



# ENVIS NEWSLETTER

**MICROORGANISMS AND IMPACT ON PUBLIC HEALTH**

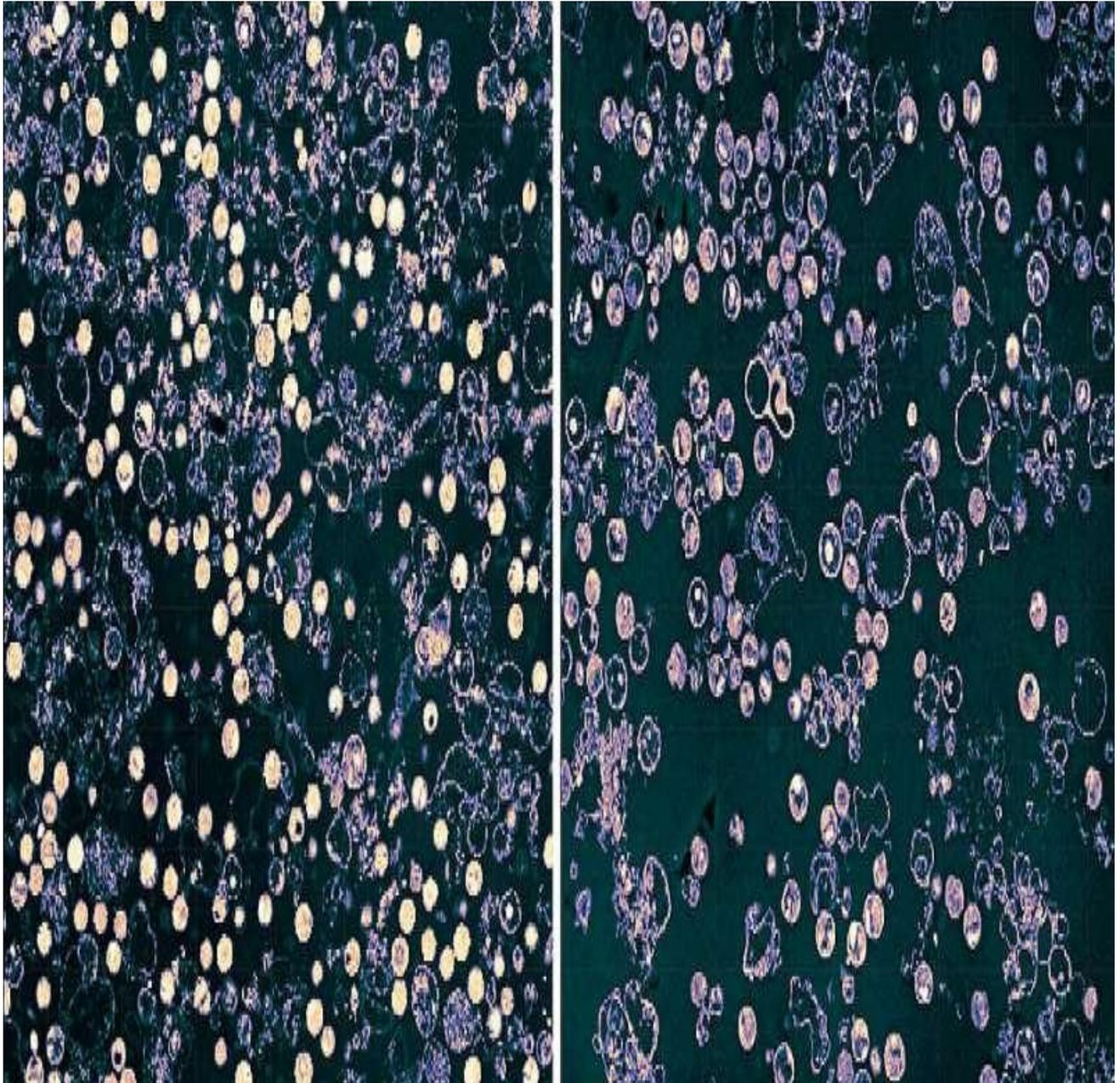
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**27<sup>th</sup> September 2020**

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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.

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**Cover page :** Resting Chlamydia (left; bright circles), which are held without glutamine. After the addition of glutamine (right) the bacteria enter the division stages (darker circles).

(Source: [www.phys.org/news/2020-08-chlamydiae-human-cells.html](http://www.phys.org/news/2020-08-chlamydiae-human-cells.html))

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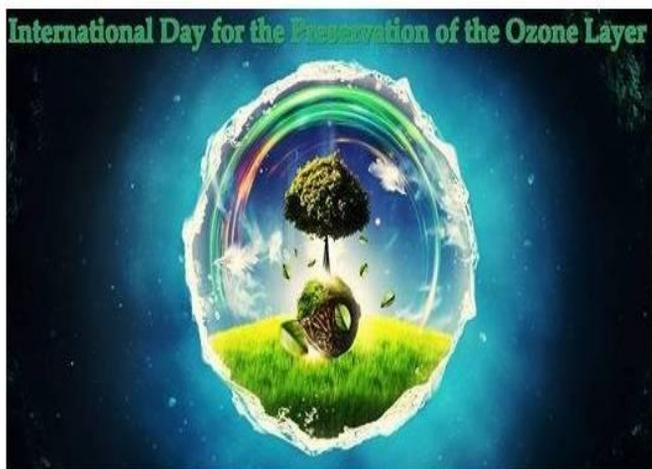
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16<sup>th</sup> September 2020

Dear Readers,

Greetings!

After the gradual lifting up of lockdown since June 08 2020 things are slowly returning back to normal, we must be aware and take necessary precautions and not let our guard down in the nations fight against the deadly viral disease COVID-19. This global pandemic though worse has left us with strong questions on how healthy is our life and our environment. It is time we should ensure that we are taking steps for betterment of this world for future generations to sustain. I believe all of us are aware of these facts and our DzUM ENVIS Newsletter has always put fourth these in its contents to the readers. This issue contains a review article on design and applications of microbial communities along with topics such as facts on the offspring of older mothers less likely to live long and prosper, process of chlamydiae replication in human cells, information on researchers collaboration on a strategy for sustainable aquaculture and about a novel natural dye for screening cell viability. Hope you find this issue very useful.

Dr. C. Arulvasu

Kindly send your feedback @

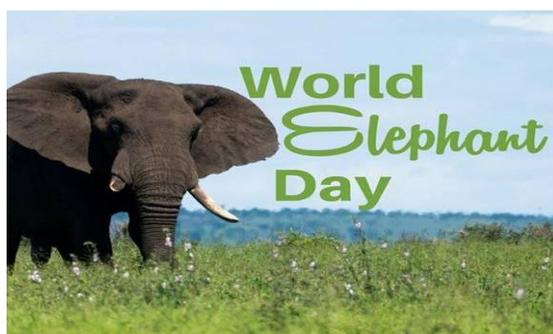
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29<sup>th</sup> JULY, 2020



12<sup>th</sup> AUGUST 2020

## Introduction

The demeanors of microbial community have been widely exploited by the scientific population for industrial development, ameliorative and therapeutic researches. In order to achieve these scientists greatly rely on genetic engineering, an exemplary tool to design microbial communities that suits the human needs. Such altered communities manifest improved functions that can be employed for a wide range of applications. These developments have exalted the community design approach which includes selective proliferation, excerpption of suitable communities, combinatorial evaluation, and *in silico* modeling of microbiome. Combining the community design with computational approach will greatly advantage the development of synthetic community. The present reveiw herein discusses the role of these synthetic microbial community with respect to human needs, effective techniques in designing synthetic communities and also highlights the need for sophisticated techniques to overcome the problems involved in evaluating the designed communities.

## Role of synthetic microbial communities

Primary sectors such as health care, agriculture and industry are positively influenced by the microbial community under various aspects. Conspicuously, in the health sector the role of human microbiome in the human physiology, immunity, development and nutrition has gained much introspection. For instance, the human gut health can be ameliorated by means of microbially synthesized butyrate which contributes as a major energy source (Donohoe *et al.*, 2011) and anti-inflammatory agent (Canani *et al.*, 2011). The microbiome also plays a major role in the human immune system by its effect on lymphoid development and T cell differentiation (Hooper *et al.*, 2012; Kabat *et al.*, 2014). Whereas, in the industrial sector the microbiome endows its influence in waste water treatment (Pitt *et al.*, 1981; Daims *et al.*, 2001) and biofuels production (Abate *et al.*, 1996;

Mamma *et al.*, 1996). In the agricultural sector ingression of nitrogen (Franche *et al.*, 2009; Rovira, 1991) and phosphorus (Afzal, 2008) by the plants have been convalesced by the environmental microbiomes. All these multitude function renders microbial communities as an effective contrivance in the primary and health sectors with respect to microbiome-based technologies and therapeutics (Mimee *et al.*, 2016; Marchesi *et al.*, 2016). Specially engineered microbial communities can be effectively maneuvered for clinical and industrial applications. These engineered microbes can be developed by various techniques one of which includes manipulating environmental aspects to improve functional abilities. This approach has widely been used in fermentation technologies.

## Designing synthetic microbial communities

Previous reports in this field have proclaimed that substrate composition (Cui *et al.*, 2009; Pholchan *et al.*, 2010; Bassin *et al.*, 2012), aeration (Simova *et al.*, 2003), pH (Cui *et al.*, 2009; Fang and Liu 2002) and temperature (Zoetemeyer *et al.*, 1982) are the major environmental factors that can be manipulated to design microbial community that suits the human needs. Another approach to develop engineered microbes involves excerpption of suitable communities by removing undesired communities. Most recently, antibiotics follow this approach to eliminate harmful pathogens from the human body and in contrary to this approach, probiotics exerts beneficial microbes to improve the human gut health (Walsh *et al.*, 2014; Derrien *et al.*, 2015). However, to unveil the propensity of the engineered communities more sophisticated techniques must be utilized to have complete control over the engineered microbes and this is a must, especially while using combinations of microbes. Moreover, complete control over the engineered organisms can effectively modulate the human microbiome and surpass the side effect accompanying the antibiotics (Bartlett *et al.*, 2006; Theriot *et al.*, 2014) and also overcome uncertainties in the probiotic engraftment (Zmora *et al.*, 2018; Maldonado-Go *et al.*, 2016).

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## A Combinatorial Approach

These synthetic microbial communities can be highly effective while using combinatorial approach where merged microbial metabolism can improve the production and degradation of target compounds in an industrial setup (Bader *et al.*, 2010). Overall, the synthetic microbial community caters a malleable and influential approach that bolster the ability of researchers to design the microbial community as a whole rather than focusing only on the existing communities. However, the major impediment underlying this approach includes selection of suitable microbial combinations that can effectively alter the targeted function. In order to completely exploit this rational design to the benefit of human needs, more sophisticated techniques must be employed and various researches are underway that underlines these needs.

### Applications

Various advantages evinced by the synthetic communities also include its potential to co-exist with communities that can never be achieved in the natural environment. Such combinatorial benefits enhance the metabolic activity there by leading to a better or entirely new function that cannot be achieved by naturally prevailing communities. This pragmatic approach is highly effective in biodiesel production and synthesis of bio active compounds (Bader *et al.*, 2010). The enhanced metabolic activities of the combinatorial synthetic communities have been successfully exploited for the production of various resources that include hydrogen (Asada *et al.*, 2006), acetic acid (Collet *et al.*, 2005; Kondo and Kondo 1996; Talabardon *et al.*, 2000) and lactic acid (Taniguchi *et al.*, 2004; Roble *et al.*, 2003). Degradation of polycyclic aromatic hydrocarbons (Boonchan *et al.*, 2000) and cellulose (Haruta *et al.*, 2002; Poszytek *et al.*, 2016) has also been successfully carried out by this approach. Treatment of textile effluent has been made easy by this combinatorial approach whereby the researchers have combined three different species which can successfully degrade the textile effluents thereby improving the water quality (Ayed *et al.*, 2010).

### Techniques to overcome complications

Increasing the number of species in combinatorial approach also allows exponential increase in number of

complications which makes the combinatorial evaluation difficult. Fractional Factorial Design (FFD) is an effective technique that can overcome this problem and drastically reduce the number of combinatorial evaluations. FFD effectively evaluates impacts of external factors such as substrate composition (Prakasham *et al.*, 2007; Skonieczny and Yargeau 2009; Jimé'nez *et al.*, 2014; Molina-Barahona *et al.*, 2004), pH (Skonieczny and Yargeau 2009; Kikot *et al.*, 2010), temperature (Prakasham *et al.*, 2007) and heavy metal toxicity (Kikot *et al.*, 2010) on the community functions. Apart from combinatorial evaluation, performance of individual species can also be evaluated using FFD or similar techniques. In a recent study, scientists have successfully evaluated the individual performance of every single community present in a random gut community subset (Faith *et al.*, 2014). Though the study was based on random community subset, it is well evident from results that FFD can be effectively utilized in a similar manner on synthetic combinatorial communities. Effectual use of FFD in textile effluent treatment has been reported already (Chen *et al.*, 2009; Chen *et al.*, 2011). The individual and interactive inter species impacts on total organic carbon (TOC) degradation along with substrate utilization have been appraised in the above mentioned studies. These studies ushered the scientists to develop synthetic combinations to improve the degradation capacity. The intriguing results suggested that combination of less number of species (3 or 4) rendered the combination more effective than a baseline mixture (6 or more).

On contrary, treating the microbial consortia on the whole as a single unit has also been proven effective. This technique is specifically used for consortium with proven emergent functions. The marine consortium used above-mentioned approach to develop synthetic combinatorial community that can effectively fix CO<sub>2</sub> in the marine environment (Hu *et al.*, 2014; 91. Hu *et al.*, 2016). This approach has also successfully improved the lignocellulolytic enzyme activity by designing a synthetic consortium from a preexisting consortium with cellulolytic activity (Poszytek *et al.*, 2016). Apart from reducing the number of community members in the consortium this technique also allows to include new species in the consortium that cannot be isolated. These techniques allow the research community to

effectively evaluate and improve the functional abilities of a pre-existing synthetic consortium without drastically altering the combinatorial evaluations.

### Conclusion:

The fast growing population makes it mandatory to synthesize compounds of human interest rapidly. Exploiting synthetic communities seems to be the most efficient approach to effectively synthesize these compounds and these are considered advantageous over the natural communities due to their efficiency and rapidity. Combining two or more synthetic communities makes it easy to perform complicated synthesis in highly robust environmental fluctuations. However, the rate of success highly depends upon selection and evaluation of suitable communities that can be combined to improve the target functions. Hence, there arises a need to overcome the difficulties that accompanies the combinatorial approach. In order to overcome these complications development of sophisticated computational techniques have become the need of the hour. The present review underlines the importance of these techniques that can assist the research community to choose the suitable consortium and also have complete control over the selected communities thereby minimizing side effects and improve the efficiency of synthesis.

### References

Abate C., Callieri D., Rodríguez E. and Garro O (1996). Ethanol production by a mixed culture of flocculent strains of *Zymomonas mobilis* and *Saccharomyces* sp. *Appl Microbiol Biotechnol*, **45**: 580 - 583.

Afzal A (2008). Rhizobium and phosphate solubilizing bacteria improve the yield and phosphorus uptake in wheat (*Triticum aestivum*). *Int J Agric Biol*, **10**: 85 - 88.

Asada Y., Tokumoto M., Aihara Y., Oku M., Ishimi K., Wakayama T., Miyake J., Tomiyama M and Kohno H (2006). Hydrogen production by cocultures of *Lactobacillus* and a photosynthetic bacterium, *Rhodobacter sphaeroides* RV. *Int J Hydrogen Energy*, **31**: 1509 - 1513.

Ayed L., Achour S., Khelifi E., Cheref A and Bakhrouf A (2010). Use of active consortia of constructed ternary bacterial cultures via mixture design for Congo Red decolorization enhancement. *Chem Eng J*, **162**: 495 - 502.

Bader J., Mast-Gerlach E., Popovic MK., Bajpai R and Stahl U (2010). Relevance of microbial coculture fermentations in biotechnology. *J Appl Microbiol*, **109**: 371 - 387.

Bartlett JG (2006) Narrative review: the new epidemic of *Clostridium difficile*-associated enteric disease. *Ann Intern Med*, **145**: 758.

Bassin JP., Kleerebezem R., Rosado AS., van Loosdrecht MCM and Dezotti M (2012) Effect of different operational conditions on biofilm development, nitrification, and nitrifying microbial population in moving-bed biofilm reactors. *Environ Sci Technol*, **46**: 1546 - 1555.

Boonchan S, Britz ML, Stanley GA: Degradation and mineralization of high-molecular-weight polycyclic aromatic hydrocarbons by defined fungal-bacterial cocultures. *Appl Environ Microbiol.*, 2000, **66**: 1007-1019.

Canani RB., Di Costanzo M., Leone L., Pedata M., Meli R and Calignano A (2011). Potential beneficial effects of butyrate in intestinal and extraintestinal diseases. *World J Gastroenterol*, **17**: 1519 - 1528.

Chen Y., Lin C-J., Jones G., Fu S and Zhan H (2011). Application of statistical design for the optimization of microbial community of synthetic domestic wastewater. *Biodegradation*, **22**: 205 - 213.

Chen Y., Lin C-J., Jones G., Fu S and Zhan H (2009). Enhancing biodegradation of wastewater by microbial consortia with fractional factorial design. *J Hazard Mater*, **171**: 948 - 953.

Collet C., Gaudard O., Péringer P and Schwitzgübel J-P (2005). Acetate production from lactose by *Clostridium thermolacticum* and hydrogen-scavenging microorganisms in continuous culture effect of hydrogen partial pressure. *J Biotechnol*, **118**: 328 - 338.

Cui M., Yuan Z., Zhi X and Shen J (2009). Optimization of biohydrogen production from beer lees using anaerobic mixed bacteria. *Int J Hydrogen Energy*, **34**: 7971 - 7978.

Daims H., Nielsen JL., Nielsen PH., Schleifer KH and Wagner M (2001). In situ characterization of Nitrospira-like nitrite-oxidizing bacteria active in wastewater treatment plants. *Appl Environ Microbiol*, **67**: 5273 - 5284.

Derrien M and van Hylckama Vlieg JET (2015). Fate, activity, and impact of ingested bacteria within the human gut microbiota. *Trends Microbiol*, **23**: 354 - 366.

Donohoe DR., Garge N., Zhang X., Sun W., O'Connell TM., Bunker MK and Bultman SJ (2011). The microbiome and butyrate regulate energy metabolism and autophagy in the mammalian colon. *Cell Metab*, **13**: 517 - 526.

Faith JJ., Ahern PP., Ridaura VK., Cheng J and Gordon JI (2014). Identifying gut microbe-host phenotype relationships using combinatorial communities in gnotobiotic mice. *Sci Transl Med*, **6**: 220.

Fang HHP and Liu H (2002). Effect of pH on hydrogen production from glucose by a mixed culture. *Bioresour Technol*, **82**: 87 - 93.

Franch C., Lindström K and Elmerich C (2009). Nitrogen-fixing bacteria associated with leguminous and non-leguminous plants. *Plant Soil*, **321**: 35 - 59.

Haruta S., Cui Z., Huang Z., Li M., Ishii M and Igarashi Y (2002). Construction of a stable microbial community with high cellulose-degradation ability. *Appl Microbiol Biotechnol*, **59**: 529 - 534.

- Hooper LV., Littman DR and Macpherson AJ (2012). Interactions between the microbiota and the immune system. *Science*, **336**: 1268 - 1273.
- Hu J., Wang L., Zhang S., Le Y and Fu X (2014). Feasibility of a two-step culture method to improve the CO<sub>2</sub>-fixing efficiency of nonphotosynthetic microbial community and simultaneously decrease the spontaneous oxidative precipitates from mixed electron donors. *Appl Biochem Biotechnol*, **173**: 2307 - 2320.
- Hu J., Xue Y., Li J., Wang L., Zhang S., Wang Y-N, and Gao M-T (2016). Characterization of a designed synthetic autotrophic– heterotrophic consortia for fixing CO<sub>2</sub> without light. *RSC Adv*, **6**: 78161 - 78169.
- Jime´nez J., Guardia-Puebla Y., Romero-Romero O., Cisneros- Ortiz ME., Guerra G., Morgan-Sagastume JM and Noyola A (2014). Methanogenic activity optimization using the response surface methodology, during the anaerobic co-digestion of agriculture and industrial wastes. Microbial community diversity. *Biomass Bioenergy*, **71**:84 – 97.
- Kabat AM., Srinivasan N and Maloy KJ (2014). Modulation of immune development and function by intestinal microbiota. *Trends Immunol*, **35**: 507 - 517.
- Kikot P., Viera M., Mignone C and Donati E (2010). Study of the effect of pH and dissolved heavy metals on the growth of sulfate-reducing bacteria by a fractional factorial design. *Hydrometallurgy*, **104**: 494 - 500.
- Kondo T and Kondo M (1996). Efficient production of acetic acid from glucose in a mixed culture of *Zymomonas mobilis* and *Acetobacter* sp. *J Ferment Bioeng*, **81**: 42 - 46.
- Maldonado-Go´mez MX., Mart´nez I., Bottacini F., O’Callaghan A., Ventura M., van Sinderen D., Hillmann B, Vangay P., Knights D and Hutkins RW et al (2016). Stable engraftment of *Bifidobacterium longum* AH1206 in the human gut depends on individualized features of the resident microbiome. *Cell Host Microbe*, **20**: 515 - 526.
- Mamma D., Koullas D., Fountoukidis G., Kekos D., Macris BJ and Koukios E (1996). Bioethanol from sweet sorghum: simultaneous saccharification and fermentation of carbohydrates by a mixed microbial culture. *Process Biochem*, **31**: 377 - 381.
- Marchesi JR., Adams DH., Fava F., Hermes GDA., Hirschfield GM., Hold G., Quraishi MN., Kinross J., Smidt H and Tuohy KM et al. (2016). The gut microbiota and host health: a new clinical frontier. *Gut*, **65**: 330 - 339.
- Mimee M., Citorik RJ and Lu TK (2016). Microbiome therapeutics - advances and challenges. *Adv Drug Deliv Rev*, **105**: 44 - 54.
- Molina-Barahona L., Rodri´guez-Va´zquez R., Herna´ndez- Velasco M., Vega-Jarqu´n C., Zapata-Pe´rez O., Mendoza-Cantu´ A and Albores A (2004). Diesel removal from contaminated soils by biostimulation and supplementation with crop residues. *Appl Soil Ecol*, **27**: 165 - 175.
- Pholchan MK., de C. Baptista J., Davenport RJ and Curtis TP (2010). Systematic study of the effect of operating variables on reactor performance and microbial diversity in laboratory- scale activated sludge reactors. *Water Res*, **44**: 1341 - 1352.
- Pitt WW., Hancher CW and Patton BD (1981). Biological reduction of nitrates in wastewaters from nuclear processing using a fluidized-bed bioreactor. *Nucl Chem Waste Manag*, **2**: 57 - 70.
- Poszytek K., Cieczkowska M., Sklodowska A and Drewniak L (2016). Microbial consortium with high cellulolytic activity (MCHCA) for enhanced biogas production. *Front Microbiol*, **7**: 324.
- Prakasham RS., Rao CS., Rao RS., Lakshmi GS and Sarma PN (2007). Lasparaginase production by isolated *Staphylococcus* sp. - 6A: design of experiment considering interaction effect for process parameter optimization. *J Appl Microbiol*, **102**: 1382 - 1391.
- Roble ND., Ogbonna JC and Tanaka H (2003). L-Lactic acid production from raw cassava starch in a circulating loop bioreactor with cells immobilized in loofa (*Luffa cylindrica*). *Biotechnol Lett*, **25**: 1093 - 1098.
- Rovira AD (1991). Rhizosphere research - 85 years of progress and frustration. In *The Rhizosphere and Plant Growth*. Edited by Keister DL, Cregan PB. Netherlands: Springer; 3 - 13.
- Simova ED., Frengova GI and Beshkova DM (2003). Effect of aeration on the production of carotenoid pigments by *Rhodotorula rubralactobacillus casei* subsp. *casei* co-cultures in whey ultrafiltrate. *Z Naturforsch*, **58**: 225 - 229.
- Skonieczny MT and Yargeau V (2009). Biohydrogen production from wastewater by *Clostridium beijerinckii*: effect of pH and substrate concentration. *Int J Hydrogen Energy*, **34**: 3288 - 3294.
- Talabardon M., Schwitzguebel J-P., Peringer P and Yang S-T (2000). Acetic acid production from lactose by an anaerobic thermophilic coculture immobilized in a fibrous-bed bioreactor. *Biotechnol Prog*, **16**: 1008 - 1017.
- Taniguchi M., Tokunaga T., Horiuchi K., Hoshino K., Sakai K and Tanaka T (2004). Production of L-lactic acid from a mixture of xylose and glucose by co-cultivation of lactic acid bacteria. *Appl Microbiol Biotechnol*, **66**: 160 - 165.
- Theriot CM., Koenigsknecht MJ., Carlson PE., Hatton GE., Nelson AM., Li B., Huffnagle GB., Z Li J and Young VB (2014). Antibiotic induced shifts in the mouse gut microbiome and metabolome increase susceptibility to *Clostridium difficile* infection. *Nat Commun*, **5**: 3114.
- Walsh CJ., Guinane CM., O’Toole PW and Cotter PD (2014). Beneficial modulation of the gut microbiota. *FEBS Lett*, **588**: 4120 - 4130.
- Zmora N., Zilberman-Schapira G., Suez J., Mor U., Dori-Bachash M., Bashiardes S., Kotler E., Zur M, Regev-Lehavi D and Brik RB-Z et al. (2018). Personalized gut mucosal colonization resistance to empiric probiotics is associated with unique host and microbiome features. *Cell*, **174**: 1388 - 1405.e21.
- Zoetemeyer RJ., Arnoldy P., Cohen A and Boelhouwer C (1982). Influence of temperature on the anaerobic acidification of glucose in a mixed culture forming part of a two-stage digestion process. *Water Res*, **16**: 313- 321.

### Why are the offspring of older mothers less fit to live long and prosper?

The offspring of older mothers do not fare as well as those of younger mothers, in humans and many other species. They are not as healthy, or they do not live as long, or they have fewer offspring themselves. A longstanding puzzle is why evolution would maintain this maternal effect in so many species, since these late-born offspring are less fit to survive and reproduce.

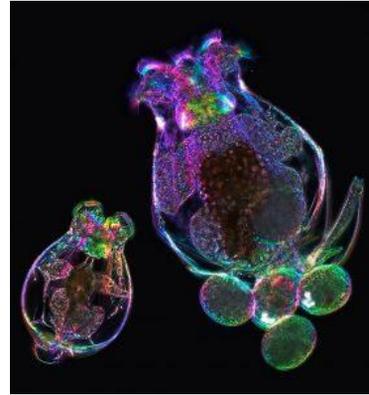
In a new study in rotifers (microscopic invertebrates), scientists tested the evolutionary fitness of older-mother offspring in several real and simulated environments, including the relative luxury of laboratory culture, under threat of predation in the wild, or with reduced food supply. They confirmed that this effect of older maternal age, called maternal effect senescence, does reduce evolutionary fitness of the offspring in all environments, primarily through reduced fertility during their peak reproductive period. They also suggest an evolutionary mechanism for why this may occur. The study, led by Kristin Gribble of the Marine Biological Laboratory and Christina Hernández of Woods Hole Oceanographic Institution, is published in *Proceedings of the National Academy of Sciences*.

Gribble's study is unique in that it combines laboratory data from their prior work with mathematical modelling to address a longstanding question in the evolution of aging. He said natural selection should weed out these less-fit offspring of older mothers, so why do we see this phenomenon across so many species?

To address this, Hernández and collaborators built mathematical models to calculate, for the first time, the strength of natural selection pressure on the survival and fertility of offspring populations as functions of the age of their mothers. They found this pressure, called the selection gradient, declines with maternal age.

Gribble added "Because of this, maternal effect senescence will persist and continue to evolve in the population, even though it results in decreased fitness". They don't yet fully understand the genetic mechanisms that cause offspring quality to decrease with maternal age.

The models that the team developed can be applied to a wide range of species to evaluate the fitness consequences of maternal effect senescence. Gribble said as long as one have experimental data, as they did, on lifespan and fecundity of offspring from mothers of different ages, one can address this question in many organisms.



**Figure: Mother rotifer (*Brachionus manjavacas*) carrying four eggs (right) and newly-hatched daughter (left). Image of live rotifers acquired using polychromatic polarization and phase contrast.**

**Image Credit: Michael Shribak, Evgeny Ivashkin, Kristin Gribble**

**Source: [www.mbl.edu](http://www.mbl.edu)**

### Scientists reveal why tummy bugs are so good at swimming through gut

Researchers have solved the mystery of why a species of bacteria that causes food poisoning can swim faster in stickier liquids, such as within guts. The findings could potentially help scientists halt the bacteria in its tracks, because they show how the shape of the bacteria's body and the components that help it swim are all dependent on each other to work. This means any disruption to one part could stop the bacteria getting through to the gut.

*Campylobacter jejuni* is responsible for millions of food poisoning cases every year and a key step in its invasion of the body is swimming through the viscous (sticky) mucous layer of the guts. Researchers have observed that *C. jejuni* swims faster in viscous liquids than in less-viscous liquids, like water, but until now they did not know why. Now, researchers from Imperial College London, Gakushuin University in Tokyo and the University of Texas Southwestern Medical Center have filmed *C. jejuni* in action to uncover the mystery. Their results are published in the

## Two opposing motors

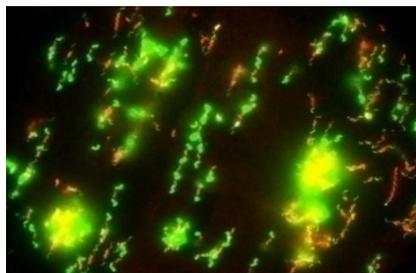
*C. jejuni* uses its two opposing tails, called flagella, to help it move. It has a flagellum at each end of its body that spin around to propel itself through liquid. However, the opposing flagella have confused scientists. Co-first author Dr. Eli Cohen, from the Department of Life Sciences at Imperial, said it seemed very strange that the bacteria had a tail at both ends. It was like having two opposing motors at either end of a ship. It was only then they watched the bacteria in action that they could see how the two tails work cleverly together to help the bacteria move through the body.

The team created *C. jejuni* strains that have fluorescent flagella and used high-speed microscopy to see what happened as they swam around. They discovered that to move forward, the bacteria wrap their leading flagella around their helically shaped bodies, meaning both flagella were then pointing in the same direction and providing unified thrust. To change direction, they changed which flagella were wrapped around their body, enabling quick 180 degree turns and potential escape from confined spaces.

## Sticky situations

They also found that the process of wrapping the flagella was easier when swimming through viscous liquids; the stickiness helping push the leading flagella back around the body. In less-viscous liquids neither flagella were able to wrap around the body.

Lead researcher Dr. Morgan Beeby, from the Department of Life Sciences at Imperial said their study kills two birds with one stone: in setting out to understand how *C. jejuni* moves, they resolved the apparent paradoxes of how it



**Figure:** *C. Jejuni* cell bodies (red) and flagella (green).

**Image Credit:** Eli Cohen / Imperial College London

swims in one direction with opposing flagella and how it swims faster in more viscous liquid. As well as solving some long-standing mysteries, the research could also help researchers find new way to prevent infection by *C. jejuni*, by

targeting any of its interconnected structures that help it move around. The research also revealed that the helical shape of the bacteria body is crucial for allowing the flagella to wrap around it, showing how the two components are reliant on each other.

**Source:** [www.imperial.ac.uk](http://www.imperial.ac.uk)

## Researchers discover how chlamydiae multiply in human cells

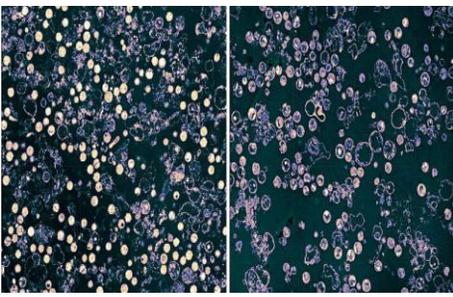
Chlamydia are bacteria that cause venereal diseases. In humans, they can only survive if they enter the cells. This is the only place where they find the necessary metabolites for their reproduction and this happens in a relatively simple way: The bacteria create a small bubble in the cell and divide in it over several generations.

What is the decisive step that initiates the reproduction of the bacteria? It has not been known so far. Researchers from Julius-Maximilians-Universität Würzburg (JMU) in Bavaria, Germany, have now discovered it. This is important because the first step in the reproduction of the pathogens is likely to be a good target for drugs.

## Glutamine import into the host cell increases

In the case of chlamydia, the first step is to reprogram the metabolism of their human host cells. The cells then increasingly import the amino acid glutamine from their environment. If this does not work, for example because the glutamine import system is out of order, the bacterial pathogens are no longer able to proliferate. This was reported by a JMU team led by Dr. Karthika Rajeeve, who has meanwhile been awarded a professorship at the Aarhus University in Denmark and Professor Thomas Rudel in the journal *Nature Microbiology*.

Professor Rudel explained Chlamydiae need a lot of glutamine to synthesize the ring-shaped molecule peptidoglycan, generally a building material of the cell wall and use it for the construction of a new wall that is drawn into the bacterial cell during division. Next, the JMU team hopes to clarify the importance of the glutamine metabolism in chronic chlamydiae infections. This might provide information that might help to better understand the development of severe diseases as a result of the infection.



**Figure: Resting Chlamydia (left; bright circles), which are held without glutamine. After the addition of glutamine (right) the bacteria enter the division stages (darker circles).**

**Image Credit: Lehrstuhl für Mikrobiologie/Universität Würzburg**

**Source:** [www.phys.org](http://www.phys.org)

### ONLINE REPORTS

#### **Researchers collaborate on a strategy for sustainable aquaculture, the world's fastest growing food sector**

As the population grows and the global standard of living improves, humanity's appetite for seafood is increasing. In 2020 seafood consumption reached an all-time high, with an average of 20kg consumed annually by every person on the planet. Up to now most of this was caught in the world's freshwaters and oceans. But things are changing, and today half of all seafood consumed comes from farmed sources, called aquaculture. The sector is expected to double by 2050 to supply the increasing global demand.

UC Santa Barbara Assistant Professor Halley E. Froehlich has contributed to an evaluation of the complex interactions between human, environmental and animal health parameters of this budding industry, a view scientists call the One Health framework. The study, published in the journal *Nature Food*, brings together a diverse team of scientists, economists, sociologists and policy specialists led by the Centre for Sustainable Aquaculture Futures, a joint initiative between the University of Exeter and the United Kingdom's Centre for Environment, Fisheries and Aquaculture Science.

Froehlich, a faculty member in the department of environmental studies and of ecology, evolution, and marine biology said aquaculture is now being more widely recognized as an important part of our global food system and it will continue to grow. So, the question is, how do we

plot that course in a more sustainable way?

Aquaculture has played a major role in lifting millions of people out of poverty in many low and middle-income nations, but it faces a range of sustainability challenges. These include environmental degradation, overuse of antibiotics, release of disease agents and the requirement of wild-caught fish meal and fish oil to produce feed. Parts of the industry also engage in poor labour practices and gender inequality.

Negative societal impressions created by such examples mask aquaculture's potentially significant benefits. Farming cold-blooded animals is very efficient from a nutrient perspective. Many species, such as oysters, do not even require feeding. In addition, aquaculture can operate on a smaller footprint than many other forms of food production.

The new paper uses the One Health framework to lay out a set of metrics to include in national aquaculture strategies across the globe to improve sustainability as the industry expands. These include concepts like access to nutritious food and quality employment, the health of wild fish stocks and ecosystems and maintaining a small environmental footprint and resilience to climate change.

Communication, cooperation and coordination will be critical to the sustainable development of aquaculture as the sector grows. "If you don't have that knowledge transfer, for instance, from scientists to policy-makers or farmers to scientists, these types of framework structures won't go anywhere" Froehlich said.

With that in mind, the authors collaborated widely on this report. Senior co-author Charles Tyler from the University of Exeter said the paper results from extensive interaction between a wide range of academic experts in aquaculture, health, environmental and social sciences, economists, industry stakeholders and policy groups.

The paper presents a strategy for developing aquaculture as well as the benchmarks to which we will measure its sustainability and success. Lead author, Grant Stentiford of the Centre for Environment, Fisheries and Aquaculture Science said this is an important paper acknowledging that aquaculture is set to deliver most of our seafood by 2050, but also that sustainability must be designed-in at every level. The One Health approach offers a tool for governments to consider when designing policies. He hopes it will become a blueprint for how government and industry can interact on these issues in

the future. Most importantly, considering aquaculture's evolution from a subject studied by specialists to an important food sector requires now a much broader interaction with policy and society than arguably has occurred in the past.

Some of these principles are already being applied in the European Union and in Norway, according to Froehlich, who has begun shifting her focus toward the industry in the United States, especially California. She is currently in the middle of a Sea Grant project collecting the most comprehensive dataset of marine aquaculture information from across all coastal states in the U.S. This includes practices, policies, and the hidden interactions with fisheries that influence how aquaculture is conducted in each state.

"Aquaculture is everywhere and nowhere at the same time," Froehlich said. "People don't realize how integrated it is into so many facets of marine ecology, conservation biology, and fisheries".



**Figure: Farmed Maine oysters on the half shell.**

**Image Credit: Halley E. Froehlich**

**Source:** [www.w.phys.org](http://www.w.phys.org)

### **Lending color to dead cells - A novel natural dye for screening cell viability**

Scientists discover a natural food pigment that can distinguish between living and dead cells in cell cultures. Conducting studies *in vitro*, a Latin term that literally means in the glass, is essential in the fields of medicine and biology. Working with *in vitro* cultures is a relatively cost-effective and easily repeatable way of gaining insight into the interactions between cells or microorganisms and specific chemical compounds, such as drugs, nutrients, and toxins. However, to properly assess the toxicity of a compound, a reliable and efficient way to distinguish live cells from cells killed due to toxicity is necessary.

Researchers have elucidated several methods to tell live and dead cells apart and one popular approach is the dye exclusion test (DET) using synthetic dyes. In conventional

DET, a dye such as trypan blue or methylene blue selectively permeates and stains dead cells, distinguishing them from live cells. This seems simple enough, but these synthetic dyes have been known to damage living cells in the culture as well. This renders them unusable for long-term studies with a single culture.

Fortunately, as is described in a study published in the journal *MDPI Biology*, a team of scientists from the Tokyo University of Science, Japan comprising Assistant Professor Ryoma Tagawa, Professor Yoshikazu Higami, Professor Eiji Tokunaga, and Assistant Professor Kyohei Yamashita recently discovered an alternative to DET with synthetic dyes: DET using a natural pigment made from *Monascus purpureus* (MP), a mold species traditionally used in Asia for the production of fermented foods. According to Dr. Yamashita, lead author of this and two other studies on MP, its discovery as a tool for distinguishing dead cells was as a case of serendipity.

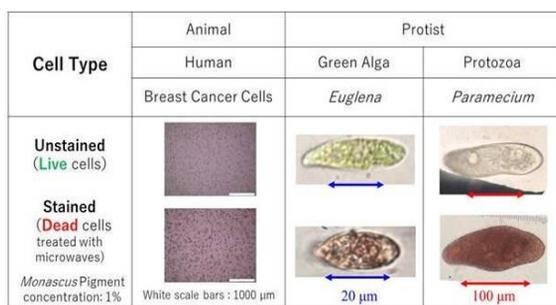
Dr. Yamashita and a colleague were working alongside Dr. Koji Yamada and Dr. Kengo Suzuki from *Euglena Co., Ltd.* to find effective ways of culturing *Euglena gracilis*, a type of single-cell algae, in foods, when they stumbled upon the usefulness of MP and another natural dye called anthocyanin pigment for studying cell health over time. The results of their study are published in *PeerJ* in the world's first report on the application of natural food pigments in cell viability assays. Dr. Yamashita then went on to lead another study demonstrating the applicability of MP in DET for another single-cell organism species with a vastly different structure, *Paramecium*.

In their most recent study, the one published in *MDPI Biology*, Dr. Yamashita and colleagues proved that MP can be used to ascertain the viability of breast cancer cells. They found that, unlike trypan blue, MP does not damage living cells and is robust against a typical chemotherapy drug cisplatin. Moreover, MP took only ten minutes to stain dead cells and costs a tenth of what trypan blue does. Considering all this, Dr. Yamashita remarks: "The proposed natural pigment enables the long-term monitoring of the life and death of cells, which may bring about improvements in the efficiency of biomass production, basic research on metabolic mechanisms, and applied research in fields such as breeding."

In addition to its use as a reagent to monitor the life and death of cells, Dr. Yamashita notes that the pigment is also nutritious to living cells and has antioxidative characteristics, which is useful for boosting culture efficiency and performing quality control in the food industry, where safe fermentation is critical. It is also safe to humans and the environment.

This applicability of MP to completely different kinds of cells breast cancer, Euglena and Paramecium has made Dr. Yamashita very optimistic about its potential. He states "Our natural pigment could be the tool that opens up new research fields involving the determination of the causes behind the death of cells. Moreover, natural pigments are highly likely to have useful properties that have not yet been found, and there is much room for exploration."

There is certainly a bright and colourful future ahead for this promising natural dye!



**Figure: Staining with Monascus pigment solution. Live cells exclude stain, but dead cells incorporate stain.**

**Image Credit: Tokyo University of Science**

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

## NEWS

### Secondary variant of *Photorhabdus luminescens* interacts with plant roots

One of the basic approaches in organic farming is to use organisms beneficial to the system to combat pests. The bacterium *Photorhabdus luminescens* is one such beneficial organism. In the case of insect larvae infestation, the bacterium produces a variety of different toxins which quickly kill the larvae. Yet, it seems this is not the only ability of *Photorhabdus* that can be exploited for organic plant cultivation. A research team led by Professor Ralf Heermann at Johannes Gutenberg University Mainz (JGU) has discovered additional properties that could significantly

extend its range of uses. They have identified a new form of the bacterium that was previously unknown which has a direct relationship with the roots of plants. The researchers think that here it promotes plant growth primarily by releasing substances which combat plant-damaging fungi.

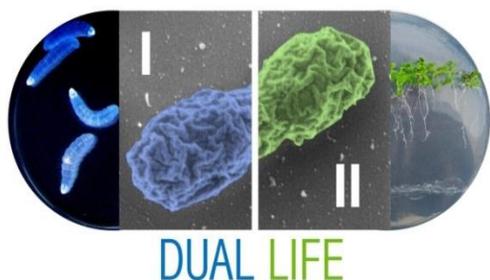
Bacteria of the *Photorhabdus luminescens* family are close relatives of the plague pathogen *Yersinia pestis*. However, they do not pose a danger to humans, but rather stand out for a different characteristic: The insect larvae they kill become luminescent. As well as harmful toxins, for reasons that are as yet unclear, *Photorhabdus* also produces the enzyme luciferase, which causes the body of the victim to glow as it decays. This form of *Photorhabdus* lives in close symbiosis with small nematodes that penetrate into insect larvae and release the bacteria inside them. But it appears that the newly identified variant does not need a host. Researchers were surprised to find that a large proportion of the population was developing differently and looked into why this was.

Heermann's team first used molecular biological techniques to analyze the transcriptome, i.e., the total number of gene transcripts in a cell and found that there were actually two variants. According to the results, the new variant differs on a number of levels as it is more mobile and sensitive, reacts to plant exudates and is attracted towards them. All this pointing to the fact that this bacterial variant interacts more intensely with plants. In the next stage, the research team looked at the interaction more closely. They discovered that the new variant bacterium changes its metabolism to increase the utilization of sugar instead of protein and produces substances that inhibit the growth of fungi that are pathogenic to plants. "A completely different set of natural substances is produced when this bacterium comes into contact with plants," Heermann added.

### Second bacterial variant offers new prospects for organic farming

The researchers do not know yet why there is this second variant of *Photorhabdus luminescens*, which, despite being genetically identical to its primary form, behaves differently and also does not produce luciferase. The two first authors of the paper published in Applied and Environmental Microbiology, Dr. Alice Regaiolo and Nazzareno Dominelli, postulate that the purpose of this is to ensure there is a variant

of *Photorhabdusluminescens* that can survive and fend for itself even if the other variant is unable to prosper because the host nematodes do not find any insects. In any case, there may be completely new prospects for sustainable crop protection in agriculture: The bacteria could be used to combat pests and also promote plant growth. The question now arises of whether other pathogenic bacteria also lead such a "dual life". So far, this has been the first time that this phenomenon was observed.



**Figure: The "dual life" of the insect-pathogenic bacterium *Photorhabdusluminescens*: The primary variant (I) of the bacterium lives in symbiosis with its hosts, nematodes, which attack and kill insect larvae. Because this variant is bioluminescent, the larvae it kills glow with a blue light (left). The genetically identical secondary variant (II) cannot interact with nematodes, remains in the soil after an infection cycle, and instead interacts with plant roots (right).**

**Image Credit: ill. NazzarenoDominelli, Ralf Heermann**

**Source: [www.bioengineer.org](http://www.bioengineer.org)**

### Abstracts of Recent Publications

**01. Science of The Total Environment, 2020, 737, Pages: 140245.**

**The responses of soil enzyme activities, microbial biomass and microbial community structure to nine years of varied zinc application rates.**

Yu-Min Liu, Wen-Qing Cao, Xiu-Xiu Chen, Bao-Gang Yu, Ming Lang, Xin-Ping Chen and Chun-Qin Zou .

*College of Resources and Environmental Sciences, National Academy of Agriculture Green Development, Key Laboratory of Plant-Soil Interactions, Ministry of Education, China Agricultural University, Beijing 100193, China.*

Zinc (Zn) fertilizer application can certainly improve the production and nutritional quality of cereal crops. However, Zn accumulation in the soil may lead to some deleterious environmental impacts in agroecosystems. The effects of long-term Zn application on soil microbial properties remain unclear, but it is imperative to understand such effects. In this study, we collected soil samples from a nine-year field experiment in a wheat-maize system that continuously received Zn applied at various rates (0, 2.3, 5.7, 11.4, 22.7 and 34.1 kg ha<sup>-1</sup>) to evaluate the soil enzymes, microbial biomass and microbial community structure. The results showed that Zn application at the rate of 5.7 kg ha<sup>-1</sup> significantly increased the activities of urease, invertase, alkaline phosphatase and catalase in the soil, while the rate of 34.1 kg ha<sup>-1</sup> significantly decreased the evaluated enzyme activities. The microbial biomass carbon (C) and nitrogen (N) were not affected by Zn application rates, although an increase in the microbial biomass C was observed in the 11.4 kg ha<sup>-1</sup> treatment. Moreover, the alpha diversity of the bacterial and fungal communities did not vary among the nil Zn, optimal Zn (5.7 kg ha<sup>-1</sup>) and excess Zn (34.1 kg ha<sup>-1</sup>) treatments. However, the bacterial communities in the soil receiving the optimal and excess Zn application rates were slightly changed. Compared to the nil Zn treatment, the other Zn application rates increased the relative abundances of the *Rhodospirillales*, *Gaiellales* and *Frankiales* orders and decreased the abundance of the *Latescibacteria* phylum. The redundancy analysis further indicated that the soil bacterial community composition significantly correlated with the concentrations of soil DTPA-Zn and total Zn. These results highlight the importance of optimal Zn application in achieving high production and high grain quality while concurrently promoting soil microbial activity, improving the bacterial community and further maintaining the sustainability of the agroecological environment.

**Keywords:** Enzyme activity, Microbial biomass, Bacteria and fungi, Community structure, Zinc application.

**02. Science of The Total Environment, 2020, 726, Pages: 137961.**

**A review of biochemical and thermochemical energy conversion routes of wastewater grown algal biomass**

Poonam Choudhary, Paula Peixoto Assemany, Farah Naaz, Arghya Bhattacharya, Jackeline de Siqueira Castro, Eduardo de Aguiar do Couto Couto, Maria Lúcia Calijuri, Kamal Kishore Pant, Anushree Malik.

*Applied Microbiology Laboratory, Centre for Rural Development and Technology, IIT Delhi, 110016, India.*

Microalgae are recognized as a potential source of biomass for obtaining bioenergy. However, the lack of studies towards economic viability and environmental sustainability of the entire production chain limits its large-scale application. The use of wastewaters economizes natural resources used for algal biomass cultivation. However, desirable biomass characteristics for a good fuel may be impaired when wastewaters are used, namely low lipid content and high ash and protein contents. Thus, the choice of wastewaters with more favorable characteristics may be one way of obtaining a more balanced macromolecular composition of the algal biomass and therefore, a more suitable feedstock for the desired energetic route. The exploration of biorefinery concept and the use of wastewaters as culture medium are considered as the main strategic tools in the search of this viability. Considering the economics of overall process, direct utilization of wet biomass using hydrothermal liquefaction or hydrothermal carbonization and anaerobic digestion is recommended. Among the explored routes, anaerobic digestion is the most studied process. However, some main challenges remain as little explored, such as a low energy pretreatment and suitable and large-scale reactors for algal biomass digestion. On the other hand, thermochemical conversion routes offer better valorization of the algal biomass but have higher costs. A biorefinery combining anaerobic digestion, hydrothermal carbonization and hydrothermal liquefaction processes would provide the maximum possible output from the biomass depending on its characteristics. Therefore, the choice must be made in an integrated way, aiming at optimizing the quality of the final product to be obtained. Life cycle assessment studies are critical for scaling up of any algal biomass valorization technique for sustainability. Although there are limitations, suitable integrations of these processes would enable to make an economically feasible process which require further study.

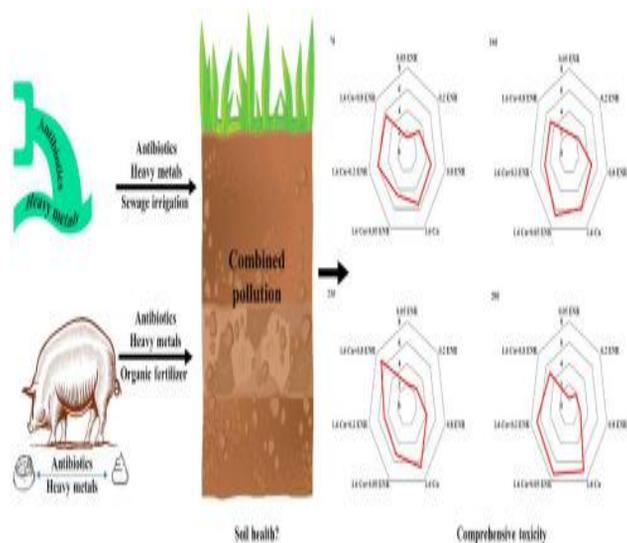
**Keywords:** Hydrothermal liquefaction, Hydrothermal carbonization, Anaerobic digestion, Biorefinery, Life cycle analysis

### 03. Chemosphere, 2020.

#### Effects of interaction between enrofloxacin and copper on soil enzyme activity and evaluation of comprehensive toxicity.

Rui Yang, Jinhua Wang, Lusheng Zhu, Jun Wang, Lili Yang, Shushuai Mao, Jeremy L.Conkle, Yangyang Chen, Young MoKim.

Antibiotics are detected in association with heavy metals in the soil. However, interactions between antibiotics and heavy metals on soil enzyme activity have yet to be studied thoroughly. In this study, soil enzyme activity (urease, sucrase, phosphatase, and Rubisco) were measured after exposure to soils dosed with copper (Cu) and/or enrofloxacin (ENR) over 28 days. Enzyme responses to ENR only treatments varied, but Cu exhibited a strong negative response from all soil enzymes except Rubisco. An interaction between the effects of the two pollutants on soil enzymes was observed in the combined contamination treatments. Greater comprehensive toxicity to soil enzyme activity was observed in combined treatment groups compared to other groups. We anticipate our studies can provide a scientific theoretical basis for the combined pollution of antibiotics and heavy metals in soil.



**Keywords:** Enrofloxacin, Copper, Soil enzymatic activity, Interaction, Comprehensive toxicity.

## E - Resources

### NATIONAL

ICMR-National Institute of Virology (NIV)

<https://www.niv.co.in/>

National Institute of Immunology (NII)

<http://www.nii.res.in/>

Rajiv Gandhi Centre for Biotechnology

<https://rgcb.res.in/>

National Institute of Science Communication and Information

Resources (NISCAIR)

<https://www.niscair.res.in/>

### INTERNATIONAL

Australian Society for Microbiology

<https://www.theasm.org.au/>

IUMS International Union of Microbiological Societies

<https://www.iums.org/>

Society for Industrial Microbiology and Biotechnology

<https://www.simbhq.org/>

Soil Science Society of America (SSSA)

<https://www.soils.org/>

## EVENTS

### Conferences / Seminars / Meetings 2020-2021

**14<sup>th</sup> International Conference on Clinical Microbiology and Epidemiology.** December 24 - 25, 2020. **Venue:** Vienna , **Austria.**

**Website:** <https://waset.org/clinical-microbiology-and-epidemiology-conference-in-december-2020-in-vienna>

**14<sup>th</sup> International Conference on Multispecialty Pathology.** December 24 - 25. **Venue:** Vienna, **Austria.**

**Website:** <https://waset.org/multispecialty-pathology-conference-in-december-2020-in-vienna>

**4<sup>th</sup> World Summit on Virology, Vaccines & Emerging Diseases.** January 08 - 09, 2021. **Venue:** Bangkok, **Thailand.**

**Website:** <https://virologycongress.conferenceseries.com/>

**14<sup>th</sup>Annual Meet on Bacteriology & Applied Microbiology.** February 26- 27, 2021. **Venue:** Tokai, **Japan.**

**Website:** <https://bacteriology.conferenceseries.com/asiapacific/>

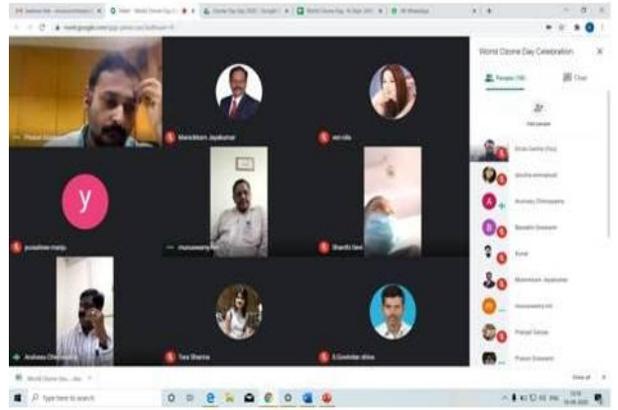
## Biodiversity: where the world is making progress—and where it's not

The future of biodiversity hangs in the balance. World leaders are gathering to review international targets and make new pledges for action to stem wildlife declines. Depending on whether you are a glass half-full or half-empty person, you are likely to have different views on their progress so far.

More than 175 countries agreed to 20 targets under the banner of the Convention for Biological Diversity, which was signed in 1992. The most recent plan, published in 2010, was to halt the extinction of species and populations by 2020 to prevent the destruction of global ecosystems and to staunch the loss of genetic diversity, the variety within the DNA of species' populations, which helps them adapt to a changing environment.

But the targets were missed. An optimist might say that's because they were laudably ambitious, and we are making good progress nonetheless. The protection of land particularly rich in biodiversity has increased from 29% to 44% in just a decade, which is a huge policy achievement. On the other hand, we failed to halt global biodiversity loss during a previous round of global targets ending in 2010 and, a decade later, we are still far behind where we need to be. A recent UN report compiled detailed assessments of the world's progress towards each of the 20 targets. It highlights some small victories and where the greatest gulfs exist between present action and necessary ambition.

# International Day for the Preservation of the Ozone Layer, 16<sup>th</sup> September, 2020



# World Rivers day 27<sup>th</sup> September 2020 (Fourth Sunday of September, every year)

