



ENVIS NEWSLETTER

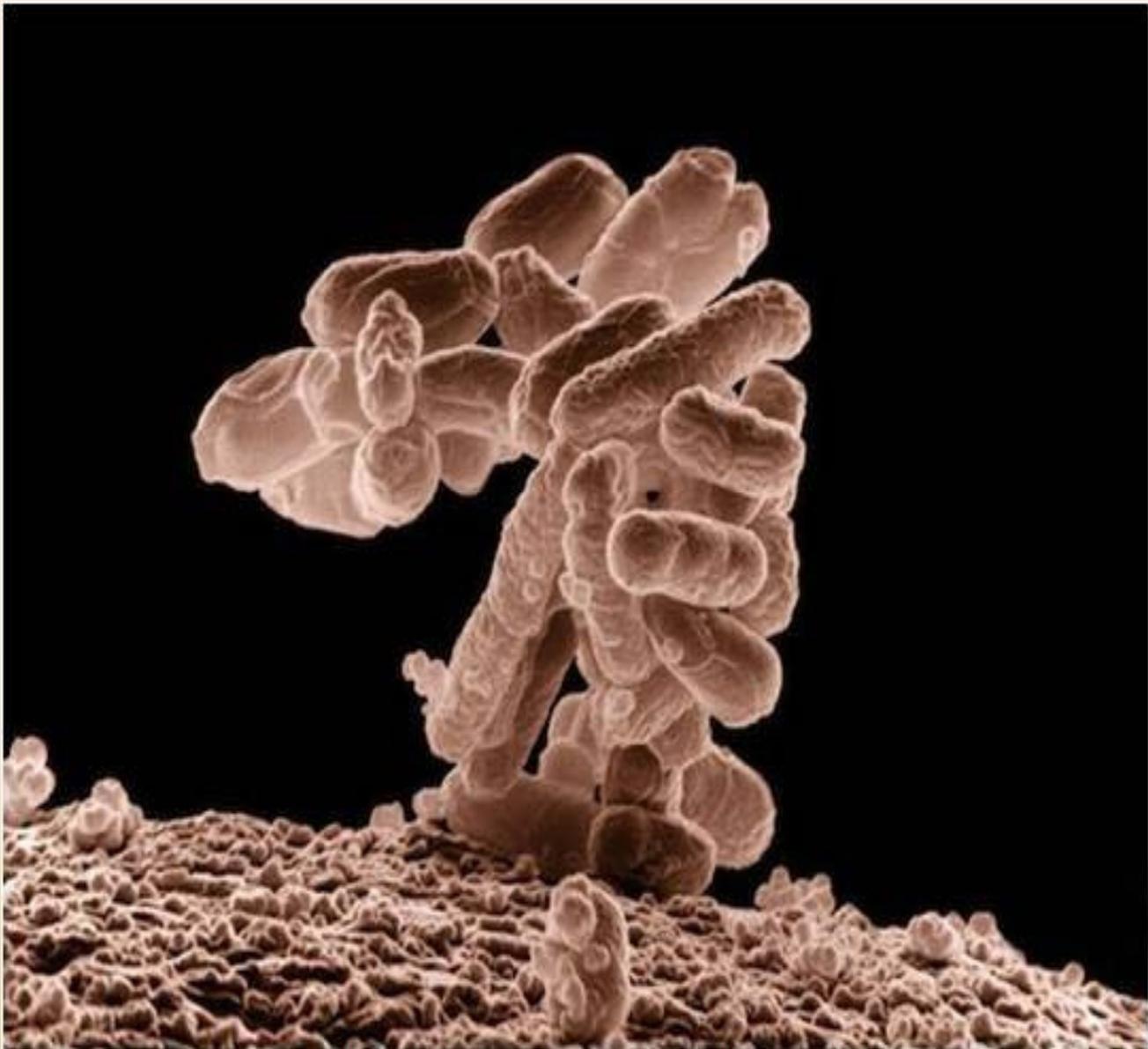
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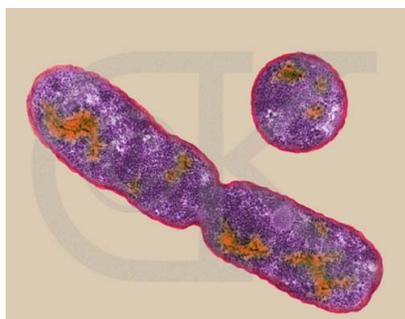
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Bacterial reproduction

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.

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Cover page : Glowing bioluminescent bacteria

ENVIS Newsletter
on
Microorganisms and Environment Management

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Dear Readers,

Contaminants to the environment causing ecological problems leading to imbalance in nature is of global concern. Understanding adverse effects of contaminants leads to improved regulation, management and control. The ideal solution for pollution abatement is the use of biological systems. Bioremediation, the most effective innovative technology, includes bio-stimulation (stimulating viable native microbial population), bio-augmentation (artificially introduction of viable population), phytoremediation (plants) and phycoremediation (microalgae), its central thrust depends on microbes. Phycoremediation is environmental friendly and has been widely used for the disposal of industrial wastes.

Nowadays marine microorganisms have fascinated many biologists of their unique, biologically active secondary metabolites especially from **fungi**. Many secondary metabolites from marine sources tend to be more highly bioactive against many types of tumor and viruses compared to the terrestrial derived bio-products. In spite of the sea's vast potential identified, this domain remains relatively unexplored.

In this issue, you will find articles on the developments, importance and current practices of phycoremediation for industrial effluent and also on the natural functions of secondary metabolites from endophytic fungi of marine resources especially from mangrove origin. Other interesting features of this issue takes you through an exciting scenario where **bacteria collaborate to sense arsenic** and **bioluminescent bacteria may illuminate your house** are path breaking developments to utilize microorganisms for the larger benefit of mankind.

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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Microalgae for potential phycoremediation of Industrial effluent - A case study

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Introduction

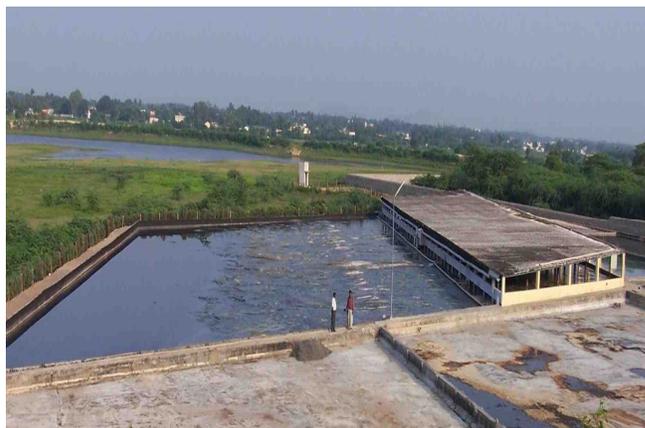
Microalgae are the most primitive and the first photosynthetic micro organisms to colonize earth. They are the primary producers in aquatic ecosystems and contribute to the oxygen levels in the atmosphere. Microalgae take up nutrients, evolve oxygen and effectively sequester CO₂. Being simple organisms micro algae can adapt to any kind of extreme conditions. They can degrade a wide range of chemicals and remove most of the heavy metals. This ability of micro algae has found applications in dealing with pollution caused by industrial effluents. VIAT has been successfully implementing micro algae based technology to manage a variety of industrial effluents all over India for the past 10 years. These industries have been treating effluents in a conventional way which involves the use of chemicals at every stage of treatment process resulting in huge amount of sludge. Algae based technology avoids all these chemicals at the same time effectively bring down vital parameters to acceptable levels.

Phycoremediation

Phycoremediation is the process in which algae are employed to remediate environmental pollution. Olguin (2003) defines phycoremediation involves the use of macroalgae or microalgae for effective removal or biotransformation of pollutants, including nutrients and xenobiotics from wastewater and CO₂ from waste air. Large-scale phycoremediation of industrial effluent has been done successfully in some industries in India (Sivasubramanian, 2006; Sivasubramanian *et al.*, 2009; Sivasubramanian, 2010; Sivasubramanian *et al.*, 2010; Hanumantha Rao *et al.*, 2010). Using algae based treatment technology, efficient pH correction, sludge reduction and reduction of BOD and COD could be achieved by avoiding toxic chemicals by these industries. During effluent treatment process huge amount of valuable algal biomass is also being generated by these industries.

1. World's first phycoremediation plant at Ranipet, India

Large-scale phycoremediation plant is in operation at SNAP Natural and Alginate Products, Ranipet, India from September 2006. The industry generates 30 to 40 KL of highly acidic effluent every day which is being pH corrected and evaporated using algae based treatment technology developed by Sivasubramanian *et al.* (2009). There is 100% reduction in sludge by phycoremediation.



Phycoremediation plant at SNAP industries, Ranipet, India.

Phycoremediation plant is used to treat the acidic effluent from this alginate industry. The liquid effluent is highly acidic. Conventionally, sodium hydroxide has been used for the neutralization of the acidic effluent which results in an increase in total dissolved solids and the generation of solid waste. The study was conducted in three stages. In the first stage, the solar ponds used for evaporating the effluent were converted into high rate algal ponds with *Chroococcus turgidus*, a blue green alga. Based on the results of pilot plant studies, a full scaling up of the slope tank was made.

2. Phycovolatilization of heavy metals

Use of algae to treat industrial effluents containing heavy metals is an alternative to the biosorbents and physical and chemical methods. In this study, effluent from a leather-processing chemical industry in Ranipet, Tamil Nadu, India, was treated for the removal of heavy metals using the microalga, *Chlorella vulgaris*, which was isolated from the effluent itself. The results of the study showed that after 8 hours, *C. vulgaris* exhibited a better adsorption capacity under sunlight compared to laboratory conditions (i.e., 30.6 mg/g dry weight vs 10.5 mg/g dry weight, respectively). Similarly, reduction of heavy metals and mass balance in pilot-scale field studies conducted in a high-rate

algal pond showed that the microalga, apart from adsorption, complexation, and entrapment mechanisms, is likely to possess phycovolatilization capability probably via biotransformation processes (Hanumantha Rao *et al.*, 2010).

3. Effluent from confectionery industry

A Confectionery industry in Tamilnadu, India generates 50 – 70 kilo liters of effluent per day. The plant effluent generated is divided into two streams viz., industrial effluent stream from the production process and sewage effluent stream from the human activities. These are mixed prior to sending to the equalization tank. The effluent for phycoremediation treatment is taken after it goes through the DAF(Dissolved air floatation) in the conventional treatment method. pH is conventionally corrected by adding caustic soda at the equalization tank stage which results in doubling of total dissolved solids (TDS). After pH correction the effluent is sent to buffer tank and anaerobic reactors (AR) to digest rest of the organic compounds. After digestion in AR effluent goes through a series of clarifiers and sand filter and finally taken to reverse osmosis (R/O) for recycling.

Effluent Characteristics

The characteristic raw effluent produced by this confectionery industry is characterized by its organic content, which is composed of easily biodegradable compounds such as sugars, sweeteners, casein, vegetable oils, acacia gums, condensed milk, food coloring and flavoring agents, etc. This confectionery industry is using major ingredients such as sugar and sweeteners, natural colors, acacia gum, sugar substitutes, gum base and flavors for all type of confectionery products. They use number of chemicals during the process and they all become a part of the effluent. This liquid effluent is acidic in pH, dominated by yeast cell population.

Algal treatment

Chlorella vulgaris grows very well in the raw effluent. It utilizes sugar present in the effluent. The effluent becomes less turbid and this reduces the load for the anaerobic reactors. Phycoremediation helps to correct pH, reduce sugar levels, reduces BOD and COD. Effluent is added and removed from the algal treatment tank @ 3500 L/h which is the flow rate requirement to anaerobic digesters. Algal biomass reaches to 1.5 g dry weight/L.

4. Effluent from soft drink manufacturing industry

Soft drink manufacturing units in India use ground water for the production. The ground water is filtered and softened using chemicals and sent to R/O and nano filtration (N/F) for further TDS reduction. The effluent generated by the industry includes R/O reject, reject from N/F, utilities, cleaning, softener regeneration, bottle wash and cleaning in process (CIP). In some units the treated effluent is sent to R/O for recycling. The effluent is treated with conventional chemical and physical methods. Removal of nutrients especially nitrates and phosphates are the major problem faced by this industry. The effluent contains high inorganic nutrients (nitrates and phosphates) and low pH. Microalgal technology is effectively employed to remove nitrates and phosphates. The effluent has all the essential nutrients for algal growth. Algae employed could remove nutrients (nitrate and phosphate) at a rapid rate well within the requirement of the industry.

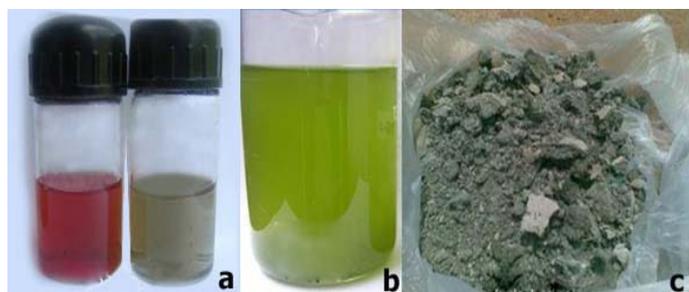
5. Effluent from textile dyeing industries

Phycoremediation technology is employed in a few textile dyeing industries by the author and his team. Two textile dyeing industries were selected for the present discussion (one near Chennai and the second at Ahmedabad). In Chennai-industry the effluent is generated from various sources like dye bath, mercerizer, wash water, desizing water and printing. The industry generates around 200 KL of effluent per day. The effluent is treated with conventional physical and chemical methods resulting in huge amount of sludge and water effluent. The dyeing industrial effluents is rich in various dyes with high pH and TDS, because of various chemicals being used, like sodium bicarbonate, sodium chloride etc. The industry at Ahmedabad generates around 84,000 m³ effluents every day. The effluent generated is highly alkaline and treated with conventional chemical methods. Dye removal, reduction of BOD and COD are the major problems associated with effluent treatment. These effluents contain various dyes and high pH, TDS, BOD and COD because of various chemicals being used, like sodium bicarbonate, sodium chloride etc.

Phycoremediation of textile dyeing effluents

Effective color removal, pH correction, BOD and COD reduction and sludge reduction are achieved by algal treatment on both the industries. Effluent provides all the necessary nutrients for the algal growth. Cell number is

maintained around $250 \times 10^4/\text{ml}$ (0.75 g dry weight/L). In the Chennai unit the algal biomass is harvested, dried and used as fuel. The dried algal pellet has a high calorific value.



Phycoremediation of textile dyeing effluent and algal biomass production (a) Decolorization and degradation of effluent before (left) and after (right) treatment with microalgae. (b) algal growth (c) dried algal cake

Algal biomass production in textile dyeing effluent

Both the effluents from the textile dyeing industry support very good growth of algae (*Chlorococcum humicola*). The treated effluent after harvesting algal biomass is sent to R/O for recycling. The R/O reject is fed into phycoremediation plant as source of nutrients. The biomass generated was harvested and analyzed for assessing the quality. When compared to the control (lab grown biomass) effluent grown biomass exhibits higher values for most of the biochemicals. The FAME (fatty acid methyl esters) analysis showed the existence of a single fatty acid in major composition indicating it is highly suitable for biodiesel production and a very little unsaturation is a good sign of hope in the process of biodiesel production from algae and the alga *Chlorococcum humicola* has a great potential of being a feed stock for biodiesel production.

Conclusions

VIAT has been implementing algae based technology to treat a wide range of effluents for the past 10 years. A few case studies have been summarized above to give readers an idea about the efficiency of phycoremediation and the benefits we can derive if the technology is developed and executed properly. VIAT is right now involved in several projects in India and abroad. One of the major applications of algal technology is to treat acidic industrial effluents. Apart from this algal technology can be effectively employed to remove color, odour, COD, BOD and sludge from the effluents.

Integrating algal biomass production with phycoremediation seems to address most of the economics and problems associated with mass cultivation. Apart from cleaning

the environment from the onslaught of ever increasing pollution, valuable and cheaper biomass is generated from wastewater, effluents and sludge if appropriate algal species are identified and grown in industrial wastes.

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Bacteria can communicate with each other through nanotubes

Bacteria are known to communicate in nature primarily via the secretion and receipt of extracellular signaling molecules. This communication enables bacteria to execute sophisticated tasks such as dealing with antibiotic production and secretion of virulence factors. Researchers at the Hebrew University of Jerusalem identified a previously uncharacterized type of bacterial communication mediated by nanotubes that bridge neighboring cells. These nanotubes connect bacteria of the same and different species. Via these tubes, bacteria are able to exchange small molecules, proteins and even small genetic elements (known as plasmids). The better molecular understanding of nanotube formation could lead to the development of novel strategies to fight against pathogenic bacteria

Source: www.sciencedaily.com

Endophytic fungi from Mangrove: A source of secondary metabolites

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Introduction

The ocean is considered to be a source of potential drugs. India is consecrated with a more than 8000 kms of coastline, possessing over 2 million sqkms of Exclusive Economic Zone (EEZ). Indian coastline has every type of marine habitats like inter-tidal, rocky, muddy and sandy shores, coral reefs and mangrove forest. However, the potential of this domain as the basis for new biotechnologies remains largely unexplored. A few selected research institutes in India are engaged in the exploration of life saving drug from marine sources. Many International research institutes and pharma based companies have recognized the significances of this area and acknowledged the importance of establishing interdisciplinary research centers focusing on marine natural products. Similar efforts should be made in India in order to explore biotechnological potential of our country's untapped marine biodiversity.

Marine natural products have attracted the attention of biologists and chemists over for the last five decades. Several of the compounds isolated from marine source exhibit biological activity. Most of these molecules are still in preclinical or early clinical development from marine associated microbes. In recent years, marine natural product bio-prospecting has yielded a considerable number of drug candidates.

Endophytic fungi are now recognized as a new and relatively unexplored source of bioactive compounds. Chiefly mangrove endophytic fungi have rich metabolites because symbiotic associations between fungi and photosynthetic organisms are both ancient and ubiquitous protecting host against various aggressions. Endophytes are growing intercellularly and asymptotically within living tissues establishing mutual relationship with the host plant. Most of the endophytic fungi have a wide range of plant host diversity. This paper reviews the biodiversity and novel metabolites production of endophytic fungi of mangrove.

Diversity of mangrove endophytic fungi

Endophytic fungi are reported from plants growing in various environments including tropic, temperate, xerophytes and aquatic. Marine fungi do not form a traditional taxonomic grouping (Raghukumar, 2008), but rather form an ecological grouping. Within the marine fungi there are two sub-divisions are found i.e. obligate and facultative marine fungi (de Vita-Marques *et al.*, 2008). According to Raghukumar (2008), 800 species of obligate marine fungi have been reported, comprising mostly of Ascomycetes and only 56 species have been discovered for facultative marine fungi (de Vita-Marques *et al.*, 2008).

A wide range of parasitic and saprophytic fungi have been reported from mangrove environment either living on the tissue, as epiphytes, rather than within. But few studies have investigated the endophytes from mangrove. Yang *et al.* (2006) reported 290 strains of endophytic fungi obtained from Fugong in Fujian Province, China. They reported that the dominant genera were *Penicillium* sp., *Alternaria* sp., *Dothiorell* sp and non-sporulating groups. Several studies on fungi associated with mangrove detritus have been published. There are a few studies on the endophytic fungi of mangrove plants and most of them are confined to endophytes from Pichavaram mangrove (Kumaresan and Suryanarayanan, 2002).

Bioactive compounds from mangrove endophytic fungi

Complex interactions between the host and the endophyte, such as the provision of various types of defensive substances (secondary metabolites) by the endophyte, have led to further research of these organisms. Some of these endophytes produce bioactive substances that are products of the host-microbial interactions. The most well-known example being that of taxol, a multibillion dollar anti-cancer compound produced in yew plant *Taxus brevifolia* by the terrestrial endophytic fungus *Taxomyces andreanae* (Strobel, 2002).

Endophytic fungus *Dothiorella* sp. isolated from mangrove plant of *Avicennia marina* have antimicrobial and cytotoxicity effect against human epidermal carcinoma of oral cavity, KB cell line (carcinoma cell line) and human Burkitt's lymphoma (Xu *et al.*, 2005).

Similarly, *Pestalotiopsis* sp. isolated from the leaves of *Rhizophora mucronata*, produced various bioactive compounds such as pestalotiopyrones, pestalotiopisorin, pestalotiollides A, pestalotiopin A, and four amides namely pestalotiopamides, nigrosporapyrone, 2- anhydromevalonic acid, and ρ - hydroxyl benzaldehyde.

Mangrove endophytic fungi *Phomopsis* sp. from *Hibiscus tiliaceus* derived a new substance namely A-seco-oleane-type triterpenes. The structurally related A-seco-oleane in mangrove endophytes may play an important role in protecting the host plant against environmental infections. Cytosporones, coumarins and alkaloid compounds derived from endophytic fungi of *Pestalotiopsis* sp isolated from *Rhizophora mucronata*. Isoflavones isolated from mangrove endophytic fungi *Fusarium* sp. and subsequently, mangrove endophytic fungi *Penicillium chermesinum* exhibited cytotoxicity activity against cancer cell lines. Conversely, toxin and acids such as paeciloxocins were isolated from the mangrove fungus *Paecilomyces* sp. Paeciloxocin A exhibited strong cytotoxicity against the hepG2 cell line (Chen *et al.*, 2010). In addition Xia *et al.* (2008) reported two new acids with a known compound, purpactin A were isolated from mangrove endophytic fungus (No. ZZF13).

Conclusion

Diversity of mangrove endophytic fungi with its unique physiological adaptations to the extreme marine environment provides a fruitful source for the discovery of new life saving drug. Although substantial progress has been made in identifying novel drug from the marine sources, great endeavors are still needed to explore these molecules for clinical applications.

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Research Reports

Bacteria collaborate to sense arsenic

Living cells can be exploited to sense and process environmental stimuli, including poorly defined microenvironments, biological markers of disease, defects in materials and complex small molecules. But obtaining a reliable signal from individual cells has proved a challenge. Prindle *et al* report a solution to this problem: a sensor composed of millions of bacterial cells that communicate with each other over long distances (up to 2.4 centimetres). The cells respond to the presence of arsenic by altering the rate at which they produce synchronized pulses of fluorescence.

Cells have been engineered to sense many environmental signals, including light, chemicals, touch, metal ions and pH. For example, sensors have been made in which human olfactory receptors are expressed in yeast cells. Most cellular sensors are based on a protein or messenger RNA that responds to a signal by causing the expression of a gene. Such genetic sensors often suffer from low dynamic range (that is, there is little change in output between the absence and

presence of a signal) and nonspecificity (they are activated by multiple signals). Furthermore, because cells are living systems, individual responses may vary because of stochastic effects or differences in growth states.

Prindle *et al.* have addressed the problem of dynamic range by applying the principles of signal processing to a biosensor based on genetic circuits. Such circuits use biochemical interactions to produce functions analogous to their electronic counterparts. Previously, the same group built a robust genetic oscillator - a network of genes and proteins that produced regular pulses of molecules and used this as a time-keeping mechanism to control cell-cell communication between bacteria. This yielded populations of bacteria that expressed a fluorescent protein in unison, and so produced synchronized pulses of light.

Theoretically, such an oscillator would enable a sensor to use the frequency of oscillations as signals, making the sensor less sensitive to environmental noise and exposure time than systems based on steady-state signals. A problem with the previous oscillator, however, was that cell-cell coupling relied on the diffusion of a small molecule through cellular media, a process that is too slow to allow rapid, long-range coupling of millions of cells. Molecular diffusion in the gas phase is much faster, so Prindle *et al.* used this mechanism to accelerate the coupling between separate colonies of bacteria.

In this way, the authors were able to couple 2.5 million cells of the bacterium *Escherichia coli*, which were arranged as an array of colonies across a distance of 5 millimetres. As in the previously reported oscillator, the output of the system was the coordinated, oscillating expression of a fluorescent protein, which the authors detected using a microscope. The period of the oscillations was quite long (more than an hour), but the degree of synchronization was high and the colonies produced light pulses within 2 minutes of each other.

To demonstrate a potential application of their system, Prindle *et al.* 'rewired' their network to incorporate elements that respond to arsenic. The resulting system acted as an arsenic sensor: once the concentration of arsenic reached a threshold value, the amplitude and period of the oscillations increased significantly. This produced a device with a large dynamic range. What's more, because the device averaged the outputs of a population of cells, noise was reduced and the sensor's response was decoupled from the growth state of individual cells. The authors scaled up their device so that it included more than

12,000 communicating bacterial colonies, covering an area of 2.4×1.2 centimetres.

Several advances, yet to be achieved, would improve the ability to connect this living sensor to an electronic system. One problem is that the minimum response time of the sensor to an input signal is slow, because gene expression which takes about 20 minutes to occur is required. Another issue is that the output involves fluorescence, which is awkward for electronic devices to use; the ideal output would be a direct electrical signal. To this end, cells have been metabolically engineered so that they can be induced to release electrons, which can then be read by an electronic sensor. The electron-transport system found in bacterial nanowires (extracellular appendages that conduct electricity) has also been harnessed to link cells to an electronic system. Nevertheless, these strategies still require the expression of a gene that triggers electron flux, so the resulting sensors are relatively slow to respond to signals.

More broadly, there are several collaborative research efforts aiming to develop better toolboxes for building interfaces between cellular and electronic components. One such project is to build a millimetre-scale robot that swims like a lamprey, using a combination of human muscle cells, yeast-based sensors, an electronic brain and flexible materials (nicknamed 'cyberplasm'). Another project is to develop genetic sensors, along with genetic circuits to apply signal processing within the cell and new approaches to link cellular outputs to an electronic system, with the ultimate objective of controlling robots. As the integration of cellular and electronic systems matures, it will be interesting to see how circuitry in future devices is divided between biological and electronic components.

Source: Nature

Bacteriophages mobilize the antibiotic resistance of bacteria in the environment

The role of bacteriophages viruses that infect bacteria could be crucial in the transfer of antibiotic resistance genes between bacteria, and this process could favour the emergence of resistant bacterial strains in the natural environment.

This is one of the main conclusions of an article published in the journal *Antimicrobial Agents and Chemotherapy* by the researchers Maite Muniesa, Joan Jofre, 7

Marta Colomer-Lluch and Lejla Imamovic, from the Generalitat-supported Health-Related Water Microbiology (MARS) Research Group, part of the Department of Microbiology at the Faculty of Biology of the University of Barcelona (UB).

Antibiotic resistance, a global problem

Antibiotic resistance, which is the focus of the World Health Organization's 2011 World Health Day, is caused by multiple factors, including antimicrobial abuse and acquisition of resistance genes. It is currently believed that the origin of some forms of resistance lies in the transfer of genes between microorganisms in the natural environment.

“Resistance to antibiotics is one of the main problems encountered in the treatment of infectious diseases across the world,” explain the lecturer Maite Muniesa, from the UB's Department of Microbiology. “Traditionally, most scientific studies of multi-resistance genes have focused on plasmids, which are circular, covalently closed DNA molecules that act as the principal vehicle for inter-bacterial gene transmission.”

The article focuses on samples of faecal waste from different animals (cattle, pigs and poultry) from farms in Catalonia, some of which have not been treated with antibiotics. Specifically, the experts behind the study analyse the horizontal transfer of pathogenicity genes between enteric bacteria by bacteriophages: the genes *bla*TEM and *bla*CTX-M, involved in resistance to betalactamic antibiotics, and *mecA*, associated with methicillin resistance in *staphylococci*, which are responsible for a large proportion of hospital infections.

Bacteriophages as messengers

It is clearly described in scientific literature that bacteriophages are highly efficient vectors for the inter-cellular transfer of DNA fragments. But what role do phages play in the emergence of new bacterial resistances? As a step towards answering this question, the study shows for the first time that bacteriophages contain antibiotic resistance genes and are potentially excellent vehicles for the propagation of bacterial resistance genes in the environment.

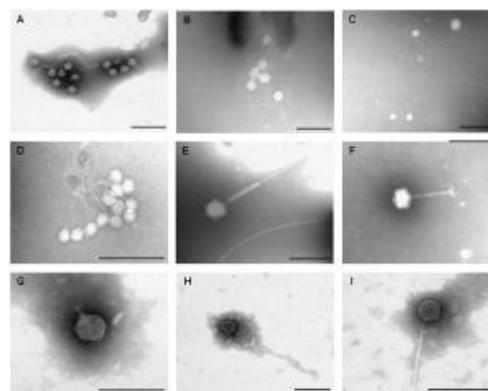
As Professor Joan Jofre notes, “bacteriophages facilitate the transfer of antibiotic resistance genes between different biomes, and the potential scope of this process in the natural environment has not yet been described.” In their role as mobilizers of antimicrobial resistance genes, explains Maite Muniesa, “bacteriophages are more durable than plasmids and, surprisingly, can be found in high concentrations in the natural

environment. What we need to do now is identify the types of viruses that are transferring the resistance genes between bacteria.”

New resistances, new scientific challenges

Antibiotic resistances detected in the clinical setting are also genetically present in bacteria found in the natural environment. Despite the numerous measures taken to control the use of antibiotics in agriculture, new forms of antimicrobial resistance continue to emerge. According to experts, the evidence suggests that the appearance of new resistances is not simply the result of selective pressure from antibiotics but is also due to the mobilization of resistance genes in the environment, a natural process in which the biological role of phages cannot be ignored.

The new study brings an ecological perspective to the problem and defines the boundaries that restrict the emergence of new antimicrobial resistances in the natural environment. Moving forwards, this research area could contribute to the detection of resistances that have not been described in the clinical setting and, by extension, broaden research into new antimicrobial agents. “In the field of antimicrobial resistance, we must remember that there are many factors to consider which are not being taken into account. For example, certain antibiotic treatments targeting bacteria are also capable of activating the mobilization of different types of genes by bacteriophages. In this field of research, it is something that must be given particular consideration,” warns Professor Joan Jofre.



Electron micrographs of bacteriophages present in sewage and river water. The role of bacteriophages could be crucial in the transfer of antibiotic resistance genes between bacteria.

(ImageCredit: Marta Colomer-Lluch *et al.* PLoS One, DOI: 10.1371/journal.pone.0017549)

Source: www.sciencedaily.com

Space bound bacteria inspire Earthbound remedies

WASHINGTON - Recent research aboard the space shuttle is giving scientists a better understanding of how infectious disease occurs in space and could someday improve astronaut health and provide novel treatments for people on Earth. “With our space-based research efforts, including the International Space Station, we are not only continuing our human presence in space, but we are engaged in science that can make a real difference in people’s lives here on Earth,” said NASA Administrator Charles Bolden. “NASA’s leadership in human spaceflight allows us to conduct innovative and groundbreaking science that reveals the unknown and unlocks the mysteries of how disease-causing agents work.”

The research involves an opportunistic pathogen known as *Pseudomonas aeruginosa*, the same bacterium that caused astronaut Fred Haise to become sick during the Apollo 13 mission to the moon in 1970.

Scientists studying the bacterium aboard the shuttle hope to unlock the mysteries of how disease-causing agents work. They believe the research can lead to advanced vaccines and therapies to better fight infections. The findings are based on flight experiments with microbial pathogens on NASA shuttle missions to the International Space Station and appear in a recent edition of the journal *Applied and Environmental Microbiology*.

“For the first time, we are able to see that two very different species of bacteria *Salmonella* and *Pseudomonas* share the same basic regulating mechanism, or master control switch, that micro-manages many of the microbes responses to the spaceflight environment,” said Cheryl Nickerson, Associate Professor at the Center for Infectious Diseases and Vaccinology, the Biodesign Institute at Arizona State University (ASU) in Tempe. “We have shown that spaceflight affects common regulators in both bacteria that invariably cause disease in healthy individuals [*Salmonella*] and those that cause disease only in people with compromised immune systems [*Pseudomonas*].”

By studying the global gene expression patterns in bacterial pathogens like *Pseudomonas* and *Salmonella*, Nickerson’s team learned more about how they react to reduced gravity.

Pseudomonas aeruginosa can coexist as a benign microbe in healthy individuals, but poses a serious threat to people with compromised immune systems. It is the leading cause of death for those suffering from cystic fibrosis and is a serious risk to burn victims. However, a high enough dosage of *Salmonella typhimurium* always will cause disease, even in healthy individuals.

During the initial study in 2006, two bacterial pathogens, *Salmonella typhimurium* and *Pseudomonas aeruginosa*, and one fungal pathogen, *Candida albicans* were launched to the station aboard shuttles. They were allowed to grow in appropriately contained vessels for several days. Nickerson’s team was the first to evaluate global gene and protein expression (how the bacteria react at the molecular level) and virulence changes in microbes in response to reduced gravity.

“We discovered that aspects of the environment that microbes encountered during spaceflight appeared to mimic key conditions that pathogens normally encounter in our bodies during the natural course of infection, particularly in the respiratory system, gastrointestinal system and urogenital tract,” Nickerson said. NASA’s Advanced Capabilities Division Director, Benjamin Neumann added that, “This means that in addition to safeguarding future space travelers, such research may aid the quest for better therapeutics against pathogens here on Earth.”

The initial study and follow-on space experiments show that spaceflight creates a low fluid shear environment, where liquids exert little force as they flow over the surface of cells. The low fluid shear environment of spaceflight affects the molecular genetic regulators that can make microbes more infectious. These same regulators might function in a similar way to regulate microbial virulence during the course of infection in the human body.

“We have now shown that spaceflight conditions modified molecular pathways that are known to be involved in the virulence of *Pseudomonas aeruginosa*,” said Aurelie Crabbe, a researcher in Dr. Nickerson’s lab at ASU and the lead author of the paper. “Future work will establish whether *Pseudomonas* also exhibits increased virulence following spaceflight as did *Salmonella*.”

NASA's Fundamental Space Biology Program sponsored and funded the research conducted by Crabbe and Nickerson along with their colleagues at the Biodesign Institute at ASU. They collaborated with the University of Colorado School of Medicine, University of Arizona, Belgian Nuclear Research Center, Villanova University, Tulane University, Affymetrix Inc, and NASA scientists.

Source: www.sciencedaily.com

Glowing, blinking bacteria reveal how cells synchronize biological clocks

Biologists have long known that organisms from bacteria to humans use the 24 hour cycle of light and darkness to set their biological clocks. But exactly how these clocks are synchronized at the molecular level to perform the interactions within a population of cells that depend on the precise timing of circadian rhythms is less well understood.

To better understand that process, biologists and bioengineers at UC San Diego created a model biological system consisting of glowing, blinking *E. coli* bacteria. This simple circadian system, the researchers report in the issue of *Science*, allowed them to study in detail how a population of cells synchronizes their biological clocks and enabled the researchers for the first time to describe this process mathematically.

"The cells in our bodies are entrained, or synchronized, by light and would drift out of phase if not for sunlight," said Jeff Hasty, a Professor of biology and bioengineering at UC San Diego who headed the research team. "But understanding the phenomenon of entrainment has been difficult because it's difficult to make measurements. The dynamics of the process involve many components and it's tricky to precisely characterize how it works. Synthetic biology provides an excellent tool for reducing the complexity of such systems in order to quantitatively understand them from the ground up. It's reductionism at its finest."

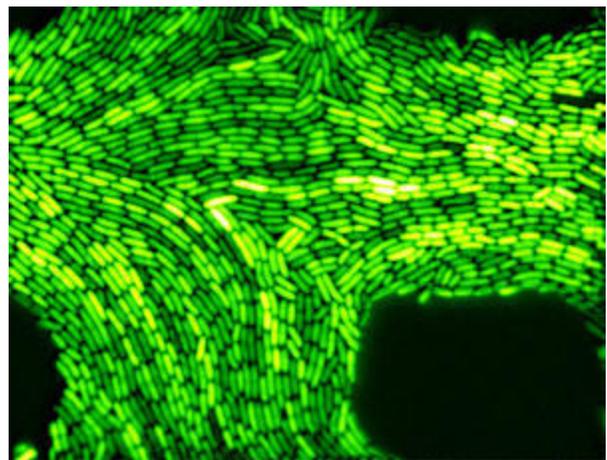
To study the process of entrainment at the genetic level, Hasty and his team of researchers at UC San Diego's Biocircuits Institute combined techniques from synthetic biology, microfluidic technology and computational modeling to build a microfluidic chip with a series of chambers containing populations of *E. coli* bacteria. Within each bacterium, the

genetic machinery responsible for the biological clock oscillations was tied to green fluorescent protein, which caused the bacteria to periodically fluoresce.

To simulate day and night cycles, the researchers modified the bacteria to glow and blink whenever arabinose a chemical that triggered the oscillatory clock mechanisms of the bacteria was flushed through the microfluidic chip. In this way, the scientists were able to simulate periodic day-night cycles over a period of only minutes instead of days to better understand how a population of cells synchronizes its biological clocks.

Hasty said a similar microfluidic system in principal could be constructed with mammalian cells to study how human cells synchronize with light and darkness. Such genetic model systems would have important future applications since scientists have discovered that problems with the biological clock can result in many common medical problems from diabetes to sleep disorders.

Other members of Hasty's team included Lev Tsimring, Associate director of the BioCircuits Institute, and bioengineering graduate students Octavio Mondragon, Tal Danino and Jangir Selimkhanov. Their research was supported by grants from the National Institutes of Health and General Medicine and the San Diego Center for Systems Biology.



Green fluorescent protein causes the *E. coli* to glow when the cells' clock is activated.

(Credit: UC San Diego)

Source: www.sciencedaily.com

Bio fertilizers for tree cultivation

Excessive use of chemical fertilizers has generated several environmental problems. To overcome these, bio fertilizers can be used as they are natural, beneficial, eco friendly and user friendly.

They are considered important in growth improvement and establishment of forest tree seedlings as the media used to raise seedlings in nursery as well as planting sites are generally low in nutrients and beneficial microbial populations.

It is very essential to improve the seedling health and quality planting stock of every forest tree species at the nursery level for successful establishment in the field. The following group of bacteria and fungi are major bio fertilizers being used in tree cultivation. Arbuscular mycorrhizal (AM) fungi are symbiotic associations between tree roots and soil fungi that play a key role in nutrient cycling in the ecosystem and also protect plants against environmental stress.

Nitrogen fixing bacteria

Some bacteria are capable of nitrogen fixation from the atmospheric nitrogen pool. The major types of N_2 fixing bacteria are *Azospirillum*, *Rhizobium* and *Frankia*. *Azospirillum* is free living in soils so that it can be cultured and produced in artificial medium only.

It can be used at the rate of 5 gm / tree seedlings of all tree crops. *Rhizobium* is host specific nitrogen fixing bacteria normally associated with leguminous trees. About 5g of *rhizobium* /tree seedlings of leguminous tree crops is required for nitrogen fixation and growth improvement.

Phosphate solubilising

Most of the Indian soils are deficient in phosphorus and its requirement is met by the addition of phosphate fertilizers in the form of aluminium phosphate or iron phosphate. But these fertilizers are becoming costly and may have adverse effect on forest trees. Hence, phosphate solubilising bacteria (PSB) have to be used. PSB also can be used at the rate of 5gm to all tree seedlings and are capable of solubilising 50-60 per cent of rock phosphorus in the soil. Care should be taken while using biofertilizers. They should not be mixed with chemical fungicides or insecticides and are to be used with prolonged shelf life forms.

Source: The Hindu, Sep 01, 2011.

Found: Bacteria that can convert carbon into food

Washington: Scientists have identified some mysterious organisms in the dark depths of the ocean which they believe are converting carbon dioxide into a form useful for life. The bugs, which the scientists call “twilight” microbes, could be the missing link of global carbon cycle as they are found turning inorganic carbon into useable food some 2,625 feet below the ocean surface, LiveScience reported.

The job of capturing carbon crucial to sustaining life on Earth is usually carried out by plants that use sunlight as energy. But light doesn't penetrate below 656 feet of ocean, so plants can't do this job. To survive, living cells must convert carbon dioxide into molecules that can form cellular structures or be used in metabolic processes, the scientists said.

Simple, single-celled organisms called archaea that often live in extreme conditions were thought to be responsible for much of the dark ocean's carbon fixation. But there was evidence that archaea could not account for the total amount of carbon fixation going on there.

“Our study discovered specific types of bacteria and their likely energy sources that may be responsible for this component of the dark ocean carbon cycle,” said study author Ramunas Stepanauska.

Source: The Times of India, September, 03, 2011.

Microbes, nuclear waste and power

With implications that could eventually benefit sites forever changed by nuclear contamination, researchers at Michigan State University have unravelled the mystery of how microbes generate electricity while cleaning up nuclear waste and other toxic metals.

Details of the process, which can be improved and patented, are published in the current issue of the Proceedings of the National Academy of Sciences.

“*Geobacter* bacteria are tiny micro-organisms that can play a major role in cleaning up polluted sites around the world,” said Gemma Reguera, who is an MSU

(Michigan State University) AgBio Research scientist. “Uranium contamination can be produced at any step in the production of nuclear fuel, and this process safely prevents its mobility and the hazard for exposure.”

The ability of *Geobacter* to immobilize uranium has been well documented. However, identifying the *Geobacter*'s conductive pili or nanowires as doing the yeoman's share of the work is a new revelation, according to a Michigan State University press release.

Nanowires, hair-like appendages found on the outside of *Geobacter*'s, are the managers of electrical activity during a cleanup. “Our findings clearly identify nanowires as being the primary catalyst for uranium reduction,” Reguera said. “They are essentially performing nature's version of electroplating with uranium, effectively immobilizing the radioactive material and preventing it from leaching into groundwater.”

Source: The Hindu, Sep 08, 2011.

Abstracts

001. Anthony L. Andrady. Department of Chemical and Biomolecular Engineering, North Carolina State University, Raleigh, NC 27695, USA. **Microplastics in the marine environment.** Marine Pollution Bulletin, 2011, **62** (8), 1596 - 1605.

This review discusses the mechanisms of generation and potential impacts of microplastics in the ocean environment. Weathering degradation of plastics on the beaches results in their surface embrittlement and microcracking, yielding microparticles that are carried into water by wind or wave action. Unlike inorganic fines present in sea water, microplastics concentrate persistent organic pollutants (POPs) by partition. The relevant distribution coefficients for common POPs are several orders of magnitude in favour of the plastic medium. Consequently, the microparticles laden with high levels of POPs can be ingested by marine biota. Bioavailability and the efficiency of transfer of the ingested POPs across trophic levels are not known and the potential damage posed by these to the marine ecosystem has yet to be quantified and modelled. Given the increasing levels of plastic pollution of the oceans it is important to better understand the impact of microplastics in the ocean food web.

Keywords: Microplastics, Nanoplastics, POPs, Plastics, Food web

002. Alberto Hernandez-Eligio, Mildred Castellanos, Soledad Moreno and Guadalupe Espín. **Transcriptional activation of the *Azotobacter vinelandii* polyhydroxybutyrate biosynthetic genes *phbBAC* by PhbR and RpoS.** Microbiology, 2011, **157** (11), 3014 - 3023.

We previously showed that in *Azotobacter vinelandii*, accumulation of polyhydroxybutyrate (PHB) occurs mainly during the stationary phase, and that a mutation in *phbR*, encoding a transcriptional regulator of the AraC family, reduces PHB accumulation. In this study, we characterized the roles of PhbR and RpoS, a central regulator during stationary phase in bacteria, in the regulation of expression of the PHB biosynthetic operon *phbBAC* and *phbR*. We showed that inactivation of *rpoS* reduced PHB accumulation, similar to the *phbR* mutation, and inactivation of both *rpoS* and *phbR* resulted in an inability to produce PHB. We carried out expression studies with the wild-type, and the *rpoS*, *phbR* and double *rpoS-phbR* mutant strains, using quantitative RT-PCR, as well as *phbB::gusA* and *phbR::gusA* gene fusions. These studies showed that both PhbR and RpoS act as activators of *phbB* and *phbR*, and revealed a role for PhbR as an autoactivator. We also demonstrated that PhbR binds specifically to two almost identical 18 bp sites, TGTCACCAA-N₄-CACTA and TGTCACCAA-N₄-CAGTA, present in the *phbB* promoter region. The activation of *phbB* and *phbR* transcription by RpoS reported here is in agreement with the observation that accumulation of PHB in *A. vinelandii* occurs mainly during the stationary phase.

Keywords: *Azotobacter vinelandii*, polyhydroxybutyrate, polyhydroxybutyrate biosynthetic genes.



NATIONAL

Microbial Type Culture Collection and Gene Bank
www.mtcc.imtech.res.in

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

National Centre for Cell Science
www.nccs.res.in

National Facility for Marine Cyanobacteria
<http://www.bdu.ac.in/centers/nfmc/>

INTERNATIONAL

Coimbra Collection of Algae
woc.uc.pt/botanica/

China General Microbiological Culture Collection Center (CGMCC)
www.im.ac.cn/en/sklomr/08.php

World Federation for Culture Collections (WFCC)
<http://www.wfcc.info/index.php/collections/display/>

Collection of Aquatic Important Microorganisms
www.sgm.ac.uk

EVENTS

Conferences / Seminars / Meetings 2011 - 2012

National Conference on Marine Environmental Challenges and Coastal Zone Management Strategy. February 13 - 14, 2012. **Venue:** Department of Marine Science, Bharathidasan University, Thiruchirapalli – 620 024, Tamilnadu, **India.**

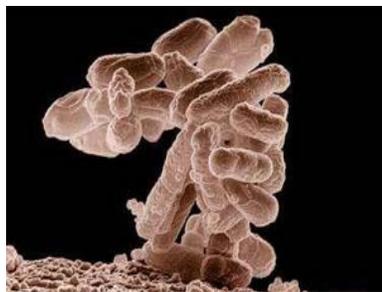
National Workshop on Microbial Diversity: DNA to Database. February 22 - 24, 2012. **Venue:** Bioinformatics Infrastructure Facility, Department of Biotechnology, Alagappa University, Karaikudi – 630 003, Tamil Nadu, **India.**
Website: www.alagappabiotech.org

“E-waste Management using Biological Tools: An Eco - friendly approach”. March 8 - 9, 2012. **Venue:** Loyola Institute of Frontier Energy (LIFE), Loyola College, Nungambakkam, Chennai-600 034, Tamil Nadu, **India.**
Website: www.loyolacollege.edu/life.html

Annual Conference of the Association for General and Applied Microbiology (VAAM). March 18 - 21, 2012. **Venue:** Tubingen, **Germany.** **Website:** <http://www.conventus.de>

3rd TNO Beneficial Microbes Conference. March 26 - 28, 2012. **Venue:** NH Conference Centre Leeuwenhorst, **The Netherlands.** **Website:** http://www.bastiaanse-communication.com/html/bc_2012.html

Environmental Microbiology and Biotechnology Conference 2012. April 10 – 12, 2012. **Venue:** Facoltà di Ingegneria - via Terracini 28, Bologna, **Italy.**
Website: http://www.efb-entral.org/index.php/Main/events/environmental_microbiology_biotechnology_conference_2012



Glowing bioluminescent bacteria

Soon, bacteria-powered light may illuminate your house

Researchers in a leading electronic company has come up with a more greener and power-efficient lighting system, which will use glowing bioluminescent bacteria to illuminate your house. The bioluminescent bacteria, which flourishes on waste generated in the average home, is housed in hand-blown glass cells, clustered together to form a lamp. Each cell is joined to the lamp's reservoir base by thin silicon tubes that pipe methane gas from composted bathroom solids and vegetable scraps via a kitchen dodad that digests bio-waste. Till the time proper nutrients are supplied, the bio-light's living bacteria can be powered indefinitely. Although the light is not bright enough to fully replace conventional lighting, it does make people conscious of household forms of wasted energy that could be tapped.

Source: Indian Express, November 29, 2011.

**Honor to a renowned microbiologist!
Hearty Congratulations!**



Honorable Chief Minister of Tamil Nadu **Dr. J. Jayalalithaa** Presented '**Life Time Achievement Award**' to **Prof. Dr. S. P. Thyagarajan**, Ph.D., D.Sc., formerly **Vice-Chancellor of Madras University** and presently **Pro-Chancellor and Chief Advisor (Research)** Sri Ramachandra University, Chennai for his **meritorious services in medical microbiology**.



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