



ENVIS NEWSLETTER

MICROORGANISMS AND IMPACT ON PUBLIC HEALTH

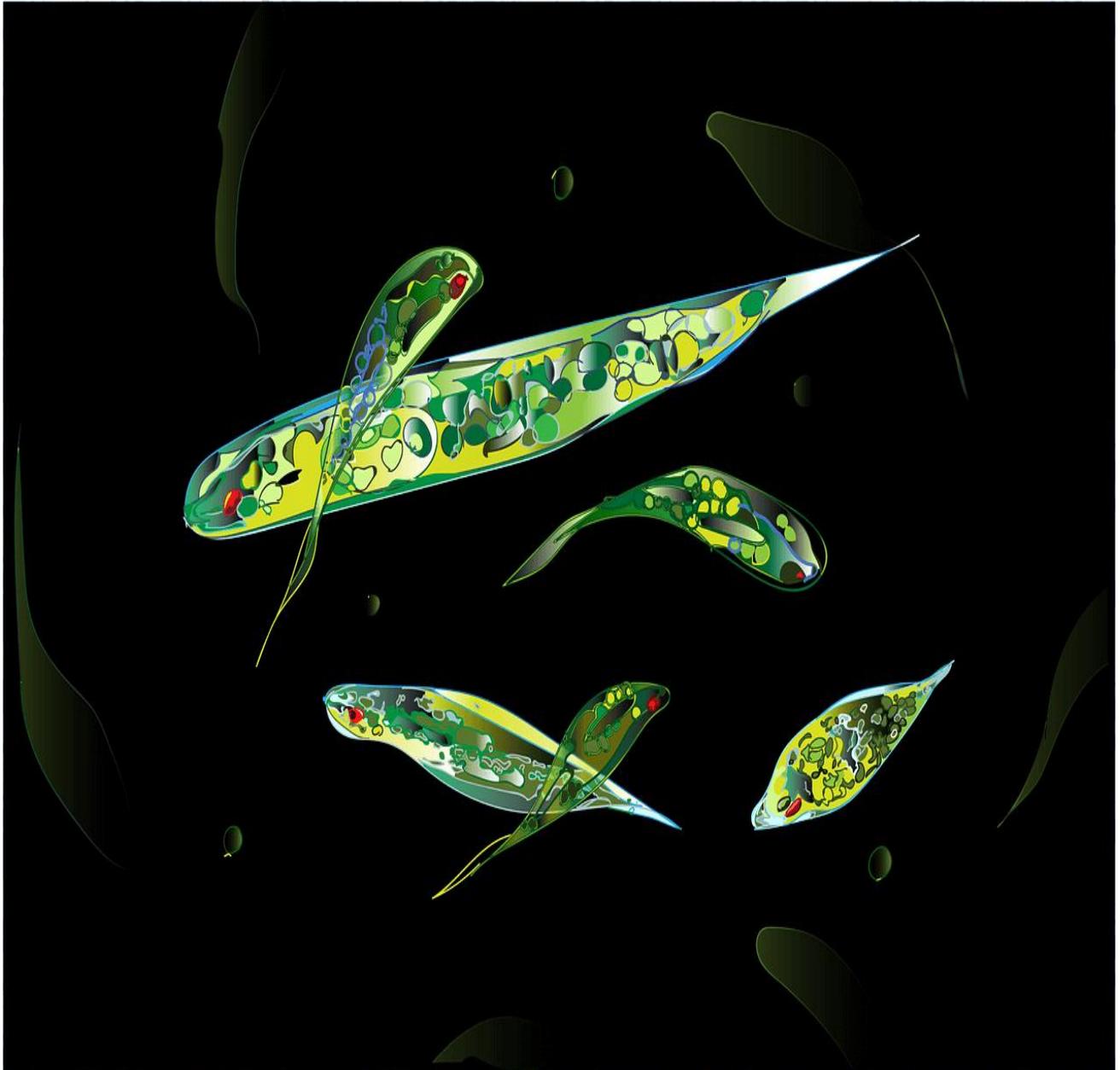
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**World
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**Wetlands and
climate change**

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ENVIS Newsletter on 'Microorganisms and Impact on Public Health', a quarterly publication, brings out original research articles, reviews, reports, research highlights, news-scan etc., related to the thematic area of the ENVIS Centre. In order to disseminate the cutting-edge research findings to user community, ENVIS Centre on Microorganisms and Impact on Public Health invites original research and review articles, notes, research and meeting reports, details of forthcoming conferences / seminars / symposia / trainings / workshops for publication in the newsletter.

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

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CONTENTS

Page No.

SCIENTIFIC ARTICLE

- Potential algal species for phycoremediation of pharmaceutical industrial effluents from Kandigai, Kanchipuram district, Tamil Nadu 2

G. K. Saravanan, R. Banupriya L. Ramya and S. Elumalai

RESEARCH REPORTS

- Plants, fungi and bacteria work together to clean polluted land 5

- Researchers remove harmful hormones from Las Vegas wastewater using green algae 5

- Gut microbiome protects against acute arsenic toxicity 7

ONLINE REPORTS

- Heavy metal planet fragment survives destruction from dead star 8

- Using tiny organisms to unlock big environmental mysteries 9

NEWS

- Climate-driven evolution in trees alters their ecosystems 10

- Novel insights into soil biodiversity, Earth's global engine 11

- The paper mulberry coevolved with soil microbes to humanity's benefit 11

- ABSTRACT OF RECENT PUBLICATION 12

E - RESOURCES

EVENTS

From the Coordinator's Desk!

Dear Readers,

Greetings!

Since industrialization, highly toxic organic and inorganic compounds such as fuels, polychlorinated biphenyls (PCBs), polycyclic aromatic hydrocarbons (PAHs), pesticides, dyes, heavy metals etc. have been synthesized and released in the environment for direct or indirect application. Removal of these contaminants and restoring the environment is a difficult task. Though various methods are available, the catabolic versatility from biological process of microorganisms, plants, insects etc. to degrade or convert such pollutants is ecofriendly and reliable, by a process known as bioremediation and biodegradation. Keeping this in mind, researchers have identified many potential organisms that could be used for environmental remediation yet it is only upto laboratory levels and requires practical demonstration to assign its efficiency in fields. An article in the present issue has identified two algae that could be used in remediation being isolated from the polluted environment.

In addition, other interesting topics such as microorganisms working together to clean polluted land, removal of EDCs from waste water using algae, protection against arsenic toxicity by gut microbiome, climate change in evolution of ecosystems and many more are included.

Dr. C. Arulvasu

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3rd MARCH, 2019

Potential Algal Species for Phycoremediation of Pharmaceutical Industrial Effluents from Kandigai, Kanchipuram District, Tamil Nadu

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Scenedesmus sp.
Phycoremediation

ABSTRACT

Water pollution is recognized as a major threat to aquatic ecosystems globally. Phycoremediation is cost effective and a continuous treatment technique that uses microalgae to clean up the polluted water from pharma industry. In the present study, two predominant fresh water microalgae *Chlorella* sp. and *Scenedesmus* sp. were isolated from the pharmaceutical industrial effluents of Kanchipuram district that are potential phycoremediators both as individuals and as consortium for these contaminated waters.. Preliminary results revealed that these microalgal species to be highly efficient in reducing BOD, COD, TSS, TDS, and metals like sulphate, zinc and copper from pharmaceutical industrial effluents. Therefore, both the species can be used as eco-friendly adsorbent in the treatment of polluted waste water.

Introduction

Heavy metals are metallic elements and metalloids that have relatively high density compared to water. In recent years, there has been an increasing ecological and global public health concern associated with environmental contamination by heavy metals and toxic effluents. Assuming heaviness and toxicity are interrelated an exponential increase of their use in several industrial, agricultural, domestic and technological applications has increased risk of exposure to these elements. Environmental pollution is very prominent in point source areas such as mining, foundries, smelters and other metal-based industrial operations. Toxic metals sometimes imitate the action of an essential element in organisms, interfering with their metabolic process. Waste waters from the above industries are recognized as a major threat to aquatic ecosystems globally (Oswald and Gotaas, 1957). Some of the pollutants like lead (Pb), arsenic (As), mercury (Hg), chromium (Cr) especially hexavalent chromium, nickel (Ni), barium (Ba), cadmium (Cd), cobalt (Co), selenium (Se), vanadium (V), oils and grease, pesticides, are very harmful and toxic even in ppb (parts per billion) range to ppm (Kaplan *et al.*, 1987).

Most pharmaceutical effluents are known to contain varying concentrations of organic compounds and total solids including heavy metals such as lead, mercury, cadmium, nickel, chromium and other toxic organic chemicals or phenolic compounds that are mutagenic and carcinogenic to humans (Idris *et al.*, 2013). Bioremediation

using biological systems of the contaminated sites to catalyze the degradation or transformation of various chemicals to non toxic forms is an ideal approach to deal with water pollution. Algal bioremediation is most effective in waste water treatment as an inexpensive biomaterial for removal of contaminants. Hence, development of biological based treatment system is considered as economically cheaper and environment friendly (Prabha *et al.*, 2016).

Microalgae are best known for biological treatment and have capability to grow in nutrient rich waste waters thus contributing to reducing pollutants and help in the maintenance of environmental sustainability and carbon neutrality (Mohan *et al.*, 2011). Waste water treatment using microalgae is gaining prominence, due to its potential in efficiently uptaking the nutrients and organics by heterotrophic nutritional requirement coupled with the production of potentially valuable biomass, which can be further used in several processes to generate value added products (Park *et al.*, 2011; Mohan *et al.*, 2015 & 2016). Based on the above background, an attempt was made for bioremediation of waste water through identification of potential algal species from the polluted water itself.

Materials and Methods

Kandigai in Kanchipuram district of Tamil Nadu is a pharmaceutical industrial region with polluted water bodies by these industrial effluents. Water samples were collected and cultured to identify algal diversity present in it. Temperature and pH were recorded from collection sites using YSI Multi parameter water quality instrument.

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The samples were subjected to microscopic studies by simple wet mount preparation and cultured for microalgae isolation in Bold Basal Medium (BBM). Samples 1ml each were serially diluted from 10^{-1} to 10^{-10} and from each dilution 0.01 ml of samples were transferred to BBM containing 2% agar in Petri plates. The plates were incubated at room temperature for 10 days and observed for growth. Later discrete green colonies were selected and transferred to liquid medium (BBM) and maintained for 21 days at room temperature.

The growth rate experiments were done for isolated algal species at temperature of 28°C with cycles of light: dark (12:12h) illumination, measuring cell density at constant intervals using Spectrophotometer (Hitachi U 2900) at wavelength of 680nm and their dry weights were estimated. Effluents were treated with selected algal cultures in BBM with different ratios such as 100:400, 200:300, 250:250, 300:200 and 400:100 v/v respectively. The same experiment was repeated with combination of algal mixture in equal volume to determine the effectiveness of consortium in treatment of pharma effluents.

The physico-chemical parameters were analyzed for both raw and microalgae treated effluents following APHA standard methods (APHA, AWWA, and WEF. 1998). Microalgae were estimated for pigments such as Chlorophyll a, b and β -carotene following methods of Jeffrey and Humphrey (1975) and MacKinney (1941) using different wavelengths of UV visible spectrophotometer (Hitachi U-2900). Bio-Chemical analysis such as carbohydrate (Dubois *et al.*, 1956), protein (Bradford, 1976) and lipid (Folch *et al.*, 1957) was also determined for selected microalgae. The absorption of metals by microalgae was studied using Scanning Electron Microscopy.

Results & Discussion

The physico-chemical parameters of water samples such as temperature ranged from 28°C to 32°C, pH between 5.8 to 6.7, dissolved oxygen (DO)

in range of 4.1 to 9.52 mg/L, chemical oxygen demand (COD) and biological oxygen demand (BOD) were in average about 1240 mg/L and 374 mg/L respectively. The effluent samples predominantly contained two micro algae *Chlorella* sp. and *Scenedesmus* sp. However, other algal species though present were in lesser numbers. Hence, further studies were carried out using *Chlorella* sp. and *Scenedesmus* sp that had quick adaptation and high growth rates.

Chlorella sp., *Scenedesmus* sp. and consortium showed biomass productivity of 622.88 ± 14.03 mg dry weight L^{-1} , 142.50 ± 4.52 mg dry weight L^{-1} and 680.88 ± 98.03 mg dry weight L^{-1} respectively after 21 days of incubation. The percentage of protein content in these microalgae ranged from 18 – 45 % of dry matter. The highest percent of the protein was measured in the *Scenedesmus* sp. ($45.10 \pm 0.70\%$) followed by consortium ($39.00 \pm 0.62\%$) and least in *Chlorella* sp. (18.65 ± 0.70 %). Carbohydrate content was quantitatively evaluated and was found to be high in Consortium of micro algal samples $17.12 \mu g ml^{-1}$ followed by *Chlorella* sp. and *Scenedesmus* sp. as $15.07 \mu g ml^{-1}$ and $15.67 \mu g ml^{-1}$ respectively. The total lipid contents for these microalgae ranged from 18.89 ± 1.2 % to 40.49 ± 2.58 % of the dry weight. Maximum lipid content was observed in the Consortium ($40.49 \pm 2.58\%$) followed by *Chlorella* sp. (38.10 ± 2.58 %) and *Scenedesmus* sp. (18.89 ± 1.2 %) suggesting that the members of the class Trebouxiophyceae accumulated higher lipid content than the Chlorophyceae members (Figure 1).

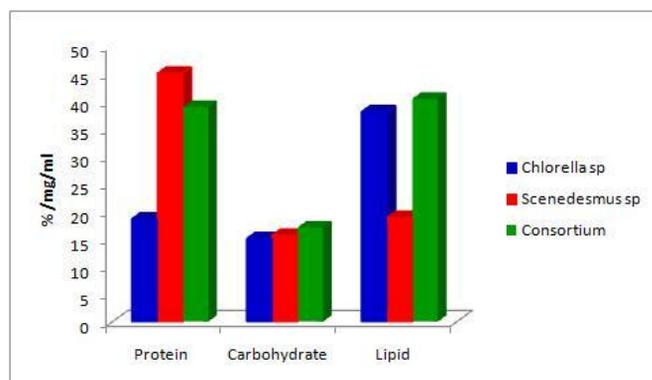


Figure 1: Graph showing the biochemical composition of selected microalgal species isolated from effluent water samples of pharmaceutical industry.

Photosynthetic pigment chlorophyll a was quantitatively high in consortium (18.12 $\mu\text{g ml}^{-1}$) followed by *Chlorella* sp. (15.343 $\mu\text{g ml}^{-1}$) and *Scenedesmus* sp. (11.16 $\mu\text{g ml}^{-1}$). Chlorophyll b content was found high in *Chlorella* sp. (25.134 $\mu\text{g ml}^{-1}$) compared with Consortium (23.31 $\mu\text{g ml}^{-1}$) and *Scenedesmus* sp. (16.13 $\mu\text{g ml}^{-1}$). Carotene content was accumulated high in consortium (192.15 mg ml^{-1}) compared with *Chlorella* sp. (185.23 mg ml^{-1}) and *Scenedesmus* sp. (145.8 mg ml^{-1}) (Figure 2).

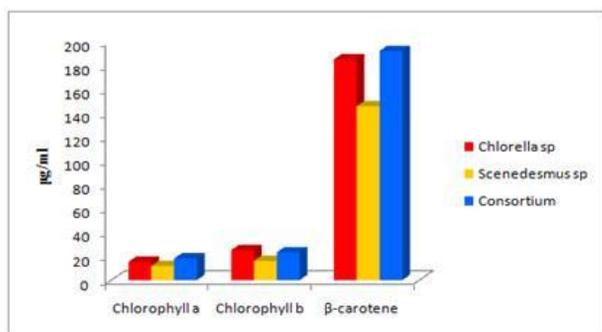


Figure 2: The graph showing the quantitative analysis of pigment composition of selected microalgal strains.

The morphology of two different micro algae were examined through scanning electron microscopy (SEM) from treated effluents. It was found that there was a change in the morphology of structure indicating that algae has taken up metals from the treated samples, a process known as bioaccumulation. The pharmaceutical industry has shown great interest in the use of algae as a source of biochemically active substances. At present, outcome and toxicity of pharmaceutical residues in the aquatic environment pose difficulties. The pharmaceutical waste water effluent sample collected from Kandigai was found to contain numerous species out of which *Chlorella* sp. and *Scenedesmus* sp. were predominant with bioremediation capabilities.

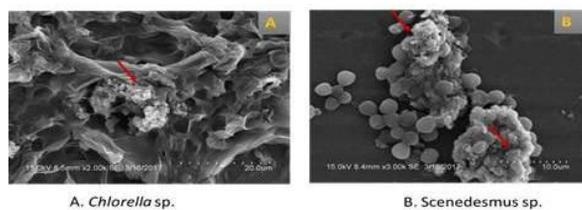


Figure 3: The scanning electron microscopic image of selected micro algae *A. chlorella* sp. and *B. scenedesmus* sp. The marked places show changes in morphology due to bioaccumulation of metals from samples.

Conclusion

Pharmaceutical manufacturers must operate under strict regulations by FDA in different countries and ought to maintain acceptable water quality standards for use, discharge or reuse. Growing microalgae on wastewater offers new insights for the microalgae industry as well as the wastewater treatment industry. The selected microalgae like *Chlorella* sp., *Scenedesmus* sp. and consortium is applied in treating the pharmaceutical wastewater and it will help in reducing the toxicity and facilitate recycling and reutilization of polluted water. The use of wastewaters for cultivating microalgae is necessary in order to reduce the cost of microalgae production. Furthermore, India being a tropical country with plenty of sunshine it is well suited for implementation of Phycoremediation as a technology and also can be carried out at an industrial scale for effective utilization of biomass.

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RESEARCH REPORTS

Plants, fungi and bacteria work together to clean polluted land

Highly complex interactions among roots, fungi and bacteria underlie the ability of some trees to clean polluted land, according to a novel study by bioinformatics and plant-biology experts.

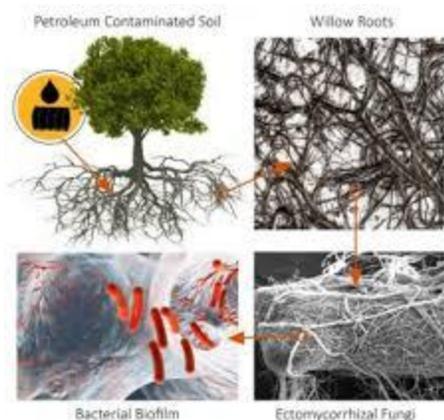
Fast-growing trees, such as willows, are known to tolerate and even rejuvenate soil contaminated with petroleum by-products or heavy metals. The clean-up of soil in this way is known as phytoremediation, and the process is commonly attributed to “secondary metabolism” the production of specialized compounds in plants that helps them to cope us with environmental stress.

New findings by the Montreal researchers, published in the journal *Microbiome*, suggest that a more intricate symbiosis of microbial life underpins willows' ability to thrive in these stressful conditions. Using advanced techniques for analyzing the

simultaneous expression of genes from multiple organisms in an ecosystem, the scientists examined the roots of willows grown on a polluted site in suburban Montreal. They found that complex interactions among a range of ectomycorrhizal fungi which form symbiotic sheaths around the roots of plants and certain bacteria appeared to drive the degradation of hydrocarbons in the ground.

“We normally approach genetics by limiting the investigation to single organisms or domains of life,” says Emmanuel Gonzalez, lead author of the study and bioinformatics specialist at the Canadian Centre for Computational Genomics at McGill. “What was so surprising here was that, by looking for the genetics of all the life below-ground, the biological picture actually became easier to see. This also suggests that such complex mutualistic interactions may be the natural norm outside of the laboratory.”

Nicholas Brereton, a research fellow at Université de Montréal's Plant Biology Research Institute and senior author of the study, adds that “our initial mind-set was that bioinformatics and biology could be more profoundly integrated to see the diversity of function within a challenged root system. This quite quickly led to technical improvements in how we could observe gene expression across multiple life-forms, leading to new environmental biology discoveries. We hope these findings showcase how powerful cross-disciplinary dialogue can be for revealing the incredibly intricate solutions present in the natural world.”



Source: www.sciencedaily.com

Researchers remove harmful hormones from Las Vegas wastewater using green algae

A common species of freshwater green algae is capable of removing certain endocrine disrupting chemicals (EDCs) from wastewater, according to new research. Researchers explored 5

the potential for use of a species of freshwater green algae called *Nannochloris* to remove EDCs from treated wastewater.

EDCs are natural hormones and can also be found in many plastics and pharmaceuticals. They are known to be harmful to wildlife, and to humans in large concentrations, resulting in negative health effects such as lowered fertility and increased incidence of certain cancers. They have been found in trace amounts (parts per trillion to parts per billion) in treated wastewater, and also have been detected in water samples collected from Lake Mead.

In a new study published in the journal *Environmental Pollution*, DRI researchers Xuelian Bai, Ph.D., and Kumud Acharya, Ph.D., explore the potential for use of a species of freshwater green algae called *Nannochloris* to remove EDCs from treated wastewater.

“This type of algae is very commonly found in any freshwater ecosystem around the world, but its potential for use in wastewater treatment hadn't been studied extensively,” explained Bai, lead author and Assistant Research Professor of environmental sciences with the Division of Hydrologic Sciences at DRI. “We wanted to explore whether this species might be a good candidate for use in an algal pond or constructed wetland to help remove wastewater contaminants.”

During a seven-day laboratory experiment, the researchers grew *Nannochloris* algal cultures in two types of treated wastewater effluents collected from the Clark County Water Reclamation District in Las Vegas, and measured changes in the concentration of seven common EDCs.

In wastewater samples that had been treated using an ultrafiltration technique, the researchers found that the algae grew rapidly and significantly improved the removal rate of three EDCs (17 β -estradiol, 17 α -ethinylestradiol and salicylic acid), with approximately 60 percent of each contaminant removed over the course of seven days. In wastewater that had been treated using ozonation, the algae did not grow as well and had no significant impact on EDC concentrations.

One of the EDCs examined in the study, triclosan, disappeared completely from the ultrafiltration water after seven days, and only 38 percent remained in the ozonation water after seven days but this happened regardless of the presence of algae, and was attributed to breakdown by photolysis (exposure to light).

“Use of algae for removing heavy metals and other inorganic contaminants have been extensively studied in the past, but for

removing organic pollutants has just started,” said Acharya, Interim Vice President for Research and Executive Director of Hydrologic Sciences at DRI. “Our research shows both some of the potential and also some of the limitations for using *Nannochloris* to remove EDCs from wastewater.”

Although these tests took place under laboratory conditions, a previous study by Bai and Acharya published in November 2018 in the journal *Environmental Science and Pollution Research* examined the impacts of these same seven EDCs on quagga mussels (*Dreissena bugensis*) collected from Lake Mead. Their results showed that several of the EDCs (testosterone, bisphenol A, triclosan, and salicylic acid) were accumulating in the body tissues of the mussels.

“Algae sit at the base of the food web, thereby providing food for organisms in higher trophic levels such as quagga mussels and other zooplanktons,” Bai said. “Our study clearly shows that there is potential for these contaminants to biomagnify, or build up at higher levels of the food chain in the aquatic ecosystem.”

Bai is now working on a new study looking for antibiotic resistance in genes collected from the Las Vegas Wash, as well as a study of microplastics in the Las Vegas Wash and Lake Mead. Although Las Vegas's treated wastewater meets Clean Water Act standards, Bai hopes that her research will draw public attention to the fact that treated wastewater is not 100 percent clean, and will also be helpful to utility managers as they develop new ways to remove untreated contaminants from wastewater prior to release.



Image: Samples of *Nannochloris* grow in the Environmental Engineering Laboratory at the Desert Research Institute in Las Vegas. This species of green algae was found to be capable of removing certain types of endocrine disrupting chemicals from treated wastewater.

Image credit: Xuelian Bai/DRI.

“Most wastewater treatment plants are not designed to remove these unregulated contaminants in lower concentrations, but we know they may cause health effects to aquatic species and even humans, in large concentrations,” Bai said. “This is concerning in places where wastewater is recycled for use in agriculture or released back into drinking water sources.”

Source: www.sciencedaily.com

Gut microbiome protects against acute arsenic toxicity

New research shows that the gut microbiome is essential for full protection against acute arsenic poisoning.

Research conducted at Montana State University shows that microbes in the human gut play an important role in protecting against arsenic toxicity, a problem that affects an estimated 200 million people who are exposed to arsenic through contaminated drinking water.

For the past five years, MSU doctoral candidate Michael Coryell has worked with his adviser, Seth Walk, and committee member, Timothy McDermott, to find how the human gut microbiome affects arsenic after it has been ingested. Now, Coryell is the lead author of a paper published in Dec. 21, 2018 in the journal *Nature Communications* that details his findings of how the gut microbiome is essential for full protection against acute arsenic toxicity.

With arsenic topping the federal Agency for Toxic Substances and Disease Registry's list of the most toxic chemicals for the past 20 years, the research is particularly important because even chronic low levels can lead to cancer or cardiovascular disease later in life.

Coryell, a doctoral candidate in microbiology and immunology and fellow in the Molecular Biosciences Program in MSU's College of Agriculture and the College of Letters and Science, said he is hopeful his work will contribute to the development of probiotic and microbiome-focused therapies that can mitigate the risk for arsenic toxicity.

“One of the next big challenges for microbiome researchers will be translating laboratory findings like this into real-world solutions,” said Coryell, who in 2016 won a Ruth L. Kirschstein Individual Predoctoral National Research Service Award from the National Institutes of Health.

Past studies have shown that microbes in the environment can biochemically transform naturally occurring arsenic in soil or

rocks either into less toxic or more toxic forms a topic McDermott researches in MSU's Department of Land Resources and Environmental Sciences in the College of Agriculture.

What researchers don't know as much about is what microbes in the human gut do with arsenic before it is absorbed into the body, said Walk, associate professor in MSU's Department of Microbiology and Immunology and senior author of the paper.

“There are many factors that influence disease a person's environment, diet, genetics but we can only evaluate some of those things in human studies by observing different genotypes of people who have different diets or drink water from different sources,” Walk said.

Coryell used laboratory mice to create experimental controls to sort out the variables' influences. He found that antibiotics disrupted the gut microbiome, allowing more arsenic to accumulate in the tissues, rather than being excreted.

“That was an interesting finding because it showed that even though there was some microbial activity in the gut, the mice were not as good at getting rid of the arsenic and were probably taking more of it into their system and building up more in their tissues,” Coryell said.

Mice raised without any microorganisms were similarly affected, Coryell said. But when organisms from the human microbiome were introduced, they had a protective effect.

“That was a big advance,” Walk said, “because we were able to look at the germ-free mice and put back the microbiomes we wanted to examine from different people. We found that depending on which microbiome the mice got, they were protected to varying degrees.”

Those results suggest that the microbiome of some people may be more protective than others, Walk said, and may answer the question of why some people who drink from a shared water source tainted with arsenic develop disease later in life while others don't.

“That idea really hasn't been incorporated into any epidemiological study or model,” Walk said. Folks are moving into this field, but what our data shows pretty definitively is that both the microbiome and its composition matter.

“So, in order to predict how likely certain individuals are to develop disease, we need to account for the microbiome and just how protective it is,” he said. “These results help us

to establish that foundation.”

A better understanding of how the microbiome protects against toxins like arsenic could benefit communities or villages with contaminated water sources through probiotic or other microbiome therapies, especially since it is not always practical or possible to replace a water source, Walk said.

“Microbiome research is moving to microbiome-focused therapies for what we know it plays a role in, and clean food and water is a big topic here in Montana and around the world,” he said.

Source: www.sciencedaily.com

ONLINE REPORTS

Heavy metal planet fragment survives destruction from dead star

A fragment of a planet that has survived the death of its star has been discovered by astronomers in a disc of debris formed from destroyed planets, which the star ultimately consumes.

The iron and nickel rich planetesimal survived a system-wide cataclysm that followed the death of its host star, SDSS J122859.93+104032.9. Believed to have once been part of a larger planet, its survival is all the more astonishing as it orbits closer to its star than previously thought possible, going around it once every two hours.

The discovery, reported in the journal *Science*, is the first time that scientists have used spectroscopy to discover a solid body in orbit around a white dwarf, using subtle variations in the emitted light to identify additional gas that the planetesimal is generating.

Using the Gran Telescopio Canarias in La Palma, the scientists studied a debris disc orbiting a white dwarf 410 light years away, formed by the disruption of rocky bodies composed of elements such as iron, magnesium, silicon, and oxygen the four key building blocks of the Earth and most rocky bodies. Within that disc they discovered a ring of gas streaming from a solid body, like a comet's tail. This gas could either be generated by the body itself or by evaporating dust as it collides with small debris within the disc.

The astronomers estimate that this body has to be at least a kilometre in size, but could be as large as a few hundred kilometres in diameter, comparable to the largest asteroids known in our Solar System.

White dwarfs are the remains of stars like our sun that have

burnt all their fuel and shed their outer layers, leaving behind a dense core which slowly cools over time. This particular star has shrunk so dramatically that the planetesimal orbits within its sun's original radius. Evidence suggests that it was once part of a larger body further out in its solar system and is likely to have been a planet torn apart as the star began its cooling process.

Lead author Dr Christopher Manser, a Research Fellow in the Department of Physics, said: The star would have originally been about two solar masses, but now the white dwarf is only 70% of the mass of our Sun. It is also very small roughly the size of the Earth and this makes the star, and in general all white dwarfs, extremely dense.

“The white dwarf's gravity is so strong about 100,000 times that of the Earth's that a typical asteroid will be ripped apart by gravitational forces if it passes too close to the white dwarf.”

Professor Boris Gaensicke, co-author from the Department of Physics, adds: The planetesimal we have discovered is deep into the gravitational well of the white dwarf, much closer to it than we would expect to find anything still alive. That is only possible because it must be very dense and/or very likely to have internal strength that holds it together, so we propose that it is composed largely of iron and nickel.

“If it was pure iron it could survive where it lives now, but equally it could be a body that is rich in iron but with internal strength to hold it together, which is consistent with the planetesimal being a fairly massive fragment of a planet core. If correct, the original body was at least hundreds of kilometres in diameter because it is only at that point planets begin to differentiate like oil on water and have heavier elements sink to form a metallic core.”

The discovery offers a hint as to what planets may reside in other solar systems, and a glimpse into the future of our own.

Dr Christopher Manser said: As stars age they grow into red giants, which ‘clean out’ much of the inner part of their planetary system. In our Solar System, the Sun will expand up to where the Earth currently orbits, and will wipe out Earth, Mercury, and Venus. Mars and beyond will survive and will move further out.

“The general consensus is that 5-6 billion years from now, our Solar System will be a white dwarf in place of the Sun, 8

orbited by Mars, Jupiter, Saturn, the outer planets, as well as asteroids and comets. Gravitational interactions are likely to happen in such remnants of planetary systems, meaning the bigger planets can easily nudge the smaller bodies onto an orbit that takes them close to the white dwarf, where they get shredded by its enormous gravity.

Learning about the masses of asteroids, or planetary fragments that can reach a white dwarf can tell us something about the planets that we know must be further out in this system, but we currently have no way to detect.

“Our discovery is only the second solid planetesimal found in a tight orbit around a white dwarf, with the previous one found because debris passing in front of the star blocked some of its light that is the “transit method” widely used to discover exoplanets around Sun-like stars. To find such transits, the geometry under which we view them has to be very finely tuned, which means that each system observed for several hours mostly leads to nothing. The spectroscopic method we developed in this research can detect close-in planetesimals without the need for a specific alignment. We already know of several other systems with debris discs very similar to SDSS J122859.93+104032.9, which we will study next. We are confident that we will discover additional planetesimals orbiting white dwarfs, which will then allow us to learn more about their general properties.”

Source: www.sciencedaily.com

Using tiny organisms to unlock big environmental mysteries

Biological processes that influence climate and the environment, such as carbon fixation or nitrogen recycling are parts of these planet-wide processes are actually driven by the tangible actions of organisms at every scale of life, beginning at the smallest: the microorganisms living in the air, soil, and water. And now researchers have made it easier than ever to study these microbial communities by creating an optimized DNA analysis technique.

When you hear about the biological processes that influence climate and the environment, such as carbon fixation or nitrogen recycling, it is easy to think of them as abstract and incomprehensibly large-scale phenomena. Yet parts of these planet-wide processes are actually driven by the tangible actions of organisms at every scale of life, beginning at the smallest: the microorganisms living in the air, soil, and water.

So, if you want to understand how an ecosystem be it a tropical forest, an agricultural zone, or a watershed will fare in the face of natural and human-induced changes, you need to understand what the microbes in that community are up to. But how do you examine the roles that a diverse group of creatures play if you can't even see them without a microscope?

The best way to do this is to look at their genes, and researchers from Lawrence Berkeley National Laboratory (Berkeley Lab) have developed a new DNA analysis technique that reveals a very interesting, and previously hard-to-study, aspect of a microbial community's genome.

As described in the journal *mBio*, a team led by Aindrila Mukhopadhyay has optimized existing methods to isolate plasmids the small packages of DNA that enable microorganisms like bacteria to quickly acquire and share genes. Often, these DNA molecules, which are separate from the chromosomes, encode functions that can confer a survival advantage in certain situations.

“When you want to learn about a microbial community, focusing specifically on their plasmids allows you to get a sense of the suite of capabilities that a community wants to keep mobile perhaps because they are needed periodically,” said Mukhopadhyay, a senior scientist in Berkeley Lab's Biological Systems and Engineering Division and because a microbial community's collection of plasmid-based genes, aptly called the plasmidome, changes in response to evolutionary pressure much faster than chromosomal genes, looking at this combined pool of genetic information helps scientists construct a vivid picture of the environment beyond that moment in time.

“Studying plasmids is like looking inside someone's backpack to see what they're keeping handy to use themselves and potentially share with another person,” Mukhopadhyay elaborated. “Say you look inside and find an umbrella. It may not be raining at the time, but the umbrella suggests that it rains from time to time.”

Existing DNA sequencing and analysis techniques, however, make it hard to separate the plasmidome from the vast library of chromosomal genetic code present in a microbiome sample. To make this task easier, the team worked out a method to detect plasmids of different sizes in bacterial communities of varying density, particularly very low-density environments like groundwater.

After refining their approach, the scientists applied it to groundwater samples from different wells at the Oak Ridge Field Research Center (ORFRC), a site that is contaminated with heavy metals. Scientists working with ENIGMA a multi-institute research consortium focused on advancing our fundamental understanding of complex microbial communities conduct many studies using the unique ORFRC site.

The researchers were intrigued to find that these samples contained hundreds of plasmids, some of which were the largest plasmids reported in any plasmidome study. Furthermore, they discovered that although the types and abundances of bacteria fluctuated dramatically across groundwater samples, the plasmids were often similar. Interestingly, the plasmids found at the highest frequency across samples encoded mercury-resistance genes, yet there was no detectable mercury contamination in the groundwater studied. The presence of these genes reflects the history of this site and shows that its microscopic residents are prepared if mercury is re-encountered.

Moving forward, the team is hopeful that other scientists will use their approach, the details of which are openly shared in the paper, to yield fresh insight into the variety of interesting and influential microbiomes on Earth, including the ones inside our bodies.

“As we study more and more microbiomes, we gain key knowledge that could ultimately be used to manipulate communities for some benefit, such as environmental clean-up, sewage treatment, or improving our health. Other federally funded projects are working toward these goals, and our discovery could be valuable to their work,” said Mukhopadhyay. “Currently, most of these organisms are very different than the lab organisms whose functions and genetics are well documented, and getting a genetic handle on a new species is a big task.”

“But these mobile genetic packages present a way to manipulate these organisms naturally,” added Ankita Kothari, a Biological Systems and Engineering Division project scientist and the lead author of the paper. “So, if you want to examine an ecosystem at a molecular level and you need genetic tools to do that, the answer could be in the plasmidome already.”

This work was a highly collaborative effort between Berkeley Lab researchers and groups at ORFRC and the DOE Systems Biology Knowledgebase (KBase). The other contributing authors on this study are Yu-Wei Wu, John-Marc

Chandonia, Marimikel Charrier, Lara Rajeev, Andrea Rocha, Dominique Joyner, Terry Hazen, and Steven Singer. The work was conducted as part of ENIGMA, a multi-institute research consortium focused on studying the impact of microbial communities on their ecosystems. ENIGMA is led by Berkeley Lab and funded by the Department of Energy's Office of Science.

Source: www.sciencedaily.com

NEWS

Climate-driven evolution in trees alters their ecosystems

A new study explores how climate, evolution, plants, and soils are linked. The research is the first to show how climate-driven evolution in tree populations alters the way trees directly interact with their immediate soil environment.

By surveying 17 naturally occurring populations of narrowleaf cottonwood trees (*Populus angustifolia*), the researchers discovered that tree populations in warmer places have less genetic variation. This difference, in turn, has consequences for their soil microbial communities and soil chemical composition.

“Future climate change could reduce the potential for adaptation in plants, especially in less genetically varied populations. In order to cope up with these stressful conditions, plants may be developing a stronger relationship with their soil microbiome and nutrients. It may be a mechanism for persistence in a changing world,” said Ian Ware, PhD candidate in UT's Department of Ecology and Evolutionary Biology and lead author of the study.

Warmer temperatures in southern tree populations have resulted in earlier bud break and leaf-out the time period in which buds, then leaves, become present on the growing plant. This evolution reduces genetic variation and alters the way tree populations interact with their soil environment.

“We show that as climates become warmer and drier, population-level genetic variation decreases and trees have a larger impact on their associated soil microbes and soil nutrient pools,” said Ware.

The finding suggests a mechanism for how these plants continue to exist in stressful climates.

“Understanding how plant-soil-microbe linkages evolve in response to changes in climate across habitats may provide 10

information on the forces that drive local adaptation with consequences for nitrogen availability and soil carbon storage,” Ware said. “These findings have direct implications for climate change conservation and restoration practices, such as assisted migration and population management.”

Source: www.sciencedaily.com

Novel insights into soil biodiversity, Earth's global engine

New findings indicate changes in soil biodiversity are driven by changes in plant cover and soil acidification during ecosystem development.

A Virginia Tech professor was part of an international team of researchers that discovered new advances about the major ecological patterns driving the changes in soil biodiversity that occur over millions of years.

The study published in the journal *Proceedings of the National Academy of Sciences* provides critical insights on the factors that control changes in the biodiversity of soil bacteria, fungi, protists, and invertebrates over many millennia. The findings indicate that these changes in soil biodiversity are driven by changes in plant cover and soil acidification during ecosystem development.

“This research provides a new framework for understanding soil and ecosystem biodiversity, which is fundamental to maintaining our global biosphere and managing for future global change” said Mark A. Williams, an associate professor in the School of Plant and Environmental Sciences in the Virginia Tech College of Agriculture and Life Sciences.

Soil microbes and animals, from tiny soil bacteria to earthworms, are unsung heroes in our environment, providing hundreds of billions of dollars in ecosystem services. These organisms are critical in maintaining the global biosphere and human existence. As a thought experiment during classes, Williams often asks his students what would happen if all of these diverse organisms were to become extinct. “Humans would die, too”, is the typical answer.

These soil organisms provide clean drinking water, regulation of the atmosphere, and nutrients that allow for productive and sustainable crop and natural ecosystems. Soil animals and microbes are the most abundant and diverse

organisms on Earth. Still, little is known about their relationships to ecosystem change and natural history.

“We sought to understand how soil biodiversity changes over millions of years, and whether ecological patterns would help explain aspects of ecosystem and global ecology,” Williams said.

Two major ecological patterns explain the changes in soil biodiversity from centuries to many millennia.

In less productive ecosystems, increases in soil biodiversity followed increases in plant cover, which provide food for soil microbes and animals. In more productive ecosystems, however, where resource availability is more abundant, acidification during soil development was often associated which declines in soil biodiversity. Interestingly, these patterns, which had not yet been observed, are different from those reported for other communities, such as plants and large fauna.

Source: www.sciencedaily.com

The paper mulberry coevolved with soil microbes to humanity's benefit

The paper mulberry evolved its uniquely fibrous inner bark around 31 million years ago, long before the woody tree was first used for bookmaking during China's Tang dynasty. This adaptation, which makes the nutrient-rich plant easy to pass through foraging animals, may have been its way of feeding nearby soil microbes. Botanists in China discovered this connection in the first analysis of the *Broussonetia papyrifera* genome.

Using comparative genetics, the research team also found that the paper mulberry tree developed a complex set of flavonoids. These compounds, commonly used in Chinese traditional medicine, can help a plant's roots attract nitrogen-fixing bacteria such as *Pseudomonas* and *Rhizobia*, which in turn promote leaf and stem growth (a tactic commonly used by legumes), and enhance the paper mulberry's ability to adapt to a wide range of environments.

“The unique traits of paper mulberry are consistent with the ancient Chinese philosophy of mutual promotion and restraint, suggesting that paper mulberry is a very complex and remarkable tree species,” write the authors, led by botanist Shihua Shen of the Key Laboratory of Plant Resources, Chinese Academy of Sciences. “Both humans and livestock 11

can benefit from the symbiosis of paper mulberry and microbes.”

The paper mulberry tree, which has over 30,000 genes, is native to Asia and has a long history of application. The bark of paper mulberry is the main raw material of Cai Lun papermaking, one of the four great inventions in ancient China. The tree's leaves are the raw materials for high-quality protein feed. Being rich in flavonoids, the paper mulberry forms relationships with various beneficial soil bacteria.

“The paper mulberry is a very important multi-purpose resource plant,” says Shen. “However, the lack of systematic research and artificial domestication hinder the development and utilization of plant, which is far behind other economic crops. We hope that this study will promote the breeding of new paper mulberry strains with higher yield and high quality.”

The research team plans to continue investigating the molecular mechanisms that lead to economically important traits such as pulping, papermaking, and the creation of feedstock, medicine, and food.

Source: www.sciencedaily.com

Abstract of Recent Publication

01. Ultrasonics Sonochemistry, 2019, Vol. 53, Pages: 202 - 213.

Combined hydrodynamic cavitation based processes as an efficient treatment option for real industrial effluent.

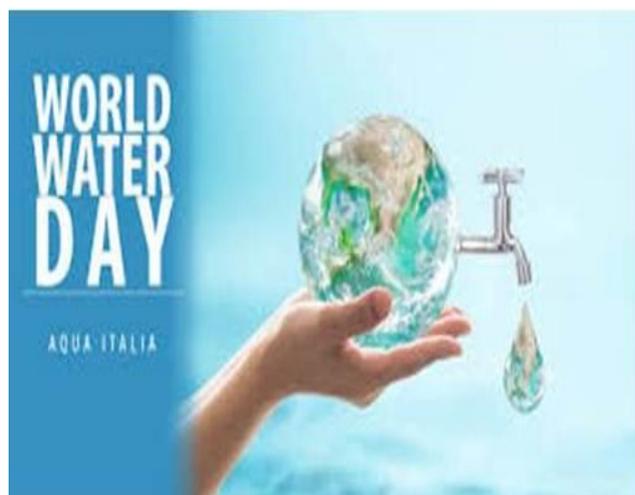
Pooja Thanekar, Parag R. Gogate.

Department of Chemical Engineering, Institute of Chemical Technology, Matunga, Mumbai 40019, India.

In the present work, hydrodynamic cavitation (HC) operated alone and in combination with chemical oxidants has been applied for the treatment of real industrial effluent obtained from a local industry. Initially, the analysis of literature related to the hybrid methods involving hydrodynamic cavitation has been presented along with recommendations for the selection of important operating conditions for the HC operated individually and in combination with oxidation processes based on hydrogen peroxide (H_2O_2), ozone (O_3) and persulphate (KPS). Subsequently, the treatment of real industrial effluent has also been investigated in details

using HC alone and in combined mode with other oxidation processes focusing on the main objective of COD reduction. The reduction in the COD achieved using individual treatment of HC under the optimized conditions of inlet pressure as 4 bar and pH as 4 was only 7.9%. The application of different hybrid approaches based on HC such as $HC + H_2O_2$, $HC + O_3$, $HC + KPS$ and $HC + H_2O_2 + O_3$ established higher COD reduction as compared to only HC. The maximum extent of COD reduction as 60.8% was achieved using $HC + H_2O_2 + O_3$ combination whereas, relatively lower extent of COD was achieved for operations of $HC + H_2O_2$, $HC + O_3$ and $HC + KPS$ with the actual COD reduction being 40.3%, 38.7% and 8.5% respectively. It was also observed that 30.4%, 28.2%, 15.6%, and 4.7% of TOC reduction was obtained for the combined processes of $HC + H_2O_2 + O_3$, $HC + H_2O_2$, $HC + O_3$, and $HC + KPS$ respectively. Based on the kinetic study, it was established that the degradation fitted the first order kinetics for all the approaches. The combined processes of HC with oxidants were also compared with ultrasound reactors (both individual and combined operation) in terms of COD reduction, cavitation yield calculations, and treatment cost. HC reactors were established to be more energy efficient and also significantly cost effective, much lower than ultrasonic reactors.

Keywords: Real industrial effluent; Hydrodynamic cavitation; Ultrasonic reactors; Advanced oxidation processes; Cavitation yield; Total treatment cost.



22nd MARCH 2019

NATIONAL

Indian Institute of Ecology and Environment
<http://www.ecology.edu>

Indian Institute of Ecology and Environment
<https://www.itis.gov>

Industrial Toxicology Research Centre
<http://iitrindia.org>

Central Institute of Freshwater Aquaculture
<http://cifa.nic.in>

INTERNATIONAL

Microbial Ecology in States of Health and Disease
<http://www.e-booksdirectory.com/details.php?ebook=9802>

International Federation for Cell Biology
<http://www.ifcbiol.com>

Soil Science Society of America
<https://www.soils.org>

World Federation for Culture Collections
<http://www.wfcc.info/index.php/committees/wdcm/>

EVENTS
Conferences / Seminars / Meetings 2019

Applied Bioinformatics and Public Health Microbiology. June 05 - 07, 2019 . **Venue:** Wellcome Genome Campus, **UK.**
Website: <https://coursesandconferences.wellcomegenomecampus.org/our-events/applied-bioinformatics-public-health-microbiology-2019/>

CSM 2019 Canadian Society of Microbiologists. June 10 - 13, 2019. **Venue:** Quebec, **Canada.** **Website:**
https://www.csm-scm.org/english/conf_upcoming_details.asp?PageID=52

8th Congress of European Microbiologists. July 07 - 11, 2019. **Venue:** Glasgow, **UK.** **Website:** <https://fems2019.org>

ASV 2019 American Society for Virology. July 20 - 24, 2019. **Venue:** Minneapolis, MN, **USA.** **Website:**
<https://www.asv.org/asv-2019/>

International Forest Day - 21st March, 2019



Rehabilitation and Ecological Benefits of Mangrove Plantation - Muttukadu Backwater - 2019

