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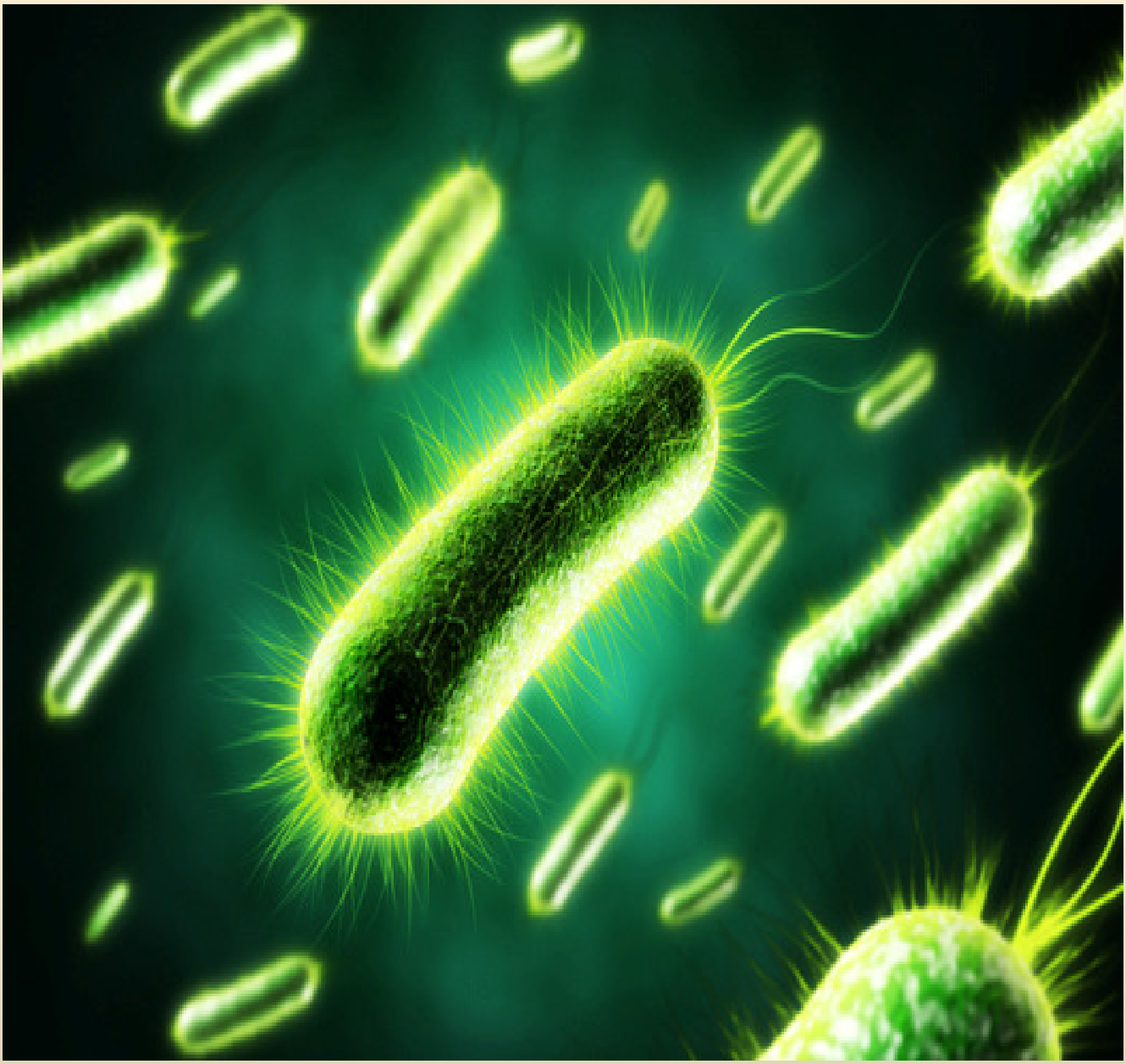

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ENVIS Newsletter on Microorganisms and Environment Management, a quarterly publication, brings out original research articles, reviews, reports, research highlights, news-scan etc., related to the thematic area of the ENVIS Centre. In order to disseminate the cutting-edge research to user community, ENVIS Centre on Microorganisms and Environment Management invites original research and review articles, notes, research and meeting reports. Details of forthcoming conferences / seminars / symposia / trainings / workshops also will be considered for publication in the newsletter.

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Cover page : *Geobacter* - Wired bacteria clean up nuclear waste.

(Image Credit : iStockphoto)

ENVIS Newsletter
on
Microorganisms and Environment Management

Contents

Dear Readers,

The ever increasing global population needs more and more energy resources, but most of these resources are limited and exploited. Specifically, population growth is intensifying the demand for consumption of nonrenewable energy sources such as oil, coal and natural gas. The imbalance in the environment further worsens the impacts of climate change and lead to depletion of natural resources. Sustainability and sustainable development may therefore help to overcome the demand of non renewable energy by the production of biofuels such as bioelectricity, biogas, etc.

Besides, new emerging technologies are underway to produce energy from wastes without exploiting the fossil fuels. Energy from wastes is a recent technique to produce electricity directly through combustion, or produce a combustible fuel commodity, such as methane, methanol, ethanol or synthetic fuels by microbial fuel cells. This issue contains article on tetrodotoxin producing bacteria isolated from pufferfish, electricity from biofuel wastes, and methane gas production by electricity through the microbes. Other fascinating informations on microbes are also included.

We sincerely look forward to your suggestions and feedbacks. Please do mail us at.

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Prof. N. Munuswamy

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World Population Day, July 11th 2012

Tetrodotoxin Producing Bacteria from the Copepod Infecting Pufferfish

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Abstract

The copepod *Pseudocaligus fugu* (Siphonostomatoida: Caligidae) is a common parasite, collected from the body surface of the pufferfish *Takifugu* spp. in Japan. It was endowed with number of bacterial colonies, revealed through scanning electron microscopy (SEM) and by experiments. On the basis of bacterial colonies isolated, two types of isolates showed a high affinity for adhesion to the shrimp carapace. These two types were identified through 16S rRNA sequence analysis as *Shewanella woodyi* and *Roseobacter* sp. Representative isolates of these two adhesive bacteria were examined for tetrodotoxin (TTX) production by High Performance Liquid Chromatography (HPLC)–Fluorometric system, Gas chromatography–Mass Spectrometry (GC-MS) and Liquid Chromatography–Mass Spectrometry (LC-MS). From these results, it is evident that TTX and anhydroTTX are present in the isolate of *Roseobacter* sp. indicating the bacterial origin of TTX.

Introduction

In the marine fish aquaculture industry, parasitic copepods are causing serious consequences and important as pathogens particularly the “sea lice” belonging to the family Caligidae these copepod cause mortality or acting as disease agents, by creating a portal for entry of bacterial or other pathogens (Rosenberg, 2008). It is successful only through their feeding behavior on host mucus, tissues and blood. They could easily transmit disease -causing agents to other hosts (Cusack and Cone, 1986). Furthermore, it has been found that parasitic copepods are endowed with an abundance of bacteria on their exoskeleton (Venmathi Maran *et al*., 2011) which had been reported from the body surface of marine planktonic copepods also the attachment and abundance of bacteria can be host specific or site specific (Sochard *et al*., 1979). However, the significance of bacterial adhesion onto the surfaces of copepods or any living aquatic organisms has not been studied in detail.

Tetrodotoxin (TTX), known as pufferfish toxin, is one of the most potent non-protein neurotoxin because of frequent involvement in fatal food poisoning. It has a unique chemical structure and has specific action of blocking sodium channels of excitable membranes. The toxin derives its name from the pufferfish family Tetraodontidae, but past studies have revealed its wide distribution in both terrestrial and marine animals of vertebrate species which includes goby, newt and frog, and invertebrate species like octopus, gastropod mollusk, crab, starfish, nemertean and turbellarian (Noguchi *et al*., 2006). The origin of TTX and its biological significance in TTX-bearing animals have been investigated for a long time (Matsumura, 1995).

The puffers of the genus *Takifugu* (Actinopterygii: Tetraodontidae) is common in the Far East Asian countries, considered as delicacy and commercially important (Venmathi Maran *et al*., 2011). It has been proven that liver, ovary and other viscera of the fish are endowed with high level of TTX, and however varies depending on its species (Noguchi *et al.,* 2006). Most of the puffers are infected with an ectoparasitic copepod *P. fugu* (Venmathi Maran *et al*., 2011), which has revealed accumulation of TTX (Ikeda *et al*., 2006). Interestingly, the abundance of rod-shaped bacteria that adhere to the body surface of *P. fugu* was noted. Although marine bacteria are likely to be a source of TTX, there has been no clear evidence to support the bacterial origin of TTX. On this basis, the adhesive bacteria on *P. fugu* were speculated that to be the producers of TTX. Thus the present study documents the characteristic feature of bacteria associated with the copepod, in producing TTX.

Observation of bacteria on copepod

The puffers *Takifugu* spp. (called as ‘fugu’ in Japanese) were collected from the central part of the Seto Inland Sea of Japan (Fig.1A). The infected parasitic copepod *P. fugu* was removed from the body surface of those pufferfish (Fig.1B). The copepods were desalinated by transferring into the distilled water for 1-3 hours and processed further to reveal the attachment of bacteria over the whole body of copepod through scanning electron microscope (SEM). Attached bacteria were observed throughout the body surface of the copepod *P. fugu* (Fig. 2A). These bacteria were rod-shaped, approximately 1.2–2.8 µm size in length with slimy materials and some bacteria were observed in dense

masses on the cephalothorax (Fig. 2A).

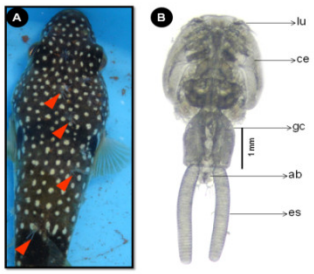

Fig. 1A. Pufferfish infected with the parasitic copepod *Pseudocaligus fugu*; B. Ovigerous *Pseudocaligus fugu*, lu: lunule; ce: cephalothorax; gc: genital complex; ab: abdomen; es: egg sac.

Adhesion of bacteria

The bacteria present on copepods were cultured and isolated on Marine Agar 2216 at 25 ˚C for 24h and subjected to the adhesion experiment using the shrimp carapace. There were several colony types attached on the carapace. Of those, only two types of bacteria showed a high degree of adhesion to the shrimp carapace. The level was evaluated based on the abundance and density of bacteria attached. The other types of bacteria showed less adhesion (attached sparsely). Control showed no bacterial attachment but slimy substances.

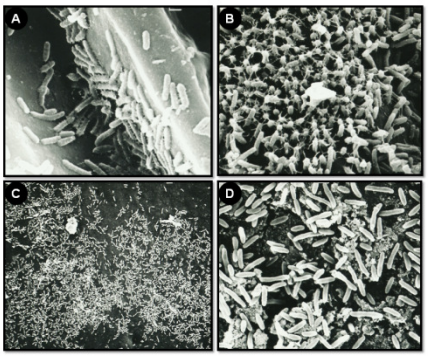

Fig. 2. Scanning electron micrographs of bacteria: A. Attached on the cephalothorax of the parasitic copepod; B. First type isolate; C. Second type isolate; D. The same at higher magnification.

Identification

The two bacterial isolate which showed high adhesion to the shrimp carapace were characterized by morphological and biochemical tests, and identified at generic level by 16S rRNA sequence analyses. The highly adhesive bacteria, were Gram-negative, oxidase-positive, short rods (1.2-2.8 µm in length). For the genus level identification, 16S rRNA sequence of both the isolates were amplified and sequencing was done. Through BLAST search, it was found that both of N- and C-terminus nucleotide sequences of the 16S rRNA gene of one of the bacterial isolate perfectly matched (100 % similarity) with only those of *Shewanella woodyi* (Fig. 2B). Other isolate, matched (99 % similarity) with *Roseobacter* sp. (Fig. 2C & D).

Analyses of TTX

Along with authentic TTX standards, both the extracts were examined for TTX and related substances by high performance liquid chromatography (HPLC). A small amount of these Fr. I and II mentioned above were subjected to gas chromatography –mass spectrometry (GC-MS) and liquid chromatography–mass spectrometry. As authentic toxins, TTX standard containing several percent of 4epi-TTX and anhydrotetrodotoxin (anhyTTX) was prepared from the ribbon worm *Cephalothrix* sp. (Asakawa *et al*., 2000). HPLC analysis of *Roseobacter* sp., two peaks, with retention times (Rt) of 14.1 and 16.3 min, corresponded well to the retention times of TTX and anhyTTX, respectively. TTX and anhyTTX, were detected from the culture supernatant of *Roseobacter* sp., by HPLC and GC-MS. Mass spectral analysis showed a protonated molecule ion of $(M+H)^+$ at m/z 320 and the other ion of $(M+H-H_2O)^+$ at m/z 302.

Discussion

Naturally-occurring rod-shaped bacteria are seen on both dorsal and lateral parts of the cephalothorax of *P. fugu*. It was reported that *Vibrio* spp. predominantly attached on the body surface of the planktonic copepods and in gut (Sochard *et al*., 1979) in contrast to our study on parasitic copepods. Multiplication of *Vibrio* takes place on the body surface, thereby enhancing the possibility of disease. After colonization by bacteria, multiplication takes place on the copepod surface rather than in the water samples. After multiplication, the cells are joined by additionally attaching cells and leads to the formation of microcolonies (Nagasawa, 1986).

The adhesion of bacteria to the parasitic copepod has considerable ecological significance. These bacteria, with their high adhesive ability, could colonize and degrade the chitinous material comprising the cuticle of the copepod. Usually, nutrient less location are selected by bacteria for their attachment. In the adhesion experiment, only two types of bacteria were virulent with high adhesive affinity to the carapace. The present method, experimental infection of bacteria-free shrimp carapace, is useful to determine whether the isolates have a high adhesive ability or not

(Venmathi Maran *et al.,* 2007).

The γ-proteobacteria *S. woodyi,* a Gram-negative, facultatively anaerobic, motile, short rod was first isolated from the squid ink and sea water samples from depths of 200-300m in the Alboran Sea. During the last decade, the genus *Shewanella* has received significant attention due to its important role in co-metabolic bioremediation of halogenated organic pollutants. The α-proteobacteria *Roseobacter* is a Gram-negative, aerobic, motile rod (Holt *et al.,* 1994). *Roseobacter* species are ecologically significant because they play a major role in the production of toxin in dinoflagellates. When the non-toxic dinoflagellate *Alexandrium tamaranse* mixed with *Roseobacter* sp., it can produce the toxin.

The TTX-bearing animals are considered not to synthesize the toxin by themselves but to accumulate TTX through food chain starting from the marine bacteria that produce TTX. It is strongly suggested that bacteria like *Vibrio*, *Pseudomonas*, *Shewanella*, *Alteromonas* and others have been shown to produce TTX, although the produced amount of TTX was very small. In addition to TTX, bacterial production of anhyTTX was also reported. Although TTX-productivity of the bacteria isolated from the positive strain is much less, due to the culture conditions. Research on the mechanism of TTX synthesis and also on optimization of culture conditions in laboratory could be helpful. However, it was reported that *Vibrio alginolyticus* produced 213 MU of TTX in the medium containing 1% NaCl and 1% Phytone peptone in 72 hr culture. These facts suggested that bacteria are closely related to the toxification of pufferfish. More research is needed on aspects such as, whether puffer fish accumulate the TTX-producing bacteria through the food or come from the environment (Noguchi *et al.,* 2006).

The bacteria *Shewanella alga* and *Alteromonas tetraodonis* isolated from a red alga *Jania* sp. produce TTX. *Shewanella putrefaciens* from the pufferfish *Takifugu niphobles* and many other marine bacteria isolated from TTX-bearing organisms have also been reported to produce TTX. In relation to that, the two high adhesive types of bacteria have been isolated from *P. fugu* for TTX. Though *Shewanella* is known as a TTX producer (Simidu *et al.,* 1987), TTX and its derivatives are not detected in *S. woodyi*. On the other hand, *Roseobacter* sp. exhibited productivity of TTX Though some *Roseobacter* strains are known to be toxic, for the first time it is reported that the genus *Roseobacter* as a tetrodotoxin producer (Venmathi Maran *et al.,* 2007).

In general, TTX produced in the host puffers mainly due to the bacteria and also by the ingestion of toxic diets. In this study, our earlier hypothesis was that the isolated bacteria would be a pathogen for the fishes and could act as a vector however, the results shown that they are not pathogenic. On the other hand, they are involved in the production of TTX. At present, *Roseobacter* strain is considered as a TTX producer and its analog, anhydro-TTX for the first time. Even though, other bacteria *Shewanella* was not positive in HPLC analysis, still presume that they could be involved in the production of TTX, since previous studies suggested *Shewanella* as the toxin producer. Although, we investigated only in limited strains for TTX, the results indicate that TTX-producing bacteria are quite widespread among various attached bacterial groups. The exact mechanism of the synthesis of TTX by bacteria and the role of TTX in the bacteria themselves are still unknown. It seems reasonable to postulate that TTX is synthesized solely by bacteria which could be transferred from the host puffer to the parasite. More research is needed to elucidate the mechanism of TTX synthesis and the role of TTX in bacteria (Venmathi Maran *et al.,* 2011).

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I am thankful to Professors S. Ohtsuka, T. Nakai and M. Asakawa, Hiroshima University, for their support during this study. I also thank Korea Research Council of Fundamental Science and Technology (KRCF) and Korea Institute of Ocean Science and Technology (KIOST) projects (PK08080) for financial support to prepare the article.

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Biofuel waste product recycled for electricity

A by-product of biofuel manufacture can power microbial fuel cells to generate electricity cheaply and efficiently, according to scientists presenting their work at the Society for General Microbiology's Autumn Conference. The work could help to develop self-powered devices that would depollute waste water and be used to survey weather in extreme environments.

Distillers Dried Grain with Solubles (DDGS) is a waste product from bioethanol production that is commonly used as a low-cost animal feed. Researchers from the University of Surrey incorporated DDGS together with bacteria-inoculated sludge from a waste water treatment plant in their microbial fuel cell. The design of the fuel cell meant that the bacteria, which used the DDGS for their growth, were physically separated from their oxygen supply. This meant that the bacteria were forced into sending electrons around a circuit leading to a supply of oxygen. By tapping into this electron flow, electricity could be generated from the waste.

Microbial fuel cells offer the ability to convert a wide range of complex organic waste products into electrical energy, making it an attractive target technology for renewable energy. Finding cost-efficient starting products is necessary to help commercialize the process, explained Lisa Buddrus who is carrying out the research. "DDGS is potentially one of the most abundant waste products in the UK. As the biofuel industry expands the supply of DDGS will become more abundant," she said. "The next step for us is to identify the electrogenic bacterial species that grow on DDGS. Furthermore, by looking at genetics across this microbial community, we will be able to better understand the metabolic processes and essential genes involved in electron liberation and transfer." she said.

As well as being low-cost, microbial fuel cells that use DDGS are very eco friendly. The waste that is left following electricity extraction is of greater value, as it is less reactive with oxygen, making it less polluting. "We've found something really useful from a waste product without affecting its value as animal feed and at the same time improving its environmental status. This is something we place great importance on and within our group we have a team solely

dedicated to reducing polluting potential," said Professor Mike Bushell who is leading the group.

A lot of microbial fuel cell research focuses on developing environmental sensors in remote locations. "Self-powered sensors in remote places such as deserts or oceans can be used to provide important data for monitoring weather or pollution. Other applications in focus for microbial fuel cells include treating waste water to produce green electricity and clean up the water at the same time," explained Professor Bushell.

Source: www.sciencedaily.com

Scientists use microbes to make 'Clean' Methane

Microbes that convert electricity into methane gas could become an important source of renewable energy, according to scientists from Stanford and Pennsylvania State universities.

Researchers at both campuses are raising colonies of microorganisms, called methanogens, which have the remarkable ability to turn electrical energy into pure methane, the key ingredient in natural gas. The scientists' goal is to create large microbial factories that will transform clean electricity from solar, wind or nuclear power into renewable methane fuel and other valuable chemical compounds for industry.

"Most of today's methane is derived from natural gas, a fossil fuel," said Alfred Spormann, a professor of chemical engineering and of civil and environmental engineering at Stanford. "And many important organic molecules used in industry are made from petroleum. Our microbial approach would eliminate the need for using these fossil resources."

While methane itself is a formidable greenhouse gas, it is 20 times more potent than CO_2, the microbial methane would be safely captured and stored, thus minimizing leakage into the atmosphere, Spormann said.

"The whole microbial process is carbon neutral," he explained. "All of the CO_2 released during combustion is derived from the atmosphere, and all of the electrical energy comes from renewables or nuclear power, which are also CO_2-free."

He also added methane-producing microbes, could help to solve one of the biggest challenges for large-scale renewable energy: What to do with surplus electricity generated by photovoltaic power stations and wind farms.

"Right now there is no good way to store electricity," Spormann said. "However, we know that some methanogens can produce methane directly from an electrical current. In other words, they metabolize electrical energy into chemical energy in the form of methane, which can be stored. Understanding how this metabolic process works is the focus of our research. If we can engineer methanogens to produce methane at scale, it will be a game changer."

'Green' methane

Burning natural gas accelerates global warming by releasing CO_2 that's been trapped underground for millennia. The Stanford and Penn State team is taking a "greener" approach to methane production. Instead of drilling rigs and pumps, the scientists envision large bioreactors filled with methanogens single-cell organisms that resemble bacteria but belong to a genetically distinct group of microbes called archaea.

By human standards, a methanogen's lifestyle is extreme. It cannot grow in the presence of oxygen. Instead, it regularly dines on atmospheric CO_2 and electrons borrowed from hydrogen gas. The byproduct of this microbial meal is pure methane, which methanogens excrete into the atmosphere.

The researchers plan to use this methane to fuel airplanes, ships and vehicles. In this ideal scenario, cultures of methanogens would be fed a constant supply of electrons generated from emission-free power sources, such as solar cells, wind turbines and nuclear reactors. The microbes would use these clean electrons to metabolize CO_2 into methane, which can then be stockpiled and distributed via existing natural gas facilities and pipelines when needed.

When the microbial methane is burnt as a fuel, CO_2 would be recycled back into the atmosphere where it is originated from unlike conventional natural gas combustion, which contributes to global warming.

"Microbial methane is much more ecofriendly than ethanol and other biofuels," Spormann said. "Corn ethanol, for example, requires acres of cropland as well as fertilizers, pesticides, irrigation and fermentation. Methanogens are much more efficient, because they metabolize methane in just a few quick steps."

Microbial communities

For this new technology to become commercially viable, a number of fundamental challenges must be addressed. "While conceptually simple, there are significant hurdles to overcome before electricity-to-methane technology can be deployed at a large scale," said Bruce Logan, a professor of civil and environmental engineering at Penn State. "That's because the underlying science of how these organisms convert electrons into chemical energy is poorly understood."

In 2009, Logan's lab was the first to demonstrate that a methanogen strain known as *Methanobacterium palustre* could convert an electrical current directly into methane. For the experiment, Logan and his Penn State colleagues built a reverse battery with positive and negative electrodes placed in a beaker of nutrient-enriched water.

The researchers spread a biofilm mixture of *M. palustre* and other microbial species onto the cathode. When an electrical current was applied, the *M. palustre* began churning out methane gas. "The microbes were about 80 percent efficient in converting electricity to methane," Logan said.

The rate of methane production remained high as long as the mixed microbial community was intact. But, when a previously isolated strain of pure *M. palustre* was placed on the cathode alone, the rate plummeted, suggesting that methanogens separated from other microbial species are less efficient than those living in a natural community.

"Microbial communities are complex," Spormann added. "For example, oxygen-consuming bacteria can help to stabilize the community by preventing the build-up of oxygen gas, which methanogens cannot tolerate. Other microbes compete with methanogens for electrons. We want to identify the composition of different communities and see how they evolve together over time."

Microbial zoo

To accomplish that goal, Spormann has been feeding electricity to laboratory cultures consisting of mixed strains of archaea and bacteria. This microbial zoo includes bacterial species that compete with methanogens for CO_2, which the bacteria uses to make acetate an important ingredient in vinegar, textiles and a variety of industrial chemicals. "There might be organisms that are perfect for making acetate or methane but haven't been identified yet," Spormann said. "We need to tap into the unknown, novel organisms that are out there."

At Penn State, Logan's lab is designing and testing advanced cathode technologies that will encourage the growth of methanogens and maximize methane production. The Penn State team is also studying new materials for electrodes, including a carbon-mesh fabric that could eliminate the need for platinum and other precious metal catalysts.

"Many of these materials have only been studied in bacterial systems but not in communities with methanogens or other archaea," Logan said. "Our ultimate goal is to create a cost-effective system that reliably and robustly produces methane from clean electrical energy. It's high-risk, high-reward research, but new approaches are needed for energy storage and for making useful organic molecules without fossil fuels."

The Stanford-Penn State research effort is funded by a three-year grant from the Global Climate and Energy Project at Stanford.

Post-doctoral fellow Svenja Lohner, left, and Professor Alfred Spormann. Their research, along with the work of others, could help solve one of the biggest challenges for large-scale renewable energy: What to do with surplus electricity generated by photovoltaic power stations and wind farms.

(**Image Credit:** Linda A. Cicero / Stanford News Service)

Source: www.sciencedaily.com

Viruses help scientists battle pathogenic bacteria and improve water supply

Infectious bacteria received a taste of their own medicine from University of Missouri researchers who used viruses to infect and kill colonies of *Pseudomonas aeruginosa*, common disease-causing bacteria. The viruses, known as bacteriophages, could be used to efficiently sanitize water treatment facilities and may aid in the fight against deadly antibiotic-resistant bacteria.

Source: www.phys.org

Microbiologist patents process to improve biofuel production

Biofuel production can be an expensive process that requires considerable use of fossil fuels, but a Missouri University of Science and Technology microbiologist's patented process could reduce the cost and the reliance on fossil fuels, while streamlining the process.

The process involves a microbe that thrives in extreme conditions. Dr. Melanie Mormile, a professor of biological sciences at Missouri S&T, has found a particular bacterium, called *Halanaerobium hydrogeniformans*, that can be used to streamline biofuel production. Because the bacterium thrives in high-alkaline, high-salt conditions, it can eliminate the need to neutralize the pH of the biomass, a step required in the alkali treatment of biomass for production of hydrogen fuel and other biofuels. Mormile and her fellow researchers have been awarded two patents for developing a biofuel production process that uses the bacterium.

"In the development of biofuels, a lot of energy is required to break down the biomass to the point where bacteria can ferment it to form ethanol or, in our case, hydrogen and other useful products," Mormile says.

The conventional method of biofuel production involves the steam blasting of switchgrass and straw to separate lignin, an unnecessary byproduct, from the cellulose that is needed to create the biofuel. The process requires electricity, produced by either coal or natural gas, to generate the steam. That process releases considerable amounts of CO_2, while remaining dependent on fossil fuels. The degradation of the lignin produces compounds that inhibit fermentation and lead to overall low hydrogen yields. Treating the switchgrass and straw with an alkaline substance removes the lignin with limited formation of the harmful compounds, but the resulting slurry is highly alkaline and very salty. Before the discovery of *H. hydrogeniformans*, a neutralization step was required before the fermentation process could begin. Using Mormile's bacterium, that step can be eliminated.

"This shows promise in producing hydrogen from alkaline pre-treated biomass," Mormile says. "With alkaline pre-treatment, you don't have to apply heat, and using our bacterium will allow you to skip the neutralization process. It makes this a less expensive and more efficient process."

Mormile's team is getting results.

"We are seeing hydrogen production similar to a genetically modified organism and we haven't begun to tweak the genome of this bacterium yet."

Mormile is now looking for ways to optimize growth of the organism and minimize the cost. She is working with Dr. Oliver Sitton, Associate Professor of Chemical and Biochemical Engineering at Missouri S&T, to optimize growth of the bacterium in a bioreactor.

"We have shown that we can produce hydrogen in a lab-scale reactor," Mormile says. "The next step in the project is to find the best growth medium and optimize the hydrogen production from this organism."

"We realize this isn't going to solve all the transportation fuel problems, but we'd like to see this develop into regionalized solutions," Mormile explains. "Farm communities could take agricultural waste, perform the alkaline pretreatment, feed it to an onsite reactor and produce hydrogen fuel directly for use on the farm."

Mormile studies extremophiles life forms that exist in extreme conditions. The *H. hydrogeniformans* bacterium used in Mormile's hydrogen fuel production study came from Soap Lake in Washington State.

Soap Lake is unique in that, it has not turned over in more than 2,000 years because of its high salinity. Its water has the same pH as ammonia and is 10 times saltier than seawater.

"Normally, lakes turn over twice a year due to temperature changes in the water," Mormile explains. "Throughout the year, material like dead algae with all their nutrients accumulate at the bottom of the lake. During the summer months, the bottom of the lake stays cool while the surface gets warm, trapping the nutrients at the bottom. As fall approaches, the temperature throughout the whole lake becomes the same and mixing or turnover can occur." Soap Lake's shape and high bottom salt content prevent it from turning over, trapping those nutrients.

"The bottom section of the lake contains so much salt it's like syrup," said Mormile. In the future, Mormile hopes to return to Soap Lake to look for more new organisms.

"This process is only one step," Mormile says. "We know our bacteria can't break down cellulose, a crystalline molecule that provides structure for plants and trees. So we want to find bacterium that can break the cellulose into smaller components that our fermenting bacteria can utilize."

Also named on the patents are Dr. Dwayne Elias of the biosciences division of Oak Ridge National Laboratory, Matthew B. Begemann of the Microbiology Doctoral Training Program at the University of Wisconsin-Madison, and Dr. Judy D. Wall of the University of Missouri-Columbia biochemistry department.

Source: www.sciencedaily.com

New coating evicts biofilms for good

Biofilms may no longer have any solid ground upon which to stand. A team of Harvard scientists has developed a slick way to prevent the troublesome bacterial communities from ever forming on a surface. Biofilms stick to just about everything, from copper pipes to steel ship hulls to glass catheters. The slimy coatings are more than just a nuisance, resulting in decreased energy efficiency, contamination of water and food supplies, and especially in medical settings persistent infections. Even cavities in teeth are the unwelcome result of bacterial colonies.

In a study published in the Proceedings of the National Academy of Sciences (PNAS), lead coauthors Joanna Aizenberg, Alexander Epstein, and Tak-Sing Wong coated solid surfaces with an immobilized liquid film to trick the bacteria into thinking they had nowhere to attach and grow.

"People have tried all sorts of things to deter biofilm build-up textured surfaces, chemical coatings, and antibiotics, for example," says Aizenberg, Amy Smith Berylson Professor of Materials Science at the Harvard School of Engineering and Applied Sciences (SEAS) and a Core Faculty Member at the Wyss Institute for Biologically Inspired Engineering at Harvard. "In all those cases, the solutions are short-lived at best. The surface treatments wear off, become covered with dirt, or the bacteria even deposit their own coatings on top of the coating intended to prevent them. In the end, bacteria manage to settle and grow on just about any solid surface we can come up with."

Taking a completely different approach, the researchers used their recently developed technology, dubbed SLIPS (Slippery-Liquid-Infused Porous Surfaces) to effectively create a hybrid surface that is smooth and slippery due to the liquid layer that is immobilized on it.

It was first described in the September 22, 2011, issue of the journal Nature, the super-slippery surfaces have been shown to repel both water- and oil-based liquids and even prevent ice or frost from forming.

"By creating a liquid-infused structured surface, we deprive bacteria of the static interface they need to get a grip and grow together into biofilms," says Epstein, a recent Ph.D. graduate who worked in Aizenberg's lab at the time of the study.

"In essence, we turned a once bacteria-friendly solid surface into a liquid one. As a result, biofilms cannot cling to the material, and even if they do form, they easily 'slip' off under mild flow conditions," adds Wong, a researcher at SEAS and a Croucher Foundation Postdoctoral Fellow at the Wyss Institute.

Aizenberg and her collaborators reported that SLIPS reduced by 96-99% the formation of three of the most notorious, disease-causing biofilms *Pseudomonas aeruginosa*, *Escherichia coli,* and *Staphylococcus aureus* over a 7-day period.

The technology works in both a static environment and under flow, or natural conditions, making it ideally suited for coating implanted medical devices that interact with bodily fluids. The coated surfaces can also combat bacterial growth in environments with extreme pH levels, intense ultraviolet light, and high salinity.

SLIPS is also nontoxic, readily scalable, and most importantly self-cleaning, needing nothing more than gravity or a gentle flow of liquid to stay unsoiled. As previously demonstrated with a wide variety of liquids and solids, including blood, oil, and ice, everything seems to slip off surfaces treated with the technology.

To date, this may be the first successful test of a nontoxic synthetic surface that can almost completely prevent the formation of biofilms over an extended period of time. The approach may find application in medical, industrial, and consumer products and settings.

In future studies, the researchers aim to better understand the mechanisms involved in preventing biofilms. In particular, they are interested in whether any bacteria transiently attach to the interface and then slip off, if they just float above the surface, or if any individuals can remain loosely attached.

"Biofilms have been amazing at outsmarting us. And even when we can attack them, we often make the situation worse with toxins or chemicals. With some very cool, nature-inspired design tricks we are excited about the possibility that biofilms may have finally met their match," concludes Aizenberg.

Aizenberg and Epstein's coauthors included Rebecca A. Belisle, research fellow at SEAS, and Emily Marie Boggs '3, an undergraduate biomedical engineering concentrator at Harvard College. The authors acknowledge support from the Department of Defense Office of Naval Research; the Croucher Foundation; and the Wyss Institute for Biologically Inspired Engineering at Harvard University.

The word "SLIPS" is coated with the SLIPS technology to show its ability to repel liquids and solids and even prevent ice or frost from forming. The slippery discovery has now been shown to prevent more than 99 percent of harmful bacterial slime from forming on surfaces.
(**Image Credit:** Joanna Aizenberg, Rebecca Belisle, and Tak-Sing Wong)

Source: www.sciencedaily.com

NEWS

NASA claim of arsenic-friendly life form untrue

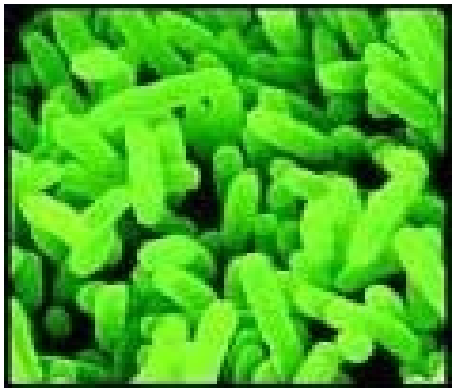
WASHINGTON: The claim by NASA scientists that they have discovered a new form of bacteria which thrive on arsenic has been disapproved by two new studies, which say the bugs can't substitute arsenic for phosphorus to survive.

Two scientific papers, published in the journal Science, refuted the 2010 NASA finding that bacterium called GFAJ-1 not only tolerates arsenic but actually incorporates the poison into its DNA, swapping out phosphorus. "Contrary to an original report, the new research clearly shows that the bacterium, GFAJ-1, cannot substitute arsenic for phosphorus to survive," the journal said.

"If true, that finding would have important implications for our understanding of life's basic requirements since all known forms of life on earth use six elements : oxygen, carbon, hydrogen, nitrogen, phosphorus and sulphur," it said.

If an organism on earth were found to survive without one of these building blocks, it could mean that life on other planets (as well as our own) is more adaptable than expected. Felisa Wolfe-Simon, who led the NASA study, acknowledged very low levels of phosphate within their study samples; but, they concluded the contamination would've been insufficient to allow GFAJ-1 to grow.

Now, the two separate studies find that Wolfe-Simon's medium did contain enough phosphate contamination to support GFAJ-1's growth. It's just that GFAJ-1, a well-adapted extremophile living in a high-arsenic environment, is thrifty, and is likely capable of scavenging phosphate under harsh conditions, helping to explain why it can grow even when arsenic is present in its cells, the new studies claimed.



Source: The Times of India, July 10, 2012.

3D motion of common cold virus offers hope for improved drugs using Australia's fastest supercomputer

Melbourne researchers are now simulating in 3D, the motion of the complete human rhinovirus, the most frequent cause of the common cold, on Australia's fastest supercomputer, paving the way for new drug development.

Rhinovirus infection is linked to about 70 per cent of all asthma exacerbations with more than 50 per cent of these patients requiring hospitalisation. Furthermore, over 35 per cent of patients with acute chronic obstructive pulmonary disease (COPD) are hospitalised each year due to respiratory viruses including rhinovirus.

A new antiviral drug to treat rhinovirus infections is being developed by Melbourne company Biota Holdings Ltd, targeted for those with these existing conditions where the common cold is a serious threat to their health and could prove fatal. A team of researchers led by Professor Michael Parker from St Vincent's Institute of Medical Research (SVI) and the University of Melbourne is now using information on how the new drug works to create a 3D simulation of the complete rhinovirus using Australia's fastest supercomputer.

"Our recently published work with Biota shows that the drug binds to the shell that surrounds the virus, called the capsid. But that work doesn't explain in precise detail how the drug and other similar acting compounds work," Professor Parker said.

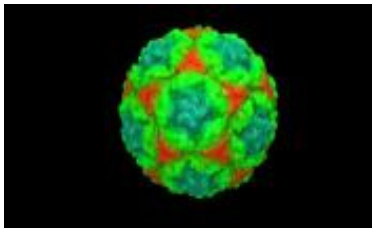
Professor Parker and his team are working on the newly installed IBM Blue Gene/Q at the University of Melbourne with computational biologists from IBM and the Victorian Life Sciences Computation Initiative (VLSCI). In production from 1 July 2012, the IBM Blue Gene/Q is the most powerful supercomputer dedicated to life sciences research in the Southern Hemisphere and currently ranked the fastest in Australia.

"The IBM Blue Gene/Q will provide us with extraordinary 3D computer simulations of the whole virus in a time frame not even dreamt of before," Professor Parker said. "Supercomputer technology enables us to delve deeper in the mechanisms at play inside a human cell, particularly how drugs work at a molecular level.

"This work offers exciting opportunities for speeding up the discovery and development of new antiviral treatments and hopefully save many lives around the world," he said. Professor Parker said that previously we have only been able to run smaller simulations on just parts of the virus. Professor James McCluskey Deputy Vice-Chancellor (Research) at the University of Melbourne said: "The work on rhinovirus is an example of how new approaches to treat disease will become possible with the capacity of the IBM Blue Gene Q, exactly how we hoped this extraordinary asset would be utilised by the Victorian research community in collaboration with IBM."

"This is a terrific facility for Victorian life science researchers, further strengthening Victoria's reputation as a leading biotechnology centre," he said. Dr John Wagner, Manager, IBM Research Collaboratory for Life Sciences-Melbourne, co-located at VLSCI, said these types of simulations are the way of the future for drug discovery.

"This is the way we do biology in the 21st Century," he said. The newly operational IBM Blue Gene/Q hosted by the University of Melbourne at the VLSCI is ranked 31st on the prestigious global TOP500 list. The TOP500 table nominates the 500 most powerful computer systems in the world. The VLSCI is an initiative of the Victorian Government in partnership with the University of Melbourne and the IBM Life Sciences Research Collaboratory, Melbourne.

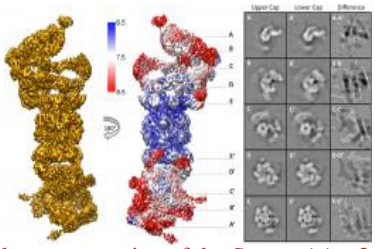


This is a surface rendering of the common cold virus.

Source: Biology News Net, July 17, 2012

Making a molecular micromap: Imaging the yeast 26S proteasome at near-atomic resolution

Biological systems are characterized by a form of molecular recycling and unneeded or damaged proteins biochemically marked for destruction undergo controlled degradation by having their peptide bonds broken by proteasomes. Recently, scientists at the Max-Planck Institute of Biochemistry in Germany used cryo-electron microscopy (cryo-EM) single particle analysis and molecular dynamics techniques to map the *Saccharomyces cerevisiae* 26S proteasome. The researchers then used this map to build a near-atomic resolution structural model of the proteasome. The Max Planck team showed that cryo-electron microscopy allowed them to successfully model the 26S core complex where X-ray crystallography studies conducted over the past 20 years have not.



Single particle reconstruction of the *S. cerevisiae* 26S proteasome without imposed symmetry (A–E), using a cryo-electron microscope.

Source: www.phys.org

Abstracts

001. González R, García-Balboa C, Rouco M, Lopez-Rodas V, Costas E. Genetica, Facultad de Veterinaria, Universidad Complutense, 28040, Madrid, Spain. **Adaptation of microalgae to lindane: a new approach for bioremediation.** Aquatic Toxicology, 2012, **109**, 25 - 32.

Lindane is especially worrisome because its persistence in aquatic ecosystems, tendency to bioaccumulation and toxicity. We studied the adaptation of freshwater cyanobacteria and microalgae to resist lindane using an experimental model to distinguish if lindane-resistant cells had their origin in random spontaneous pre-selective mutations (which occur prior to the lindane exposure), or if lindane-resistant cells arose by a mechanism of physiological acclimation during the exposure to the selective agent. Although further research is needed to determine the different mechanisms contributing to the bio-elimination of lindane, this study, however, provides an approach to the bioremediation abilities of the lindane-resistant cells. Wild type strains of the experimental organisms were exposed to increasing lindane levels to estimate lethal concentrations. Growth of wild-type cells was completely inhibited at 5mg/L concentration of lindane. However, after further incubation in lindane for several weeks, occasionally the growth of rare lindane-resistant cells was found. A fluctuation analysis demonstrated that lindane-resistant cells arise only by rare spontaneous mutations that occur randomly prior to exposure to lindane (lindane-resistance did not occur as a result of physiological mechanisms). The rate of mutation from lindane sensitivity to resistance was between 1.48×10^{-5} and 2.35×10^{-7} mutations per cell per generation. Lindane-resistant mutants exhibited a diminished fitness in the absence of lindane, but only these variants were able to grow at lindane concentrations higher than 5mg/L (until concentrations as high as 40 mg/L). Lindane-resistant mutants may be maintained in uncontaminated waters as the result of a balance between new resistant mutants arising from spontaneous mutation and resistant cells eliminated by natural selection waters via clone selection. The lindane-resistant cells were also used to test the potential of microalgae to remove lindane. Three concentrations (4, 15 and 40 mg/L) were chosen as a model. In these exposures the lindane-resistant cells showed a great capacity to remove lindane (until 99% lindane was eliminated). Apparently, bioremediation based on lindane-resistant cells could be a great opportunity for cleaning up of lindane- and other chlorinated organics-polluted habitats.

Keywords: Adaptation, Bioremediation, Lindane, Microalgae, Mutation.

002. Alguacil Mdel M, Torrecillas E, Hernández G, Roldán A. CSIC-Centro de Edafología y Biología Aplicada del Segura, Department of Soil and Water Conservation, Campus de Espinardo, Murcia, Spain. **Changes in the diversity of soil arbuscular mycorrhizal fungi after cultivation for biofuel production in a guantanamo (cuba) tropical system.** PLoS One. 2012, **7** (4). 1 - 8.

The arbuscular mycorrhizal fungi (AMF) are a key, integral component of the stability, sustainability and functioning of ecosystems. In this study, we characterised the AMF biodiversity in a native vegetation soil and in a soil cultivated with *Jatropha curcas* or *Ricinus communis*, in a tropical system in Guantanamo (Cuba), in order to verify if a change of land use to biofuel plant production had any effect on the AMF communities. We also asses whether some soil properties related with the soil fertility (total N, Organic C, microbial biomass C, aggregate stability percentage, pH and electrical conductivity) were changed with the cultivation of both crop species. The AM fungal small sub-unit (SSU) rRNA genes were subjected to PCR, cloning, sequencing and phylogenetic analyses. Twenty AM fungal sequence types were identified: 19 belong to the Glomeraceae and one to the Paraglomeraceae. Two AMF sequence types related to cultured AMF species (Glo G3 for *Glomus sinuosum* and Glo G6 for *Glomus intraradices-G. fasciculatum-G. irregulare*) did not occur in the soil cultivated with *J. curcas* and *R. communis*. The soil properties (total N, Organic C and microbial biomass C) were higher in the soil cultivated with the two plant species. The diversity of the AMF community decreased in the soil of both crops, with respect to the native vegetation soil, and varied significantly depending on the crop species planted. Thus, *R. communis* soil showed higher AMF diversity than *J. curcas* soil. In conclusion, *R. communis* could be more suitable for the long-term conservation and sustainable management of these tropical ecosytems.

Keywords: arbuscular mycorrhizal fungi, native vegetation soil, fungal small sub-unit, mycorrhizal fungi.

E - Resources on Microorganisms

NATIONAL

Centre for Excellence in Genomic Sciences
http://www.genomicsmku.org/

National Fungal Culture Collection of India
http://www.aripune.org/NFCCI.html

North Bengal University Bacterial Culture Repository Unit
http://nrrl.ncaur.usda.gov/

National Collection of Industrial Microorganisms
www.ncl-india.org/ncim/

National Facility for Marine Cyanobacteria
http://www.nfmc.res.in/

INTERNATIONAL

Bacillus Genetic Stock Center
http://www.bgsc.org/

Plymouth Culture Collection of Marine Microalgae
http://www.mba.ac.uk/culture-collection/

IBT Culture Collection of Fungi
http://fbd.dtu.dk/straincollection/

Collection of Environmental and laboratory microbial Strains
http://www.tymri.ut.ee/214568

Culture Collection of Algae at the University of Cologne
http://www.ccac.uni-koeln.de/

EVENTS
Conferences / Seminars / Meetings 2012 - 2013

3rd International Conference on Microbial Communication. November 5 - 8, 2012. **Venue:** Jena, **Germany.**
Website: http://www.micom-conference.de/

Marine Microbiology and Biotechnology: Biodiscovery, Biodiversity and Bioremediation. November 14 - 16, 2012.
Venue: Western Gateway Building, University College Cork, Cork, **Ireland.**
Website: http://www.ucc.ie/en/mmbiotech2012/

IInd International Conference on Antimicrobial Research. November 21 – 23, 2012. Venue: Lisbon, **Portugal**.
Website: http://www.formatex.org/icar2012/index.html

Annual Conference of the Assiociation for General and Applied Microbiology (VAAM). March 10 - 13, 2013.
Venue: Messe Bremen, **Germany**. **Website:** http://www.clocate.com/conference/Annual-Conference-of-the-Association-for-General-and-Applied-Microbiology-VAAM-2013/30740/

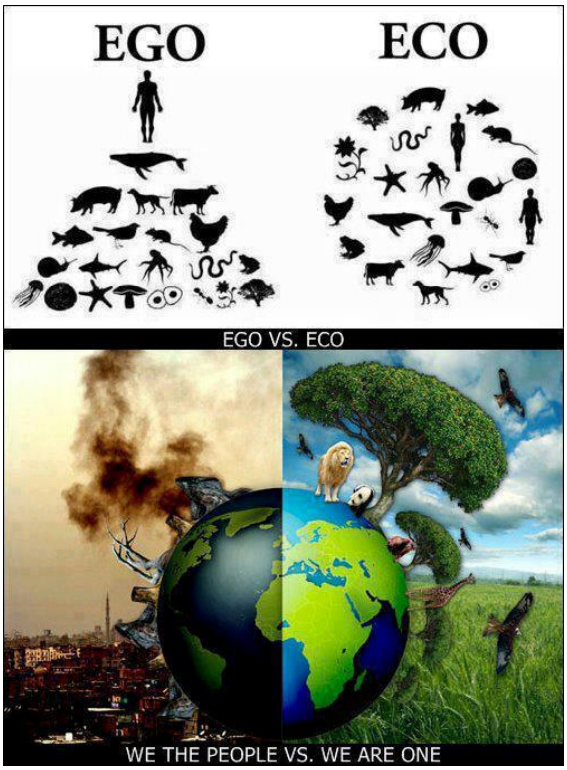
TEHRAN (FNA) - When it comes to germ-busting power, the eyes have it, according to a discovery by researchers that could lead to new, inexpensive antimicrobial drugs.

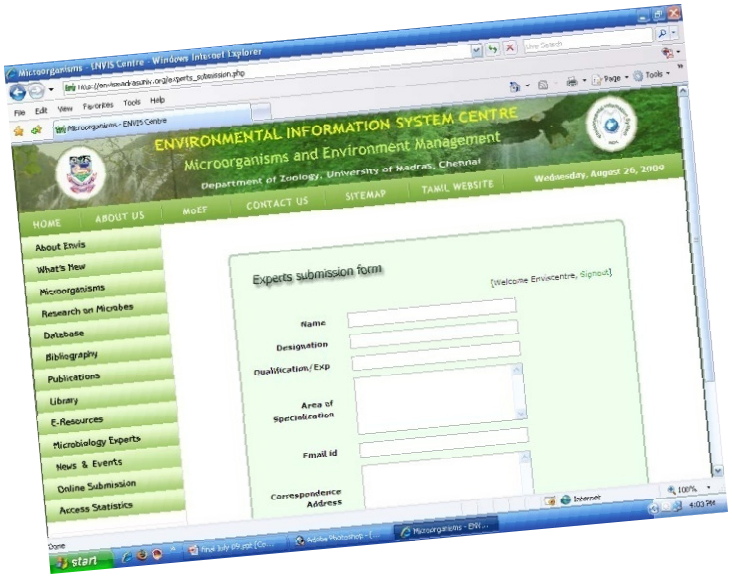
Eye proteins have germ - Killing power

Proteins in the eye can help to keep pathogens at bay, finds a new UC Berkeley study. A team of UC Berkeley vision scientists has found that small fragments of keratin proteins in the eye play a key role in warding off pathogens. The researchers also put synthetic versions of these keratin fragments to the test against an array of nasty pathogens. These synthetic molecules effectively zapped bacteria that can lead to flesh-eating disease and strep throat (*Streptococcus pyogenes*), diarrhoa (*Escherichia coli*), staph infections (*Staphylococcus aureus*) and cystic fibrosis lung infections (*Pseudomonas aeruginosa*).

Source: www.english.farsnews.com

Participation of ENVIS CENTRE at National Evaluation Meeting, Bhopal (29th & 30th Aug 2012)





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