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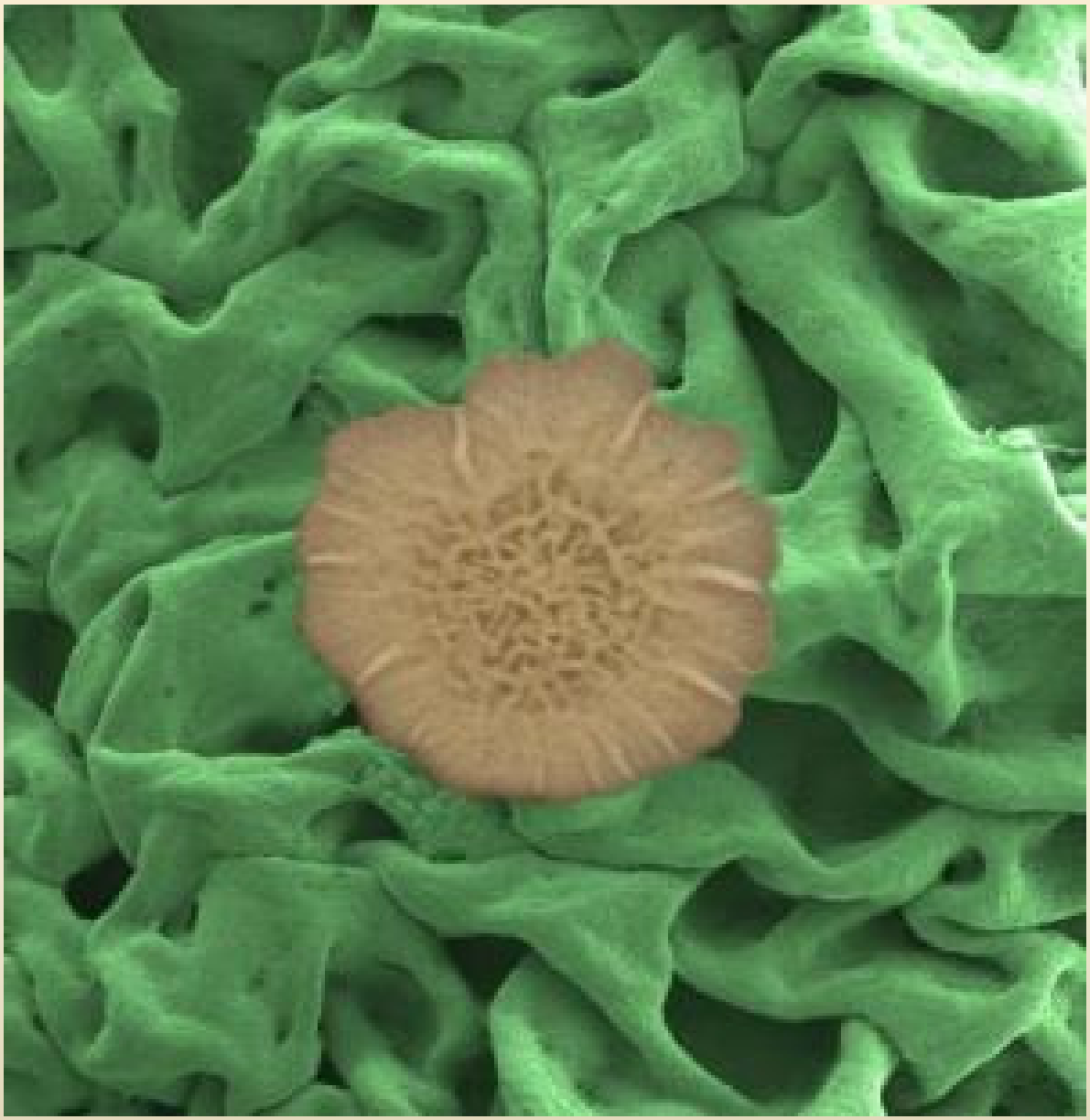

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ENVIS Newsletter on Microorganisms and Environment Management, a quarterly publication, publishes original research articles, reviews, reports, research highlights, news-scan etc., related to the thematic area of the ENVIS Centre. In order to disseminate 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.

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Cover page : Slimy bacterial biofilm surface with *Bacillus subtilis* colony superimposed at the center

Courtesy : Laboratory of Joanna Aizenberg, Harvard School of Engineering and Applied Sciences, USA.

ENVIS Newsletter
on
Microorganisms and Environment Management

Contents

Dear Readers,

Happy New Year 2011!

Welcome to the **International year of Forests, 2011**. The livelihood of over 1.6 billion people depend on forests and it is a home to 80% of our terrestrial biodiversity. It is our major concern to strengthen the conservation and sustainable development of all types of forests for the benefit of current and future generations.

Forests play a vital role in the global carbon cycle: they act as carbon stores, absorbing greenhouse gases and maintaining forest ecosystems, thus helping to increase our resilience to climate change. A healthy natural forest is a self - sustaining system made up of a complex web of relationships. Besides, plants in the forest interact with the soil and its microbes which are important parts of the overall ecosystem. Microbes, especially bacteria and fungi, are of great importance because of their mutualistic/ symbiotic association.

This issue carries articles on plant microbe associations for ecological restoration and the importance of *Acinetobacter* as a nosocomial pathogen; other information on genomic comparison of ocean microbes and bioremediation of oil spill by bacteria are note worthy.

We sincerely look forward to your suggestions and feedback. Please do mail us at www.envismadrasuniv.org/send_feedback.php.

Prof. N.Munuswamy

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World Environment Day - 5th June 2011

Stressed and degraded habitats - a repository of novel plant-microbe associations useful for ecological restoration

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Alteration in the natural plant communities is the first visible symptom of degraded habitats. Such habitats are characterized by reduction in biodiversity (above and below ground) and a multitude of abiotic stresses (nutrients, moisture, etc.). The key ecological functions responsible for sustenance of the ecosystem are also lost (Boyer and Wratten, 2010). The loss of these functions is primarily due to changes in soil properties (physico-chemical and biological) which determine the productivity of the ecosystem. Ecologically significant functional groups of soil bacteria affect the soil structure, nutrient availability and organic matter content which in turn determine the plant recruitment, establishment and hence the productivity of stressed and degraded habitats (Sharma *et al*., 2010; Rau *et al*., 2009). Therefore, stress-induced changes in above-ground biodiversity are primarily due to loss of below-ground biodiversity (Bardgett *et al*., 2005). Consequent loss of above and below ground biodiversity creates an extremely harsh environment which is non-conducive for natural regeneration of the native ecosystem. In fact, such places become a favourite place for weedy exotic species which further adds to the stress on the habitat. Due to such alterations in the native ecosystems, an array of ecosystem goods and services available to mankind also get diminished, which affect the quality of life (Wainger and Price, 2004). Therefore, such stressed-habitats are an ecological and economic burden on society.

Ecological restoration of degraded habitats has been recognized as one of the components of sustainable development which ensures long-term supply of the ecosystem services for mankind, minimizes the rate of climate change and increases the socio-economic status of native communities (Schmidhuber and Tubiello, 2007). Wild grasses have been considered the 'nurse species', which can colonize extreme habitats. They are bottom-up control species and regulate ecosystem functioning. These species can thrive in nutritionally poor habitats, contribute to soil formation by enhancing the decomposable biomass and are able to coexist and give way to other native species making rapid ecosystem development (Sharma *et al*., 2010; Rau *et al*., 2009). Wild grasses are among the few naturally colonizing native species at such sites but their spread is generally slow, therefore the sites remain mostly barren even after several decades. Establishment of wild grasses having economic and ecological significance would be a viable strategy to convert the degraded habitats into biologically and sociologically significant habitats. Presence of ecologically diverse functional group of rhizobacteria might contribute to the ecological success of the wild grasses. Therefore, the spread of wild grasses could be facilitated by using ecologically diverse functional group of rhizobacteria, which contribute to ecological success of the wild grasses. They help the host plant and process the habitat directly and indirectly by:

(i) nutrient enrichment (release of phosphate, iron etc. from insoluble mineral complexes, fixation of atmospheric nitrogen, etc.), (ii) biological storage of phosphate and iron (polyphosphate and hemophores etc.), (iii) chelation and mobilization of nutrients to the host plant (siderophore production), (iv) enhancing nutrient acquisition and colonization potential of host plant (production of phytohormones, reduction of stressed-ethylene by production of 1-aminocyclopropane-1-carboxylate deaminase), and

(v) protecting the host plant from biotic stresses such as pests and pathogens (production of HCN, siderophore and antibiotics etc.) (Rau *et al*., 2009). However, limited studies are available on rhizosphere microbes of wild grasses of arid and semi-arid regions.

Keeping this in view, field surveys of stressed/degraded habitats in Delhi region were carried out and *Saccharum munja* and *S. ravennae* were identified as among the naturally colonizing native wild grasses (Fig. 1). They are perennial wild grasses which are excellent soil binders due to their extensive root network system and forms tall thick clumps with high biomass tufts. Moreover, it is also an integral component of the socio-economic fabric (used for making rope, hand fans, baskets, broom, mats, shield for crop protection etc.) of the native people (Sharma *et al*., 2005). To

fasten the colonization of these grasses at stressed sites, there is an urge to identify and characterize its rhizobacteria. Therefore, the study reported: (i) the diversity in rhizobacteria of these grasses colonizing selected stressed sites; (ii) the variations in plant growth promoting traits and tolerance to different metals among rhizobacteria; and (iii) the significance of rhizobacteria in the establishment of these grasses in stressed environment.

Fig. 1. *Saccharum munja* (A) and *S. ravennae* (B) native wild grasses naturally colonizing abandoned Bhatti mine and fly ash dump (Delhi), respectively

Characterization of the rhizobacteria of native grasses naturally colonizing abandoned mine sites may help in identification of microbial inoculants for ecological-restoration programmes. Eighty one strains of *Saccharum munja* rhizobacteria isolated from an abandoned mine located on Aravalli mountain and 50 from bulk-region were identified using 16S rRNA sequence analyses. Based on chemical and biological-assays they were categorized into ecologically diverse functional groups (siderophore-, IAA-, ACC-deaminase-, HCN-, polyphosphate producers; phosphate-solubilizer; antagonistic). Eight genera, 25 species from rhizosphere and 2 genera, and 5 species from bulk-region were dominated by *Bacillus* spp. (*B. barbaricus, B. cereus, B. firmus, B. flexus, B. foraminis, B. licheniformis, B. megaterium, B. pumilus, B. subtilis, B. thuringiensis)* and *Paenibacillus* spp. (*P. alvei, P. apiarius, P. lautus, P. lentimorbus, P. polymyxa, P. popillae*). Siderophore-producers were common in, rhizosphere and bulk soil, whereas IAA producers, N_2-fixers and $FePO_4$-solubilizers dominated rhizosphere samples. During the reproductive phase (winter) of *S. munja*, siderophore-, ACC-deaminase and polyP-producers were predominant; however dominance of HCN-producers in summer might be associated with termite-infestation. *In vivo* ability of selected rhizobacteria (*B. megaterium* BOSm201*, B. subtilis* BGSm253*, B. pumilus* BGSm157*, P. alvei* BGSm255*, P. putida* BOSm217*, P. aeruginosa* BGSm306) to enhance seed-germination and seedling-growth of *S. munja* in mine-spoil suggest their significance in natural colonization and potential for ecological restoration of Bhatti mine (Sharma *et al*., 2010).

Metal-rich fly ash dumps may serve as repository of ecologically useful multi-functional rhizobacteria having potential use in the development of vegetation at the dumps. Therefore, bacteria from the rhizosphere of a wild perennial grass (*S. ravennae*) colonizing Indraprastha and Badarpur fly ash dumps of Delhi region were purified, identified and functionally characterized. The fly ash had low levels of nutrients, moisture and organic matter coupled with toxic levels of heavy metals (As, Cd, Cr, Cu, Hg, Ni, Pb and Zn). Both the dumps were mostly barren except for a few patches of *Saccharum ravennae* and some weedy species. Sixty five dominant, morphologically distinct rhizobacteria were purified, which belonged to 18 genera and 38 species. Gram-positive bacteria were dominating in the fly ash environment. *Bacillus* spp. and *Paenibacillus* spp. were common at both the dumps. Multi-metal tolerance was shown by diverse bacterial taxa. The minimum inhibitory concentration (MIC) was highest for As (12.5 – 20.0 mM) and Pb (7.5 – 10.0 mM), although many rhizobacteria also possessed significant tolerance to Cr, Zn, Ni, Cu, Co and Cd. The tolerance profiles of rhizobacteria to different metals may be ranked in the decreasing order as As > Pb > Cr > Zn > Ni > Cu > Co > Cd > Hg. Majority of rhizobacteria showed good siderophore activity. Multiple-metal tolerance was also coupled with high siderophore production in some of the isolates (*Microbacterium barkeri* IPSr74, *Serratia marcescens* IPSr90 and IPSr82, *Enterococcus casseliflavus* BPSr32, *Bacillus* sp. IPSr80, *Pseudomonas aeruginosa* BPSr43 and *Brochothrix campestris* BPSr3). Most of the bacteria could grow on nitrogen-deficient medium. However, the dominant nitrogen fixers reported from the rhizosphere of other *Saccharum* species were not detected. *S. marcescens* IPSr90 was the only rhizobacterium, which showed ACC-deaminase (ACCD) activity. Proportion of phosphate solubilizing bacteria was high. Considerable improvement in the seedling establishment, plant weight and shoot length in rhizobacterial inoculated plants of *S. ravennae* in fly ash environment

indicated the significance of rhizobacteria in its colonization and spread to the dumps. Representative rhizobacteria, with high MIC (for most of the metals) and good plant growth promoting (PGP) traits comparable to commercially useful bacterial inoculants were identified as *S. marcescens* IPSr82 and IPSr90, *P. aeruginosa* BPSr43, *Paenibacillus larvae* BPSr106, *Arthrobacter ureafaciens* BPSr55, *Paenibacillus azotofixans* BPSr107 and *E. casseliflavus* BPSr32. *S. ravennae* and some of these rhizobacteria may be potentially useful for the development of inoculation technologies for conversion of barren fly ash dumps into ecologically and economically productive habitats (Rau *et al*., 2009).

In conclusion, the stressed and degraded habitats harbour ecologically unique wild grasses which support taxonomically and functionally diverse group of rhizobacteria. These rhizobacteria possess multiple plant growth promoting traits and show tolerance towards a range of toxic heavy metals. They are involved in the natural colonization and spread of these grasses on stressed habitats. Wild grasses and their associated plant growth promoting rhizobacteria may be potentially useful for the development of ecological restoration technologies to convert barren, stressed - and degraded-habitats into ecologically and economically productive habitats.

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Acinetobacter baumannii: emerging nosocomial pathogen

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INTRODUCTION

Infections that occur during hospitalization but are not present or incubating upon hospital admission are defined as nosocomial (*nosos* = disease, *komeo* = to take care of). Nosocomial infections are one of the major health problems confronting clinicians in intensive care units. Contribution of *Acinetobacter baumannii* to nosocomial infections has been increasing abruptly over the last 30 years and due to this reason, it is a problem of immediate concern. *A. baumannii,* a very common hospital pathogen in ICUs and wards has been identified as one of the six important and highly drug resistant hospital pathogens by the "Infectious Disease Society of America"(IDSA) (Boucher *et al*., 2009). Figure 1 shows the prevalence of *A. baumannii* among the nosocomial infectious bacteria.

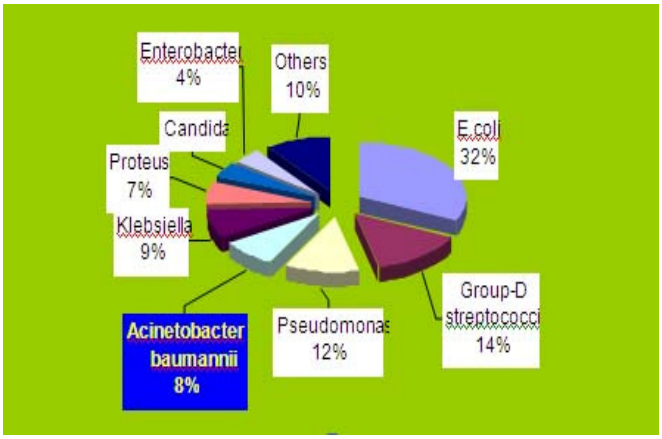

Fig. 1. PIE distribution of Nosocomial infection producing organisms.

Taxonomy features of *Acinetobacter baumannii*

In the taxonomy of bad bugs, *Acinetobacter baumannii* is classified as an opportunistic pathogen. *A. baumannii* belong to the lineage of *Proteobacteria-Gammaproteobacteria-Pseudomonadales-Moraxellaceae*. *A. baumannii* is a pleomorphic, metabolically versatile, ubiquitous, nonfermentative, catalase positive, oxidase negative, aerobic gram-negative pathogen, commonly isolated from the hospital environment and hospitalized patients.

A. baumannii do not have a fastidious growth requirement and are able to grow at various temperatures and pH conditions. These bacteria can grow in simple mineral medium containing ammonium or nitrate salts and a single carbon and energy source such as acetate, lactate or pyruvate. Their optimal temperature of growth is in the range of 35 - 45^{0}C. The capacity to grow at 44^{0}C serves as a distinguishing characteristic between *A. baumannii* and other genospecies.

Nosocomial Infections associated with *A. baumannii*

A. baumannii has recently emerged as an important nosocomial pathogen, mostly involving patients with impaired host defenses, especially in intensive care units, neonatal units and neurosurgical wards. They can cause infections in hospital patients, especially those who are already very ill, such as patients in intensive care units. It preys exclusively on the weakest of the weak and the sickest of the sick, slipping into the body through open wounds, catheters, and breathing tubes. *A. baumannii* has been isolated from various types of opportunistic infections, including septicemia, pneumonia, endocarditis, meningitis, skin and wound infection, and urinary tract infections (Kapil *et al.*, 1998). Infections caused by *A. baumannii* usually involve organ systems with a high fluid content (e.g., respiratory tract, peritoneal fluid and urinary tract), manifesting as nosocomial pneumonia, infections associated with continuous ambulatory peritoneal dialysis (CAPD), or catheter-associated bacterimia. Studies on *A. baumannii* in various countries have shown a predominance of isolation from urine (21-27%) and tracheal-bronchial secretions (30-40%) (Villers *et al.*,1998). Reports on bloodstream infections from military medical hospitals for treating service members injured in Afghanistan and the Iraq/Kuwait region, together with similar reports during the Vietnam war, have raised the possibility of environmental contamination of wounds as a potential source (Davis *et al.*, 2005).

In newborns, the elderly, burn victims, patients with depressed immune systems, and those on ventilators, *A. baumannii* infections can cause death. Death by *A. baumannii* can take many forms: catastrophic fever, pneumonia, meningitis, infections of the spine and sepsis of the blood. Patients who survive face longer hospital stays, more surgery, and severe complications. Patients with *A. baumannii* pneumonias occurring in the context of an outbreak in the intensive care unit (ICU) generally have a history of preceding contact with respiratory support monitors or equipment. It is believed by some clinicians that the recovery of *A. baumannii* in the hospitalized patient is an indicator of severe illness, with an associated mortality of approximately 30%.

Penetrance of *A. baumannii* in hospital settings

During the last two decades, hospital acquired infections involving multi-resistant *A. baumannii* isolates have been reported, often in association with contamination of the hospital equipment or cross-contamination by the colonized hands of patient attending personnel. It is often difficult to distinguish between infection and colonization with *A. baumannii*. Healthy people can carry the bacteria on their skin with no serious ill effects - a process known as colonization. Colonization poses no threat to people who are not already ill, but colonized health care workers and hospital visitors can carry the bacteria into neighboring wards and other medical facilities. Therefore, entrance of *A. baumannii* in hospital, through a colonized patient is the most likely mode. Adherence to host cells, as demonstrated in an in vitro model using bronchial epithelial cells is considered to be a first step in the colonization process. Figure 2 shows the factors that contribute to *A. baumannii* as environmental persistence and host infection and colonization. Once it enters a hospital ward, *A. baumannii* can spread from the colonized patient to the environment and other susceptible patients. The direct environment of the patient can become contaminated by excreta, air droplets and scales of skin. *A. baumannii* is often cultured from hospitalized patients sputum or respiratory secretions, wounds, and urine.

A. baumannii also colonizes irrigating solutions and intravenous solutions. *A. baumannii* does not have fastidious growth requirements and is able to grow at various temperatures and pH conditions. Hence, the contaminated

environment can become a reservoir from which the organism can spread. The versatile organism exploits a variety of both carbon and energy sources. These properties explain the ability of *Acinetobacter* species to persist in either moist or dry conditions in the hospital environment, thereby contributing to transmission. This hardiness, combined with its intrinsic resistance to many antimicrobial agents, contributes to the organism's fitness and enables it to spread in the hospital setting.

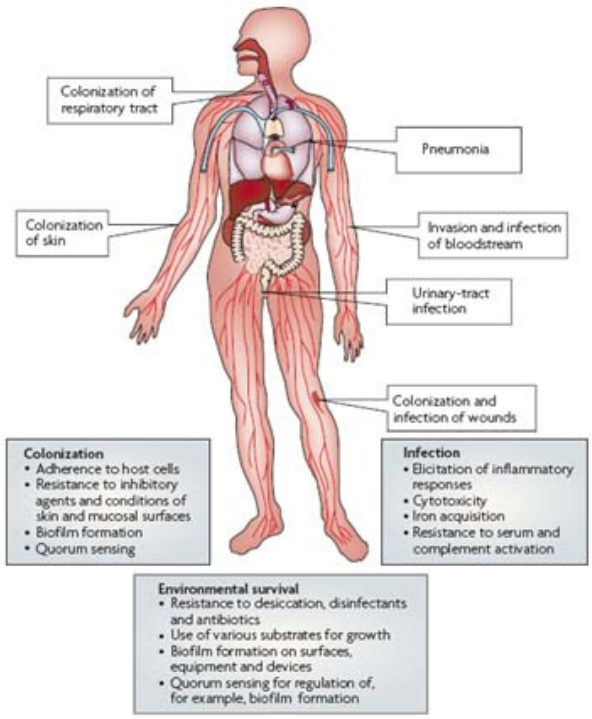

Fig. 2. The factors that contribute to *Acinetobacter baumannii* environmental persistence and host infection and colonization

Pathogenic factors associated with *A. baumannii* infections

Outgrowth on mucosal surfaces and medical devices, such as intravascular catheters and endotracheal tubes can result in biofilm formation, which enhances the risk of infection of the bloodstream and airways. Experimental studies have identified various factors that could have a role in *A. baumannii* infection, for example, lipopolysaccharide has been shown to elicit a proinflammatory response in animal models (Knapp *et al.*, 2006). Furthermore, the *A. baumannii* outer membrane protein A has been demonstrated to cause cell death in vitro (Choi *et al.*, 2008). Iron-acquisition mechanisms and resistance to the bactericidal activity of human serum are considered to be important for survival in the blood during bloodstream infections. Environmental survival and growth require attributes such as resistance to desiccation, versatility in growth requirements, biofilm forming capacity and probably, quorum-sensing activity (Smith *et al.*, 2007). Finally, adequate stress response mechanisms are thought to be required for adaptation to different conditions.

Global Scenario of resistance patterns of *A. baumannii*

Among all the bacterial pathogens, which are associated with the infections in hospitals, *A. baumannii* has a large contribution in all around the world. *A. baumannii* was also considered as the main culprit for the death of soldiers during Iraq war and globally, most of the clinical attentions were insight after the disaster of war (Davis *et al.*, 2005). Many reports have come regarding the outbreaks and pathology of *A. baumannii* (Boucher *et al.,* 2009). About twelve hundred references are cited since 1987 and approximately one quarter of the PubMed citations for "nosocomial *Acinetobacter*" appeared in 2005 and 2009. An increasing number of reports globally suggest that *A. baumannii* have become important nosocomial pathogens, which account for about 8-10% of gram negative bacterial infections.

Effective treatments for *A. baumannii* infections

Few antibiotics are effective for the treatment of *A. baumannii* infections because of the resistance accumulated by isolates and the frequency of multidrug-resistant strains (Davis *et al.*, 2005). The group of antibiotics, which usually are used by clinicians all around the world are β-lactams, aminoglycosides and quinolones. Currently many nosocomial isolates are resistant to all these major classes of antibiotics and therefore, these strains are referred to as Multi Drug Resistant (MDR) organisms. The most challenging part of these strains is the extensive antimicrobial drug resistance. Today, resistance has rendered most of the original antibiotics obsolete for many infections, mandating an increased reliance on synthetic drugs. Almost 25 years ago, researchers observed acquired resistance of *A. baumannii* to antimicrobial drugs commonly used at that time, among them being aminopenicillins, ureidopenicillins, first and second generation cephalosporins, cephamycins, most aminoglycosides, chloramphenicol, and tetracycline.

As *A. baumannii* infections are often difficult to treat, a combination therapy is usually done for effective treatment. The combination of antibiotics include ampicilin-sulbactam, combinations of imipenem and clavanate, imipenem + tobramicin, polymyxin B + sulbactam etc. Clinical data are too few to recommend the use of specific combination regimens for the treatment of infections caused by MDR strains of *A. baumannii*, but combination therapy might be considered by clinicians in order to achieve synergistic activity and to maximize antimicrobial effectiveness (as well as to minimize the possibility of emergence of further resistance) in severely ill patients for whom therapeutic options are otherwise limited.

Resistance mechanisms

One of the biggest issues with treating *A. baumannii* is that the bacterium is naturally resistant to a number of antibiotics, making it challenging to find a drug regime which will effectively attack it in an infected patient. Generally, *A. baumannii* exploits all the stratagems via multigenic phenomenon to escape from mortal effects of antibiotics. Documented mechanisms of resistance in *A. baumannii* are aminoglycosides-modifying enzymes, broad-spectrum β-lactamases, altered penicillin-binding proteins, quantitative and/or qualitative changes in outer membrane porins (Vashist and Rajeswari, 2006). Differential expression of membrane proteins in susceptible and highly resistant strains of *A. baumannii* from different parts of the world clearly show a strong association with the emergence of the resistance phenotype (Vashist *et al.,* 2010). All the above features of *A. baumannii* make this organism special for urgent medical investigations. More effective preventive measures are needed to cure the *A. baumannii* infections and to combat the spread of these MDR organisms.

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Killer paper for next-generation food packaging

Recently scientists have been exploring the use of silver nanoparticles, each 1/50,000 the width of a human hair as germ-fighting coatings for plastics, fabrics and metals. Paper coated with silver nanoparticles could provide an alternative to common food preservation methods such as radiation, heat treatment, and low temperature storage. The coated paper showed potent antibacterial activity against *Escherichia coli* and *Staphylococcus aureus*, two causes of bacterial food poisoning, killing all of the bacteria in just three hours.

Source: www.sciencedaily.com

Genomic comparison of ocean microbes reveals East-West divide in populations

Much as an anthropologist can study populations of people to learn about their physical attributes, their environs and social structures, some marine microbiologists read the genome of microbes to glean information about the microbes themselves, their environments and lifestyles.

Using a relatively new methodology called comparative population genomics, these scientists compare the entire genomes of different populations of the same microbe to see which genes are "housekeeping" or core genes essential to all populations and which are population-specific. Scientists are able to read a genome and translate the genes into proteins that serve particular functions. Population-specific genes sometimes tell a very clear story about the environment, for instance, temperature and the availability of light and particular elements, and over time, they can point to the microbes' evolutionary adaptation to changes in the ecosystem. Occasionally, as was the case with recent research at MIT (Massachusetts Institute of Technology), the population-specific genes reveal this information with crystal clarity, even providing unmistakable clues about lifestyle.

Professor Sallie (Penny) W. Chisholm of MIT's Department of Civil and Environmental Engineering (CEE) and former doctoral student Maureen Coleman compared the genetic makeup of two populations of the same oceanic photosynthetic bacterium, *Prochlorococcus*, one living in the Atlantic Ocean and one in the Pacific.

They found that although a continent separates the populations, they differ significantly in only one respect: those in the Atlantic have many more genes specifically related to the scavenging of phosphorus, an essential element for these microbes. And just as the variations in the beaks of Darwin's finches were evolutionary adaptations related to food availability, so too are the variations in the *Prochlorococcus* genes related to phosphorous gathering. Both are examples of a powerful evolutionary force at work.

"We expected to see some difference in the genes related to phosphorous, because the Atlantic Ocean has a lower concentration of phosphorus than the Pacific, so Atlantic populations of *Prochlorococcus* carry many more genes involved in extracting phosphorus from the seawater. They need more creative ways of gathering it. But we didn't expect it to be the only difference," said Chisholm. "This indicates that phosphorus availability is the dominant selective force in defining these populations."

The researchers also noted that the microbes in the Atlantic Ocean had increased numbers of phosphorous-related genes that helped them neutralize arsenic, an element they sometimes take up by mistake when they are scavenging for phosphorous. This finding "buttresses the assertion" that this is the result of a strong selective process, Chisholm said. "We're really diagnosing the ecosystem using a specific species of microbe as a reporter," said Chisholm. "We're letting the cells tell us what they have to deal with in their environment."

She and Coleman also compared the genomes of two populations of a neighboring bacterium, *Pelagibacter*, and found that genes related to phosphorus gathering in that bacterium appear in far greater numbers in the Atlantic Ocean population, but with a twist. These microbes have a somewhat different repertoire of phosphorus-related genes, suggesting subtle differences between these two microbial groups with respect to how they scavenge phosphorus. This could reflect an adaptive behavior known as "niche partitioning," which allows cells sharing a microenvironment to apportion resources according to a cell's "lifestyle" rather than all competing for the same element or same form of that element.

To obtain these findings, which were published in the online Early Edition of the Proceedings of the National Academy of Sciences in the week of Oct. 11, the two scientists used the complete genomes of 13 strains of lab-cultured *Prochlorococcus* and *Pelagibacter* as reference genes, and compared these with the genes of well-documented wild microbe populations gathered at long-term oceanographic study stations near Bermuda (BATS) and Hawaii (HOTS). The work was funded by the Gordon and Betty Moore Foundation, the National Science Foundation and the U.S. Department of Energy.The next step in this research is to make similar studies at different depths and locations to study the effects of temperature and chemical gradients on the genomes of microbial populations.

"How fast marine microbes adapt to environmental change is a big unknown," said Coleman, who is now a postdoctoral associate at Caltech. "One way to address this is to sample the population genomes over time, with parallel environmental monitoring. We might then be able to catch evolution in action. Long term study sites like HOT and BATS are crucial for this effort."

Scientists on the R/V Kilo Moana oceanographic research ship lower a rosette holding 24 bottles that capture samples at different ocean depths in the Pacific Ocean.

(**Image Credit:** Maureen Coleman)

Source: www.sciencedaily.com

UV light nearly doubles vacuum's effectiveness in reducing carpet microbes

New research suggests that the addition of ultraviolet light to the brushing and suction of a vacuum cleaner can almost double the removal of potentially infectious microorganisms from a carpet's surface when compared to vacuuming alone.

Researchers say the findings suggest that incorporating the germicidal properties of UV light into vacuuming might have promise in reducing allergens and pathogens from carpets, as well.

"What this tells us is there is a commercial vacuum with UV technology that's effective at reducing surface microbes. This has promise for public health, but we need more data," said Timothy Buckley, associate professor and chair of environmental health sciences at Ohio State University and senior author of the study.

"Carpets are notorious as a source for exposure to a lot of bad stuff, including chemicals, allergens and microbes. We need tools that are effective and practical to reduce the associated public health risk. This vacuum technology appears to be a step in the right direction."The research appears online in the journal Environmental Science & Technology.

For this study, Buckley and colleagues tested a commercially available upright vacuum cleaner, evaluating separately and in combination the standard beater-bar, or rotating brush, as well as a lamp that emits germicidal radiation. UV-C light with a wavelength of 253.7 nanometers has been studied extensively for its disinfection properties in water, air and food and on a variety of surfaces. This is the first study of its effects on carpet surfaces.

The Ohio State research group selected multiple 3-by-3-foot sections of carpeting of different types from three settings: a commercial tight-loop carpet in a university conference room, and medium Berber carpet with longer, dense loops in a common room of an apartment complex and a single-family home.

Researchers collected samples from each carpet section using contact plates that were pressed onto the flooring to lift microbes from the carpet surfaces. They collected samples from various locations on each test site to obtain a representative sample of the species present on the carpets.

After sampling, the plates were incubated for 24 hours in a lab and the number of colonies was counted. The plates contained growth media particularly suited for fungi commonly found in indoor environments, including *Penicillium* and *Zygomycetes.*

Each treatment was tested separately by collecting multiple samples from each 3-by-3-foot section before and after treatment: vacuuming alone, the application of UV-C light alone, or a combination of UV-C light and vacuuming. In each case, the carpets were vacuumed at a speed of 1.8 feet per second for two minutes.

Overall, vacuuming alone reduced microbes by 78 percent, UV-C light alone produced a 60 percent reduction in microbes, and the combination of beater-bar vacuuming and UV-C light reduced microbes on the carpet surfaces by 87 percent. When looking at the microbe quantities, the researchers found that, on average, vacuuming alone removed 7.3 colony-forming units of microbes per contact plate and the UV-C light removed 6.6 colony-forming units per plate. The combination of UV-C light and vacuuming yielded the largest reduction in colony-forming units: 13 per plate.

"We concluded that the combined UV-C-equipped vacuum produced approximately the sum of the individual effects, and therefore the UV-C was responsible for an approximate doubling of the vacuum cleaner's effectiveness in reducing the surface-bound microbial load," Buckley said.

Surfaces in residential settings, and especially carpets, are seen as potentially posing health risks because they are reservoirs for the accumulation of a variety of contaminants. Those most susceptible to infection, including the elderly, asthmatics, the very young and people with compromised immune systems, might be at particular risk because they spend most of their time indoors, Buckley noted.

"The best next step would be to test this UV-C vacuum technology in some environments that are high risk, where we could sample for specific pathogens," Buckley said. "The home environment would be particularly important, because that's where people spend the lion's share of their time and are likely to be in close contact with carpet."

Most natural UV-C rays from the sun are absorbed in the atmosphere, but long-term exposure to artificial UV-C sources can cause skin and eye damage. The vacuum has been engineered to prevent exposure to harmful radiation from the UV-C lamp, Buckley said.

Upright vacuum retail prices generally range from about $100 to $900. The equipment in this study falls within that range. This work was supported through a contract with Halo Technologies Inc. of Des Plaines, Ill., which supplied the vacuum technology. Co-authors of the study include Eric Lutz, Smita Sharma and Bruce Casto of the Division of Environmental Health Sciences and Glen Needham of the Department of Entomology, all at Ohio State.

Source: www.sciencedaily.com

ONLINE REPORTS ON MICROORGANISMS

Detecting pathogens in waterways: an improved approach

U.S. Department of Agriculture (USDA) scientists have come up with a way to detect pathogenic *Escherichia coli* and *Salmonella* bacteria in waterways at lower levels than any previous method. Similar methods have been developed to detect pathogenic *E. coli* in meat products, but the approach by scientists with USDA's Agricultural Research Service (ARS) represents a first for waterways.

ARS is USDA's principal intramural scientific research agency, and this research supports the USDA priority of ensuring food safety.

When health officials test a public beach or lake for *Salmonella* or *E. coli* 0157:H7, they use two types of non-pathogenic bacteria, *Enterococci* and generic *E. coli*, as indicators. But while the indicators are often detected in contaminated waterways, their abundance doesn't guarantee the presence of either pathogen, according to Michael Jenkins, a microbiologist at the ARS J. Phil Campbell Sr. Natural Resource Conservation Center in Watkinsville, Ga.

These indicator organisms are often reliable, but investigators have detected the indicators in pathogen-free waters and have failed to find them in waters that contained sufficient levels of the pathogens to make someone sick.

The indicators are used as signals because both pathogens are hard to detect directly at levels that will make someone ill: just 100 cells of *Salmonella* and just 10 to 100 cells of *E. coli* 0157:H7, the toxic strain of the bacterium. Organic matter in a water sample will throw off current PCR (polymerase chain reaction) technology when it is used as a tool for detection. *Salmonella* and *E. coli* outbreaks are often attributed to agricultural operations, so improving ways to track down sources of outbreaks is a major priority.

Jenkins and his ARS colleagues Dinku Endale and Dwight Fisher at Watkinsville combined techniques previously developed to assess water quality and detect pathogens in laboratory settings: a water filtration technique to concentrate the pathogens; a special medium for growing and measuring the number of pathogenic cells; a biochemical testing process; and PCR technology.

They collected water samples from a pond at the Watkinsville site, ran them through a special filter, removed the filter contents and used a centrifuge to spin the filtered contents into a pellet form. They used the suspended pellets to develop cell cultures, confirmed their identity with a genetic method, and determined the concentration found in the original samples.

Their results, published in the Journal of Applied Microbiology, showed the process can be used to detect just a few cells of pathogenic *E. coli* and *Salmonella* in a

10-liter water sample, lower levels than any previously detected. Because the system involves collecting cell cultures, it also may lead to developing culture collections that, like a fingerprint database, could be used to identify bacterial strains that are potential sources of future outbreaks.

Source: www.sciencedaily.com

Like humans, amoebae pack a lunch before they travel

Some amoebae do what many people do. Before they travel, they pack a lunch. In results of a study reported in the journal Nature, evolutionary biologists Joan Strassmann and David Queller of Rice University show that long-studied social amoebae *Dictyostellum discoideum* (commonly known as slime molds) increase their odds of survival through a rudimentary form of agriculture.

Research by lead author Debra Brock, a graduate student at Rice, found that some amoebae sequester their food, particular strains of bacteria, for later use.

"We now know that primitively social slime molds have genetic variation in their ability to farm beneficial bacteria as a food source," says George Gilchrist, program director in the National Science Foundation's Division of Environmental Biology, which funded the research. "But the catch is that with the benefits of a portable food source, comes the cost of harbouring harmful bacteria."

After these "farmer" amoebae aggregate into a slug, they migrate in search of nourishment and form a fruiting body, or a stalk of dead amoebae topped by a sorus, a structure containing fertile spores. Then they release the bacteria - containing spores to the environment as feedstock for continued growth. The findings run counter to the presumption that all "Dicty" eat everything in sight before they enter the social spore - forming stage.

Non-farmer amoebae do eat everything, but farmers were found to leave food uneaten, and their slugs don't travel as far. Perhaps because they don't have to. The advantages of going hungry now to ensure a good food supply later are clear, as farmers are able to thrive in environments in which non-farmers find little food. The researchers found that about a third of wild - collected Dicty are farmers. Instead of consuming all the bacteria they encounter, these amoebae eat less and incorporate bacteria into their migratory systems.

Brock showed that carrying bacteria is a genetic trait by eliminating all living bacteria from four farmers and with four non-farmers as the control group by treating them with antibiotics.

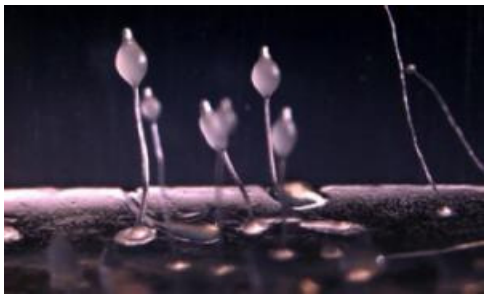
All amoebae were grown on dead bacteria; tests confirmed that they were free of live bacteria. When the eight clones were then fed live bacteria, the farmers all regained their abilities to seed bacteria colonies, while the non-farmers did not.

Dicty farmers are always farmers; non-farmers never learn. Rice graduate student Tracy Douglas co-authored the paper with Brock, Queller and Strassmann. She confirmed that farmers and non-farmers belong to the same species and do not form a distinct evolved group. Still, mysteries remain.

The researchers want to know what genetic differences separate farmers from non-farmers. They also wonder why farmer clones don't migrate as far as their counterparts. It might be a consequence of bacterial interference, they say, or an evolved response, since farmers carry the seeds of their own food supply and don't need to go as far.

Also, some seemingly useless or even harmful bacteria are not consumed as food, but may serve an as-yet-undetermined function, Brock says. That has implications for treating disease as it may, for instance, provide clues to the way tuberculosis bacteria invade cells, says Strassmann, infecting the host while resisting attempts to break them down.

The results demonstrate the importance of working in natural environments with wild organisms whose complex ties to their living environment have not been broken.

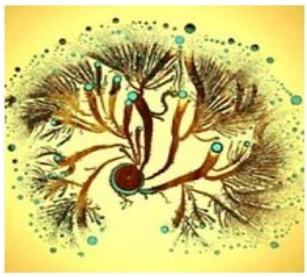


This is an alternate view of amoebae fruiting bodies, with spores and bacteria

(**Image Credit:** Owen Gilbert)

Source: www.sciencedaily.com

The Genius of Bacteria



A "smart community"of *Paenibacillus vortex* bacteria.

IQ scores are used to assess the intelligence of human beings. Now an international team of Tel Aviv University has developed a "Social - IQ score" for bacteria. The international team was first to sequence the genome of pattern-forming bacteria, the *Paenibacillus vortex* (Vortex). While sequencing the genome, the team developed the first "Bacteria Social - IQ Score" and found that Vortex and two other *Paenibacillus* strains have the world's highest Social - IQ scores among all 500 sequenced bacteria. When compared to human IQ Score it is higher and this information can also be directly applied in "green" agriculture or biological control, where bacteria advanced offense strategies and toxic agents can be used to fight harmful bacteria, fungi and even higher organisms.

(**Image Credit:** Prof. Eshel Ben-Jacob.)

Source: www.sciencedaily.com

News

Bacteria ate up methane from Gulf spill, say scientists

Bacteria consumed the methane released from the Deepwater Horizon oil spill in the Gulf of Mexico within about four months, say scientists.

"It was remarkable. We had gone out there assuming that there would be plenty of methane still there and the fact was that it was all gone," Discovery News quoted John Kessler of Texas A & M University in College Station, as saying .

The team had seen a different picture when they sampled the area in June 2010, before the July 15 sealing of the well. Methane levels were high, dissolved in plumes about two-thirds of the way to the sea floor, and decomposition rates were low.

"It seemed that methane would be there for a much longer time period, possibly several years," said Kessler.

But when the team returned in three cruises between Aug. 18 and Oct. 4, expecting to track the slow degradation of methane, they found that it all was gone. Concentrations had returned to background levels.

Source: Indian Express, January 07, 2011.

Abstract

Magdalena Mulet, Zoyla David, Balbina Nogales, Rafael Bosch, Jorge Lalucat, and Elena García-Valdés. Microbiologia, Departament de Biologia, Institut Mediterrani d'Estudis Avançats (CSIC-UIB), Universitat de les Illes Balears, 07122 Palma de Mallorca, Illes Balears, Spain.
***Pseudomonas* diversity in crude-oil-contaminated intertidal sand samples obtained after the prestige oil spill.** Applied and Environmental Microbiology, **77** (3), 2011, 1076 - 1085.

The Galicia seashore, in northwestern Spain, was one of the shorelines affected by the Prestige oil spill in November 2002. The diversity of autochthonous *Pseudomonas* populations present at two beaches (Carnota municipality) was analyzed using culture-independent and culture-dependent methods. The first analysis involved the screening of an *rpoD* gene library. The second involved the isolation of 94 *Pseudomonas* strains that were able to grow on selective media by direct plating or after serial enrichments on several carbon sources: biphenyl, gentisate, hexadecane, methylnaphthalene, naphthalene, phenanthrene, salicylate, xylene, and succinate. Eight denitrifying *Pseudomonas* strains were also isolated by their ability to grow anaerobically with nitrate. The calculated coverage index for *Pseudomonas* species was 89% when clones and isolates were considered together, and there were 29 phylospecies detected. The most abundant were members of the species *P. stutzeri*, *P. putida*, *P. anguilliseptica*, and *P. oleovorans*. Thirty-one isolates could not be identified at the species level and were considered representatives of 16 putative novel *Pseudomonas* species. One isolate was considered representative of a novel *P. stutzeri* genomovar. Concordant results were obtained when the diversities of the cloned DNA library and the cultured strains were compared. The clone library obtained by the *rpoD* PCR method was a useful tool for evaluating *Pseudomonas* communities and also for microdiversity studies of *Pseudomonas* populations.

Keywords: Prestige oil spill*;* autochthonous *Pseudomonas*; crude-oil-contaminated*; P. stutzeri; P. putida; P. anguilliseptica; P. oleovorans.*

E - Resources on Microorganisms

NATIONAL

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

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

Institute of Microbial Technology
www.imtech.res.in

National Institute of Science Communication and Information Resources
www.niscair.res.in

Indian Institute of Ecology and Environment
www.ecology.edu/iiee/iiee.htm

INTERNATIONAL

The Culture Collection of Algae and Protozoa
www.ccap.ac.uk

Federation of European Microbiological Societies
www.fems-microbiology.org/website/nl/default.asp

International Union of Microbiological Societies
www.iums.org

Society for General Microbiology
www.sgm.ac.uk

Culture Collection, University of Göteborg
www.ccug.gu.se

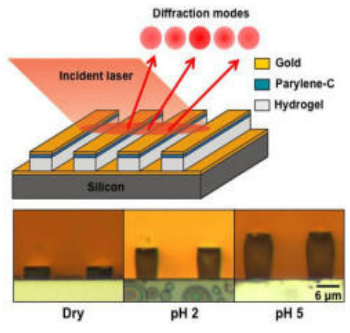
EVENTS
Conferences / Seminars / Meetings 2011

Annual Conference of the Association for General and Applied Microbiology. April 3 – 6, 2011. **Venue:** Karlsruhe, **Germany**. **Website:** www.vaam2011.de.

Emerging Topics in Microbial Pathogenesis. April 12 – 14, 2011. **Venue:** Gartenpavilion, Juliusspital Würzburg, Klinikstraße 1, 97070 Würzburg, **Germany. Website:** www.fems-leopoldina-2011.uni-wuerzburg.de.

Ecology of Soil Microorganisms: Microbes as Important Drivers of Soil Processes. April 14, 2011 - May 1, 2011. **Venue:** Top Hotel**,** Prague, Blazimska 1781/4, Prague 4, **Czech republic.**
Website: www.biologicals.cz/conferences/index.php?conference_id=7.

11th Conference of Bacterial Genetics and Ecology. May 29, 2011 - June 2, 2011. **Venue:** Corfu, **Greece.**
Website: www.bageco11.org.



Diffraction based Sensor

New type of biological and chemical sensor

Researchers introduced a new type of "diffraction - based" sensor made of thin stripes of a gelatinous material called a hydrogel, which expands and contracts depending on the acidity of its environment. The new type biological and chemical sensor has few moving parts and works by precisely determining pH and revealing the identity of substances in liquid environment such as water or blood. The microscopic images at the bottom show how the hydrogel stripes expand with decreasing acidity.

(**Credit:** Brick Nanotechnology Center, Purdue University.)
Source: www.sciencedaily.com

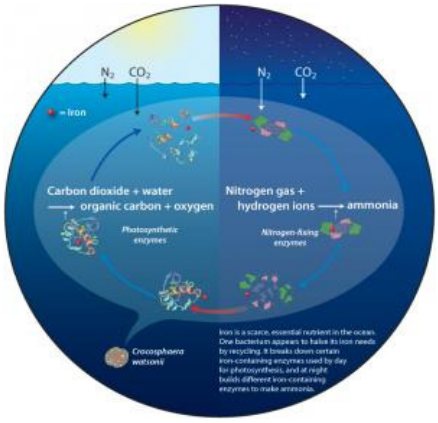
Petri dish with bacteria

Bacteria can have a 'Sense of Smell'

Bacteria are well - known to be the cause of some of the most repugnant smells on Earth, but now a team of marine microbiologists at Newcastle University have discovered for the first time that bacteria have a molecular "nose" that is able to detect airborne, smell-producing chemicals such as ammonia in the environment. Bacteria respond to this smell by producing a biofilm or slime, the individual bacteria joining together to colonise an area in a bid to push out any potential competitor.

(**Image Credit:** iStockphoto/Alexander Raths)

Source: www.sciencedaily.com



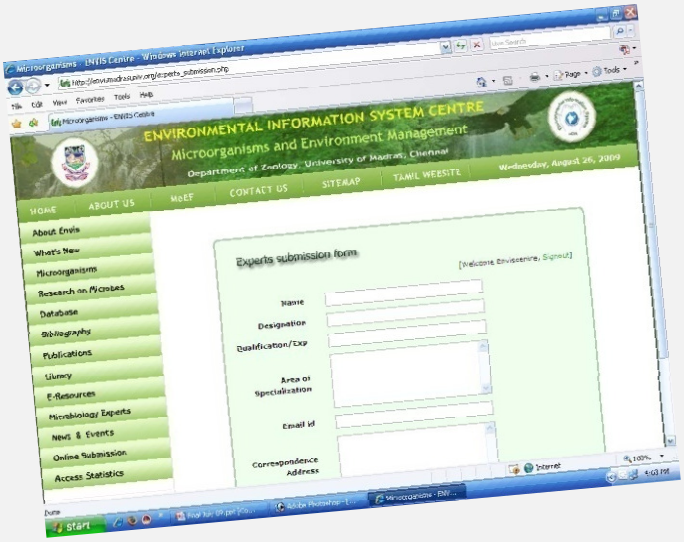
'Hot-Bunking' bacterium recycles iron to boost Ocean metabolism

Iron is a scarce, but essential nutrient in the ocean. The marine bacterium, *Crocosphaera watsonii* that launches the ocean food web survives by using a remarkable biochemical trick. By day, it uses iron in enzymes for photosynthesis to make carbohydrates; then by night, it appears to reuse the same iron in different enzymes to produce organic nitrogen for proteins.

(**Image Credit:** Jack Cook, Woods Hole Oceanographic Institution)

Source: www.sciencedaily.com

Environmental Information System
INDIA



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