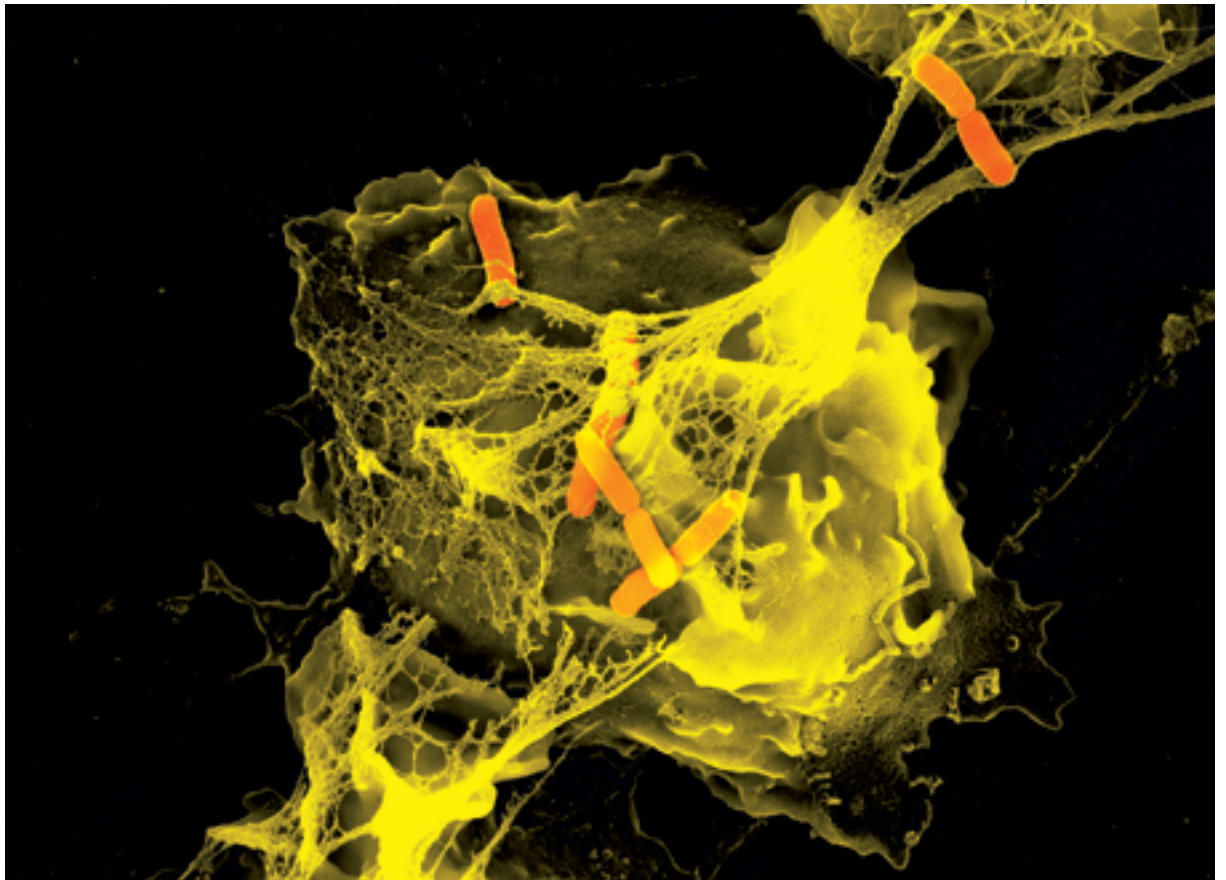




RESEARCH *in Brief*



INFECTION BIOLOGY

Immune Cells that Cast Nets

Neutrophils are the immune system's first line of defense: this type of white blood cell "engulfs" bacteria that invade the body, and destroys them inside the cell. Scientists at the Max Planck Institute for Infection Biology in Berlin discovered that neutrophils have a second, truly unusual defense strategy

in their arsenal: they form filamentous structures outside the cell body – much like nets, where pathogens become entangled and are rendered harmless (SCIENCE, March 5, 2004).

Between 50 and 80 percent of the white blood cells in human blood are neutrophils. Their

cell bodies contain membrane-bound vesicles known as granules, which house an extensive array of enzymatic and chemical antimicrobial agents. When a neutrophil comes across a pathogen, the latter is, so to speak, eaten up and then, with the help of such agents, killed and "digested."

The Director of the Department

The nets of stimulated neutrophils and the *Shigella* trapped therein (orange) under the scanning electron microscope.

of Cellular Microbiology at the Max Planck Institute for Infection Biology in Berlin, Arturo Zychlinsky, and a microscopy team headed by Volker Brinkmann discovered that neutrophils can also grasp onto and destroy bacteria extracellularly: using different microscopes, the researchers were able to demonstrate that neutrophils form fine fibers outside of the cells.

The scientists in Berlin have termed these structures "neutrophil extracellular traps," or NETs, which are exceedingly sophisticated and not only entangle, but also disarm and kill bacteria. The mesh of these nets is composed of chromatin, a composite of deoxyribonucleic acid and proteins, which is normally found only in the nuclei of eukaryotic cells. The majority of the proteins in chromatin are histones, which are poisonous to bacteria. In addition, the NETs contain immune agents from the neutrophilic granules. Both meth-

ods of attack can explain the recent findings made in cooperation with Yvette Weinrauch from New York University, which show that NETs can kill bacteria with great efficiency, including various forms of *Shigella* (the pathogen that causes bacterial dysentery), *Salmonella* (typhoid fever) and *Staphylococcus*, the etiological agent of many diseases from ear infections to toxic shock syndrome. ●

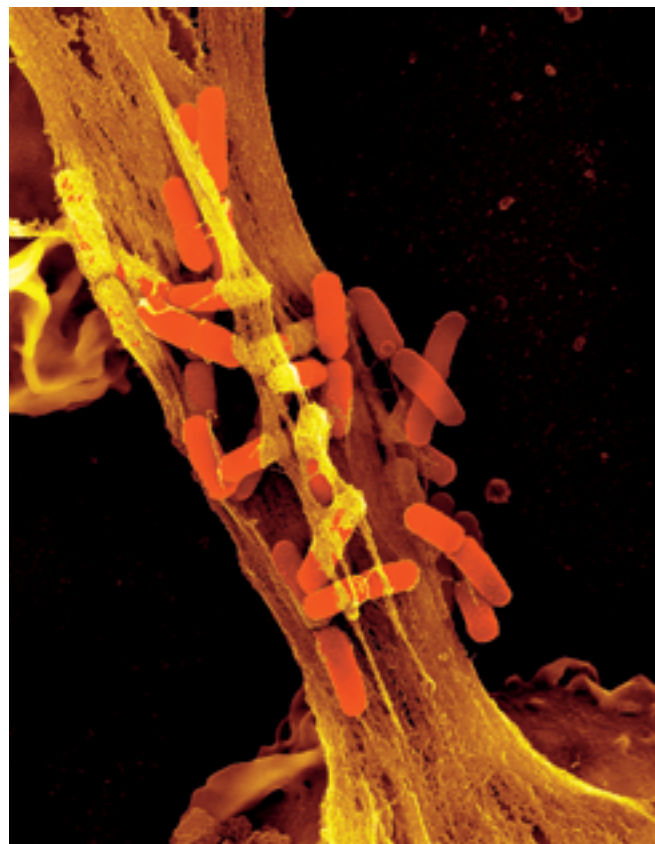


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Fiber net bundle with *Shigella* (orange).



BIOLOGICAL CYBERNETICS

Seeing by Learning

Cross-linkage of nerve cells in the higher cognitive regions of the brain enables people to remember other people, objects and events. Thanks to the plasticity of such networks, we can continuously store new content. Researchers at the Max Planck Institute for Biological Cybernetics in Tübingen have now discovered that learning also has a feedback effect on the neurons of the brain's visual centers themselves. And that this optimizes interaction and feedback between sensory and associative brain areas, in addition to the "upward" information flow from visual areas (PLOS BIOLOGY, February 17, 2004).

Primates' brains recognize familiar objects and persons with great accuracy, even when embedded in complex and dynamic settings. This ability is largely based on the fact that learning and neuronal plasticity enable the brain, also during adulthood, to constantly adapt itself and continually optimize the perception process – this is why, as experience shows, repeated observation improves our ability to recognize objects. It has long been unclear, however, how the brain coordinates such improvements. Visual signals initially travel from the eyes to the primary visual cortex and from there further into nearby "lower" processing areas in which visual features are analyzed. Together, these regions form the brain's so-called visual centers. Injury to these centers results in blindness. From here, visual signals are sent to "higher" cognitive brain areas in the temporal and frontal lobes, which are involved in representing objects



The natural image of a lion (right) was mixed with "visual white noise" (left) to create a version of the natural image that is blurred and difficult to recognize (center).

FIG. 1. ROBERT SHALENGER/US FISH AND WILDLIFE SERVICE

and persons. Injuries to these regions mean that objects and persons can still be seen, but no longer recognized.

Scientists have established that learning alters the activity and cross-linkage of neurons in higher brain centers in adulthood. It is assumed that such modifications constitute the internal representation of learned contents. On the other hand, the properties of the visual centers, according to standard opinion, are no longer capable of change. Recently, however, scientists came across the first evidence that learning also modifies visual centers; however, the extent and behavioral relevance of the learning effects remained unclear. Gregor Rainer, Han Lee and Nikos Logothetis from the Max Planck Institute for Biological Cybernetics have now been able to show that learning does indeed strongly influence the activity of sensory brain centers. The cognitive scientists were able to empirically investigate such effects by training monkeys to identify computer images of specific objects from their "natural" environment, which, with the aid of interpolation techniques, could then be made less recognizable to varying degrees.

The scientists presented the monkeys with individual images of "natural" objects – including, for example, birds and humans – each blurred to a greater or lesser extent. Shortly afterwards, a second image was shown to the monkeys, whose task it was to signal whether

the second image corresponded with the first. The neuronal activity in the lower visual processing regions was simultaneously recorded. The result: In new and non-blurred images, the activity of the neurons showed little change, whereas in blurred images, the activity increased dramatically. In addition, the greater the activity and informational content of the neurons, the more the monkeys' ability to detect partially recognizable images improved.

But just how do individual neurons in the lower visual centers manage to improve recognition of blurred images? After identifying a group of neurons that responded and fired more strongly to blurred stimuli, the scientists investigated the monkeys' eye movements to find out how the animals were able to recognize already familiar objects. The results showed that, subsequent to learning, eye movements scanning the original images overlapped considerably with those scanning their blurred counterparts. The monkeys had obviously learned to concentrate their attention on particularly striking properties of the images, allowing them to recognize the blurred versions of the original images.

The experiments show that the recognition of ill-defined images is greatly improved by learning, and that such improved performance is dependent on the neurons in the lower visual processing regions. These neurons compensate for

indistinct visual contents by coordinating different regions of the brain and constructing a learning-dependent increase in information on visual stimuli. Lower visual processing areas are therefore fundamental in resolving ambiguities in the contents of perception, and achieve this by interacting with higher brain regions – this is how even unclear images are interpreted correctly in the end.

These discoveries prove that learning also leads to changes in the informational content and the activity of neurons in lower visual centers. Seeing and recognition, according to Rainer and his colleagues, are dynamic processes that are fundamentally contributed to by the interactions between lower sensory brain regions and higher cognitive regions. In the course of such interactions, the continuous signals from the retina are processed against the brain's expectations and experiences. This integration between input and expectations already occurs in the lower visual centers. As a result, we see that which we have learned to recognize. ●



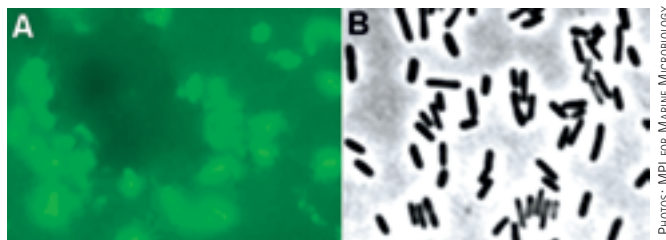
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MARINE MICROBIOLOGY

Tracking Down Iron-Eating Bacteria

Iron rusts: This has been known since at least the beginning of the Iron Age, for almost four thousand years. However, it was not until modern times that chemists were able to understand and explain why it rusts. Somewhat later, in 1930, it was discovered that iron can also be attacked and destroyed by microorganisms – through so-called bio-corrosion. And now scientists at the Max Planck Institutes for Marine Microbiology (Bremen) and for Iron Research (Düsseldorf), together with the Institute for Material Testing in Bremen, have detected new kinds of bacteria that attack iron in a particularly aggressive but as yet unexplained way (NATURE, February 26, 2004).



Microscopic image of novel sulfate-reducing bacteria that corrode iron. A: Bacteria cells directly from corroding iron that have been chemically fixed and made to glow under the microscope using a molecular-biological detection method, a fluorescing DNA probe.

B: The same bacteria species, but in a living state, in an artificial medium.

Iron is one of mankind's oldest and most used basic materials – and even in modern industrial societies, easily the most important utility metal. Besides the numerous technical advantages that have earned the material its leading position, this metal exhibits one rather "ignorable" characteristic: in damp air, as well as in water containing oxygen, it is oxidized and turns into rust – a porous, crumbly mass made up of brownish iron oxides with bound water molecules. Such corrosion can be prevented or at least delayed by numerous methods, such as making iron alloys – that is, adding other metals to it – or sealing it off from destructive forces with

protective coatings that keep out water and oxygen. Simply excluding air, and thus oxygen, already helps considerably, as demonstrated by the long lifespan of iron water pipes – even though water alone can also attack iron, albeit very slowly. However, this slow corrosion in air-free water can be greatly accelerated by certain bacteria, so-called anaerobes that multiply in oxygen-free media and gain their metabolic energy from the reduction of sulfate with a number of natural reductants. These anaerobic bacteria reduce sulfate dissolved in natural water to hydrogen sulfide, a poisonous and aggressive gas that smells like rotten eggs, and that then attacks iron. This creates coal-black corrosion products, compounds of sulfur and iron

as found in poorly aerated drainage system pipes. A second method of "anaerobic bio-corrosion" similarly used by sulfate-reducing bacteria should, according to a theory developed in 1930, function via hydrogen generated during slow underwater electrochemical corrosion on iron surfaces. This so-called cathodic hydrogen should be consumed by these bacteria to reduce sulfate, and should thus be continuously used up – which would have the effect of promoting and accelerating iron corrosion in water in the absence of air.

However, these eminently plausible theories fail as measured against the "voracity" shown by

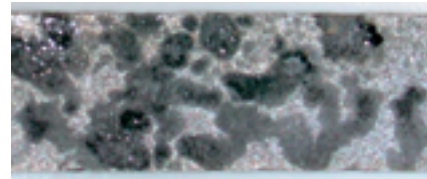


Image of an afflicted iron surface. The corrosion resulting from the newly discovered sulfate-reducing bacteria is clearly visible.

the kind of sulfate-reducing bacteria recently discovered by scientists at the Max Planck Institute for Marine Microbiology, the Max Planck Institute for Iron Research and the Institute for Material Testing in Bremen. Under the influence of these bacteria, iron corrodes underwater much more rapidly than can be accounted for by the use of cathodic hydrogen. Consequently, these newly discovered bacteria may play a considerable, but until now overlooked role in the corrosion of iron under air-free conditions. A detailed understanding of the "lifestyle" of these microorganisms has still not been achieved, as their metal-attached growth and study in the lab in pure cultures is a time-consuming task. However, the results available to date support the idea that these bacteria circumvent the laborious process of cathodic hydrogen formation and consumption, and instead capture electrons directly from the iron – in other words, they create a shortcut via an "electric current" that then leads to the iron's rapid corrosion. How they manage this will hopefully be revealed by further analyses of cultured bacteria – which will then perhaps also show whether and how the destructive handiwork of these microscopic iron-eaters can be controlled. ●



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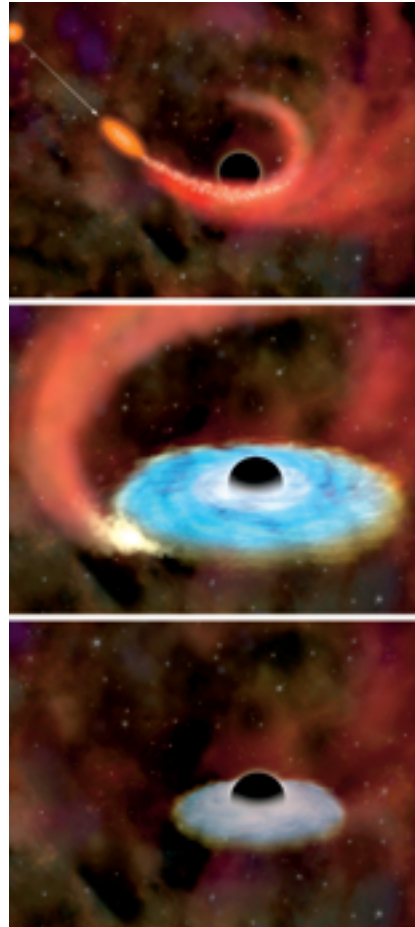
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EXTRATERRESTRIAL PHYSICS

Star Falls into Gravitational Trap

Recent observations have now substantiated the theory long held by astronomers that black holes may be lurking at the center of "inconspicuous," inactive galaxies. Researchers at the Max Planck Institute for Extraterrestrial Physics in Garching, along with colleagues from Columbia University and the European Space Agency (ESA), recorded a gigantic burst of X-rays from the center of an optically unremarkable galaxy. The astrophysicists believe this event bears witness to the destruction of a star that came too close to a black hole at the galaxy's center – subsequently being crushed and drawn into its "gravitational gullet" (ASTROPHYSICAL JOURNAL, March 1, 2004).

Such a scenario had long been postulated by British astrophysicist Sir Martin Rees, who regarded it as potential proof of the existence of black holes in the center of normally quiescent galaxies. The galaxy with the catalog number RXJ 1242-1119, in which this process was first observed, came to the attention of scientists at the Max Planck Institute in Garching as long ago as 1992. At the time, the X-ray satellite ROSAT located the optically unremarkable galaxy as a strong X-ray source. A recent survey by the Hubble space telescope, along with NASA's Chandra satellite and the ESA's XMM-Newton satellite, led to a surprising discovery: the galaxy's X-ray intensity has dropped by a factor of 200 since 1992, but the center is still shining more brightly in the "X-ray sky" than that of a "normal" galaxy. It is considered certain that the origin of this radiation lies in a black hole at the center of the galaxy. In addition, researchers



A star is ripped apart by the tidal effect of a black hole (top). Part of the stellar debris is then sucked in by the black hole (center) and heats up tremendously. This leads to a gigantic radiation outbreak that gradually subsides again with time (bottom).

believe the outbreak was caused by a star that came too close to this "massive monster," was initially deformed and finally ripped apart by its gravitation. Part of the star's mass was then consumed by the black hole – its remains heating up tremendously in the process and emitting intense X-ray radiation. Only the "afterglow" of this spectacular event can now be observed. At its brightest, the

black hole must have devoured a mass approximately the size of the Earth every 10 minutes, estimates Stefanie Komossa of the Max Planck Institute in Garching. Were the same to happen in our galaxy – at the center of the Milky Way – it would, viewed with "X-ray vision," appear almost as bright as the Sun.

Black holes are particularly interesting for astrophysicists, as such exotic objects are intimately connected with both the origin and the development of galaxies and, by association, with the universe as a whole. Bursts of radiation, as described above, originating when a star is "swallowed," offer one of the – very few – possibilities of detecting

and studying black holes. These flashes briefly light up the backdrop surrounding black holes. Such "light echoes" can then be used to establish important information about conditions at the centers of galaxies, as well as about processes occurring in close proximity to black holes' domain of activity: a ray of light in regions of space that are still shrouded in darkness and mystery, if you will. ●



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BIOPHYSICAL CHEMISTRY

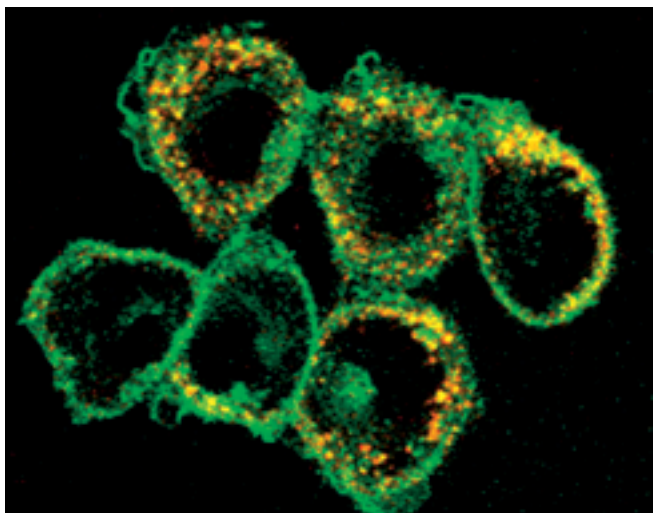
The Small and the Beautiful

With the help of semiconductor nanocrystals, researchers at the Max Planck Institute for Biophysical Chemistry in Göttingen, Germany are now able to capture movies of signal transmission processes involved in the control of gene expression. This breakthrough is expected to speed up the development of new cancer-curing drugs. Quantum dots (or QDs) can be used as nano-sized markers to visualize DNA sequences, proteins or other molecules and track them in the cell. The complexes consisting of QDs and specific ligands, in this case a cellular growth factor, bind

ten-millionth of a millimeter in diameter that fluoresce in several different colors upon excitation with a laser source. These crystals enabled the researchers to deliver real-time video clips of signal transmission in the so-called erbB receptor family, important targets for many anti-tumor drugs, such as antibodies directed against breast cancer. Among other processes, the movies capture the uptake and subsequent redistribution of the receptor-growth factor complexes into the interior of the cell.

"The *in vivo* measurements reported in our study revealed new insights into cellular processes and interactions that

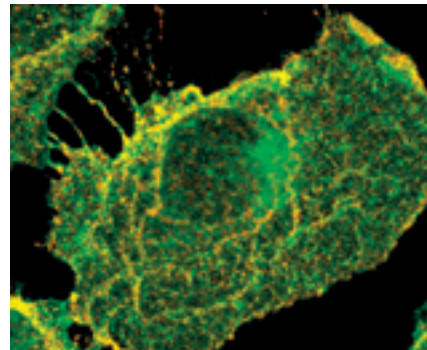
Living cells expressing epidermal growth factor receptor fused to green fluorescent protein (green) bind and are activated by epidermal growth factor complexed to quantum dots (red). The growth factor-receptor complex becomes quickly internalized into vesicles that appear yellow by the superposition of the two colored signals recorded at ambient temperature on a confocal microscope.



to target molecules such as receptors on the cell surface. The QDs glow in a variety of colors and are up to a thousand times brighter than conventional fluorescent dyes (NATURE BIOTECHNOLOGY, February 2004).

In a study published in the February issue of the acclaimed science journal NATURE BIOTECHNOLOGY, Diane Lidke and her colleagues present results of their experiments with quantum dots. These are nano-sized semiconductor crystals a mere

could previously be studied only on fixed (dead) cells," wrote the researchers, led by Dr. Thomas Jovin, chairman of the Max Planck Institute for Biophysical Chemistry's Department of Molecular Biology. "An understanding of receptor-mediated transduction is essential for rational receptor-targeted cancer therapeutics. Quantitative approaches based on multiple combinations of quantum dots and ligands will be invaluable for such investigations." In the same issue of NATURE BIOTECHNOLOGY, two lead-



PHOTOS: MPI FOR BIOPHYSICAL CHEMISTRY

ing experts in live-cell imaging reviewed the results of the study. "Semiconductor nanocrystals can track movements of individual receptors on the surface of living cells with unmatched spatial and temporal resolution," wrote Gal Gur and Yosef Yarden of Israel's Weizmann Institute of Science. "[Other] imaging methodologies have limited spatial and temporal resolution and either require complex manipulation or are able to provide only very brief snapshots of receptor dynamics."

Conventional tools, such as fluorescent dyes and polymer spheres, bleach too quickly – sometimes within seconds – to be of use for extended video images of living cells, according to the researchers. Quantum dots, on the other hand, are not only very photostable but also very bright, making it possible to trace many elements of the cell for minutes or even hours at a time. Today, the length of observation time is a critical factor for the study of cellular processes, since rapid changes can occur over a time span of seconds or minutes. ●

Cells expressing the epidermal growth factor receptor erbB1 – green fluorescent protein eGFP (green) fusion protein after a short incubation with complexes of epidermal growth factor (EGF) and quantum dots (QD, red) nanoparticles. The EGF-QD complexes are seen binding to the cell surface. Notice in particular the binding of EGF-QDs to the filopodia (cell extensions) and the ruffling of the cell membrane due to activation of the receptor by the EGF-QD binding.



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MOLECULAR GENETICS

Chatty Finches

Mutations in the gene known as FOXP2 are associated with a specific speech deficit, affecting articulation and language comprehension. Apparently FOXP2 plays a central role in speech development. Neurobiologists now report that the gene could also play a key role in the ability of birds to learn song. Scientists from the Max Planck Institute for Molecular Genetics in Berlin and from Duke University in the U.S. discovered an almost identical version of FOXP2 in songbirds and could then show that the corresponding protein was expressed in brain regions that are critical for song learning (JOURNAL OF NEUROSCIENCE, March 31, 2004).

In 2002, Svante Pääbo's group at the Max Planck Institute for Evolutionary Anthropology in Leipzig compared the DNA sequence of the intact FOXP2 gene in humans and chimpanzees. They found that the human gene carried a unique sequence variation that was estimated to have evolved roughly at the same time as language is thought to have emerged in the hominid lineage. Because FOXP2 is a transcription factor, that is, a protein that regulates the activity of many other genes, the sequence changes of FOXP2 in the hominid lineage could, in the course of evolution, have triggered a chain of events. The Leipzig team found evidence that indicates that the human version of FOXP2 was advantageous for the individuals that carried it and suspect that it could have been pivotal for the origin of human language. Young birds of many species need to learn the sounds they communicate with in a manner akin to the way infants learn to speak, which is in contrast to mice and non-human primates, which don't learn their vocalizations. Constance Scharff, head of the

Neurobiology group at the Max Planck Institute for Molecular Genetics, therefore questioned whether the songbird FOXP2 carried sequence variations similar to those found in humans. Together with Sebastian Haesler in her group, and her colleagues Erich Jarvis and Kazuhiro Wada at Duke University, they compared the expression of FOXP2 in a variety of bird brains. Among those were song-learners, such as zebra finches, canaries, chickadees, sparrows, hummingbirds and parakeets, and non-learners, such as pigeons and chickens. In addition, the scientists studied the gene in the closest relative of birds, the crocodile.

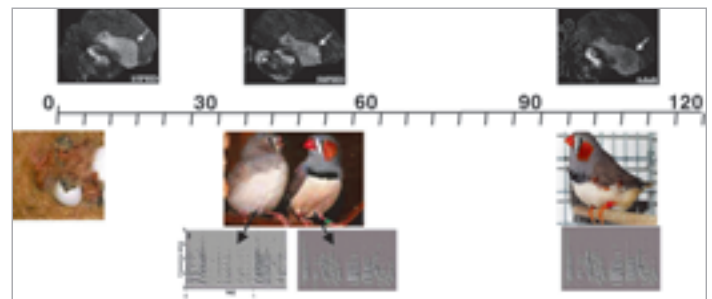
The first part of the study determined when and where the gene was expressed. Was FOXP2 expressed in brain regions that control singing?

Was it expressed during learning of song, or during singing itself? And what happens when the learning is finished? In addition, the team analyzed the sequence of the zebra finch gene and compared it to the human sequence. They found that the FOXP2 gene from finches was extremely similar to the human version, but did not carry the human-specific sequence variation. "Apparently, the human-specific version is not essential for song learning in birds," says Constance Scharff, "or other variations that exist in the songbird version of the gene helped develop this ability." In collaboration with the Leipzig team of Max Planck scientists, they are comparing FOXP2 sequences of song-learning birds with those of non-learners to see whether differences similar to those found between humans and chimps exist.

Certainly, the FOXP2 brain expression pattern the scientists now report is striking. The gene is expressed in bird brains in a manner astonishingly similar to the distribution in mammalian brains, including humans. What's more, expression in the basal ganglia, which help coordinate sequenced movements, peaks around the time of song learning, which in zebra finches occurs just once during development, but recurs seasonally in canaries. "We could show that FOXP2 levels increased in a basal ganglia region that is specialized for song learning, just at the time when song changes in both finches and canaries," Scharff explains.

Based on these findings, the scientists now hope to extend their

The expression of the FOXP2 gene in the brain of the zebra finch as a function of development stage: the regions with active FOXP2 are white; the "Area X" (white arrow), a structure that is essential for song learning, exhibits particularly high activity in the learning phase – beginning at the age of 50 days.



studies to elucidate the role this gene plays in shaping the architecture and function of brain circuits that control song learning and song production. "The discovery of FOXP2 in birds is only the beginning; there is no direct evidence yet that the gene is necessary for song learning or singing," cautions Scharff. Experiments to interfere with the expression of the gene using molecular tools to see whether it is really necessary for song learning are therefore top priority for the lab. ●



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EVOLUTIONARY ANTHROPOLOGY

The Neanderthals - a Closed Society

The analysis of fossil remains of Neanderthals and early modern humans by an international team headed by Svante Pääbo from the Max Planck Institute for Evolutionary Anthropology in Leipzig suggests that the Neanderthals did not contribute appreciably to the genetic makeup of modern man (PLoS BIOLOGY, March 2004).

In the search for the origins of modern man, researchers long had to rely on fossil finds and their morphological composition. But now modern molecular genetics techniques can garner crucial information from even the tiniest traces of DNA in fossil bones. To reconstruct the evolution of man, most molecular anthropologists use the DNA contained in the mitochondria: in contrast to DNA from the cell nucleus, this so-called mtDNA is passed on to descendants exclusively by the mother, and so conveys a picture of the purely "maternal" history.

According to one theory, early modern humans and Neanderthals are supposed to have produced common offspring. Both populations lived at approximately the same time: Neanderthals lived some 150,000 to 30,000 years ago in Europe, parts of Asia and the Middle East; modern man first appeared in Africa 100,000 to 200,000 years ago.

The team led by Svante Pääbo has now analyzed the most extensive samples of remains to date, both of Neanderthals and of early modern humans. A particular challenge in this undertaking was posed by the fact that fossil material is frequently contaminated by traces of DNA from living humans who handled the specimens. Thus, if a Neanderthal sample contains a DNA

sequence that is similar to that of an early human, there will clearly be suspicion of contamination. When Pääbo and his colleagues searched specifically for "modern DNA," they found it in every fossil sample – in Neanderthals, in early humans and even in the teeth of cave bears.

Therefore, the researchers concentrated their search on, not human DNA, but rather exclusively Neanderthal DNA to find indications of intermingling between the two populations. The mtDNA of modern man differs considerably from that found in four Neanderthal samples that were sequenced previously. Pääbo's group used a technique that measures the amino acid content of a bone, which gives an indication whether it might still contain DNA. They developed this technique themselves in their labs, and the advantage is that it allows a DNA-independent assessment about a bone's biochemical preservation while requiring very little of the rare "raw Neanderthal material:" just 10 milligrams of fossil bone substance suffice. The scientists analyzed 24 Neanderthals and 40 early modern humans – but found that just four Neanderthals and five early modern humans were biochemically well enough preserved that they should still contain DNA.

They subsequently investigated these nine bones for mtDNA sequences similar to

those previously found in the four sequenced Neanderthal individuals.

Some of these samples were anatomically classified as a "transition" between the two groups. They originate from various parts of Europe; accordingly, it is likely that the representatives of the two populations actually did encounter one another. In the Neanderthal samples, however, the researchers discovered only mtDNA sequences that had been found in the four previously sequenced Neanderthal fossils, and that do not occur in contemporary humans; conversely, none of the five early-human samples contained mtDNA similar to that of Neanderthals.

In view of the limited quantity of early human material, Svante Pääbo does not want to rule out the possibility that there could, in fact, have been a flow of genetic material between the two populations. However, since even fossil samples that were classified as an anatomic transition between modern man and Neanderthal showed no hint of shared mtDNA, the scientists assume that, if anything, Neanderthals contributed only marginally to the gene pool of contemporary humans.



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A Neanderthal skull, found near La Chapelle in France.

Panorama

"FAT SOLVENTS" BETRAY THE TB VIRUS to the immune defense: this discovery was a major step in affording researchers at the Max Planck Institute for Infection Biology a deeper understanding of – and perhaps progress in the fight against – tuberculosis, which continues to top the list of the world's lethal infectious diseases. The tuberculosis virus, a mycobacterium, wears a kind of waxy armor consisting essentially of fat molecules (lipids). To be able to fight this virus, the immune system must first perceive and identify components of this lipid casing as antigens. This happens, as the Berlin-based researchers discovered, through so-called saposins. These protein molecules have two functions: first, they attack the lipid layer of the mycobacteria and release some of its components, and second, they make contact with so-called antigen-presenting proteins. These proteins take over the fat structures that the saponins release from the bacterial casing and then present them to the T-lymphocytes, which make up the immune defense's "records department" – and, following contact with the lipid antigens, trigger an immune reaction.

BACTERIA THAT KILL BACTERIA could be valuable for the medical field. This was the premise upon which researchers at the Max Planck Institute for Developmental Biology in Tübingen, together with colleagues from the Universities of Nottingham and Bielefeld, deciphered the complete genome of *Bdellovibrio bacteriovorus*. This predatory bacterium invades other bacteria and consumes its involuntary hosts from the inside out. The object now is to gain a better understanding of the molecular weapons (primarily enzymes) this single-celled organism employs in its attacks. This could lead to the discovery of new anti-microbial substances that operate on different mechanisms and affect different targets than those of traditional antibiotics. Moreover, it seems conceivable that *Bdellovibrio bacteriovorus* could be modified in such a way as to perhaps even be used as a "living antibiotic." After all, it attacks only single-celled organisms that have no nucleus (prokaryotes), but not eukaryotic cells of mammals, and thus of humans.

"METHANE EATERS" ON THE OCEAN FLOOR were the subject of scrutiny by researchers at the Max Planck Institutes for Terrestrial Microbiology in Marburg, for Marine Microbiology in Bremen and for Molecular Genetics in Berlin: bacteria that are capable of oxidizing, without oxygen, methane discharged from decaying organic material on the ocean floor, and extracting from it energy for their metabolism. This way of living is an unusual one, considering that methane, while requiring a mere spark to set off an explosion when exposed to air, is extremely difficult to incite to

a reaction on the cold ocean floor and with no oxygen. To be able to use it as nourishment and a source of energy, a reagent is needed, that is, a catalyst. The Max Planck researchers have now tracked down this catalyst: an enzyme containing nickel – a metal that nature, relatively speaking, rarely uses in biomolecules. The enzyme was isolated from microbe mats that cover large areas of the 200-meter-deep floor of the Black Sea, and from which methane spirals its way upward. The bacteria that use the nickel enzyme to digest and decompose methane have not, as yet, been "personally" identified. However, in view of the expansive ocean floor surfaces in which methane is converted, these microbes undoubtedly play a key role in the balance of substances in the world's oceans, and thus also in the atmosphere.

ULTRAVIOLET LIGHT GUIDES tropical rain forest bats of Central and South America to their forage, the plants that provide the nectar on which they feed: this was one of the findings of researchers at the Max Planck Research Center for Ornithology in Seewiesen, in collaboration with colleagues from the University of Erlangen and the University of Guatemala. The discovery came as a bit of a surprise, since bats – unlike other higher mammals – have no cone receptors in their retina and are thus color blind. Experiments have shown that they have only one type of rod

A flower bat hovers while "filling up" on nectar from a bromeliad in the Caribbean rain forest.

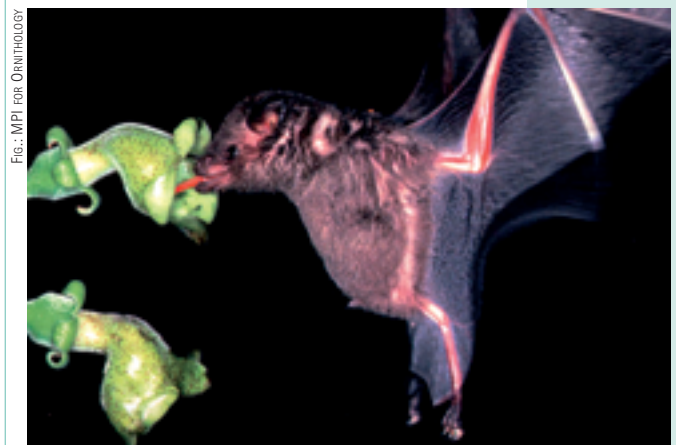


FIG.: MPI FOR ORNITHOLOGY

receptor, allowing them to distinguish between "colorless" light-dark differences at low levels of light intensity, but that these receptors are also sensitive to short-wave ultraviolet light – and thus to the rays that the petals of certain plants in the night-black rain forest reflect particularly strongly. The bat's ability to see ultraviolet may be due to the fact that, in contrast to other mammals, the bat eye lens has no filter for ultraviolet light. Nevertheless, the researchers now aim to determine whether there might not be an as yet unknown photomechanism at work here that is also utilized by other bats and perhaps even other color-blind mammals.



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