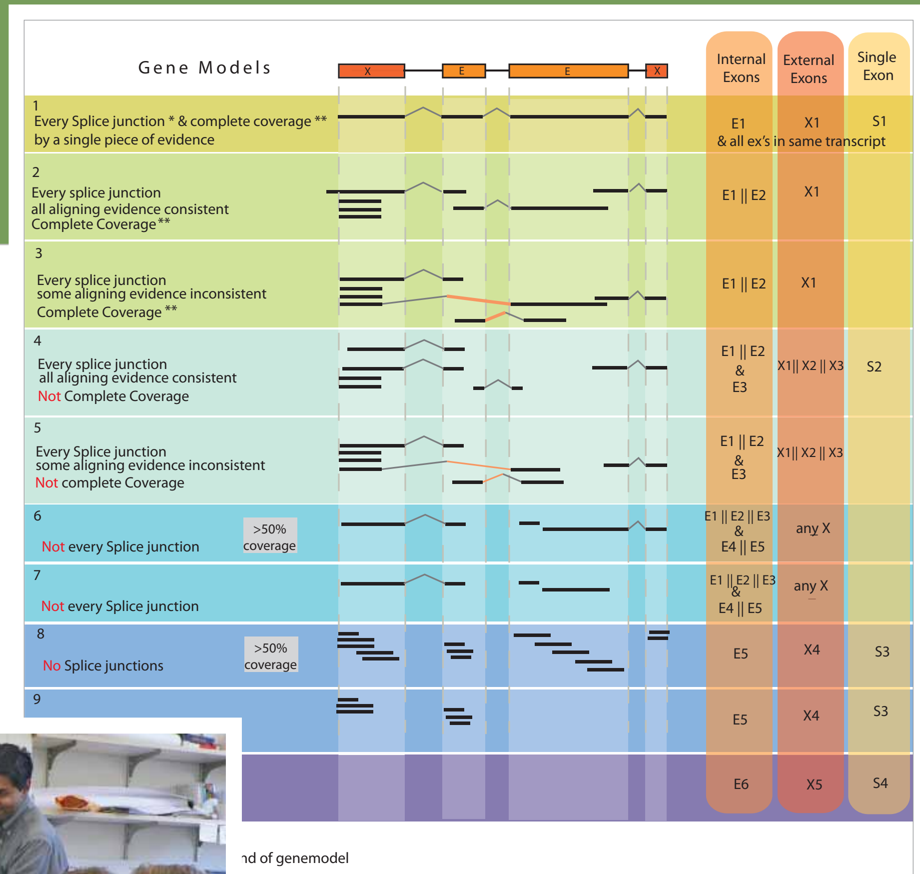
A plant the size of a golf ball has some 27 thousand protein-encoding genes, significantly more than the 20 thousand or so confirmed protein-encoding genes in humans. So what do the plant genes do? To find out, scientists use the tiny cabbage relative *Arabidopsis thaliana* to study many of the basic life processes that all plants share. Eva Huala and colleagues have been combing through the roughly 30,000 research articles about *Arabidopsis* and presenting the results in an online database called TAIR (The Arabidopsis Information Resource), http://arabidopsis.org/. TAIR, offering a large body of information on the functions carried out by many of the genes and the proteins they make, is one of the most popular biological databases in the world.

Scientists at TAIR have been working hard to keep the list of genes in the genome sequence, first published in 2000, up to date with recent discoveries. In the most current genome release, TAIR9, made public on June 19, 2009, the genome annotation team led by David Swarbreck added a confidence ranking system for each gene to reveal the experimental support for the structure of a given gene. This ranking will enable scientists working on other more recently sequenced plant genomes to know which *Arabidopsis* gene structures are reliable enough to serve as predictors of the structure of genes in other plant genomes. The TAIR9 release contains 27,379 protein-encoding genes, 926 pseudogenes (probably producing nonfunctional proteins), 3,901 genes located within transposable elements (which move around the genome), and 1,312 genes encoding various kinds of RNAs. This yields a total of 33,518 genes in all, not bad for a golf ball-sized plant.

Arabidopsis research data are important in many areas of plant biology, including crop improvement and population biology studies, as well as in basic research on plant growth and development. The TAIR Web site continues to increase in popularity with researchers around the world. On May 5, 2009, TAIR logged its 100,000,000th page view and currently averages about 35,000 different visitors to the site each month.

Eva Huala is the director of The Arabidopsis Information Resource (TAIR), one of the most widely used biological databases in the world.
Image courtesy Eva Huala

Plant Biology

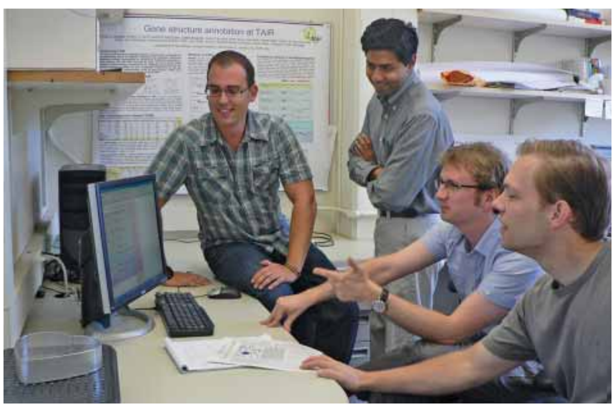


(Above) The genome annotation team's confidence ranking system (sample shown here) looks at each gene and evaluates the experimental support for its structure. The ranking reveals which *Arabidopsis* gene structures are reliable enough to serve as predictors of the gene structures in other plant genomes.

Image courtesy Eva Huala

(Below) Members of the TAIR team are viewing a confidence ranking chart. From left to right are Philippe Lamesch, Rajkumar Sasidharan, David Swarbreck, and Chris Wilks.

Image courtesy Eva Huala



Gatekeepers Get Their Due

With the explosion of information about genes and the proteins they make, it is remarkable that so little is known about how proteins interact with and within the protective membrane that surrounds a plant cell. These membrane proteins mediate acquisition of nutrients and water, secrete compounds and toxins, and, most importantly, sense aspects of their environment. They thus represent the communication interface of the cell to the outside world. They affect growth, development, and everything else. Now Sylvie Lalonde, Wolf Frommer, and a team of collaborators from UC San Diego, Penn State, and U. Maryland have attacked this information deficit head-on. As a pilot study these researchers used a high-throughput molecular screen and pinned down 900 interactions among 200 proteins out of 100,000 possible relations for the experimental plant *Arabidopsis*. They have another 3,500 genes in the pipeline to determine the complete

portfolio of interactions among membrane proteins and their partners inside the cell. Their work paves the way to a better understanding of plants and possibly to engineering them to thrive under drought or heat conditions, or otherwise to become more productive.

All of the inner workings of the cell rely on the binding of proteins. With complementary shapes, proteins dock with one another to start processes, such as telling a gene to turn on or letting in the proper nutrient. Membrane proteins make up some 20% of the proteins in *Arabidopsis*.

In the first step, the team targeted proteins that begin the communications process at the membrane to turn genes on in the nucleus. They used a screen called the mating-based protein complementation assay, or split ubiquitin system. Ubiquitin is a small protein. The scientists fused the candidate proteins onto a version of ubiquitin that is split in half. When the two candidates interact, the two halves of the ubiquitin reassemble, triggering a process that liberates a transcription factor—a protien that switches a gene on—which then goes to the nucleus. When genes are turned on in the nucleus, the researchers are alerted to the successful interaction.

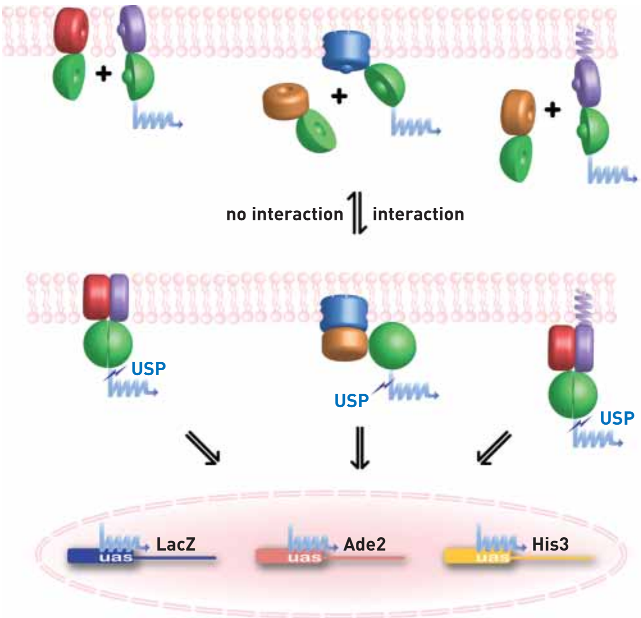
The scientists compiled a list of 8,358 candidate proteins based on information in the TAIR database, the literature, and predictive software. The ultimate goal is to test the 36 million potential interactions with a high-throughput robotics system.

This first-of-its-kind, high-throughput screen for *Arabidopsis* is just the beginning. As the library of interacting proteins grows, scientists will be able to study the details of protein interactions and how they are affected by outside forces, such as environmental changes. This project produced the first set of membrane protein interactions for any multicellular organism, and is thus relevant to crops and human medicine. □

(Above) Sam Parso and Maria Sardi are standing at the robot performing a screen.

(Below) This schematic shows what happens during three different scenarios of the screen called the mating-based protein complementation assay, or split ubiquitin system. In each case, when one protein (red or brown) interacts or docks with another (purple or blue), an ubiquitin protein is "reconstituted" (green sphere), releasing a transcription factor—a protien that switches a gene on (blue zigzag). The transcription factor then enters the nucleus of the cell (oval area), and turns genes on to alert researchers of the interaction.

Image reprinted with permission from Plant Journal 53, *610-635, 2008.*



Terrestrial Magnetism

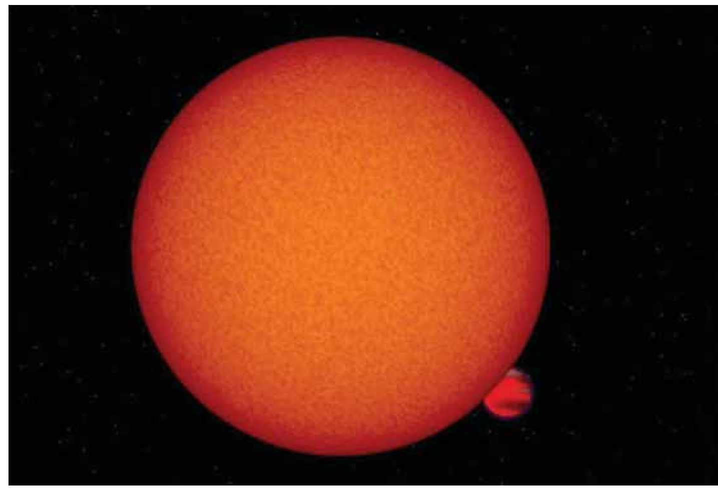
Understanding Earth, Other Planets, and Their Place in the Cosmos

A Hot Year for Exoplanets

One planet spins around its star, glowing like a kitchen burner. At over 4,400°F, OGLE-TR-56b has the hottest planetary atmosphere yet measured. Another planet, HD8606b, can be a relatively balmy 980°F, but within a few hours its eccentric orbit swings it close to its star, driving temperatures beyond 2,200°F.

Both of these extrasolar planets had their extraordinary temperatures measured by research teams that included scientists from the Department of Terrestrial Magnetism (DTM). OGLE-TR-56b is a "hot Jupiter" whose temperature was measured by Hubble Fellow Mercedes López-Morales with coauthor David Sing from Institut d'Astrophysique de Paris using over 600 images from the European Southern Observatory's Very Large Telescope and Carnegie's Magellan Baade telescope in Chile. The researchers needed the multiple images and near-ideal seeing conditions to measure accurately the change in thermal emissions when the planet was eclipsed as it went behind the star. Only about one of every 3,000 photons from the system comes from the planet. The eclipse allowed the researchers to separate the emissions of the planet from those of the star.

Along with a measurement of a different planet published simultaneously by an independent group, these were the first such measurements by ground-based instruments. Previously, all thermal emissions from extrasolar planets had been measured by NASA's Spitzer Space Telescope in Earth orbit. López-Morales notes that their ground-based temperature measurements mark an important achievement and provide a new way to continue studying exoplanet atmospheres. This is important because the work-horse Spitzer telescope has recently run out of the coolant that chills its infrared sensors, highly limiting its capabilities.

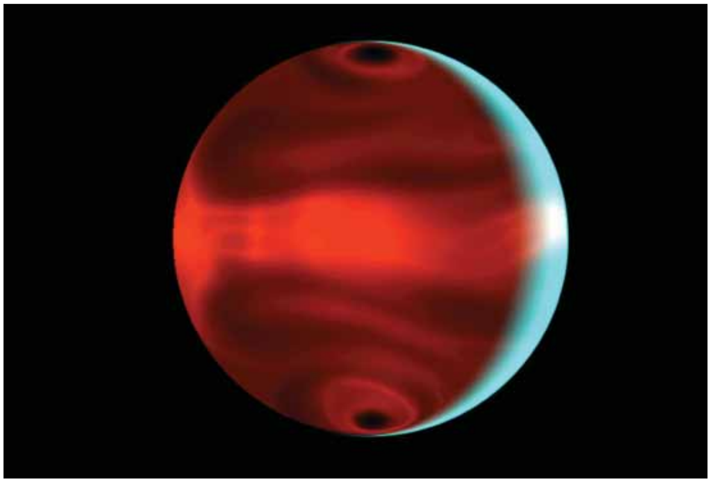


(Above) This artist's impression shows the exoplanet OGLE-TR-56b passing behind its star. At over 4400°F, the atmosphere of OGLE-TR-56b is the hottest yet observed for any exoplanet and is the first measured from ground-based instruments.

Image © D. Sing (IAP) / A&A.

(Right) Mercedes López-Morales

Image courtesy Mercedes López-Morales



(Above) The exoplanet HD8606B experiences extreme variations in temperature due to its highly eccentric orbit. This computer-generated image shows the severe weather patterns in its atmosphere during the days after its closest approach to its parent star.

Image courtesy Greg Laughlin, University of California, Santa Cruz

(Right) Paul Butler

Image courtesy Paul Butler

Paul Butler played a key role in discovering the spectacular temperature swings of HD8606b, which orbits a star 200 light-years from Earth. For this space-based study using the Spitzer Space Telescope, Butler made the precise velocity measurements of the host star, thereby enabling the planet's orbit to be calculated. As with the ground-based study, infrared observations had to be centered on the time that the planet passed behind the star, known as a secondary eclipse. The disappearance of the planet during the secondary eclipse allowed the measurements to be calibrated and the planet's temperature changes to be determined.

Both of these discoveries add to the growing store of knowledge about extrasolar planets. Butler, whose work with others has uncovered about half of the known extrasolar planets, commented, "Even after finding nearly 200 planets, the diversity and oddness of these new worlds continue to amaze and confound me."

Diamonds and Continental Geology

Diamonds form in the Earth's mantle, especially beneath the ancient, stable portions of continents called cratons. As a result, diamond prospectors have long followed Clifford's Rule: Look in the oldest parts of the craton. But DTM's Steven Shirey has found that the story is not so simple. Diamonds can have a complex history, intimately tied to the geologic evolution of continents.

Large diamonds act as inert capsules that can preserve ancient mantle minerals brought up from depths of more than 75 miles (120 kilometers) by younger volcanism. Working with visiting investigators and other colleagues over the last decade, Shirey has studied hundreds of iron sulfide inclusions in diamonds from across southern Africa. With techniques developed at DTM, he measured the ages of the inclusions using the rhenium-osmium dating system. Radioactive isotopes of rhenium decay to yield osmium at an extremely slow rate, making the system a good atomic clock to date ancient rocks and minerals. Shirey found that the inclusion age and distribution pattern document the assembly of the ancient Kaapvaal Craton by the collision of two continental blocks 2.9 billion years ago, as well as later tectonic activity at its margins extending as deep as 93 miles (150 km).

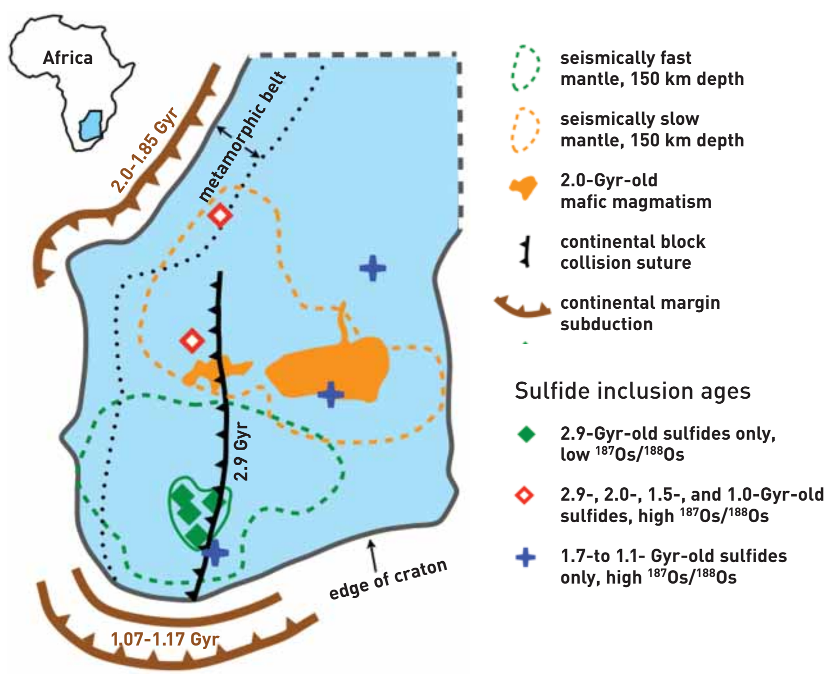
Where the two blocks came together is a fossil subduction zone that dips to the west. Shirey found that west of this zone the sulfide minerals in diamonds are most commonly 2.9 billion years old—the same age as the continental collision. East of the zone, inclusions of this age are largely missing and are younger by more than a billion years. This difference suggests a close tie between ancient subduction and diamonds: carbon-bearing fluids carried deep into or below the craton's keel by oceanic slabs percolated upward and crystallized diamonds only in that portion of the keel above the subducted slabs.

Younger diamonds were generated as the assembled craton was subjected to later subduction around its margins and to magmatism from below. These diamonds are found preferentially in areas close to past marginal subduction zones (evident today from belts of metamorphic rocks) and above areas of the mantle once invaded by magma (evident by the low velocity of seismic waves). In contrast, the 2.9-billion-year-old diamonds predominate above seismically "faster" mantle that had much less infiltration of magma. These diamond age patterns are providing the deepest new evidence yet on how continents were created and modified.

Earth's Oldest Crust

For some time, the oldest crust known on Earth was a 3.8-billion-year-old terrane in southern Greenland. In 1990, rocks from the Northwest Territories in Canada were found to be as old as 4.04 billion years. Just last year, DTM's Richard Carlson, with Ph.D. student Jonathan O'Neil, dated bedrock from northern Quebec at 4.28 billion years old, making it 250 million years older than any previously studied rocks.

These discoveries result from new geochronologic methods, similar to those pioneered at DTM in the 1950s, that allow accurate dating of rocks with long, complicated



(Above) Steven Shirey

(Right) Sketch map of the Kaapvaal-Zimbabwe Craton showing the position of key tectonic, magmatic, and mantle keel components in relation to the age and isotopic grouping of diamond inclusions. The craton's boundary is shown as a gray line (solid and dashed). The suture between its two halves is black with teeth. Relics of subduction zones around the craton's margin are shown as brown lines with teeth. Symbols show diamond mines that yielded samples for the study.

Images courtesy Steven Shirey

The point at Nuvvuagittuq, translated from Inuktitut as "point with white stripes," shows nearly 1.5 billion years of Earth history. The white rocks are 2.7 billion-year-old igneous rocks intruding older rocks, including remnants of ancient seafloor dated at 4.28 billion years by Rick Carlson and Jonathan O'Neil at DTM.
Image courtesy Rick Carlson

A film crew from the History Channel interviews DTM postdoc Jonathan O'Neil (second from right) at the field site in Nuvvuagittuq.
Image courtesy Rick Carlson

histories of heating and deformation. Carlson and O'Neil, now a postdoctoral fellow at DTM, obtained their dates by measuring minute variations in the isotopic composition of the rare Earth element neodymium in the rocks. In summer 2009 they returned to Nuvvuagittuq, as the Quebec terrane is named by the region's native Inuit, to continue exploring this small, 10-square-kilometer remnant of Earth's ancient crust.

The old Nuvvuagittuq rocks appear to represent a section of ancient seafloor, with magnesium-rich basalts similar to those found in modern oceanic crust. Some of the basalts also contain what Carlson and O'Neil interpret to be "pillow" structures that formed when hot lava cooled rapidly because of eruption under water. The terrane also includes extensive deposits of silica (now quartz) and iron oxide that likely formed as ocean water circulated through the hot rocks of newly formed oceanic crust.

Carlson and O'Neil's work on the Nuvvuagittuq rocks support conclusions from 4.36-billion-year-old mineral grains in Australia that imply that within 200 million to 300 million years of the Earth's formation its surface was already cold enough to harbor liquid water, and hence, oceans. The type of seafloor setting represented by the Nuvvuagittuq rocks today supports distinctive life forms that derive energy from chemicals in the environment, rather than from photosynthesis. Geophysical Laboratory postdoctoral fellow Dominic Papineau is among the scientists studying Nuvvuagittuq and similar sites for chemical markers of possible early life. Although definitive evidence has not yet been found, nor will it be easy to find because of the rocks' complicated metamorphic history, these ancient terranes provide new insights into Earth's earliest environments. □

First Light & The Carnegie Academy

Teaching the Art of Teaching Science

CASE Broadens Its Scope

Math for America

To help combat the disturbing international standing that American students have in science, technology, engineering, and mathematics, the Carnegie Academy for Science Education (CASE) started a new initiative in 2008. It launched a partnership with Math for America (M*f*A) and American University (AU) to create Math for America in Washington, D.C. (M*f*A DC). The goal is to improve the mathematics education of the city's public and public charter secondary school students. Bianca Abrams is the program director.

Many certified teachers in the U.S. are not trained in the specific subject they teach. Through a rigorous selection process, M*f*A DC chooses individuals with undergraduate degrees in mathematics or related disciplines to train them to become skilled mathematics teachers. Applicants must have strong undergraduate records in math and are evaluated based on undergraduate records, test scores, recommendations, personal statements, and interviews.

With stimulus funds from the American Recovery and Reinvestment Act of 2009, the National Science Foundation awarded M*f*A DC a $1.498 million grant to cover the tuition, stipend, and mentoring costs for the first 14 M*f*A Fellows. The first fellows arrived in the middle of June and finished one semester at AU, where they will spend a total of 15 months taking education and advanced math courses. They will then receive a master of arts in secondary school math teaching and be qualified for certification to teach in D.C. schools. Next summer, they will seek positions in D.C. public and charter secondary schools. In return for support, M*f*A Fellows agree to teach for four years in D.C. schools. The plan is to select and educate 34 fellows in total.

for Science Education

Biotech at Full Steam

Another 50 students graduated from McKinley Technology High School under the new D.C. Biotechnology Career Pathway Program, bringing the total of DCBiotech alumni to nearly 100. Biotechnology was also chosen by the principal of Ballou Senior High School as one of the three career-education pathways to retain as part of a redistribution of career-education options in D.C. high schools.

Ten students interned this summer at Howard University, Catholic University of America, Carnegie, and McKinley and Ballou high schools. The summer program at Ballou, cotaught by CASE codirector Julie Edmonds and CASE Teacher Fellow John Solano, was carried out in collaboration with Sarah Tishkoff's laboratory at the University of Pennsylvania. McKinley's summer program, led by coordinator of CASE programs Marlena L. Jones, employed several McKinley biotech alumni, who taught the students and shared their college experiences with them. □

(Left, top) Shown celebrating after their first semester at AU are MfA Fellows Katherine Collins, Molley Kaiyoorawongs, and Max Mikulec (left to right).

(Left, bottom) Lindsay Mann (left) and Krystn Hodge (right)

Images courtesy Bianca Abrams

McKinley students identify an unknown "infectious" microbe in a patient sample. Students work with real microbes, though not those that are actually infectious.

Image courtesy Toby Horn