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**2012 - International year of 'Marine Bio-diversity'**

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Cover page : Juvenile Crown-of-Thorns sea star hiding among corals

(Credit : S. Holzwarth)

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*Dear Readers,*

**Happy New Year 2012!**

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2	The year 2012 is designated as the 'International year of Marine Bio-diversity'. In connection with this, marine organisms have gained significant interest. Recently climate change, ocean acidification and marine pollution have accelerated the destruction of marine ecosystems. A series of reports from many countries indicate that a reduction in marine species resulting from destruction of marine ecosystems disrupts the balance of the global ecosystem. It also eliminates opportunities for development of bioengineering through use of marine genetic resources. Thus, life in the ocean is under serious threat.
5	Under these circumstances, the focus of marine biodiversity protection has to be shifted beyond the limits of national jurisdiction to include high seas and deep sea beds. The marine species outside the national jurisdiction of a country are at greater risk. In this context, countries around the world are stepping up cooperation to establish a legal mechanism for biodiversity protection and use in areas beyond the limits of national jurisdiction. Therefore Global community is under pressure to enforce laws to meet national and international commitments on sustainably to use and conserve marine biodiversity.
6	This issue brings articles concerned with the importance of marine ecosystem. Articles on the effect of climate change on marine microbial bio-films and the changing ocean microbe communities provide more information about the importance of the marine environment.
8	We sincerely look forward to your suggestions and feedbacks. Please do mail us at.
9	<a href="http://www.envismadrasuniv.org/send_feedback.php">www.envismadrasuniv.org/send_feedback.php</a>
10	<b>Prof. N. Munuswamy</b>
11	For further details, visit our website
13	<a href="http://www.envismadrasuniv.org">www.envismadrasuniv.org</a>

## Effect of global climate change on microbial biofilms

Hans-Uwe Dahms<sup>1\*</sup>, Bong-Rae Kim<sup>2</sup> and Hyung-Uk Park<sup>1,2</sup>

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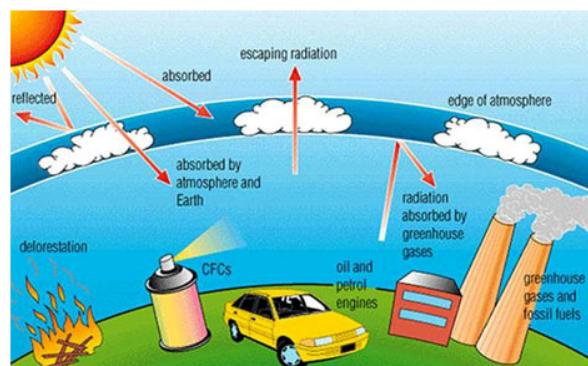
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### Introduction

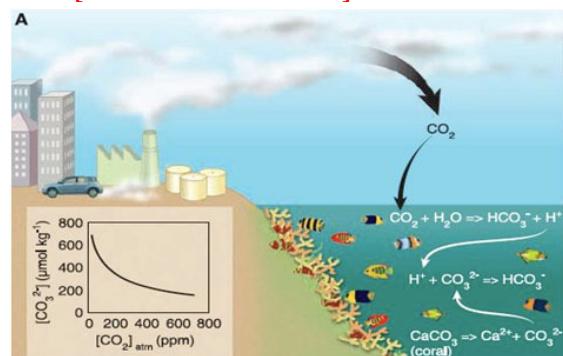
In the coming decades, the marine environment will be subject to profound changes, such as elevation of water temperature. The effects of such changes are likely to be manifested in microbial biofilms that cover all man-made or natural surfaces in the aquatic environment, which are subjected to biofouling by different species of microorganisms (Dahms *et al.*, 2007). In the process of marine biofouling, microorganisms play an important role by inducing or inhibiting settlement and metamorphosis of invertebrate larvae and algal spores (Dobretsov *et al.*, 2006). Both micro- and macrofouling in the world's oceans cause huge economic losses in the maintenance of mariculture, shipping facilities, vessels, and seawater pipelines. Moreover, an increase in biofouling subsequently increases ship fuel consumption and causes an increase in the emission of CO<sub>2</sub>, NO<sub>2</sub> and SO<sub>2</sub> gases. Large-scale increase in the emission of such green house gases can lead to considerable environmental damage by fostering global climate changes (Qian *et al.*, 2007).

Recent anthropogenically caused climate changes, which are only a fraction of predicted changes in the coming decades, have already triggered significant responses in the Earth's biota. These climatic changes are mediated primarily by greenhouse gas emissions. Atmospheric greenhouse gases trap some of the heat energy that would otherwise reradiate to space, heating up the planet in the process (Fig. 1). Ocean warming results in ice melting and increase of freshwater input, affecting nutrient input and causing a decrease of salinity in coastal regions. Increasing temperatures affect atmospheric circulation, resulting in increased up and down welling and storm intensity as well as precipitation. It has been suggested that global warming also changes El-Nino and La-Nina-like conditions that have tremendous effects on marine

life (Gorcau *et al.*, 2005) and the earth's climate (Hughes, 2003). An increase in atmospheric carbon dioxide (CO<sub>2</sub>) leads to an increase in its concentration in the oceans, where about 30% of modern CO<sub>2</sub> emissions are stored. Continuous uptake of CO<sub>2</sub> via the sea surface/ atmosphere interface is expected to decrease oceanic pH (Fig. 2). Decrease in pH will have a striking effect on marine calcifying organisms, while soft-bodied organisms may take an advantage of such changes. An increase in atmospheric CO<sub>2</sub> will also deplete the ozone layer which will elevate UV radiation fluxes (Dobretsov *et al.*, 2005; Dahms *et al.*, 2011). The number of publications that investigate the effect of global climate change on marine communities is increasing. There are no publications about the expected effect of global climate change on biofilms (or microfouling) that cover all substrates in aquatic systems.



**Fig. 1. Global warming caused by several anthropogenic activities [Credit: www.whoi.edu]**



**Fig. 2. Ocean acidification caused by several anthropogenic acids [Credit: www.whoi.edu]**

### Response of microbes to temperature and salinity

There is not much information about the effect of heat on biofouling species but it is likely that species living close to their thermal limit will be stressed and eventually die due to global warming. It is also likely that cold-water biofouling species will be replaced by warm - water species. Global warming intensifies the frequency of El-Nino and La-Nina-like conditions, which will have a tremendous effect on marine ecosystems (Fig. 3). Elevated temperatures during

La-Nina/ El-Nino events severely affect coral reefs and cause coral bleaching and mortality (Hughes, 2003). On the contrary, other species such as shrimps and scallops reproduce and survive El-Nino events better. The flow anomalies during El-Nino events have resulted in anomalous northward transport of plankton by as much as 350 km/ month. This may lead to an increase in biological invasions of warm water species and a decrease in the number of cold-water species. Elevated temperatures increase growth and the photosynthetic rate of some harmful phytoplankton species. But El-Nino events result in a critical reduction of surface nutrients that are necessary for the phytoplankton growth and subsequently affect microbiota in their growth and blooming. Therefore, high intensity of El-Nino-like conditions in future will significantly change diversity and composition of marine communities including microbial communities.

### Elevated temperature

Elevated temperature can also accelerate the transmittance of diseases between species and increase the competition between species (Fig. 4). For example, the coral pathogen *Vibrio shiloi* invades the tissues of the host corals *Oculina patagonica* and causes their bleaching (Israel *et al.*, 2001). Relatively higher water temperatures (about 28°C) will increase the infection rate by the pathogen, while low temperatures (about 16°C) will prevent bacterial growth. Thus, global warming may promote the infection of *O. patagonica* by *V. shiloi* which may significantly affect the distribution of this coral.

### Salinity dilution

Global climate change resulting in ice melting and increase of freshwater input in coastal areas will lead to a decrease of salinity in shallow waters and can affect microbial consortia due to their differential sensitivity to osmotic stress (Fig. 4).

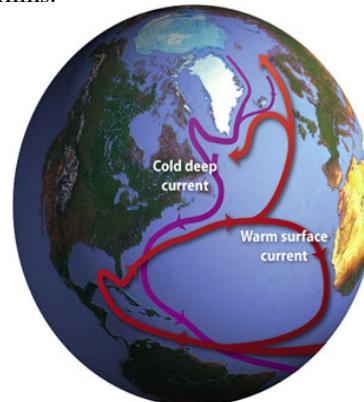
### Response to CO<sub>2</sub> and acidification

Due to anthropogenic activity CO<sub>2</sub> concentrations in the atmosphere are increasing (Fig. 2). Because the oceans are in equilibrium with the atmosphere, the predicted increase of atmospheric CO<sub>2</sub> concentrations is expected to increase CO<sub>2</sub> concentrations in the oceans, despite the fact that elevated temperature and lower pH (associated with an increase of atmospheric CO<sub>2</sub>) will decrease the solubility of CO<sub>2</sub> in seawater. In any case, it is expected that over the next

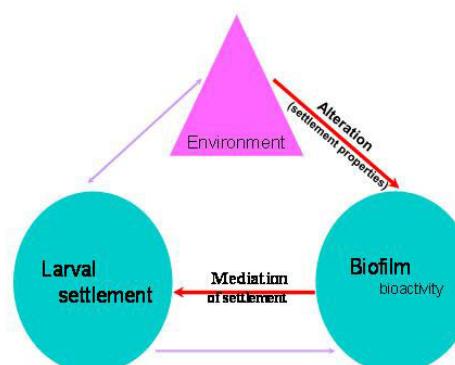
millennium, the oceans will absorb approximately 90% of the CO<sub>2</sub> emitted to the atmosphere. Increasing CO<sub>2</sub> concentrations in the marine environment are not expected to increase the productivity of marine algae. These are carbon-saturated and elevated CO<sub>2</sub> concentrations are not likely to enhance their growth. CO<sub>2</sub> dissolved in the ocean reacts with water to form carbonic acid resulting in ocean acidification. Reduction of pH due to an increase of CO<sub>2</sub> concentrations will have profound effects on the physiological reactions of marine organisms. Experiments suggested that short-term elevations of CO<sub>2</sub> resulted in reductions of protein synthesis and ion exchange in invertebrate cells.

### Sea level rise and hydrodynamics

Intertidal areas may disappear by 20-70% over the next 100 years due to increased anthropogenic activity and because of a decrease of habitat availability. Since most biofouling species are fast growing on any anthropogenic structure, they will not be affected too much by sea level rises. Both negative and positive effects of sea level rise and hydrodynamics will affect the recruitment of species and will have a dramatic effect on biofouling communities, including microbial biofilms.



**Fig. 3. Change of global oceanic circulation patterns**  
[Credit: [www.whoi.edu](http://www.whoi.edu)]



**Fig. 4. Elements of a triangle model that demarcate environmental effects on biofilms that affect larval settlement in marine substrata [after Qian *et al.*, 2007]**

## **Response to UV radiation**

An increase of CO<sub>2</sub> emissions will likely lead to further depletion of the ozone layer (Fig. 1). UVR affects primary producers by damaging organic molecules (DNA, RNA) and the inhibition of photosynthesis (Dahms *et al.*, 2011). UVR has also an indirect effect on the recruitment of algal spores and invertebrate larvae, due to its effects on bacterial communities in biofilms, which in turn may influence the settlement of propagules (Qian *et al.*, 2007). This will ultimately cause an alteration of species composition of biofouling communities.

Additionally, climate change may affect the interactions between biofouling species by changing competitor and predator-prey interactions. This includes climate driven changes in the abundance of species, which in turn affects species distribution, biodiversity, productivity, and microevolution. Global climate change can affect biofouling communities indirectly via the modification of chemical cues that are necessary for successful larval and spore settlement. It has been shown that microbial consortia in the form of biofilms are the major mediators of invertebrate larvae and algal spore settlement (Qian *et al.*, 2007). Different species of bacteria, diatoms and fungi in biofilms can induce, inhibit or have no effect on larval and algal settlement (Dahms *et al.*, 2006). The resulting effect of multi-species biofilms on larval settlement depends on species composition of biofilms and densities of different groups of microorganisms. The same microorganisms are able to produce different secondary metabolites under the same culture conditions. For example, bacteria were inhibitive to the larvae of *Balanus amphitrite* at seawater salinities of 35 and 45 PSU, but induced their settlement at 15 and 25 PSU. Environmental changes can modify the density and the composition of microbial communities, which in turn can change larval settlement. In the laboratory, larvae of different species responded differently to biofilms developed in different environmental conditions. Biofilms that were developing at relatively high temperature stimulated the settlement of the barnacle *B. amphitrite*. In contrast, the same biofilms had no effect on the larval settlement of the polychaete *Hydroides elegans*. These examples indicate that climate change may affect biofilm density, composition, production of metabolites and their effect on the recruitment of propagules, which will finally change the composition of biofouling communities (Dobretsov *et al.*, 2006).

## **Directions for upcoming research**

Microbial communities, besides other marine biota, are expected to show drastic changes in response to present and coming climate changes worldwide. Since studies on global climate changes on biofilms are rare, particularly in the natural environment, it will be necessary to investigate those effects in order to simulate their effects on natural biota as well as that in aquaculture or in anthropogenic systems. Elevated temperatures, low salinity, high wave turbulence and low pH due to increased CO<sub>2</sub> concentrations are main factors associated with global climate change. Any of them, separate or in combination, will affect the development of biofouling communities (Fig. 4). Based on the analysis of available literature, we can assume that the most drastic changes in biofouling communities are going to happen because of elevated seawater temperature and decreased pH. Possibly, in polar and temperate regions, cold-water microbiota will be replaced by alien warm-water biota. Recently, biocides and antifouling compounds have been tested using single species of microbes (Dobretsov *et al.*, 2006). To predict changes in biofilms will, however, require the development of new bioassay techniques that include several target species from different phylogenetic groups. Replacement of cold-water strains and an increase of invasive warm-water strains due to global climate change will also affect the aquaculture of marine species. The aquaculture of shellfish, such as abalone, oyster, and mussel will be affected not only because of changes in their settlement but also by pathogenic microorganisms in biofilms. In addition, UVR, acidification and elevated water temperatures affect resources of invading species. Such effects should be properly investigated and future predictions and recommendations should be made. Marine organisms can respond differently to multiple stressors and the combined effect of two or more variables will be different from the effect of an individual stressor (Dahms *et al.*, 2006). The impact of one factor can either be strengthened or weakened by another factor and the combined effect of two and more stressors may push an individual beyond a threshold that would not be reached by a single stressor. For example, high levels of UV radiation have no effect on the survival of algal spores in warm water, while spores died in treatments with high levels of UV radiation in cold water (Dahms *et al.*, 2011). Since the majority of global change studies deal with a single stressor, it will be 4

necessary in future studies to include effects of multiple stressors associated with global climate change on biofouling communities. Such factors may not only affect microbial consortia but also other biota that are influenced by them. Susceptibility of biofouling organisms to biocides may change due to climate change. Elevated CO<sub>2</sub> reduces the tolerance limits of marine organisms to certain biocides via the depression of important physiological pathways. Elevation by 5–10°C of water temperature increases the respiration of microorganisms and their sensitivity to copper. In addition, global climate change can have both direct and indirect impacts on assemblages in biofilms. Composition of microbial biofilms and their production of chemical cues can vary at different environmental conditions (Qian *et al.*, 2007). Therefore, larval and algal spore settlement on biofilms will be affected by global climate change. Due to the lack of appropriate cues, the density of some biofouling species will become low, while other species will dominate biofouling communities. Changes in microbial biofilms may finally affect the entire composition of biofouling communities. Overall, it seems that global climate change will seriously affect the productivity, development, dynamics, and composition of biofouling communities. Future studies should focus on the impact of climate change on biofouling species, populations and communities and will require multidisciplinary approaches.

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## RESEARCH REPORTS

### Marine bacteria use light to lure Plankton and fish

Not all that glitters is gold. Sometimes it is just bacteria trying to get ahead in life. Many sea creatures glow with a biologically produced light. This phenomenon, known as bioluminescence, is observed, among others, in some marine bacteria which emit a steady light once they have reached a certain level of concentration (a phenomenon called “quorum sensing”) on organic particles in ocean waters. Though this was a known occurrence, the benefits of producing light remained unclear. Now, in an article published recently in the Proceedings of the National Academy of Sciences (PNAS), researchers of the Hebrew University of Jerusalem have unraveled the mystery of why the marine bacteria glow. It has to do with what might be called “the survival of the brightest.”

The article is based on the research carried out at the Interuniversity Institute for Marine Sciences in Eilat by graduate student Margarita Zarubin, under the supervision of Prof. Amatzia Genin, Head of the Department of Evolution, Systematics and Ecology at the Hebrew University of Jerusalem in collaboration with Prof. Shimshon Belkin and his student Michael Ionescu of the Hebrew University’s Silberman Institute of Life Sciences.

Their findings show that the light emitted by the bacteria attracts predators, generally zooplankton, which ingest the bacteria but are unable to digest them. The bacteria, which **5**

continue to glow inside the zooplankton's guts, reveal the presence of the now-glowing zooplankton, which in turn, are attacked by their own predators fish who can spot them readily in the dark.

In experiments conducted by the researchers in total darkness, they found that nocturnal fish were easily able to detect the glowing zooplankton and eat them, while, on the other hand, the fish were not attracted to zooplankton that had swallowed bacteria that had undergone genetic mutation and thus did not glow. Further investigation of nocturnal fish that had fed on zooplankton showed that the luminous bacteria also survived the passage through the fish guts. "As far as the bacteria are concerned, their access to the fish digestive systems is like reaching 'paradise' a safe place, full of nutrients, and also a means of transport into the wide ocean," explained Prof. Genin.

On the other hand, the finding that some zooplankton are attracted to the glow of the bacteria and consume the luminous matter seems to be in contradiction to their own survival instincts, since it increases the chances of the zooplankton being attacked and eaten by fish. The phenomenon of quorum sensing that regulates bacterial bioluminescence can explain this finding, say the researchers. The zooplankton "know" that a light in the water indicates the presence of a rich presence of organic material on which the bacteria grow.

"In the dark, deep ocean the quantity of food is very limited, therefore it is worthwhile for the zooplankton to take the risk of becoming glowing themselves when contacting and consuming the particle with glowing bacteria, since the profit of finding rare food there is greater than the danger of exposing themselves to the relatively rare presence of predatory fish," explained Prof. Genin.



**Zooplankton after ingesting glowing bacteria**

(Image Credit: Hebrew University, Jerusalem)

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

## Viruses con bacteria into working for them

MIT (Massachusetts Institute of Technology) researchers have discovered that certain photosynthetic ocean bacteria need to beware of viruses bearing gifts: These viruses are really con artists carrying genetic material taken from their previous bacterial hosts that tricks the new host into using its own machinery to activate the genes, a process never before documented in any virus-bacteria relationship.

The con occurs when a grifter virus injects its DNA into a bacterium living in a phosphorus-starved region of the ocean. Such bacteria, stressed by the lack of phosphorus (which they use as a nutrient), have their phosphorus-gathering machinery in high gear. The virus senses the host's stress and offers what seems like a helping hand: bacterial genes nearly identical to the host's own that enable the host to gather more phosphorus. The host uses those genes, but the additional phosphorus goes primarily toward supporting the virus replication of its own DNA.

Once that process is complete (about 10 hours after infection), the virus explodes its host, releasing progeny viruses back into the ocean where they can invade other bacteria and repeat this process. The additional phosphorus-gathering genes provided by the virus keep its reproduction cycle on schedule. In essence, the virus (or phage) is co-opting a very sophisticated component of the host's regulatory machinery to enhance its own reproduction something never before documented in a virus-bacteria relationship.

"This is the first demonstration of a virus of any kind even those heavily studied in biomedical research exploiting this kind of regulatory machinery in a host cell, and it has evolved in response to the extreme selection pressures of phosphorus limitation in many parts of the global oceans," says Sallie (Penny) W. Chisholm, a Professor of Civil and Environmental Engineering (CEE) and Biology at MIT, who is principal investigator of the research and co-author of a paper published in the journal of Current Biology. "The phage have evolved the capability to sense the degree of phosphorus stress in the host they're infecting and have captured, over

evolutionary time, some components of the bacteria's machinery to overcome the limitation."

Chisholm and co-author Qinglu Zeng, a CEE postdoc, performed this research using the bacterium *Prochlorococcus* and its close relative, *Synechococcus*, which together produce about a sixth of the oxygen in Earth's atmosphere. *Prochlorococcus* is about one micron in diameter and can reach densities of up to 100 million per liter of seawater; *Synechococcus* is only slightly larger and a bit less abundant. The viruses that attack both bacteria, called cyanophages, are even more populous.

The bacterial mechanism in play is called a two-component regulatory system, which refers to the microbe's ability to sense and respond to external environmental conditions. This system prompts the bacteria to produce extra proteins that bind to phosphorus and bring it into the cell. The gene carried by the virus encodes this same protein. "Both the phage and bacterial host have the genes that produce the phosphorus-binding proteins, and we found they can both be up-regulated by the host's two-component regulatory system," says Zeng. "The positive side of infection for bacteria is that they will obtain more phosphorus binders from the phage and maybe more phosphorus, although the bacteria are dying and the phage is actually using the phosphorus for its own ends."

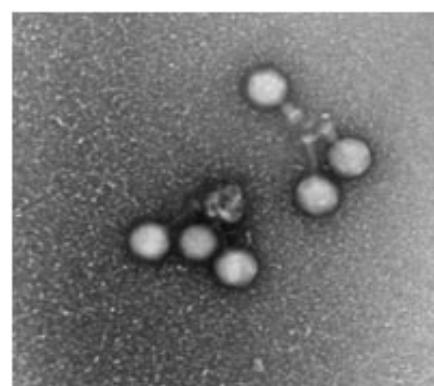
In 2010, Chisholm and Maureen Coleman, now an Assistant Professor at the University of Chicago, demonstrated that the populations of *Prochlorococcus* living in the Atlantic Ocean had adapted to the phosphorus limitations of that environment by developing more genes specifically related to the scavenging of phosphorus. This proved to be the sole difference between those populations and their counterparts living in the Pacific Ocean, which is richer in phosphorus, indicating that the variation is the result of evolutionary adaptation to the environment. The new research indicates that the phage that infect these bacteria have evolved right along with their hosts.

"These viruses the most abundant class of viruses that infect *Prochlorococcus* have acquired genes for a metabolic pathway from their host cells," says Professor David Shub a biologist at the State University of New York at Albany. "These sorts of genes are usually tightly regulated in bacteria, that is they are turned into RNA and protein only when needed by the cell. However, genes of these kinds in viruses tend to be used in a strictly programmed manner, unresponsive to changes in the

environment. Now Zeng and Chisholm have shown that these particular viral genes are regulated by the amount of phosphate in their environment, and also that they use the regulatory proteins already present in their host cells at the time of infection. The significance of this paper is the revelation of a very close evolutionary interrelationship between this particular bacterium and the viruses that seek to destroy it."

"We've come to think of this whole system as another bit of evidence for the incredible intimacy of the relationship of phage and host," says Chisholm, whose next steps are to explore the functions of all of the genes these marine phage have acquired from host cells to learn more about the selective pressures that are unique to the phage-host interactions in the open oceans. "Most of what we understand about phage and bacteria has come from model microorganisms used in biomedical research," says Chisholm. "The environment of the human body is dramatically different from that of the open oceans, and these oceanic phage have much to teach us about fundamental biological processes."

This research was supported in part by the Gordon and Betty Moore Foundation, the National Science Foundation's (NSF) CMORE program, the NSF Biological Oceanography program and the U.S. Department of Energy.



**This virus that attacks the Cyanobacteria, *Prochlorococcus* (seen here through a transmission electron micrograph), was isolated from the Atlantic Ocean near Bermuda.**

**(Image Credit: Simon Labrie and Qinglu Zeng, Chisholm Lab)**

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

### Scientists coax shy microorganisms to stand out in a crowd

The communities of marine microorganisms that make up half the biomass in the oceans and are responsible for half the photosynthesis the world over, mostly remain enigmatic. A few abundant groups have had their genomes described, but the natures and functions of the rest remain mysterious.

Understanding how the changing global environment might affect these important ecosystem players is like trying to understand how the United States works when you can only discern Texas and California while many other states remain indistinct and you only suspect the existence of ones the size of Rhode Island and Delaware.

Now University of Washington (UW) scientists have advanced a method that allowed them to single out a marine microorganism and map its genome even though the organism made up less than 10 percent of a water sample teeming with many millions of individuals from dozens of identifiable groups of microbes.

Typically researchers have had to isolate an organism and culture it in a lab before they could begin to crack its genome. “We’ve done the opposite,” said Vaughn Iverson, a UW doctoral student in oceanography and lead author of a report in the journal *Science*.

“We went to the environment, didn’t make any attempt to isolate any of the organisms in a laboratory sense and, instead, extracted the DNA from everything in the sample,” he said. “It’s a technique known as metagenomics. The UW’s innovation was to develop computational methods to simultaneously sequence all the parts and then reconstruct the chosen genome.”

The researchers determined the genome of a member of the marine group II *Euryarchaeota*, something that has defied investigators since those microorganisms were first detected about a decade ago. They are found widely across the world’s oceans so although not always abundant biologists assume they have some important function, said Virginia Armbrust, UW Professor of Oceanography and corresponding author on the *Science* paper. The resulting genome offers hints that *Euryarchaeota* might serve as a kind of cleanup crew after diatoms, another ocean microorganism, bloom and die.

“Ocean microorganisms are regulators of large biogeochemical cycles so we need to understand the different members of those communities,” Armbrust said. “As we change coastal communities for better or for worse we need to understand the players that are there.”

The genome also clarified the origin of a gene that allows marine group II *Euryarchaeota*, as well as many marine bacteria, to harvest energy directly from sunlight, with no photosynthesis involved.

The approach advanced by the UW team isn’t just useful for studying microorganisms in the oceans, but also for those found in soils and algal communities with potential for biofuels, or for understanding emerging strains of antibiotic-resistant bacteria that threaten human or animal health, Iverson said. The UW approach takes less time and money.

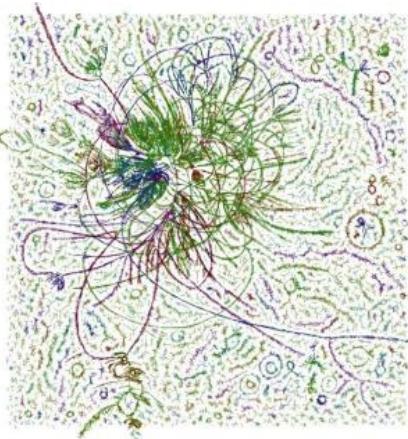
“Having to culture things to sequence them is an extra step and time consuming if they’re difficult to culture,” he said. “It becomes a chicken and egg problem. If you have never been able to study it, you don’t know what it needs. But in order to study it, you must provide the environment in the lab that it requires.” “If microbiologists can get the DNA directly and sequence it without having to culture it, that’s a big advantage.”

Metagenomics extracting DNA from whole microbial communities and sequencing it to reveal genes has been used for about a decade with marine microorganisms. Sequencing equipment and methods have leapt forward since then, thanks to many researchers and companies, the UW scientists said.

But previous techniques allowed scientists to reconstruct an organism’s genome only if the organism made up a third or more of a sample. The UW team showed how to construct the genome of marine group II *Euryarchaeota* even though it comprised only 7 percent of the cells found in 100 liters of water from Puget Sound near Seattle.

The sample was analyzed using equipment purchased with funding to Armbrust from the Gordon and Betty Moore Foundation, which also paid for Iverson’s work. The project was conducted in labs run by Armbrust and co-author Robert Morris, a UW Assistant Professor of Oceanography. Other co-authors are Christian Frazar,

Chris Berthiaume and Rhonda Morales, all with the UW. “Now you can afford to get things that are a much smaller fraction of your overall sample,” Iverson said. “That’s what’s really new to assemble something with a genome that is not closely related to anything else that is known, so there are no templates or references to work from, and to discern organisms making up less than 10 percent of a sample from a complex community.”



A graphical view of tens of millions of bases of DNA extracted from a marine microbial community found in Puget Sound, reveals the entangled genomes of bacteria, archaea and viruses. Scientists extracted 2 million of these to map the genome of one particular marine microorganism that had defied investigation.

(Image Credit: V Iverson/U of Washington)

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

#### Microbes in lava tube living in conditions like those on mars



A team of scientists from Oregon has collected microbes from ice within a lava tube in the Cascade Mountains. The microbes tolerate temperatures near freezing and low levels of oxygen, and they can grow in the absence of organic food. Under these conditions their metabolism is driven by the oxidation of iron from olivine, a common volcanic mineral found in the rocks of the lava tube. These factors make the microbes capable of living in the subsurface of Mars and other planetary bodies.

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

#### Ocean microbe communities changing, but long-term environmental impact is unclear

As oceans warm due to climate change, water layers will mix less and affect the microbes and plankton that pump carbon out of the atmosphere but researchers say it's still unclear whether these processes will further increase global warming or decrease it. The forces at work are enormous and the stakes huge, said Oregon State University (OSU) scientists in an article published in the journal Science. But inadequate ocean monitoring and lack of agreement on how to assess microbial diversity has made it difficult to reach a consensus on what the future may hold, they said.

“We’re just beginning to understand microbial diversity in the oceans and what that may mean to the environment,” said Stephen Giovannoni, an OSU Professor of microbiology. “However, a large portion of the carbon emitted from human activities ends up in the oceans, which with both their mass of water and biological processes act as a huge buffer against climate change. These are extremely important issues.”

The interest is growing, scientists say, because nearly half of the world’s photosynthesis is contributed by microbial plankton, and the process of marine carbon production and consumption is much faster than on land. A turnover of terrestrial plant biomass takes 15 years, they say, while marine turnover takes just six days.

As the ocean surface warms, evidence shows that it will become more “stratified,” or confined to layers that mix less than they did in the past. This should reduce overall ocean productivity, Giovannoni said, but so little is known about the effect on ocean microbes that the implication for carbon sequestration and global warming is less clear. Some OSU research on routine seasonal changes of microbes in the Sargasso Sea of the Atlantic Ocean suggests that different and specialized microbial communities can become more dominant when water warms. As warmer oceans become a more long-term and global phenomenon, researchers need to know more about these microbes, and whether their behavior will amplify or reduce atmospheric carbon and the greenhouse effect. It could be either, Giovannoni said.

"Some warming of surface waters may reduce carbon sequestration, which could cause a feedback loop to increase global warming," Giovannoni said. "Other forces, what we call the microbial carbon pump, could cause carbon to sink into the deep ocean and be segregated from the atmosphere for thousands of years," he said. "We know both of these processes exist, but which one will become dominant is unpredictable, because we know so little about ocean microbes."

It was only two decades ago that OSU scientists discovered SAR11, an ocean microbe and the smallest free-living cell known, but one that's now understood to dominate life in the oceans, thrives where most other cells would die and plays a huge role in carbon cycling on Earth.

Microbial action also surprised scientists just recently, Giovannoni noted, when specific microbe populations surged following the Gulf Coast oil spill and cleaned up much of the oil faster than many thought possible. And some plans to "fertilize" the ocean and sequester atmospheric carbon through marine phytoplankton growth have been put on hold, he said, because it just isn't certain what would happen.

To reduce that uncertainty, Giovannoni advocates more aggressive development and implementation of marine microbial monitoring technology around the world, to add to what scientists can already learn from study of satellite images. And the field is so new, he said, that many researchers are not even comparing the same types of data or standardizing the tools they use to assess microbial diversity a problem that needs to be addressed. Dramatic advances in DNA sequencing in recent years, Giovannoni said, should also help researchers unravel the ocean microbe mystery.

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

### Hearty bacteria help make case for life in the extreme

The bottom of a glacier is not the most hospitable place on Earth, but at least two types of bacteria happily live there, according to researchers. The bacteria *Chryseobacterium* and *Paenibacillus* showed signs of respiration in ice made in the laboratory that was designed to simulate as closely as possible the temperatures and nutrient content found at the bottom of Arctic and Antarctic glaciers, said Corien Bakermans, Assistant Professor of Microbiology, Penn State Altoona. She said that carbon dioxide levels in the laboratory-made ice containing the

bacteria, which were collected from glaciers in Greenland and Antarctica, indicated that respiration was occurring at temperatures ranging from negative 27 to positive 24 degrees Fahrenheit.

Bakermans, who worked with Mark Skidmore, Associate Professor of Geology, Montana State University, determined the level of respiration by measuring the amount of carbon dioxide in the laboratory-made ice.

While humans obtain energy from sugar, the bacteria in this experiment used acetate, a form of vinegar. Like human respiration, the microbes take in the molecules, extract energy from them and breathe out carbon dioxide as a waste product. Bakermans said the study may have implications for the search for life on other planets, like Mars, because some places on Mars are in the same temperature range as the temperature levels recorded during the experiment.

"Although there are a lot of other factors involved for life to take hold on other planets," Bakermans said, "we can still say that if microbes on Earth can do this, then there's the potential, at least, that microbes can do this on Mars." Glaciers and ice sheets represent large ecosystems that cover more than 10 percent of Earth and contain approximately 78 percent of the world's fresh water.

The researchers, who reported their findings in a recent issue of Environmental Microbiology Reports, said that respiration was reported at all temperatures examined. The respiration rate of the microbes increased as the temperature rose. While the respiration rates of the bacteria are slow compared to the human respiration, the microbes could maintain cell structure and viability throughout the observed temperature range.

The researchers also performed a staining test to measure cell viability. When cells are alive or dead, they leave a chemical footprint of those states. By applying stains to the bacteria in the laboratory-made ice, the researchers can find those chemicals and determine if the cells are alive and healthy. Bacteria seem to grow best in cracks and crevices within the ice, Bakermans said. The cracks in the ice create channels that allow water and nutrients to circulate. "It's hard for nutrients to be exchanged in the ice," Bakermans said. "But these channels appear to give the microbes access to nutrients."

The bottom of glaciers may be more hospitable for the microbes than other parts of the glacier because the areas draw warmth and nutrients from the earth, Bakermans said.

**Source:** www.sciencedaily.com

## News

### New 'killer' bacteria on the prowl

Millions of Indians are suspected to be carriers of the drug-resistant bug. After the scary New Delhi metallo-beta-lactamase-1 or the "superbug" was detected two years ago, the world is now faced with the community-acquired methicillin-resistant *Staphylococcus aureus* (ca-MRSA) bacterium that is resistant to almost all common antibiotics.

In India, where poor hygiene and the availability of over-the-counter antibiotics lead to development of resistance, an estimated 100 to 200 million people are reportedly already carriers of these virtually unbeatable killer bacteria. The killer bugs have also reached England, presumably through medical tourists who travelled to India for cosmetic surgery, and reportedly already infected several hundred people. A few cases have also turned up in Germany. The bacterium has become a serious health threat in the United States. India had protested the naming of the superbug after New Delhi and denied its presence then. Now, the ca-MRSA is all set to raise another storm.

There is only one antibiotic left a drug that is normally not even used anymore owing to its potentially fatal side effects that is still effective against these killer bacteria. In serious cases, people who become infected with these types of pathogens die of urinary tract infections, wound infections or pneumonia. And, in contrast to the highly drug-resistant hospital-acquired MRSA (ha-MRSA) strains, which primarily affect the elderly and people in hospitals and nursing homes, ca-MRSA affects healthy young people.

An article written by Philip Bethge, Veronika Hackenbroch, Laura Hoflinger, Michael Leockx and Udo Ludwig for a German news magazine Der Spiegel says the two bacteria, ha-MRSA and ca-MRSA, are only two strains from an entire arsenal of pathogens that are now resistant to almost all available antibiotics. Less than a century after the discovery of penicillin, one of the most powerful weapons ever produced by modern medicine, it threatens to become ineffective.

## Fear of 'pandemic'

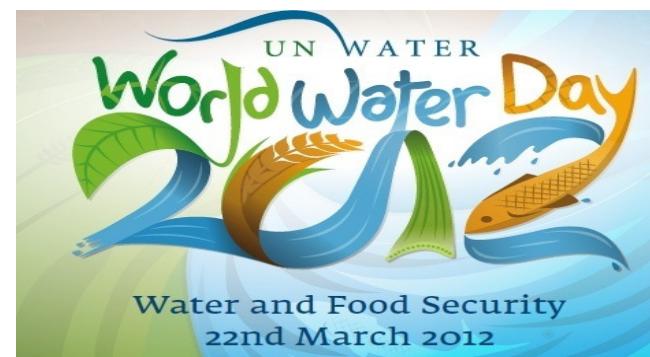
The British medical journal The Lancet warns that the drug-resistant bacteria could spark a "pandemic." And, in Germany, the dangerous pathogens are no longer only feared "hospital bugs" found in intensive care units (ICUs). Instead, they have become ubiquitous.

The bacteria are transmitted via skin, through towels, clothing or direct body contact. All it takes is a small abrasion to provide them access to a victim's bloodstream. Festering pustules develop at the infection site, at which point the pathogens are also capable of corroding the lungs. If doctors wait too long, patients can die very quickly. The dangerous bacteria have even been detected on one of Germany's high-speed ICE trains. Likewise, more than 10 per cent of the residents of German retirement homes have been reportedly colonised by MRSA bacteria. In their case, every open wound is potentially deadly. The pathogens have also been found in beef, pork and vegetables.

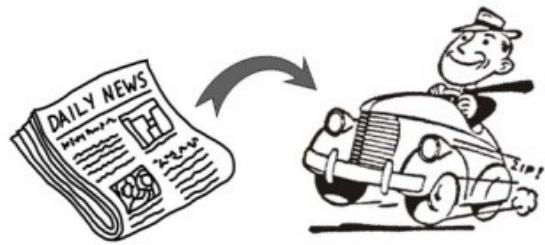
### Alarming finding

Another alarming finding is that about 3 to 5 per cent of the population carries the so-called ESBL-forming bacteria in the intestine without knowing it. Even modern antibiotics are completely ineffective against these highly resistant bacteria, the article warns. Infestation with multidrug-resistant bacteria is normally harmless to healthy individuals because their immune systems can keep the pathogens under control. Problems arise when an individual becomes seriously ill. Israel even experienced a nationwide outbreak a few years ago. Within a few months, about 1,300 people were afflicted by an extremely dangerous bacterium that killed 40 per cent of infected patients. Even today, the same bacterium still sickens some 300 people a year.

**Source:** The Hindu, January 29, 2012.



## Cars run on recycled newspaper



Scientist from Tulane University, USA have discovered a novel bacterial strain, dubbed "TU-103," that can use paper to produce butanol, a biofuel that can serve as a substitute for gasoline. They are currently experimenting with old editions of the Times Picayune, New Orleans's venerable daily newspaper, with great success. TU-103 is the first bacterial strain from nature that produces butanol directly from cellulose, an organic compound. As a biofuel, butanol is superior to ethanol and can be transported readily through existing fuel pipelines in the motor vehicles without any modification to the engine and improve mileage.

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

## Abstracts

1. Ee-Been Goh, Edward E. K. Baidoo, Jay D. Keasling and Harry R. Belle. **Engineering of Bacterial Methyl Ketone Synthesis for Biofuels.** Applied and Environmental Microbiology, **78** (1), 2012, 70 - 80.

We have engineered *Escherichia coli* to overproduce saturated and monounsaturated aliphatic methyl ketones in the C<sub>11</sub> to C<sub>15</sub> (diesel) range; this group of methyl ketones includes 2-undecanone and 2-tridecanone, which are of importance to the flavor and fragrance industry and also have favorable cetane numbers (as we report here). We describe specific improvements that resulted in a 700-fold enhancement in methyl ketone titer relative to that of a fatty acid-overproducing *E. coli* strain, including the following: (i) overproduction of  $\beta$ -ketoacyl coenzyme A (CoA) thioesters achieved by modification of the  $\beta$ -oxidation pathway (specifically, overexpression of a heterologous acyl-CoA oxidase and native FadB and chromosomal deletion of fadA) and (ii) overexpression of a native thioesterase (FadM). FadM was previously associated with oleic acid degradation, not methyl ketone synthesis, but outperformed a recently identified methyl ketone synthase (*Solanum habrochaites* MKS2 [*ShMKS2*], a thioesterase from wild tomato) in  $\beta$ -ketoacyl-CoA-overproducing strains tested. Whole-genome transcriptional (microarray) studies led to the

discovery that FadM is a valuable catalyst for enhancing methyl ketone production. The use of a two-phase system with decane enhanced methyl ketone production by 4- to 7-fold in addition to increases from genetic modifications.

**Keywords:** *Escherichia coli*, *Solanum habrochaites*, methyl ketone synthase, Bacterial methyl ketone synthesis for biofuels.

**2. Weimin Sun and Alison M. Cupples. Diversity of Five Anaerobic Toluene-Degrading Microbial Communities Investigated Using Stable Isotope Probing.** Applied and Environmental Microbiology, **78** (4), 2012, 972 - 980.

Time-series DNA-stable isotope probing (SIP) was used to identify the microbes assimilating carbon from [<sup>13</sup>C] toluene under nitrate- or sulfate-amended conditions in a range of inoculum sources, including uncontaminated and contaminated soil and wastewater treatment samples. In all, five different phylotypes were found to be responsible for toluene degradation, and these included previously identified toluene degraders as well as novel toluene-degrading microorganisms. In microcosms constructed from granular sludge and amended with nitrate, the putative toluene degraders were classified in the genus *Thauera*, whereas in nitrate-amended microcosms constructed from a different source (agricultural soil), microorganisms in the family *Comamonadaceae* (genus unclassified) were the key putative degraders. In one set of sulfate-amended microcosms (agricultural soil), the putative toluene degraders were identified as belonging to the class *Clostridia* (genus *Desulfosporosinus*), while in other sulfate-amended microcosms, the putative degraders were in the class *Deltaproteobacteria*, within the family *Syntrophobacteraceae* (digester sludge) or *Desulfobulbaceae* (contaminated soil) (genus unclassified for both). Partial benzylsuccinate synthase gene (*bssA*, the functional gene for anaerobic toluene degradation) sequences were obtained for some samples, and quantitative PCR targeting this gene, along with SIP, was further used to confirm anaerobic toluene degradation by the identified species. The study illustrates the diversity of toluene degraders across different environments and highlights the utility of ribosomal and functional gene-based SIP for linking function with identity in microbial communities.

**Keywords:** PCR, *Thauera*, *Comamonadaceae*, *Desulfosporosinus*, *Deltaproteobacteria*, *Syntrophobacteraceae*, *Desulfobulbaceae*.

## E - Resources on Microorganisms

### NATIONAL

National Fungal Culture Collection of India  
[www.aripune.org/](http://www.aripune.org/)

NII Microbial Culture Collection  
[www.niist.res.in/english/](http://www.niist.res.in/english/)

MACS Collection of Microorganisms  
[www.aripune.org/mcm.html](http://www.aripune.org/mcm.html)

NITE Biological Resource Center  
[www.bio.nite.go.jp/pamphlet/e/nbrc-e.html](http://www.bio.nite.go.jp/pamphlet/e/nbrc-e.html)

Goa University Fungus Culture Collection and Research Unit  
[wdcm.nig.ac.jp/CCINFO/CCINFO.xml?946](http://wdcm.nig.ac.jp/CCINFO/CCINFO.xml?946)

### INTERNATIONAL

Biological Institute Culture Collection of Phytopathogenic Bacteria  
[wdcm.nig.ac.jp/CCINFO/CCINFO.xml?110](http://wdcm.nig.ac.jp/CCINFO/CCINFO.xml?110)

Freshwater Algae Culture Collection  
[www.algae.ihb.ac.cn/](http://www.algae.ihb.ac.cn/)

Czech Collection of Microorganisms  
[www.sci.muni.cz/ccm/index.html](http://www.sci.muni.cz/ccm/index.html)

Iranian Fungal Culture Collection  
[www.iripp.ir](http://www.iripp.ir)

Collection of Aquatic Important Microorganisms  
[www.ciad.mx/caim/CAIM.html](http://www.ciad.mx/caim/CAIM.html)

## EVENTS

### Conferences / Seminars / Meetings 2012

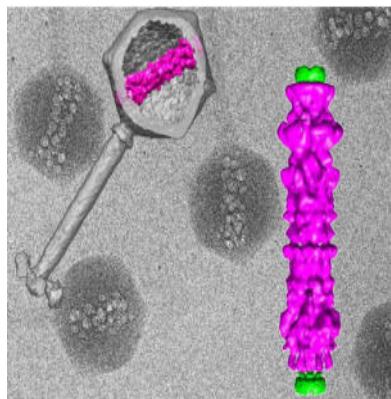
**3<sup>rd</sup> Workshop on Microbial Sulfur Metabolism**, April 15 - 18, 2012. **Venue:** NH Conference Centre Leeuwenhorst, Langelaan 3, 2211 XT Noordwijkerhout, **The Netherlands.** **Website:** [www.wmsm-3.bt.tudelft.nl/index.html](http://www.wmsm-3.bt.tudelft.nl/index.html).

**Plant-microbe interactions**, June 18 - 29, 2012. **Venue:** Norwich Research Park, NR4 7UH, Norwich, **United Kingdom.** **Website:** [www.events.embo.org/12-plant-microbe/](http://www.events.embo.org/12-plant-microbe/).

**Marine Microbes**, June 24 - 29, 2012. **Venue:** Ciocco Tuscany Resort, Lucca (Barga), **Italy.** **Website:** [www.grc.org/programs.aspx?year=2012&program=marinemicr](http://www.grc.org/programs.aspx?year=2012&program=marinemicr).

**Viruses of microbes**, July 16 - 20, 2012. **Venue:** The Royal Military Academy, Hobbemastraat 8, 1000 Brussels, **Belgium.** **Website:** [www.events.embo.org/12-virus-microbe/venue.html](http://www.events.embo.org/12-virus-microbe/venue.html).

**XV IS-MPMI Kyoto 2012. International Congress on Molecular Plant-Microbe Interactions**, July 29 - August 2, 2012. **Venue:** Kyoto International Conference Center, **Japan.** **Website:** [www.mpmi2011.umin.jp/](http://www.mpmi2011.umin.jp/).



**Cryo-electron micrographs of purified viruses with their inner structure bubbling from radiation damage. Overlaid, (left) 3D computer reconstruction of a virus's outer shell and tail in gray, with the inner structure in magenta.**

### 'Bubblegram' imaging: novel approach to view inner workings of viruses

Researchers have developed a new way to see structures within viruses that were not clearly seen before. Cryo-electron microscopy (Cryo-EM) is a technique that allows scientists to image very small particles, like structure on the surface of viruses. Despite the success of cryo-EM, scientists have been unable to clearly visualize structures inside of viruses, because higher doses of radiation is used to image them which damage the virus, destroying the fine structures that likely to be viewed. Now, researchers used high doses of radiation, and found that the inner structure could be seen as a cylinder of bubbles. While the inner structure was damaged, the team was able to superimpose the images, using three-dimensional computer reconstruction and they were able to clearly visualize the viral structure. The investigators call this technique as bubblegram imaging.

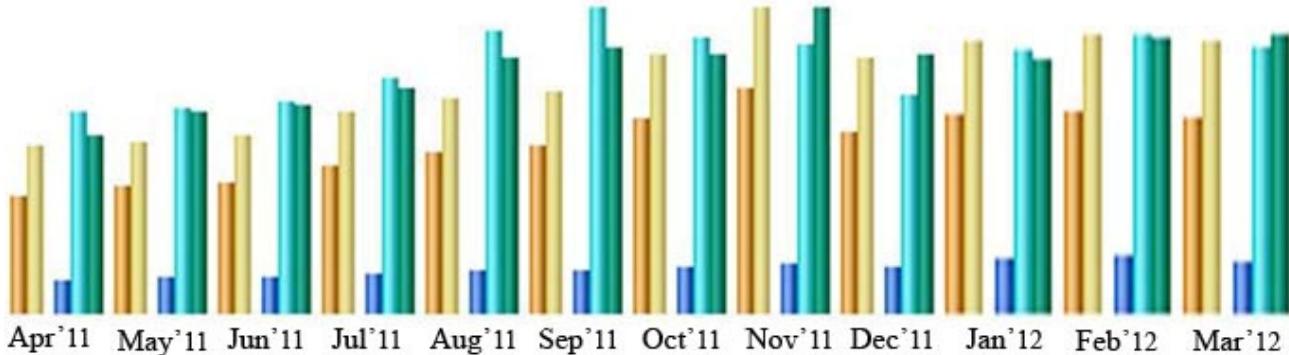
**Source:** [www.sciencedaily.com](http://www.sciencedaily.com)

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### Summary

(Apr 2011 - Mar 2012)

Unique visitors	Total number of visitors	Pages	Hits	Bandwidth
101932	139206	266606	1507222	48.69GB



Apr'11 May'11 Jun'11 Jul'11 Aug'11 Sep'11 Oct'11 Nov'11 Dec'11 Jan'12 Feb'12 Mar'12

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Happy New Year  
2012 - International Year of Marine Biodiversity  
Save the Rainforest  
ENVIS CENTRE  
Department of Zoology  
University of Madras  
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**2012**

JANUARY	FEBRUARY	MARCH	APRIL
1 2 3 4 5 6 7	8 9 10 11 12 13 14	15 16 17 18 19 20 21	22 23 24 25 26 27 28
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ENVIRONMENTAL CALENDAR 2012  
2012 - International Year of Marine Biodiversity

**January**  
30<sup>th</sup> National Cleanliness Day

**February**  
2<sup>nd</sup> World Wetlands Day

**March**  
22<sup>nd</sup> World Water Day  
23<sup>rd</sup> World Meteorological Day

**April**  
7<sup>th</sup> World Health Day

**May**  
22<sup>nd</sup> International Day for Biological Diversity

**June**  
5<sup>th</sup> World Environment Day  
8<sup>th</sup> World Oceans Day  
15<sup>th</sup> Global Wind Day

**September**  
16<sup>th</sup> International Day for the Preservation of the Ozone Layer (World Ozone Day)  
18<sup>th</sup> World Water Monitoring

**October**  
3<sup>rd</sup> World Habitat Day

**November**  
6<sup>th</sup> International Day for Preventing the Exploitation of the Environment in War and Armed Conflict

**December**  
11<sup>th</sup> International Mountain Day  
14<sup>th</sup> National Energy conservation Day

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