were participating in a dyslexia study) volunteered that they'd had trouble learning to read as children, Paulesu says.

Even though the Italian subjects were unaware of and unhindered by having dyslexia-like reading skills, under the PET scan they looked just like British and French students who struggled with reading. Compared to normal readers, dyslexics from all three countries showed less activation in parts of the temporal lobe while reading. The underutilized areas are familiar to neurologists: Patients with strokes in this area often lose the ability to read and spell, even though they still speak fluently.

The researchers aren't sure why the dyslexics seem to access this brain area less than normal readers do. Other PET studies and scattered neuropathological reports have led to speculation that, in general, dyslexics have fewer neural connections among cells in this region. Although most researchers think that's plausible, little consensus exists on more detailed explanations of how or why dyslexics' brains are different from those of normal readers, Olson says. His research suggests that genetic factors account for about half of someone's risk of developing dyslexia, although no single gene is likely to be to blame.

This research doesn't supply ready solutions for how to help dyslexic students overcome their reading disability, Paulesu says, short of moving to Italy, Turkey, or Spain, where spelling is simple and straightforward. So sympathize when English- or French-speaking students complain about having to memorize arbitrarily spelled words; they're right to feel wronged. –LAURA HELMUTH

CELL BIOLOGY

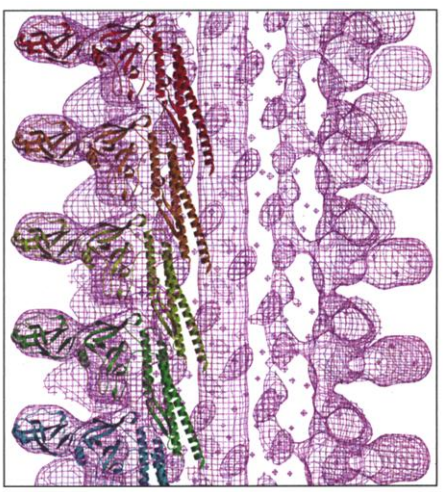
How Bacterial Flagella Flip Their Switch

Bacteria move with the agility of a tailback in American football, first cutting left, then right—all propelled by their whirling flagellar tails. Exactly how the tiny creatures achieve their feats of broken-field running has long been a mystery. New results now provide a probable solution to the puzzle.

When bacteria "run," the rotation of their flagella, long, whiplike filaments that project from the cells, is driven by motors located at the flagellar base in the bacterial membrane. The flagellar filaments are helical, and when they wind in the left-handed direction, they rotate counterclockwise. To change direction then, the bacterial cell momentarily reverses the direction of the motor, generating a torque on the flagellar filaments that flips them into right-handed helices. This causes the bacterial cell to "tumble," or change its orientation for its next run.

The mystery concerns how flagellin, the protein that makes up the filaments, achieves this dramatic structural shift. An x-ray crystallographic study of the protein described in this week's issue of *Nature* by Keiichi Namba of Matsushita's Advanced Technology Research Laboratories in Kyoto, Japan, Fadel Samatey of the Protonic NanoMachine Project, also in Kyoto, and their colleagues provides the first good look at a possible answer. It suggests that a sharp change within a very small "switch" region of flagellin is all that it takes to flip the left-handed flagellar helix into the right-handed form.

Previous structural studies, using the electron microscope and other methods, had characterized the bacterial flagellar filament to a resolution of 10 angstroms. These showed that



How they stack up. Five molecules of the protein flagellin are superimposed on a low-resolution map of a bacterial flagellar filament.

CREDIT: K. NAMBA/PROTONIC NANOMACHINE PROJECT/ERATO/JAPAN SCIENCE AND TECHNOLOGY CORP.

it is a tubular structure made up of 11 protofilaments, each formed by stacking together numerous molecules of flagellin. This protein comes in either left- or right-handed states, or L or R types, and all the molecules in a given protofilament are in the same state.

But the left- and right-handed protofilaments aren't just mirror images of one another. The repeat distance, which is the distance from any given point on one flagellin molecule to the corresponding point on the molecule above or below it, is less—by 0.8 angstroms—for the R-type protofilament. As a result, a flagellar filament containing both L and R protofilaments isn't straight but supercoils into a helix. For example, the *Salmonella* filament, which contains nine L-type and two R-type protofilaments, twists into a gentle left-handed helix. For tumbling, two of the L protofilaments are switched to the R type, and that's enough to give the filament a right-handed coil.

Researchers have long wanted to see this structural change, but that requires x-ray crystallography and they were stymied in their efforts because flagellin doesn't crys-

ScienceScope

Polytech Plum Glitzy it may not be, but Rensselaer Polytechnic Institute (RPI) in Troy, New York, has devoted admirers—including one who this week made a $360 million anonymous donation.

"A gift of this magnitude, fully unrestricted, is unprecedented," said RPI president Shirley Ann Jackson. She sees it as a vote of confidence for the Rensselaer Plan, a 5-year strategy to build stellar research programs in biotechnology—especially tissue engineering—and information technology.

Investing in Science It's a lovely problem for David Strangway, president of the Canada Foundation for Innovation (CFI). Strangway must choose between Triple-A bonds and blue chip stocks as the preferred investment vehicle for a $503 million gift from the government; the only catch is that it can't be spent until 2006–10.

The windfall is the third in the past year for CFI as the government whittles down a budget surplus (*Science*, 10 March 2000, p. 1732; 27 October 2000, p. 687). The CFI now has a war chest of $2.11 billion for competitive infrastructure grants to universities and teaching hospitals.

Although Internet stocks are definitely out, Strangway is still bullish on the prospects for solid growth. "I don't think it's unreasonable to hope that $500 million might become $670 million by the time it's needed," he says.

Dosage Details The main body that reviews U.S. gene therapy protocols plans to ramp up its scrutiny of safety reports despite complaints that it will reveal sensitive trade information.

Last week, the Recombinant DNA Advisory Committee (RAC) for the National Institutes of Health (NIH) approved a policy requiring detailed data on serious adverse effects from gene therapy experiments. The RAC has collected and made public such data for 10 years, but it wants to harmonize its requirements with those of the Food and Drug Administration (*Science*, 26 January, p. 572). A new RAC board will analyze the reports for trends. "We want to make the data more useful to everybody," says RAC chair Claudia Mickelson of MIT.

Too useful, says Michael Werner of the Biotechnology Industry Organization, who warns that forcing companies to reveal dosage levels "could be of enormous value to a competitor." The plan now goes to the NIH director.

Contributors: Michael Balter, Andrew Lawler, Constance Holden, Wayne Kondro, Jocelyn Kaiser

tallize. (The proteins link together in polymers instead.) In the current work, Namba, Samatey, and their colleagues got around that problem by clipping off the ends of the protein, thus removing the regions that form links with other flagellin molecules.

But yet another hurdle appeared: Only the R type of the protein crystallized, making it impossible to directly compare the structures of the two forms. Namba suggests that the longer L structure exists only in the filament, produced by the interaction between the protofilaments. "I don't think we will ever crystallize the L type of the protein," he says. That meant the researchers had to find another way to observe the change of the L form of flagellin to the R form.

So after determining the x-ray structure of the R-type protein, they used a computer simulation to stretch it, in 0.1-angstrom steps, into the longer L type. Up to a point, the stretching was accommodated by elastic strain throughout the structure. But then, a key hairpin fold in the protein snapped into a new position, pushing two regions of the protein farther apart and producing the L form.

While the simulation strongly suggests that Namba and his colleagues have spotted the flagellar switching mechanism, he cautions that his group has more to do to confirm that and to understand the interactions among the protofilaments. Even so, Hirokazu Hotani, a biophysicist at Nagoya University in Japan, describes the achievement as "very difficult to accomplish." He adds that the finding is important not only because it gives a clearer picture of how bacteria control their movements, but also because flagellin is the only protein known to undergo such a large degree of conformational change. And there could be a practical payoff in using the mechanism as a switch in nanomachines, although just how it might be incorporated into practical devices remains to be seen.

–DENNIS NORMILE

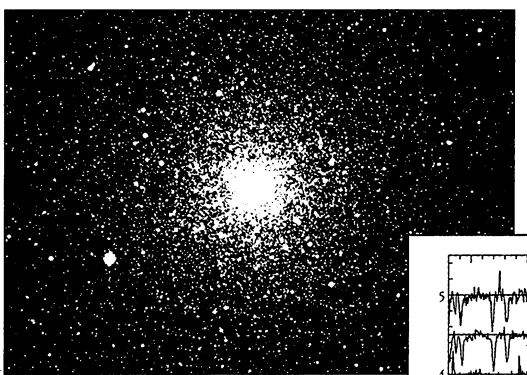
ASTRONOMY

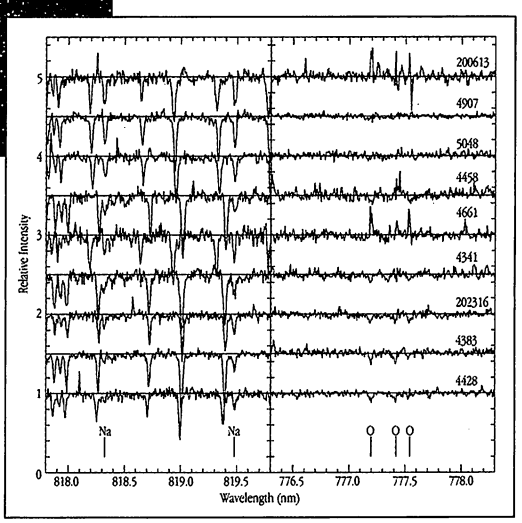
Stars Rise From Ashes In Globular Cluster

If you think cleanliness is next to godliness, avoid globular clusters. These huge, spherical concentrations of millions of old stars are among the filthiest places in the universe, according to a new study by Italian astronomers. Like houses in an industrial area, the stars in a globular cluster are polluted by the exhausts from nearby chemical plants.

In a paper to appear in *Astronomy and Astrophysics*, Raffaele Gratton of the Astronomical Observatory of Padua and his colleagues describe their discovery of polluted stars in a globular cluster known as NGC 6752, some 13,000 light-years from Earth in the southern constellation Pavo the Peacock. The cluster is about 100 light-years across and contains millions of stars, which are hundreds of times closer together than the stars in the solar neighborhood. From the Southern Hemisphere, it can easily be seen with a pair of binoculars.

Gratton and colleagues used a sensitive spectrograph on the European Southern Observatory's (ESO's) 8.2-meter Kueyen telescope in Chile (part of the Very Large Telescope) to study the chemical makeup of 18 dwarf stars—stars about the size of the sun—in NGC 6752. Because the stars in a globular cluster are believed to have formed simultaneously from the same cosmic ingredients, you would expect them to have a similar spectral fingerprint. Instead, the team found huge star-to-star variations in the composition of the stars' outer layers.





Born again. Spectrographs of dwarf stars in globular cluster NGC 6752 showed that some contain recycled ingredients.

For giant stars, that wouldn't be too surprising. Their high internal temperatures churn up their insides vigorously enough to carry the "ashes" of a star's nuclear burning processes from its core to its surface. But that can't be happening in dwarf stars, says team member Luca Pasquini of ESO in Garching, Germany, because they're not hot enough. So what causes the anomalous abundances?

One clue comes from the observations that the stars in the cluster show "anticorrelations" between certain elements. Dwarf stars that are high in oxygen tend to be low in sodium, and vice versa. A similar relation holds for magnesium and aluminum. Sodium and aluminum form relatively late in a large star's life cycle, when oxygen and magnesium tend to be depleted.

The astronomers concluded that the dwarf stars had picked up their heavy elements from hot, massive, short-lived stars that perished billions of years ago, when the cluster was young. Mixing carried the processed material from the massive stars' cores to their outer layers. Later, the dying stars ejected those layers as planetary nebulae—vast, slowly expanding shells of gas that polluted the space between the stars in the cluster and contaminated nearby dwarf stars. Pasquini thinks the "dirty" stars may have become 10% to 30% more massive because of the stellar pollution.

The new observations challenge a scenario proposed 20 years ago by Gary Da Costa of the Australian National University in Canberra and Peter Cottrell of the University of Canterbury in Christchurch, New Zealand. Da Costa and Cottrell thought the giant stars had polluted the cluster gas even before the dwarf stars formed out of it. Pasquini says it's hard to see how dwarf stars in a globular cluster could have formed much later than giant stars, as that model requires. But he acknowledges that the evidence so far is inconclusive. "We really need a better statistical sample to distinguish between the two models," he says. Da Costa agrees: "This is an important discovery. What needs to happen now is further work to understand how this process works [in detail]."

Stellar pollution has never been observed before, except in binary star systems. In the galaxy at large, astronomers say, stars are too far apart to intercept the ashes from old stars before they slowly disperse into space. But in massive globular clusters, stars are much closer together, and their combined gravity is strong enough to keep most of the "space pollution" in the neighborhood. Gratton's team also studied eight dwarf stars in a less massive cluster, NGC 6397, but found no pollution there, probably because the exhausts of dying stars have escaped the cluster altogether.

Pasquini says it's unclear how contaminants might be affecting the life cycles of the tainted stars: "We are just starting to investigate this. We'll have to run the [stellar evolution] models to see in detail what's going on."

–GOVERT SCHILLING

Govert Schilling is an astronomy writer in Utrecht, the Netherlands.

CREDITS: (LEFT TO RIGHT) AAO/DAVID MALIN; EUROPEAN SOUTHERN OBSERVATORY