



# ENVIS NEWSLETTER

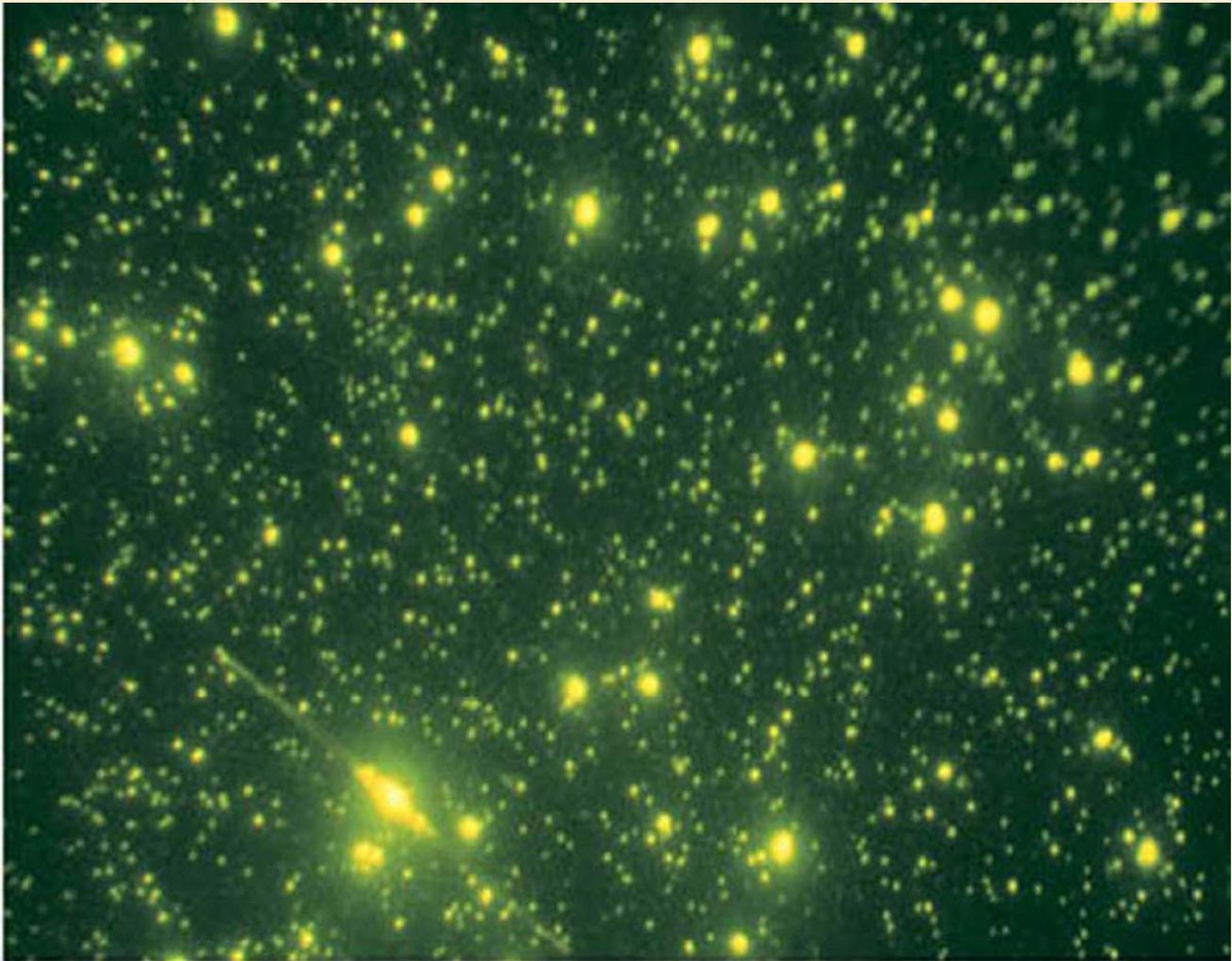
MICROORGANISMS AND ENVIRONMENT MANAGEMENT  
(Sponsored by Ministry of Environment and Forests, Government of India)



VOLUME 8

ISSUE 2

APR - JUN 2010



## ENVIS CENTRE

Department of Zoology

University of Madras, Guindy Campus, Chennai - 600 025

Telefax: 91-44-22300899; E-mail: [dzum@envis.nic.in](mailto:dzum@envis.nic.in); [enviscoordinator@gmail.com](mailto:enviscoordinator@gmail.com)

Websites: [www.envismadrasuniv.org](http://www.envismadrasuniv.org); [www.dzumenvis.nic.in](http://www.dzumenvis.nic.in); [www.envismicrobes.in](http://www.envismicrobes.in) (Tamil website)

**ISSN - 0974 - 1550**

Volume 8 | Issue 2 | Apr - Jun 2010

**EDITORS**

**Prof. N. Munuswamy**

(ENVIS Co-ordinator)

**Dr. T. Sathish Kumar**

(Scientist - D)

**ENVIS TEAM**

**Prof. N. Munuswamy** (Co-ordinator)

**Dr. T. Sathish Kumar** (Scientist - D)

**Mr. T. Tamilvanan** (Programme Officer)

**Mr. D. Siva Arun** (Programme Asstt.)

**Mr. M. Manirajan** (Data Entry Operator)

**PUBLISHED BY**

**Environmental Information System (ENVIS)**

Department of Zoology

University of Madras, Guindy Campus,

Chennai - 600 025, Tamilnadu, India.

**SPONSORED BY**

**Ministry of Environment and Forests**

Government of India

New Delhi.



*Staphylococcus epidermidis* bacteria causes biofilms on plastic devices

**INSTRUCTIONS TO CONTRIBUTORS**

ENVIS Newsletter on Microorganisms and Environment Management, a quarterly publication, publishes 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.

The articles and other information should be typed in double space with maximum of 8 - 10 typed pages. Photographs/line drawings and graphs need to be of good quality with clarity for reproduction in the newsletter. For references and other details, the standard format used in referred journals may be followed.

Articles should be sent to:

**The Co-ordinator**

**ENVIS Centre**

Department of Zoology

University of Madras

Guindy Campus, Chennai – 600 025.

Tamil Nadu, INDIA

(OR)

Send your articles by e-mail:

**enviscoordinator@gmail.com**

**dzum@envis.nic.in**

Cover page : An environmental sample containing marine viruses (small dots), bacteria (larger, brighter dots) and a diatom (long thin cell with prominent nucleus) stained with SYBR Green nucleic acid stain.

Courtesy: Jed Fuhrman, University of Southern California

**ENVIS Newsletter**  
**on**  
**Microorganisms and Environment Management**

**Contents**

**SCIENTIFIC ARTICLES**

Page No

**Marine Actinomycetes - potential but less tapped resource for antifouling compounds too !** 2

V. Gopikrishnan, M. Radhakrishnan and R. Balagurunathan

**RESEARCH NOTE**

**Effect of low - level laser irradiation on rat gut microflora** 4

A. A. Agababova and H. A. Movsesyan

**RESEARCH REPORTS**

**Soil microbes produce less atmospheric CO<sub>2</sub> than expected with climate warming** 5

**Bacterial genes that improve plant growth by 40% identified** 6

**Tiny marine microbes exert influence on Global climate: Microorganisms display a behavior characteristic of larger animals** 7

**ONLINE REPORTS ON MICROORGANISMS**

**Microbial answer to plastic pollution** 8

**Microorganisms in toxic groundwater fine - tuned to survive** 9

**NEWS**

**Martian life quest stymied by Earth microbes** 10

**ABSTRACTS OF RECENT PUBLICATIONS** 10

**E - RESOURCES ON MICROORGANISMS** 13

**EVENTS** 13

*Dear Readers,*

The clean-up of anthropogenic and xenobiotic contaminants from the environment is one of the problems currently in focus globally. It is ironic and tragic that we continue to witness the horrendous environmental fallout of the Bhopal Gas tragedy that happened 25 years ago!

We all agree that bio-degradation is a natural process. An ecosystem can be defined by its threshold assimilative capacity for xenobiotic chemicals. Appropriate bio-stimulation can convert the xenobiotic chemical into a substrate for assimilation by microorganisms, thereby creating an opportunity for restoration of the habitat. Recent advancements in technology, particularly metagenomics, bring new awareness to research on microbial diversity and technical innovation that facilitates study of physiology and ecology of environmental microorganisms. Thus microbial communities are being used for environmental clean-up and for a wealth of other services to society.

This issue also includes articles on Biofouling, a costly problem encountered in a wide spectrum of technical systems ranging from shipping industry to food industries. Our regular features included are research reports, online reports, abstracts, e-resources and events on microorganisms.

It gives us great pleasure to share our views with you. We sincerely look forward to your suggestions and feedbacks. Please do mail us at [www.envismadrasuniv.org/send\\_feedback.php](http://www.envismadrasuniv.org/send_feedback.php).

**Prof. N. Munuswamy**

For further details, visit our website

[www.envismadrasuniv.org](http://www.envismadrasuniv.org)

**World Environment Day - 5<sup>th</sup> June 2010**



**Marine Actinomycetes - potential but less tapped resource for antifouling compounds too !****V. Gopikrishnan, M. Radhakrishnan and R. Balagurunathan\***Department of Microbiology,  
Periyar University,  
Salem - 636 011, Tamilnadu, India.

\*email: rbalaguru@yahoo.com

**Introduction**

Marine biofouling is the result of the growth of microorganisms, plants and animals on surfaces immersed in the natural environment. The organisms involved in marine fouling are primarily attached or sessile forms commonly occurring in shallow waters along the coastline. The biofouling process occurs in the natural environment in sequential steps. Within minutes of immersion, a pristine surface becomes 'conditioned' through the adsorption of organic layers of macromolecules. The conditioned surface is later colonized by microorganisms, including bacteria, algae (especially diatoms), fungi and protozoa. The attachment, colonization and growth of microorganisms on the surface results in the formation of a slimy layer called biofilm. The biofilm layer can aid (or deter) the subsequent succession of 'macrofouling' species, such as barnacles, by facilitating adhesion or through the production of bioactive molecules (D'Sousa *et al.*, 2010).

**Problems of biofouling**

Biofouling is an ongoing problem for water-immersed man-made structures such as ship's hulls (Fig. 1), oceanographic instrumentation, pipelines, membranes, heat exchangers and aquaculture equipment, resulting in severe economic consequences (Schultz, 2007). Biofouling (Figs. 2 & 3) is especially economically significant on ship hulls where high levels of fouling can reduce the performance of the vessel and increase its fuel requirements. Fouling causes huge material and economic costs in maintenance of mariculture, shipping industries, naval vessels, and seawater pipelines. Governments and industry spend more than US\$ 5.7 billion annually to prevent and control marine biofouling. Biofouling can also occur in groundwater wells where build - up can limit recovery flow rates, and in the exterior and interior of ocean - laying pipes. In the latter case it has been shown to retard the

seawater flow through the pipe and has to be removed with the tube cleaning process. Biofouling also occurs on the surfaces of living marine organisms, when it is known as epibiosis.

**Fig. 1. Barnacles on ship hulls****Fig. 2. Biofouling****Fig. 3. Fouling boat****Biofouling control - Facts & Problems**

In efforts to avoid marine biofouling, antifouling paints are used, mostly with organotin like tri-n-butyltin (TBT), in which copper and organonitrogen compounds as very effective active agents. The worldwide use of TBT - based paints has caused a growing pollution in the environment and in foods on a worldwide scale and also banned the use of TBT. At present, a major challenge for the producers of coatings is to develop alternative technologies to prevent fouling on ship hulls. Safer methods of biofouling control at the research level are use of copper compounds in paints and its continued use as metal sheeting (for example Muntz metal which was specifically made for this purpose), though there is still a debate on the safety of copper. The Office of Naval Research (ONR) has developed environmentally safe biomimetic ship coatings that protect against both

barnacles and biofilms. Due to increasing restrictive regulations on the use of TBT and other polluting antifouling compounds, there is a growing need for other methods to prevent marine biofouling (Gademann, 2007).

Several physical, mechanical, chemical and biological methods for the prevention of marine biofouling have been tested in the last 40 years (Abarzua *et al.*, 1999). The production and isolation of biogenic agents from marine organisms and their embedding in non - poisonous coatings seems to be the most promising and effective method for the prevention of marine fouling. Many marine organisms especially microalgae and marine invertebrates produce biogenic agents with antibacterial, antifungal, antialgal, antiprotozoan, antilarval and antimolluscidal property to defend themselves against settlement in the marine environment and are therefore rarely fouled by other organisms. Some of these secondary metabolites possess potent antifouling activity (Clare, 1996), but their antifouling activity under laboratory and field conditions are unknown.

#### **Antifouling compounds from marine actinomycetes**

Actinomycetes are a group of Gram - positive bacteria which form filamentous structure with asexual spores and have high Guanine plus Cytosine (G+C) content in their DNA. Diversity of actinomycetes in various natural and man-made ecosystems is well documented in recent years. Actinomycetes are primarily recognized as a source for high value metabolites such as antibiotics, antivirals, anticancers, enzymes and recombinant products in which most of them are of terrestrial origin (Balagurunathan and Radhakrishnan, 2007). Recently marine derived actinomycetes are also under exploitation especially for antibiotics and anticancer agents. In the past 10 years, 659 marine bacterial compounds have been described with majority derived from actinomycetes (Williams, 2009). As marine environmental conditions are extensively different from terrestrial ones, the marine actinomycetes are different from those of terrestrial strains in producing different types of bioactive compounds. Unique compounds like salinosporamide and abyssomycin from marine actinomycete genera *Salinispora* and *Verrocosispora* add a new dimension to marine natural product research. Unfortunately actinomycetes in general and marine actinomycetes in particular are less / unexploited as antifouling compounds.

The first step in laboratory antifouling research work is the isolation of biogenic compounds and their testing on the growth of fouling organisms. Till date, antifouling compounds are reported from marine organisms like bacteria, algae and certain plants; but such reports from marine actinomycetes are scanty. An antifouling diketopiperazine was reported from deep sea bacterium *Streptomyces fungicidicus* (Li *et al.*, 2006). You *et al.* (2007) studied inhibition of *Vibrio* biofilm formation by a marine actinomycete A66, *Streptomyces albus*. Recently, Xu *et al.* (2010) isolated five structurally similar compounds from the crude extract of a marine *Streptomyces* strain obtained from deep - sea sediments. Antifouling activities of these five compounds and four other structurally - related compounds isolated from a North Sea *Streptomyces* strain against major fouling organisms were compared to probe structure - activity relationships of compounds. The functional moiety responsible for antifouling activity lies in the 2 - furanone ring and that the lipophilicity of compounds substantially affects their antifouling activities. Based on these findings, a compound with a straight alkyl side - chain was synthesized and proved itself as a very effective non - toxic, anti - larval settlement agent against three major fouling organisms. The strong antifouling activity, relatively low toxicity, and simple structures of these compounds make them promising candidates for new antifouling additives. Therefore, isolation of biogenic compounds from actinomycetes and determination of their structures could provide leads for future development of environment - friendly antifouling paints.

#### **Conclusion**

In the future, progress in the field of isolation and production of antifouling compounds is expected to involve the integration of biochemistry validated post - genomic methods and technologies and intelligent bioprocess design.

One of the most important things for developing antifouling compounds from marine actinomycetes is that they must meet the standard of the EC Biocide Directive for registered toxins. There is a need to investigate the levels of toxicity and capacities for biological degradation in the aquatic environment of actinomycetes compounds before they are used in antifouling paints and polymers for the prevention of fouling.

Moreover, it is necessary to monitor it over a long term period, once the actinomycetes compounds become incorporated into antifouling paints. This is beginning, as trials have shown that paints into which extracts of marine actinomycetes have been incorporated are effective in controlling foulers in the marine environment. However, the identification of these actinomycetes compounds with antifouling properties requires a wide range of expertise from the field of biology as well as chemistry. Due to this, antifouling compounds from marine actinomycetes with commercial potential will take time to develop. Metabolic engineering approaches are the possible way forward for future exploitation of secondary metabolites with antifouling properties from marine actinomycetes.

### References:

- Abarzua, S., Jakubowski, S., Eckert, S. and Fuchs, P. (1999) Biotechnological investigations for the prevention of marine biofouling. II. Blue Green Algae as potential producers of biogenic agents for the growth inhibition of macrofouling organisms. *Botanica Marina*. **42**, 459 - 465.
- Balagurunathan, R. and Radhakrishnan, M. (2007) Actinomycetes: Diversity and their importance - An overview in microbiology - Applications and current trends (editor) P.C.Trivedi, Pointer publishers Rajasthan. 297 - 329.
- Clare, A. S. (1996) Marine natural product antifoulants: status and potential. *Biofouling*. **9**, 211 - 229.
- D'Sousa, F., Bruin, R., Blerstekar, A., Donnelly, G., Klijnstra, J., Rentrop, C. and Wiilemsen, P. (2010) Bacterial assay for the rapid assessment of fouling and fouling release properties of coatings and materials. *J. Ind. Microbiol. Biotechnol*, **37**, 363 - 370.
- Gademann, K. (2007) Cyanobacterial natural products for the inhibition of biofilm formation and biofouling. *Chimia*, **61**, 373 - 377.
- Li, X., Dobretsov, S., Xu, Y., Xiao, X., Hung, O. S. and Qian, P. (2006) Antifouling diketopiperazines produced by a deep - sea bacterium, *Streptomyces fungicidicus*, *Biofouling*, **22**(3), 187 - 194.
- Schultz, M. P. (2007) Effects of coating roughness and biofouling on ship resistance and powering. *Biofouling*, **23**, 331 - 341.
- You, J. L., Xue, X. L., Cao, L. X., Lu, X., Wang, J., Zhang, L. X. and Zhou, S. N. (2007) Inhibition of *Vibrio* biofilm formation by a marine actinomycete strain A66. *Appl. Microbiol. Biotechnol*, DOI; 10.1007/s00253 - 007 - 1074.

Williams, P.G. (2009) Panning for chemical gold: marine bacteria as a source of new therapeutics. *Trends in Biotechnology*, **27**, 45 - 52.

Xu, Y., He, H. , Schulz, S., Liu, X., Fusetani, N. and Xiong, H. (2010) Potent antifouling compounds produced by marine *Streptomyces*. *Bioresource Technology*, **101**:1331 - 1336.

### RESEARCH NOTE

#### Effect of low - level laser irradiation on rat gut microflora

**A. A. Agababova \* and H. A. Movsesyan**

H. Buniatyan Institute of Biochemistry,  
National Academy of Sciences,  
Republic of Armenia (RA),  
5/1 Sevak St., Yerevan, 0014, RA.

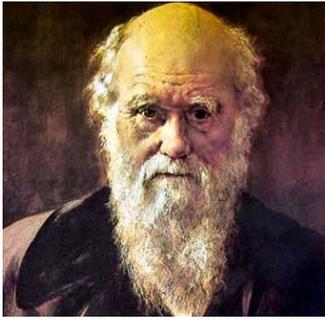
\*email: h2moska@rambler.ru

Recently, there has been an increase in the clinical application of low - level laser irradiation (LLLI) in various fields. LLLI may affect a bacterial growth, and in this study we examine the time - dependent effect of LLLI on the rat intestinal flora, particularly on the bacterium *Escherichia coli*.

Male Wistar rats were treated with a semiconductor laser (SCL) radiation (continuous wave,  $\lambda = 654$  nm, fluence = 1.27 J/cm<sup>2</sup>) for 5, 10, 20 and 30 min. The animals were decapitated immediately after a single irradiation, and feces from the lower part of the gut were examined for microflora.

After 5 min exposure to SCL, lactose - negative forms of *E. coli* and *Klebsiella pneumoniae* were observed, whilst *E. coli* growth was inhibited completely in 24 h incubated samples from gut feces. A 10 min - treatment with SCL induced a growth of *Candida* and decreased a growth of lactose - negative *E. coli* up to 80%, in contrast to *Klebsiella* whose growth was not affected. In gut microflora of 20 min - irradiated rats, were found single colonies of lactose - negative forms of *E. coli* and successfully grown *Klebsiella*, *Candida*, and several strains of *Streptococci* that were not seen in feces of control rats. A 30 - min SCL treatment caused a substantial enhancement of *Klebsiella*, and *Candida* growth, whereas all forms of *E. coli* disappeared under these conditions.

They have demonstrated that a single irradiation by coherent red light caused time - dependent changes in the intestinal microflora of healthy rats that might affect host homeostasis and the right balance of immune system kept by gut microbes.



### Soil microbes produce less atmospheric CO<sub>2</sub> than expected with climate warming

The physiology of microbes living underground could determine the amount of carbon dioxide emitted from soil on a warmer Earth, according to a study recently published online in *Nature Geoscience*.

Researchers at UC (University of California) Irvine, Colorado State University and the Yale School of Forestry & Environmental Studies found that as global temperatures increase, microbes in soil become less efficient over time at converting carbon in soil into carbon dioxide, a key contributor to climate warming.

Microbes, in the form of bacteria and fungi, use carbon for energy to breathe, or respire, and to grow in size and in number. A model developed by the researchers shows microbes exhaling carbon dioxide furiously for a short period of time in a warmer environment, leaving less carbon to grow on. As warmer temperatures are maintained, the less efficient use of carbon by the microbes causes them to decrease in number, eventually resulting in less carbon dioxide being emitted into the atmosphere.

“Microbes aren't the destructive agents of global warming that scientists had previously believed,” said Steven Allison, Assistant Professor of Ecology & Evolutionary Biology at UCI and lead author on the study. “Microbes function like humans: They take in carbon - based fuel and breathe out carbon dioxide. They are the engines that drive carbon cycling in soil. In a balanced environment, plants store carbon in the soil and microbes use that carbon to grow. The microbes then produce enzymes that convert soil carbon into atmospheric carbon dioxide.”

The study, “Soil - Carbon Response to Warming Dependent on Microbial Physiology,” contradicts the results of older models that assume microbes will continue to spew ever - increasing amounts of carbon dioxide into the atmosphere as the climate continues to warm. The new simulations suggest that if microbial efficiency declines in a warmer world, carbon dioxide emissions will fall back to pre - warming levels, a pattern seen in field experiments. But if microbes manage **5**

This year marks the 201<sup>th</sup> anniversary of Charles Darwin's birth. Darwin's ideas have influenced biology ever since, but his impact on microbiology is less well appreciated. Although it is commonly assumed that Darwin had nothing to say about microbes, he did in fact say quite a lot. He included microbes in his Beagle studies of the geographical distribution of organisms and used microscopic organisms as explicit exemplars of how adaptation did not imply increasing complexity. Darwin was both an audience of and a contributor to the natural history and experimental approaches to microbiology. The foremost microbiologists of the time corresponded with Darwin (e.g. Ferdinand Cohn, Christian Gottfried Ehrenberg). He read their work (e.g. Robert Koch's, Louis Pasteur's) and commented on it to others. Although Darwin did not draw heavily on the microbial world for observational data in his own work, he used his and others' knowledge of microorganisms to sustain his arguments about natural selection. Little was known about microbial physiology in the years in which Darwin developed his theory of natural selection. In the application of medicine, Darwin's evolutionary theory did find a temporary footing, primarily in relation to the concept of specificity and the tumultuous variation of the microbial world. Darwin often discussed microorganismal classification, origins and experimentation in his correspondence. But despite his interest in microbial phenomena, Darwin's impact on microbiological thinking of the late nineteenth century was negligible. This limited response may be connected to today's assumptions about Darwin's neglect of microbes. But today, despite the different evolutionary processes many microbes are known to undergo, Darwin's basic principle still holds sway.

(Adapted from <http://www.elsevier.com/copyright>)

to adapt to the warmth for instance, through increased enzyme activity emissions could intensify.



Fungi *Laccaria* species in Alaskan boreal forest are key drivers of the carbon cycle.

(Image Credit: Steve Allison, University of California, Irvine)

“When we developed a model based on the actual biology of soil microbes, we found that soil carbon may not be lost to the atmosphere as the climate warms,” said Matthew Wallenstein of the Natural Resource Ecology Laboratory at Colorado State University. “Conventional ecosystem models that didn't include enzymes did not make the same predictions.”

Mark Bradford, Assistant Professor of terrestrial ecosystem ecology at Yale, said there is intense debate in the scientific community over whether the loss of soil carbon will contribute to global warming. “The challenge we have in predicting this is that the microbial processes causing this loss are poorly understood,” he said. “More research in this area will help reduce uncertainties in climate prediction.”

Source: [www.sciencedaily.com](http://www.sciencedaily.com)

**Bacterial genes that improve plant growth by 40% identified**

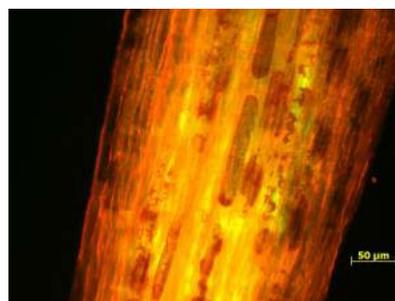
You might think bacteria that “invade” trees are there to cause certain destruction. But like the helpful bacteria that live within our guts, some microbes help plants thrive. To find out what makes these microbe - plant interactions “tick,” scientists at the U.S. Department of Energy's (DOE) Brookhaven National Laboratory decoded the genome of a plant - dwelling microbe they'd previously shown could increase plant growth by 40 percent. Their studies, described online in PLoS (Public Library of Science) Genetics, identified a wide range of genes that help explain this symbiotic success story. The work could move the approach of using bacteria as growth - promoting agents one step

closer to implementation for improved agriculture and biofuel production.

“To fuel and feed the planet for the future, we need new approaches,” said Brookhaven scientist Safiyh Taghavi, the study's lead author. “Biofuels derived from plants are an attractive alternative energy source, but many biofuel feedstock crops are in direct competition with food crops for agricultural resources such as land, water, and fertilizers. Our research is looking for ways to improve the growth of biofuel feedstock plants on land that cannot be economically used for food production. What we learn might also be put to use to increase the productivity of food crops,” she added.

The Brookhaven team has been studying a species of bacteria isolated from the roots of poplar trees. “Poplar is a model species for biofuel production, in part because of its ability to grow on marginal soils unsuitable for food crops,” said scientist Daniel (Niels) van der Lelie, who leads the research program. Previous studies by the van der Lelie-Taghavi group have shown that the bacterium *Enterobacter* (sp. 638) increases poplar growth by as much as 40 percent.

In the current study through genome sequencing performed at DOE's Joint Genome Institute, manual genome annotation in collaboration with Brookhaven biologist Sebastien Monchy, and metabolic analyses performed at the University of South Carolina in collaboration with Brookhaven plant scientist Lee Newman the scientists identified an extended set of genes that help *Enterobacter* (sp. 638) establish itself in this niche. The studies also revealed remarkable interactions between the microbe and its host that help the plant survive and thrive.



Bacteria living within poplar roots.

(Image Credit: DOE's Brookhaven National Laboratory)

Among the bacterial genes identified are ones that code for proteins that help the microbe survive and compete with other species for resources in the soil; take up nutrients released by plant roots; and move toward, adhere to, and colonize poplar root tissues. The microbes also have genes that provide benefits for the plant, including genes that may help confer drought resistance and the ability to coexist with toxic metals; genes that produce antimicrobial agents that protect plants from fungal and bacterial infections; and genes that produce plant-growth enhancing “phytohormones” and precursors that poplar cannot produce on its own.

“One of the most remarkable things about this association, which we confirmed with our metabolic assays, is that the production of these plant - growth - promoting phytohormones is directly dependent on the presence of plant - synthesized sugars, such as sucrose, in the growth medium. In addition, one metabolite (meso-2,3 butanediol) is known to elicit the induction of systemic tolerance to drought and induced systemic resistance against plant diseases,” Taghavi said. So the plant makes sugar that helps the bacteria grow and make phytohormones and other compounds that help the plants grow better and healthier.

“Interestingly, the genes that allow the bacteria to metabolize sucrose and the genes that produce the phytohormones are located on a genomic island, suggesting they may have been acquired together via natural horizontal gene transfer,” Taghavi said.

The scientists plan to continue their work by studying how these various genes are expressed during different stages of bacterial colonization of poplar. These detailed studies will further advance the scientists' understanding of the complex interactions, including the role of signaling compounds and other secondary metabolites that play a role in colonization and plant - growth promotion.

“These basic findings can eventually be translated into comprehensive strategies to exploit the use of these naturally occurring bacteria - plant relationships to improve plant establishment and biomass production. This approach can be applied to improve plant productivity for sustainable agriculture, bioenergy feedstock production on marginal lands, or to fight desertification of arid areas,” Van der Lelie said.

This research was funded by the DOE Office of Science. The DOE Joint Genome Institute unites the expertise of five national laboratories Lawrence Berkeley, Lawrence Livermore, Los Alamos, Oak Ridge, and Pacific Northwest along with the Hudson Alpha Institute for Biotechnology to advance genomics in support of the DOE missions related to clean energy generation and environmental characterization and cleanup. JGI (Joint Genome Institute) is operated for DOE by the University of California.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

**Tiny marine microbes exert influence on Global climate: Microorganisms display a behavior characteristic of larger animals**

New research indicates that the interactions of microscopic organisms around a particular organic material may alter the chemical properties of the ocean and ultimately influence global climate by affecting cloud formation in the atmosphere.

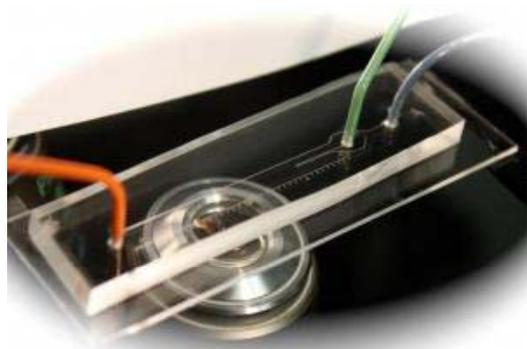
Justin Seymour, a research fellow at the University of Technology, Sydney, is the lead author of a paper published in the July 16, 2010 issue of Science that describes how a relative of the smelly chemical that sea birds and seals use to locate prey, dimethylsulfide (DMS), may serve a similar purpose at the microbial scale, helping marine microorganisms find food and cycle chemicals that are important to climate.

“We found that ecological interactions and behavioral responses taking place within volumes of a fraction of a drop of seawater can ultimately influence important ocean chemical cycling processes,” said Seymour.

Using microfluidic technology, the team of researchers led by Professor Roman Stocker of the Massachusetts Institute of Technology's Department of Civil and Environmental Engineering, recorded microbes swimming toward the chemical Dimethylsulfoniopropionate (DMSP) as it was released into a tiny channel occupied by the microbes.

The fact that the microbes actively moved toward the DMSP indicates that the tiny organisms play a role in ocean sulphur and carbon cycles, which exert a

powerful influence on Earth's climate. How fast the microorganisms consume DMSP rather than converting it into DMS is important because DMS is involved in the formation of clouds in the atmosphere. This in turn affects the heat balance of the atmosphere.



**Microchannel used to create patches of DMSP.**

**(Image Credit: Tanvir Ahmed and Roman Stocker)**

Seymour, Stocker, Professor Rafel Simó of the Institute for Marine Sciences in Barcelona, and MIT (Massachusetts Institute of Technology) graduate student Tanvir Ahmed carried out the research in the MIT laboratory of Stocker, who pioneered the use of microfluidics and video microscopy in the study of ocean microbes. The new study is the first to make a visual record of microbial behaviour in the presence of DMSP.

“It's important to be able to directly look at an environment in order to understand its ecology,” Stocker said. “We can now visualize the behavior of marine microorganisms much like ecologists have done with macro-organisms for a long time.”

To do this, the team recreated a microcosm of the ocean environment using a microfluidic device about the size of a flash drive with minuscule channels engraved in a clear rubbery material. The scientists injected DMSP into the channel in a way that mimics the bursting of an algal cell after viral infection, a common event in the ocean then. Using a camera attached to a microscope, they recorded whether and how microbes swam towards the chemical.

The researchers found that some marine microbes, including bacteria, are attracted to DMSP because they feed on it, whereas others are drawn to the chemical because it signals the presence of prey. This challenges previous theories that this chemical might be a deterrent against predators.

“Our observations clearly show that, for some plankton, DMSP acts as an attractant towards prey rather than a deterrent,” said Simó, an expert on the role of DMSP in the sulfur cycle, “By simulating the microscale patches of the chemical cue and directly monitoring the swimming responses of the predators towards these patches, we get a much more accurate perception of these important ecological interactions than can be obtained from traditional bulk approaches.”

“These scientists have used impressive technology to study interactions between organisms and their chemical environment at the scales they actually take place,” said David Garrison, Director of the National Science Foundation (NSF)'s Biological Oceanography Program. “The research will give us new insight on the workings of microbial assemblages in nature.”

The research also indicates that marine microorganisms have at least one behavioral characteristic in common with larger sea and land animals: we're all drawn to food.

The team plans to extend the research from the laboratory to the ocean environment; the team is working on an experimental system that can be used on board oceanographic ships working with bacteria collected directly from the ocean.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

**ONLINE REPORTS ON MICROORGANISMS**

**Microbial answer to plastic pollution**

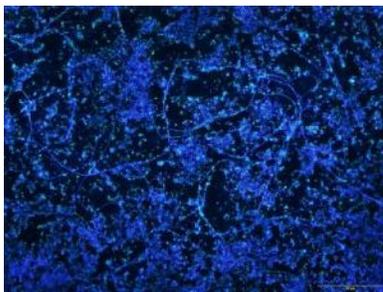
Fragments of plastic in the ocean are not just unsightly but potentially lethal to marine life. Coastal microbes may offer a smart solution to clean up plastic contamination, according to Jesse Harrison presenting his research at the Society for General Microbiology's spring meeting in Edinburgh.

The researchers from the University of Sheffield, UK and the Centre for Environment, Fisheries and Aquaculture Science (Executive agency of the UK government) have shown that the combination of marine microbes that can grow on plastic waste varies significantly from microbial groups that colonise surfaces in the wider

environment. This raises the possibility that the plastic associated marine microbes have different activities that could contribute to the breakdown of these plastics or the toxic chemicals associated with them.

Plastic waste is a long-term problem as its breakdown in the environment may require thousands of years. “Plastics form a daily part of our lives and are treated as disposable by consumers. As such, plastics comprise the most abundant and rapidly growing component of man-made litter entering the oceans,” explained Jesse Harrison.

Over time the size of plastic fragments in the oceans decreases as a result of exposure to natural forces. Tiny fragments of 5 mm or less are called “microplastics” and are particularly dangerous as they can absorb toxic chemicals which are transported to marine animals when ingested.



Microbes from the coastal seabed attached to plastic, as seen through a microscope.

(Image Credit: Jesse Harrison)

While microbes are the most numerous organisms in the marine environment, this is the first DNA - based study to investigate how they interact with plastic fragments. The new study investigated the attachment of microbes to fragments of polyethylene a plastic commonly used for shopping bags. The scientists found that the plastic was rapidly colonised by multiple species of bacteria that congregated together to form a ‘biofilm’ on its surface. Interestingly, the biofilm was only formed by certain types of marine bacteria.

The group, led by Dr. Mark Osborn at Sheffield, plans to investigate how the microbial interaction with microplastics varies across different habitats within the coastal seabed research which they believe could have huge environmental benefits. “Microbes play a key role in the sustaining of all marine life and are the most likely of all organisms to break down toxic chemicals, or even the plastics themselves,” suggested Mr Harrison. “This kind of research is also helping us unravel the

environmental impacts of plastic pollution,” he said.

Source: [www.sciencedaily.com](http://www.sciencedaily.com)

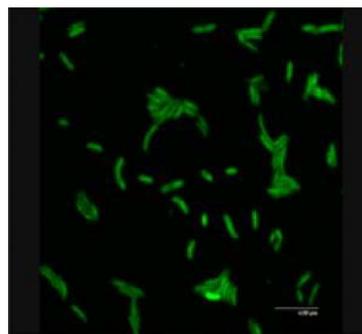
### Microorganisms in toxic groundwater fine - tuned to survive

Microorganisms can indeed live in extreme environments, but the ones that do are highly adapted to survive and little else, according to a collaboration that includes Department of Energy's (DOE's) Oak Ridge National Laboratory (ORNL) and Joint Genome Institute (JGI) and the University of Oklahoma.

The metagenomic study of a “stressed” microbial community in groundwater near a former waste disposal pond site on DOE's Oak Ridge Reservation (ORR) revealed microbes with an overabundance of genes involved in DNA recombination and repair and other defense mechanisms for dealing with contaminants and other environmental stresses.

The studies, said ORNL researcher David Watson, are ultimately aimed at developing biologically based methods for reducing the level of the contaminants in the groundwater, which at the ORR site includes nitrates, solvents and heavy metals, including uranium.

“We are looking to better understand the evolution of microbes in the groundwater plume,” Watson said. “The microbes that can break down nitrate into nitrogen can have a long-term benefit toward attenuating the plume.”



Microbes that live in contaminated groundwater.

(Image Credit: Image courtesy of DOE's Oak Ridge National Laboratory)

Watson added that researchers particularly want to better understand the genetic makeup of microbes that can metabolize oxidized forms of uranium into a form that is only slightly soluble and thus easier to precipitate and remove from the groundwater environment.

ORNL's Watson was joined in the study by the University of Oklahoma's Jizhong Zhou and Christopher Hemme; Joint Genome Institute Director Eddy Rubin and a team that included researchers from ORNL's Environmental Sciences Division, the University of Oklahoma's Institute for Environmental Genomics, Montana State University, Michigan State University and Lawrence Berkeley National Laboratory.

They found that the naturally occurring populations of microbes in the polluted groundwater which consisted of only a few cell types had “very simple” genetic structures tuned primarily to overcoming the stresses presented by the toxic soup, which has a highly acidic pH level of 3.5.

The accumulation of genes involved in resistance and responses to stress appears to be a basic survival strategy that has left the microbes with a marked loss in metabolic diversity.

The waste ponds, which are now part of the Oak Ridge Environmental Remediation Sciences Program Integrated Field Research Center, have been out of use for decades and were capped in 1983.

The research, recently published in the on-line ISME (International Society for Microbial Ecology) Journal, is sponsored by DOE's Office of Science.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

## NEWS

### Martian life quest stymied by Earth microbes

Bacteria common to spacecraft may be able to survive the harsh environs of Mars long enough to inadvertently contaminate Mars with terrestrial life according to research published in the April 2010 issue of the journal Applied and Environmental Microbiology.

#### Stated goal

The search for life on Mars remains a stated goal of NASA's Mars Exploration Program and Astrobiology Institutes. To preserve the pristine environments, the bioloads on spacecraft

headed to Mars are subject to sterilization designed to prevent the contamination of the Martian surface.

Despite sterilization efforts made to reduce the bioload on spacecraft, recent studies have shown that diverse microbial communities remain at the time of launch. The sterile nature of spacecraft assembly facilities ensures that only the most resilient species survive, including *Acinetobacter*, *Bacillus*, *Escherichia*, *Staphylococcus* and *Streptococcus*. Researchers from the University of Central Florida replicated Mars - like conditions by inducing desiccation, hypobaria, low temperatures, and UV irradiation.

#### Week-long study

During the week-long study they found that *Escherichia coli*, a potential spacecraft contaminant, may likely survive but not grow on the surface of Mars. This, if the microbe is shielded from UV irradiation by thin layers of dust or UV-protected niches in spacecraft, according to a University of Central Florida press release. “If long - term microbial survival is possible on Mars, then past and future explorations of Mars may provide the microbial inoculums for seeding Mars with terrestrial life,” say the researchers.

“Thus, a diversity of microbial species should be studied to characterise their potential for long term survival on Mars.”

**Source:** The Hindu, April 29, 2010.

### Abstracts

**001.** Ruyin Liu, Dong Li, Yingxin Gao, Yu Zhang, Song Wu, Ran Ding, Abd El - Latif Hesham and Min Yang. State Key Laboratory of Environmental Aquatic Chemistry, Research Center for Eco - Environmental Sciences, Chinese Academy of Sciences, P.O. Box 2871, Beijing 100085, China. **Microbial diversity in the anaerobic tank of a full-scale produced water treatment plant.** Process Biochemistry, 45(5), 2010, 744 - 751.

Microbial characteristics in the anaerobic tank of a full-scale produced water treatment plant capable of anaerobic hydrocarbon removal were analyzed and compared to those in the influent produced water using cultivation - independent molecular methods. Clones

related to methanogens including the methylotrophic *Methanomethylovorans thermophila* and hydrogen - and the formate-utilizing *Methanolinea tarda* were in abundance in both samples, but greater numbers of *M. tarda*-like clones were detected in the biofilm library. Both DGGE and cloning analysis results indicated that the archaea in the biofilm were derived from the influent produced water. Bacterial communities in the influent and biofilm samples were significantly different. *Epsilonproteobacteria* was the dominant bacterial group in the influent while *Nitrospira* and *Deltaproteobacteria* were the predominant groups in the biofilm. Many clones related to syntrophic bacteria were found among the *Deltaproteobacteria*. One *Deltaproteobacteria* clone was related to *Syntrophus*, which is commonly found in methanogenic hydrocarbon - degrading consortia. A number of *Deltaproteobacteria* clones were assigned to the clone cluster group TA, members of which predominate in various methanogenic consortia that degrade aromatic compounds. These results suggest that a microbial community associated with methanogenic hydrocarbon degradation may have been established in the biofilm.

**Keywords:** Produced water; Anaerobic tank; Biofilm; Archaea; Bacteria; Community.

**002.** Mal Nam Kim and Moon Gyung Yoon, Department of Biology, Sangmyung University, Seoul 110 - 743, Republic of Korea. **Isolation of strains degrading poly(Vinyl alcohol) at high temperatures and their biodegradation ability.** International Biodeterioration & Biodegradation, 64 (3), 2010, 184 - 190.

Thermophilic strains were isolated for the first time using activated sludge retrieved from wastewater treatment plant of a Poly Vinyl Alcohol (PVA) producing factory for biodegradation of PVA at relatively high temperatures. The isolated strains were identified to be *Geobacillus tepidamans*, *Brevibacillus brevis* and *Brevibacillus limnophilus*. The former strain degraded PVA for itself, while the latter 2 strains digested PVA symbiotically. PVA degradation activity of the isolated strains was assessed at first by the halo zone size formed around the colonies and finally by the modified Sturm test. The biodegradation rate of PVA was explored also in the presence of different dyes, because most of the wastewater from PVA - consuming factories contains waste dyes.

**Keywords:** Poly Vinyl Alcohol; Biodegradation; Thermophilic bacterium; *Geobacillus tepidamans*; *Brevibacillus brevis*; *Brevibacillus limnophilus*.

003. B. Rincón, F. Raposo, R. Borja , J.M. Gonzalez, M.C. Portillo and C. Saiz - Jimenez. Instituto de la Grasa, CSIC, Avda. Padre García Tejero 4, 41012 Sevilla, Spain. **Performance and microbial communities of a continuous stirred tank anaerobic reactor treating two - phases olive mill solid wastes at low organic loading rates.** Bioresource Technology, 101 (11), 2010, 3952 - 3957.

A study of the performance and microbial communities of a continuous stirred tank reactor (CSTR) treating two-phases olive mill solid wastes (OMSW) was carried out at laboratory - scale. The reactor operated at a mesophilic temperature (35 °C) and an influent substrate concentration of 162 g total Chemical Oxygen Demand (COD) L<sup>-1</sup> and 126 g volatile solids (VS) L<sup>-1</sup>. The data analyzed in this work corresponded to a range of organic loading rates (OLR) of between 0.75 and 3.00 g COD L<sup>-1</sup> d<sup>-1</sup>, getting removal efficiencies in the range of 97.0 - 95.6%. Methane production rate increased from 0.164 to 0.659 L CH<sub>4</sub> L<sub>reactor</sub><sup>-1</sup> d<sup>-1</sup> when the OLR increased within the tested range. Methane yield coefficients were 0.225 L CH<sub>4</sub> g<sup>-1</sup> COD removed and 0.290 L CH<sub>4</sub> g<sup>-1</sup> VS removed and were virtually independent of the OLR applied. A molecular characterization of the microbial communities involved in the process was also accomplished. Molecular identification of microbial species was performed by PCR amplification of 16S ribosomal RNA genes, denaturing gradient gel electrophoresis (DGGE), cloning and sequencing. Among the predominant microorganisms in the bioreactor, the Firmicutes (mainly represented by Clostridiales) were the most abundant group, followed by the Chloroflexi and the Gamma - Proteobacteria (*Pseudomonas* species as the major representative). Other bacterial groups detected in the bioreactor were the *Actinobacteria*, *Bacteroidetes* and *Deferribacteres*. Among the Archaea, the methanogen *Methanosaeta concilii* was the most representative species.

**Keywords:** Two - phases olive mill solid waste; Anaerobic digestion; Performance; Microbial community.

004. T. Hiuraa, Y. Hashidoko, Y. Kobayashi, S. Tahara. Division of Applied Bioscience, Graduate School of Agriculture, Hokkaido University, N-9, W-9, Kita-ku, Sapporo 060 - 8589, Japan. **Effective degradation of tannic acid by immobilized rumen microbes of a sika deer (*Cervus nippon yesoensis*) in winter.** *Animal Feed Science and Technology*, 155 (1), 2010, 1 - 8.

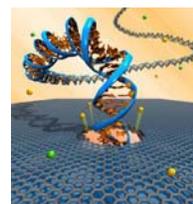
In winter seasons, wild sika deer (*Cervus nippon yesoensis*) inhabiting the Shiretoko Peninsula of Hokkaido Island, Japan, mainly graze woody materials (bark and twigs, etc.) as their feed source. Most of the tree species that they feed upon contain a high level of hydrolysable tannins within the inner bark. Tannins generally lead to low protein digestion and nutrient loss to these herbivorous mammals due to tannization of proteins. In winter months, it is speculated that wild sika deer develop a mechanism to degrade the tannins which are contained in their feed sources, but rumen fluid obtained from sika deer in winter months did not exhibit any ability to degrade tannins in liquid culture medium. However, constant degradation of hydrolysable tannin was observed when Ca - alginate gel beads were used for microbial immobilization and culturing. The gel beads that had been impregnated with  $0.6 \times 10^4$  fold - diluted rumen fluid of sika deer in winter and pre-incubated for 24 h under anaerobic conditions supplemented with a 1.5 g/L sugar were reacted with 5 g/L tannic acid solution. Under these conditions, the immobilized rumen bacteria grown in the macrogel beads effectively hydrolyzed tannic acid to release gallic acid monomers. Major bacterial colonies emerging in the Ca-alginate gel beads were identified as *Streptococcus macedonicus* and this bacterium (EC-D140) was regarded as the most likely candidate as the tannin - degrading bacterium.

**Keywords:** Winter sika deer; Rumen microbes; Tannic acid; Ca-alginate gel beads; *Streptococcus macedonicus*.

005. Gertler C, Näther DJ, Gerdts G, Malpass MC, Golyshin PN. School of Biological Sciences, Bangor University, Deiniol Road, Bangor, LL57 2UW, Gwynedd, UK. **A Mesocosm study of the changes in marine flagellate and ciliate communities in a crude oil bioremediation trial.** *Microbial Ecology*, 60(1), 2010, 180 - 191.

Protozoan grazers play an important role in controlling the density of crude - oil degrading marine communities as has been evidenced in a number of microcosm experiments. However, small bioreactors contain a low initial titre of protozoa and the growth of hydrocarbon - depleting bacteria is accompanied by the fast depletion of mineral nutrients and oxygen, which makes microcosms rather unsuitable for simulating the sequence of events after the oil spill in natural seawater environment. In the present study, the population dynamics of marine protozoan community have been analysed in a 500 l mesocosm experiment involving bioaugmented oil booms that contained oil sorbents and slow-release fertilisers. A significant increase in numbers of marine flagellates and ciliates on biofilms of oil - degrading microbes was microscopically observed as early as 8 days after the start of the experiment, when protozoa exhibited a population density peak making up to 3,000 cells ml<sup>-1</sup>. Further, the protozoan density varied throughout the experiment, but never dropped below 80 cells ml<sup>-1</sup>. An 18S rRNA gene - based fingerprinting analysis revealed several changes within the eukaryotic community over the whole course of the experiment. Initial growth of flagellates and small ciliates was followed by a predominance of larger protozoa. According to microscopic observations and SSU rRNA molecular analysis, most predominant were the ciliates belonging to Euplotidae and Scuticociliatia. This is the first study to characterise the eukaryotic communities specifically in a large - scale oil bioremediation trial using both microscopy - based and several molecular techniques.

#### A new electronic DNA sequencing



Researchers developed a new, carbon-based nanoscale platform to electrically detect single DNA molecules. Using electric fields, the tiny DNA strands are pushed through atomically-thin graphene nanopores that ultimately may sequence DNA bases by their unique electrical signature.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

## E - Resources on Microorganisms

### NATIONAL

National Institute of Virology (NIV)  
[www.niv.co.in](http://www.niv.co.in)

Amity Institute of Microbial Sciences (AIMS)  
[www.amity.edu/aims/default.htm](http://www.amity.edu/aims/default.htm)

Rajiv Gandhi Centre for Biotechnology  
[www.rgcb.res.in](http://www.rgcb.res.in)

National Facility for Marine Cyanobacteria (NFMC)  
[www.nfmc.res.in](http://www.nfmc.res.in)

National Centre for Biological Sciences  
[www.ncbs.res.in](http://www.ncbs.res.in)

### INTERNATIONAL

Microbiological Activity in Native Soils  
[www.pmac.net/mariaf.htm](http://www.pmac.net/mariaf.htm)

The Bacteriophage Ecology Group  
[www.phage.org](http://www.phage.org)

Society for Industrial Microbiology  
[www.simhq.org](http://www.simhq.org)

Federation of European Microbiological  
[www.fems-microbiology.org/website/nl/default.asp](http://www.fems-microbiology.org/website/nl/default.asp)

The Microbiology Information Portal  
[www.microbes.info](http://www.microbes.info)

## EVENTS

### Conferences / Seminars / Meetings 2010

**13th International Symposium on Microbial Ecology ISME13**, Aug 22 - 27, 2010. **Venue:** Seattle, **USA**. **Website:** [www.isme-microbes.org/isme13](http://www.isme-microbes.org/isme13).

**Bacterial Networks**, Sep 4 - 10, 2010. **Venue:** Hotel Eden Roc, Sant Feliu de Guixols (Costa Brava), **Spain**. **Website:** [www.esf.org/conferences/10335](http://www.esf.org/conferences/10335).

**International Conference on Climate Change and Environment**, Sep 22 - 24, 2010. **Venue:** Cochin University of Science and Technology, Kochi, Kerala, **India**. **Website:** [www.climate.niscair.res.in/conf.htm](http://www.climate.niscair.res.in/conf.htm).

**Power of Microbes in Industry and Environment 2010**, Sep 22 - 25, 2010. **Venue:** Malinska, Island Krk, **Croatia**. **Website:** [www.hmd-cms.hr/power2010](http://www.hmd-cms.hr/power2010).

**MICROBE 2010**, Sep 24 - 26, 2010. **Venue:** Sheffield, **UK**. **Website:** [www.microbe.org.uk/](http://www.microbe.org.uk/).

**International Workshop on Climate Change and Island Vulnerability**, Sep 26 - 28, 2010. **Venue:** Kadmat, Union Territory of Lakshadweep, **India**. **Website:** [www.climate.niscair.res.in/conf.htm](http://www.climate.niscair.res.in/conf.htm).

**3rd ASM Conference on Beneficial Microbes**, Oct 25 - 29, 2010. **Venue:** Miami, **USA**. **Website:** [www.asm.org/index.php](http://www.asm.org/index.php).



### Ocean bacteria also harvest energy from sunlight

It was long thought that Phytoplankton were the only organisms in the sea that could use sunlight for energy. Recently marine microbiologists collected 20 marine bacteria from different ocean areas, several of them have a gene in their DNA that codes for a new type of light - capturing pigment: Proteorhodopsin which converts solar energy to energy for growth and a new type of bacterial photosynthesis that takes place in the seas.

**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

## Environmental Symbols



Biodegradable

Indicates that an object is capable of being recycled



The symbol signifies that the packaging has been tested and is suitable for putting into compost collection



It means that the energy consumption of appliance is below agreed level in stand-by mode



The symbol represents Biohazard



This symbol requests that you dispose of your waste thoughtfully and do not litter



**From right: Prof. T. Balasubramanian**, Director and ENVIS In-charge, Centre of Advanced Study in Marine Biology, Annamalai University, releasing the Tamil brochure (special issue) on “Microorganisms and Environment Management” received by **Prof. N. Munuswamy**, Co-ordinator, ENVIS Centre, Department of Zoology, University of Madras and **Prof. K. Kathiresan**, Centre of Advanced Study in Marine Biology, Annamalai University.



Join with us in “Experts Directory Database”  
Send your details through:

[www.envismadrasuniv.org/experts\\_submission.php](http://www.envismadrasuniv.org/experts_submission.php)

