ENVIS CENTER
on
ENVIRONMENTAL BIOTECHNOLOGY

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ENVIS CENTRE

on

ENVIRONMENTAL BIOTECHBNOLOGY

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C O N T E N T S

BACKGROUND

Environmental Information System (ENVIS) is established in the year 1984 as a network of Information Centres. It is planned by the Ministry of Environment and Forest. Aim of this centre is to provide descriptive and environmental subject related numerical data.

This ENVIS Centre is established in the focal theme area - Environmental Biotechnology at the Department of Environmental Science, University of Kalyani, Nadia-741235, West Bengal in the year 2002.

The objective of this centre is to collect data related to the above mentioned subject, from different major libraries mainly in West Bengal and also from other states in India, through consultation with different journals, Annual Reviews, Internet and to generate a database and create a website uploaded with these information. Besides, we publish biannualy Abstract Volume on our thematic area Environmental Biotechnology under fifteen sub-heads. The volume contains abstracts of scientific articles from relavent national and international journals. Viewpoint of this abstract volume is to help the interested research workers, scientists, administrators and the general people.

This is the 28th publication of Abstract Volume of this ENVIS Centre. This contains the abstracts of research papers collected from the various areas of Environmental Biotechnology from different journals published in last six months upto June, 2016. In this issue, various topics like Bioenergy, Bioengineering, Bio-degradation, Bio-remediation, Bio-transformation etc. have been covered. We are grateful to the various libraries and their staff for their cooperation extended to us during the collection of the articles.

Abstract Format

The format of the abstract is as follows:

Abstract: The abstracts are arranged in different subheads.

Author: Name of the authors are given in the order in which they appear in the original document. These names are given in succession.

Address of Authors: Address of the author is given in parenthesis at the end of the author's name. When the address of any other author is found, it is written after wards delimited by stop(.).

Locus: The name of the journal is followed by the volume number, issue number, year of publication and the page no.

GENERAL INFORMATION

Abstract have been taken directly from source documents like research report, journals, internet, seminar proceedings, standards and patents. All the resources are published within last six months.

Abstract are broadly classified and arranged under the following 16 heads:

Bioaccumulation: Bioaccumulation means an increase in the concentration of a chemical in a biological organism over time, compared to the chemical's concentration in the environment. Compounds accumulate in living things whenever they are taken up and stored at a rate faster than they are broken down (metabolized) or excreted. Understanding the dynamic process of bioaccumulation is very important in protecting human beings and other organisms from the adverse effects of chemical exposure, and it has become a critical consideration in the regulation of chemicals.

Bioremediation: It is a clean-up technology that uses naturally occurring microorganisms to degrade hazardous substances into less toxic or nontoxic compounds. The microorganisms may:

1. Ingest and degrade organic substances as their food and energy source,

2. Degrade organic substances, such as chlorinated solvents or petroleum products, that are hazardous to living organisms, including humans, and degrade the organic contaminants into inert products.

As the microorganisms occur naturally in the environment they are likely to pose little risks of contamination.

Bio-Transformation: This is a process of Biological changes of complex compounds to simpler one or toxic to non-toxic and vice-versa. Several microorganisms are capable of transforming a varity of compounds found in nature but generally in case of synthetic compounds they are unable to show any appropriate action. Biotransfer appears to be one of the major detoxication methods known so far.

Biomarker: It is a biological response to a chemical that gives a measurement of exposure and, sometimes, of toxic effect. It can be defined as any kind of molecule which indicate the existence (past or present) of living organisms. In particular, in the fields of geology and astrobiology biomarkers are also known as biosignatures. However, in environmental science a bio-markers can also be used to indicate exposure to various environmental substances in epidemiology and toxicology.

Biofertilizer: To reduce the impact of excess chemical fertilizers in the field of agriculture the biofertilizer is being considered as a potential tool; biologically fixed nitrogen is such a source which can supply an adequate amount of Nitrogen to plants and other nutrients to some extent. Many free living and symbiotic bacteria, which fix atmospheric Nitrogen are used as biofertiliser material as a substitute for Nitrogen fertilizer. In general two types of biofertiliser are used

1. Bacterial Biofertilizer
2. Algal Biofertilizer

Biocomposting: It involves combining organic materials under conditions that enables them to decompose more quickly than they would in nature. Think about logs and leaves on the ground in a forest. The leaves will break down and disappear within a year. Logs of course will take much longer to crumble away. Composting is the process of converting all biodegradable wastes into organic manure. In composting process certain input should be made into waste to convert the process in a short time.

Biopesticide: Pest control by biological antagonism appears to be very useful tool in recent years. Bacterial pesticides are being developed. *Heliothis* complex, which lives in close association with plant roots, consists of two major crop pests budworm and ball warm. Biological insecticides against both these insects are being prepared by transfer of a gene from *Bacillus thuringiensis*

Biodegradation: It is nature's way of recycling wastes, breaking down organic matter into nutrients that can be used by other organisms. "Degradation" means decay, and the "bio-" prefix means that the decay is carried out by a huge assortment of bacteria, fungi, maggots, worms, and other organisms that eat dead material and recycle it into new forms.

In the nature, nothing is known as waste, because everything gets recycled. The waste products from one organism become the food for others, providing nutrients and energy while breaking down the waste organic matter. Some organic materials may break down much faster than others, but all will eventually decay.

By harnessing these natural forces of biodegradation, people can reduce wastes and clean up some types of environmental contaminants. Through **composting**, we accelerate natural biodegradation and convert organic wastes to a valuable resource.

Biosensor: Biosensor represents biophysical devices, which can detect the presence and measure the quantities of specific substances in a varity of environments. These specific substances may include sugars, proteins, or humas and varity of toxins in the industrial effluents. In designing a biosensor an enzyme or an antibody or even microbial cells are associated with microchip devices, which are used for quantitative estimate of a substance.

Bioengineering: It is a developing speciality featuring a multidisciplinary approach to the solution of problems in medicine and biology, based on the application of advances in science, engineering and technology. It generally engineers the biological processes through biotechnological or genetic engineering interventions. It may also be a broad-based engineering discipline that involve product design, sustainability and analysis of biological systems.

Pollen-Biotechnology: This is a new field of science dealing with the pollen chemistry and allerginicity of aerospora. This subject also covers genetic manipulation of pollen development of haploid culture. Such haploid plants have immense values in genetic research.

Biotechnology Policy Issue: Biotechnology appears to be an emerging science in present decades. Genetic manipulation and development of genetically modified organism in human welfare is now showed a potential prospect and risk. Thus, researches and application of Biotechnology in diverse field is a major policy issue in the present decades.

Agricultural Biotechnology: Over the years, tremendous success has been made in diverse field of agriculture by applying Biotechnology. It includes development of genetically modified crops, genetic improvement in sericulture practices, improvement in Biofertilizer development and similar other aspects. Production of pest and disease resistant crop is also being considered to be an emerging area of Agricultural Biotechnology.

Bioenergy: In recent decades, efforts have been made for evolving were non-polluting bioenergy sources or energy generation from organic wastes and biomass. These are all ecofreindly solutions. Biomass energy supply-demand balances have become a component of energy sector analysis and planning and is propelled huge importance in the countries. Biomass, Biogas, Hydrogen are the example of Bioenergy.

Nano Biotechnology: Bionanotechnology, nanobiotechnology, and nanobiology are terms that refer to the intersection of nanotechnology and biology. Given that the subject is one that has only emerged very recently, bionanotechnology and nanobiotechnology serve as blanket terms for various related technologies.

This discipline helps to indicate the merger of biological research with various fields of nanotechnology. Concepts that are enhanced through nanobiology include: nanodevices, nanoparticles, and nanoscale phenomena that occurs within the disciple of nanotechnology. This technical approach to biology allows scientists to imagine and create systems that can be used for biological research

Biomimicry: Biomimicry is an applied science that derives inspiration for solutions to human problems through the study of natural designs, systems and processes. Biomimicry on the other hand, which is not a science, is a more subtle way which we can benefit from nature. It is the modern, often high tech, equivalent of the

historical practices of emulating nature. . The science of biomimicry is a newly developing field but the application of biomimicry has been around since the beginning of man. The biomimetic technologies (flight controls, bio-robotics, ventilation systems, etc.) and potential technologies (fin geometry, nacre materials, etc.) improve performance. The use of biomimicry as an approach to sustainable engineering, specifically the environmental components.

ABBREVIATIONS USED IN ADDRESSES AND CITED JOURNALS

Acad	Academy	Chem	Chemistry
Adm	Administration	Cheml	Chemical
Admn	Administrative	Clinl	Clinical
Adv	Advance	Co	Company
Agri	Agriculture	Coll	College
Agricl	Agricultural	Comm	Committee
Amer	American	Commn	Commission
An	Annual	Comp	Comparative
Analyt	Analytical	Conf	Conference
Anat	Anatomy	Conv	Convention
Anim	Animal	Conserv	Conservation
Ann	Annals	Contl	Control
Appl	Applied	Contam	Contamination
Arch	Archives	Corpn	Corporation
Archaeo	Archaeology	Coun	Council
Archaeol	Archaeological	Cult	Culture
Architect	Architecture	Cultl	Cultural
Assoc	Association	Curr	Current
Asst	Assistant	Dept	Department
Atom	Atomic	Dev	Development
Bacterio	Bacteriology	Develop	Developmental
Bacteriol	Bacteriological	Dig	Digest
Bd	Board	Div	Division
Bio	Biology	Divl	Divisional
Biochem	Biochemistry	Dte	Directorate
Biocheml	Biochemical	Dy	Deputy
Bioengg	Bioengineering	Eco	Ecology
Biol	Biological	Ecol	Ecological
Biometeo	Biometeorology	Econ	Economics
Biophys	Biophysics	Ecosys	Ecosystem
Biometeol	Biometeorological	Ecotoxico	Ecotoxicology
Biotech	Biotechnique(s)	Endocrinol	Endocrinological
Biotechno	Biotechnology	Engg	Engineering
Biotechnol	Bitechnological	Engrs	Engineers
Bldg	Building	Env	Environment
Bot	Botany	Environ	Environmental
Botl	Botanical	Epidemic	Epidemiology
Br	Branch	Epidemiol	Epidemiological
Bull	Bulletin	Estd	Establishment
Cent	Centre	Ethnopharmaco	Ethnopharmacology
Centl	Central	Expt	Experiment

Exptl	Experimental	Microbiol	Microbiological
Fac	Faculty	Min	Ministry
Fd	Food	Monit	Monitoring
Fedn	Federation	Myco	Mycology
Fert	Fertiliser	Mycol	Mycological
Fmg	Farming	Nat	Natural
Gaz	Gazette	Natl	National
Genet	Genetics	N-E	North Eastern
Geo	Geology	Nut	Nutrition
Geogr	Geography	No	Number
Geogrl	Geographical	Occ	Occassional
Geol	Geological	Occupl	Occupational
Geosci	Geoscience	Oceanogr	Oceanogoraphy
Govt	Government	Org	Original
Hist	History	Orgc	Organic
Hlth	Health	Orgn	Organisation
Hort	Horticulture	Pharmaco	Pharmacology
Hosp	Hospital	Pharmacol	Pharmacological
Hydro	Hydrology	Phyl	Physical
Hydrol	Hydrological	Patho	Pathology
Immuno	Immunology	Pathol	Pathological
Immunol	Immunlogical	Petrochem	Petrochemical
Ind	Industry	Petro	Petrology
Inf	Information	PG	Post Graduate
Inst	Institute	Phys	Physics
Instn	Institution	Physio	Physiology
Int	International	Phytopath	Phytopathology
Irrig	Irrigation	Phytopathol	Phytopathological
J	Journal	Plang	Planning
Lab	Laboratory	Polln	Pollution
Lett	Letter(s)	Proc	Proceedings
Ltd	Limited	Prot	Protection
Malario	Malariology	Pub	Publication
Malariol	Malariological	Pvt	Private
Manag	Management	Qlty	Quality
Med	Medicine	Qr	Quarter
Medl	Medical	Rad	Radiation
Metab	Metabolism	Radio	Radiology
Metall	Metallurgy	Radiol	Radiological
Metallurg	Metallurgical	Rd	Road
Meteo	Meteorology	Recd	Received
Meteol	Meteorological	Reg	Region
Microbio	Microbiology	Regl	Regional

Rep	Report	Surv	Survey
Reptr	Reporter	Syst	System
Res	Research	Tax	Taxonomy
Rev	Review	Techl	Technical
Sch	School(s)	Techno	Technology
Sci	Sciences(s)	Technol	Technological
Scient	Scientific	Toxico	Toxicology
S-E	South East	Toxicol	Toxicological
Sec	Section	Transc	Transcations
Sect	Sector	Transpt	Transportation
Semin	Seminar	Trng	Training
Ser	Services	Trop	Tropical
Soc	Society	Univ	University
Socl	Social	Util	Utilisation
Stat	Statistics	Vet	Veterinary
Statl	Statistical	Zoo	Zoology
Stnd	Standard(s)	Zool	Zoological
Stud	Study/ (eis)		

Bioaccumulation

Uhram Song, Sunryung Lee. (Department of Biology and Research Institute for Basic Sciences, Jeju National University. Natural Science Building 1, Jeju Special Self-Governing Province, Jeju National University). Phytotoxicity and accumulation of zinc oxide nanoparticles on the aquatic plants *Hydrilla verticillata* and *Phragmites Australis*: leaf-type-dependent responses. Environmental Science and Pollution Research, Volume 23(9) (2016): 8539-8545

The phytotoxicity and accumulation of zinc oxide nanoparticles (ZnO NPs) on aquatic plant *Hydrilla verticillata* and *Phragmites australis* were investigated using mesocosms. The percentage of dissolved Zn in the ZnO NP treatment solutions was measured along with plant shoot growth, antioxidant enzyme activity, chlorophyll content, and Zn content. The dissolution rate of ZnO NPs in Hoagland solution was inversely related to the concentration. The submerged aquatic plant *H. verticillata*, growth was reduced during the early stages of the experiment when exposed to the highest ZnO NP concentration (1000 mg/L), whereas the emerged aquatic plant *P. australis* began to show significantly reduced growth after a few weeks. The measurements of chlorophyll content, antioxidant enzyme activity, and Zn accumulation showed that *P. australis* was adversely affected by NPs and absorbed more Zn than *H. verticillata*. The results indicated that physiological differences among aquatic plants, such as whether they use leaves or roots for nutrient and water uptake, led to differences in nanoparticle toxicity. Overall, High ZnO NP concentrations caused significant phytotoxicity on aquatic plants, and low concentrations caused unpredictable phytotoxicity. Therefore, the use and disposal of zinc oxide nanoparticles should be carefully monitored.

Keywords: Zinc oxide nanoparticles (ZnO NPs); Phytotoxicity; Aquatic plants; Submerged plant; Emerged plant; Heavy metal stress

Shanshan Di, Ledan Huang, Jinling Diao, Zhiqiang Zhou. (Beijing Advanced Innovation Center for Food Nutrition and Human Health, China Agricultural University. Department of Applied Chemistry, China Agricultural University, Department of Applied Chemistry, China Agricultural University). Selective bioaccumulation and elimination of hexachlorocyclohexane isomers in *Tubifex tubifex* (Oligochaeta, Tubificidae). Environmental Science and Pollution Research, Volume 23(7) (2016): 6990-6998

In this study, *Tubifex tubifex* worms were exposed to sediment-associated hexachlorocyclohexane (HCH) isomers to study the bioaccumulation and elimination behaviors of HCH isomers in *T. tubifex*. During a 10-day bioaccumulation experiment, bioaccumulation curves of HCHs were approximate to M-type in *T. tubifex*. The enantioselective behaviors of α-HCH enantiomers were observed in *T. tubifex*, with concentrations of (+)-α-HCH higher than that of (−)-α-HCH. The concentration of γ-HCH in *T. tubifex* was higher than that of β-HCH and α-HCH. The existence of worms can accelerate the dissipation of HCHs in sediment, and the dissipation half-lives of α-HCH, β-HCH, and γ-HCH were 8.39, 23.90, and 3.10 days, respectively. In the elimination experiment, approximately 0.053 (37.1 %), 0.074 (45.9 %), and 0.042 mg/kg$_{wwt}$ (38.4 %) α-HCH, β-HCH, and γ-HCH were depleted or excreted in *T. tubifex* on the first day, respectively. The body residues in *T. tubifex* were 0.084 (α-HCH), 0.082 (β-HCH), and 0.061 mg/kg$_{wwt}$ (γ-HCH) at the end of elimination experiment. Furthermore, the existence of *T. tubifex* could affect the overlying water quality parameters.

Keywords: *Tubifex tubifex;* HCHs; Sediment; Bioaccumulation; Dissipation; Elimination

Bioremediation

José Manuel Salgado[a], Luís Abrunhosa[a], Armando Venâncio[a], José Manuel Domínguez[b], Isabel Belo[a]. ([a] CEB-Centre of Biological Engineering, University of Minho, Braga, Portugal, [b] Department of Chemical Engineering, Sciences Faculty, University of Vigo (Campus Ourense), As Lagoas s/n, 32004 Ourense, Spain). Combined bioremediation and enzyme production by *Aspergillus* sp. in olive mill and winery wastewaters. International Biodeterioration & Biodegradation, Volume 110(2016): 16–23

Olive mill wastewaters (OMW) and vinasses (VS) are effluents produced respectively by olive mills and wineries, both sectors are of great economic importance in Mediterranean countries. These effluents cause a large environmental impact, when not properly processed, due to their high concentration of phenolic compounds, COD and colour. OMW may be treated by biological processes but, in this case, a dilution is necessary, increasing water consumption. The approach here in proposed consists on the bioremediation of OMW and VS by filamentous fungi. In a screening stage, three fungi (*Aspergillus ibericus*, *Aspergillus uvarum*, *Aspergillus niger*) were selected to bioremediate undiluted OMW, two-fold diluted OMW supplemented with nutrients, and a mixture of OMW and VS in the proportion 1:1 (v/v). Higher reductions of phenolic compounds, colour and COD were achieved mixing both residues; with *A. uvarum* providing the best results. In addition, the production of enzymes was also evaluated during this bioremediation process, detecting in all cases lipolytic, proteolytic and tannase activities. *A. ibericus*, *A. uvarum* and *A. niger* achieved the highest value of lipase (1253.7 ± 161.2 U/L), protease (3700 ± 124.3 U/L) and tannase (284.4 ± 12.1 U/L) activities, respectively. Consequently, this process is an interesting alternative to traditional processes to manage these residues, providing simultaneously high economic products, which can be employed in the same industries.

Keywords: Vinasses; Olive mill wastewater; Bioremediation; *Aspergillus* sp.; Lipases; Proteases; Tannases

Meenakshi Tiwary, Ashok K. Dubey. (Division of Biotechnology, Netaji Subhas Institute of Technology, University of Delhi, Dwarka, New Delhi 110078, India). Cypermethrin bioremediation in presence of heavy metals by a novel heavy metal tolerant strain, *Bacillus* sp. AKD1. International Biodeterioration & Biodegradation, Volume 108(2016): 42–47

An isolate, designated as *Bacillus* sp. AKD1, based on the 16S rRNA gene sequence, could transform 86% ± 3.6% of cypermethrin (initial concentration of 100 ppm) in 7 days, but biotransformation was inhibited at concentrations above 150 ppm. As determined by the Response Surface Methodology (RSM), optimum parameters for the biotransformation were: pH value of 8.0, temperature of 37.8 $^{\circ}$C and inoculum density of 4.4 mg ml^{-1} (wet wt.). Glucose, fructose and glycerol inhibited insecticide biotransformation at concentrations above 0.5%, 1.0% and 0.5 respectively (w/v). Minimum inhibitory concentrations of *Bacillus* sp. AKD1 for Co^{2+}, Cr^{6+}, Cu^{2+}, Fe^{2+}, Li^{+}, Ni^{2+}, pb^{2+}, V^{5+} and Zn^{2+} were 0.2 mM, 1.4 mM, 1.8 mM, 5.1 mM, 7.8 mM, 2.9 mM, 0.6 mM, 8.2 mM, and 0.6 mM respectively. At concentrations less than the MIC, V^{5+} and Fe^{2+} did not affect cypermethrin biotransformation, but Li+ was found to be inhibitory above 4.0 mM. The results obtained in this study have significant importance in the development of bioremediation strategy for removal of cypermethrin in cypermethrin contaminated areas co-contaminated with heavy metals.

Keywords: Bioremediation; Cypermethrin; Co-contamination; Heavy metals; Minimum inhibitory concentration

Manli Wu[a], Warren A. Dick[b], Wei Li[a], Xiaochang Wang[a], Qian Yang[a], Tingting Wang[a], Limei Xu[a], Minghui Zhang[a], Liming Chen[b]. ([a] School of Environmental and Municipal Engineering, Xi'an University of Architecture and Technology, No.13 Yanta Road, Xi'an, Shaanxi Province 710055, China, [b] School of Environment and Natural Resources, The Ohio State University, Ohio Agricultural Research and Development Center, 1680 Madison Avenue, Wooster, OH 44691, USA). **Bioaugmentation and biostimulation of hydrocarbon degradation and the microbial community in a petroleum-contaminated soil. International Biodeterioration & Biodegradation, Volume 107(2016): 158–164**

Nutrient additions can stimulate petroleum hydrocarbon degradation, but little is known about how these additions affect the microbial community involved in that degradation. A microcosm study was conducted to assess the impact of bioaugmentation with *Acinetobacter* SZ-1 strain KF453955 and biostimulation with nutrients nitrogen and phosphorus on petroleum hydrocarbon degradation efficiency and microbial community dynamics during bioremediation of an oil-contaminated soil. Soils were incubated without shaking at room temperature for 10 weeks, and petroleum hydrocarbon degradation efficiency, catalase activity, petroleum hydrocarbon degrader population, and bacterial community diversity were determined. Results showed biostimulation and bioaugmentation, respectively, promoted 60% and 34% degradation of the total petroleum hydrocarbons (TPH) after six weeks of incubation. A degradation plateau occurred in the seventh week. Catalase activity and the populations of oil degraders in soil were generally greater for biostimulation than for bioaugmentation. The inoculants survived into the seventh week for the bioaugmentation treatment, and bacterial diversity did not increase by biostimulation. The populations of TPH-degraders in soil were positively related to TPH degradation efficiency during bioremediation of petroleum-polluted soils.

Keywords: TPH; Biostimulation; Bioaugmentation; Biodegradation efficiency; Microbial community

Hirak R. Dash, Surajit Das. (Laboratory of Environmental Microbiology and Ecology (LEnME), Department of Life Science, National Institute of Technology, Rourkela, 769 008, Odisha, India). **Corrigendum to "Bioremediation of inorganic mercury through volatilization and biosorption by transgenic *Bacillus cereus* BW-03 (pPW-05)" International Biodeterioration & Biodegradation, Volume 106(2016) : 24**

Encapsulation of the transformant increased its mercury removal potential to almost 100%. Additionally, *Bacillus cereus* BW-03($_{p}$PW-05) could resist wide variations of salinity (5–30 ppt), **pH (5–8)** and mercury (5–50 ppm) and survived in mercury contaminated simulated environment up to 7 days.

Kshama Balapure[a], Kunal Jain[b], Nikhil Bhatt[a], Datta Madamwar[b]. ([a] Post Graduate Department of Microbiology, Biogas Research and Extension Centre, Gujarat Vidyapith, Sadra, 382 320, Gujarat, India, [b] Environmental Genomics and Proteomics Lab, BRD School of Biosciences, Satellite Campus, Vadtal Road, Post Box No. 39, Sardar Patel University, Vallabh Vidyanagar, 388 120, Gujarat, India). **Exploring bioremediation strategies to enhance the mineralization of textile industrial wastewater through sequential anaerobic-microaerophilic process. International Biodeterioration & Biodegradation, Volume 106(2016): 97–105**

The study exemplifies sequential anaerobic-microaerophilic bioremediation process for treatment of textile industrial wastewater having 10,000 mg l^{-1} of COD and 3330 mg l^{-1} of the BOD. The experimental results showed that, in an anaerobic phase, with cattle dung slurry as an initial feed, nearly 60% of COD and BOD was removed from textile wastewater at an optimum HRT of 2d and OLR of 5.0 kg COD $m^{-3}d^{-1}$. Further, COD and BOD removal efficiency of bacterial consortium BDN was enhanced upto 97% under microaerophilic phase, at HRT of 12 h. Moreover, optimum color removal (80%) was observed in anaerobic reactor. The combine treatment process removed 99% of color at combine HRT of 60 h. The activity of lignin peroxidase was higher as compared to other enzymes studied. The UV–vis, FTIR, ^{1}H NMR and GC–MS analyses of treated textile industrial wastewater revealed the degradation of dye compounds and formation of lower molecular weight intermediates. The toxicity of textile industrial wastewater decreased subsequently from anaerobic to microaerophilic treatment process.

Keywords: Textile wastewater; Anaerobic-microaerophilic; Mineralization; Phytotoxicity

Suvi Simpanen[a], Riikka Mäkelä[a], Juha Mikola[a], Hannu Silvennoinen[b], Martin Romantschuk[a, c]. ([a] University of Helsinki, Department of Environmental Sciences, Niemenkatu 73, 15140, Lahti, Finland, [b] Nordic Envicon Ltd, Huopalahdentie 24, 00350, Helsinki, Finland, [c] Kazan Federal University, Institute of Environmental Sciences, 420008, Kazan, Russia). **Bioremediation of creosote contaminated soil in both laboratory and field scale: Investigating the ability of methyl-β-cyclodextrin to enhance biostimulation. International Biodeterioration & Biodegradation, Volume 106(2016): 117–126**

We investigated the bioremediation of 16 polycyclic aromatic hydrocarbons (PAH) in historically creosote contaminated soil using both laboratory and field scale experiments. We found that nutrient amendments and circulation of methyl-β-cyclodextrin (CD) solution enhanced soil microbial degradation capacity. In the laboratory experiment, the degradation of lower molecular weight, 2–3 ringed PAHs was achieved already by circulating nutrient solution and the use of CD mainly increased the desorption and removal of larger, 4–5 aromatic ringed PAH compounds. The 1% CD concentration was most feasible for bioremediation as most of the extracted PAH compounds were degraded. In the 5% CD treatment, the PAH desorption from soil was too fast compared to the degradation capacity and 25% of the total PAH amount remained in the circulated solution. Similar lab-scale results have been generated earlier, but very little has been done in full field scale, and none in freezing conditions. Although freezing stopped circulation and degradation completely during the winter, PAH degradation returned during the warm period in the field test. Circulation effectiveness was lower than in the laboratory but the improved nutrient and moisture content seemed to be the main reason for decreasing soil PAH concentrations. It also appeared that PAH extraction yield in chemical analysis was increased by the CD treatment in field conditions and the results of CD-treated and non-treated soil may therefore not be directly comparable. Therefore, a positive effect of CD on PAH degradation velocity could not be statistically confirmed in the field test. Based on our results, we recommend initiating the bioremediation of PAH contaminated soil by enhancing the microbial degradation with nutrient amendments. The CD seems to be useful only at the later stage when it increases the solubilisation of strongly absorbed contaminants to some extent. More investigation is also needed of the CD effect on the PAH yield in the chemical analysis.

Keywords: Soil bioremediation; Cyclodextrin; Surfactant; Biodegradation; Biostimulation; Polycyclic aromatic hydrocarbon

Shijie Wang[a, b], Xiang Wang[a], Chao Zhang[a], Fasheng Li[a], Guanlin Guo[a]. ([a] State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing 100012, China, [b] Beijing Municipal Research Institute of Environmental Research, Beijing 100037, China). Bioremediation of oil sludge contaminated soil by landfarming with added cotton stalks. International Biodeterioration & Biodegradation, Volume 106(2016): 150–156

A field bioremediation of oil sludge contaminated soil was conducted by landfarming treatment with added cotton stalks in the Shengli oil field. The ability of landfarming treatment was evaluated to reduce petroleum hydrocarbons and restore soil quality. For 39-month landfarming, the initial concentration of total petroleum hydrocarbons (TPH) was 12.57 mg g^{-1} for oil sludge contaminated soil. The removal efficiency of TPH, saturated fraction and aromatic fraction was 68.48%, 90.04% and 85.55%, respectively. Degradation of TPH followed first order exponential decay kinetics. Soil physic-chemical properties of soil pH, saline alkali degree, nutrients, organic matters and hydrocarbon degraders were greatly improved. The results of Biolog and PCR-DGGE analysis revealed the improvement of soil microbial quantity and diversity, and the isolated predominant 23 strains showed a shift in soil community structure toward the hydrocarbon degrading species including *Streptococcus* sp., *Shewanella* sp., *Bacillus* sp., *Pseudomonas* sp., *Marinobactera* sp., *Thermoanaerobacter* sp., etc.

Keywords: Biodegradation; Oil sludge; Cotton stalk; Bacterial community

Sergio Cisneros de la Cueva, César Hernández Rodríguez Biológicas, Nicolás Oscar Soto Cruz, Juan Antonio Rojas Contreras, Javier López Miranda. (Instituto Tecnológico de Durango, Departamento de Microbiología, Escuela Nacional de Ciencias). Changes in Bacterial Populations During Bioremediation of Soil Contaminated with Petroleum Hydrocarbons. Water, Air, & Soil Pollution, Volume 227(2016): 91

An estimated 4.9 million barrels of crude oil and natural gases was released into the Gulf of Mexico during the Deepwater Horizon oil spill of 2010. The Deepwater Horizon oil spill affected the aquatic species in the Gulf of Mexico, vegetation, and the human population along the coast. To reduce the effect of the spilled oil on the environment, different remediation strategies such as chemical dispersant, and mechanical booms and skimmers were utilized. Over 2.1 million gallons of dispersants was applied to minimize the impact of the spilled oil. However, environmental and human toxicity issues arose due to the perceived toxicity of the dispersant formulations applied. After the Deepwater Horizon oil spill, various studies have been conducted to find alternative and environmentally benign oil spill response strategies. The focus of this manuscript is to demonstrate an objective and an overall picture of current research work on oil spill response methods with emphasis on dispersant and oil sorbent applications. Current trends in oil spill sorbent and dispersant formulation research are presented. Furthermore, strategies to formulate environmentally benign dispersants, as well as the possible use of photoremediation, are highlighted.

Keywords: Oil spill remediation; Oil sorbents; Dispersant application; Photoremediation; Lecithin

Yunyun Hou, Xiaoyan Liu, Xinying Zhang, Xiaoxin Hu, Liya Cao. (Laboratory of Environmental Remediation, School of Environmental and Chemical Engineering,

Shanghai University). Rhizosphere Phytoremediation with *Cyperus rotundus* for Diesel-Contaminated Wetlands. Water, Air, & Soil Pollution, Volume 227(2016): 26

Diesel spills may considerably damage the sensitive coastal wetlands along Huangpu River, Shanghai, China. In this experiment, *Cyperus rotundus*, a dominant coastal marsh plant, was cultured in diesel-contaminated soils at concentrations of 0, 1000, 5000, 10,000, 15,000 and 20,000 mg kg^{-1} to investigate its phytoremediation potential. In this study, plant biomass, removal characteristic of diesel, redox potential, and activities of urease, dehydrogenase, and polyphenoloxidase in soils were determined after 50-day pot experiments. The results demonstrated that soils planted with *Cyperus rotundus* had significantly less diesel than did unplanted soils. The residual concentrations of alkanes in soils at 10,000 mg kg^{-1} after 50 days showed that 52.9–92.0 % of Fraction a (C_{14}–C_{19}) and 47.8–64.4 % of Fraction b (C_{20}–C_{27}) were removed in unplanted soils, while more than 90 % of both Fractions a and b were removed in planted soils. The peak value of urease and dehydrogenase activities was at 15,000 mg kg^{-1} of diesel-contaminated concentration; however, the peak value of polyphenoloxidase activity appeared at 10,000 mg kg^{-1}. It was deduced that the diesel concentration between 10,000 and 15,000 mg kg^{-1} might be a limit which *Cyperus rotundus* could tolerate diesel pollution.

Keywords: Phytoremediation effect; *Cyperus rotundus;* Diesel-contaminated soil; Wetland

Saranya Kuppusamy, Palanisami Thavamani, Mallavarapu Megharaj, Ravi Naidu. (Centre for Environmental Risk Assessment and Remediation (CERAR), University of South AustraliaCooperative Research Centre for Contamination Assessment and Remediation of Environment (CRC CARE), Cooperative Research Centre for Contamination Assessment and Remediation of Environment (CRC CARE)Global Centre for Environmental Remediation (GCER), Faculty of Science and Information Technology, The University of Newcastle). Bioaugmentation with Novel Microbial Formula vs. Natural Attenuation of a Long-Term Mixed Contaminated Soil—Treatability Studies in Solid- and Slurry-Phase Microcosms. Water, Air, & Soil Pollution, Volume 227(2016): 25

Treatability studies in real contaminated soils are essential to predict the feasibility of microbial consortium augmentation for field-scale bioremediation of contaminated sites. In this study, the biodegradation of a mixture of seven PAHs in a manufactured gas plant (MGP) soil contaminated with 3967 mg kg^{-1} of total PAHs using novel acid-, metal-tolerant, N-fixing, P-solubilizing, and biosurfactant-producing LMW and HMW PAH-degrading bacterial combinations as inoculums was compared in slurry- and solid-phase microcosms over natural attenuation. Bioaugmentation of 5 % of bacterial consortia A and N in slurry- and solid-phase systems enhanced 4.6–5.7 and 9.3–10.7 % of total PAH degradation, respectively, over natural attenuation. Occurrence of 62.7–88 % of PAH biodegradation during natural attenuation in soil and slurry illustrated the accelerated rate of intrinsic metabolic activity of the autochthonous microbial community in the selected MGP soil. Monitoring of the total microbial activity and population of PAH degraders revealed that the observed biodegradation trend in MGP soil resulted from microbial mineralization. In the slurry, higher biodegradation rate constant (k) and lower half-life values ($t_{1/2}$) was observed during bioaugmentation with consortium N, highlighting the use of bioaugmentation in bioslurries/bioreactor to achieve rapid and efficient bioremediation compared to that of a static solid system. In general, natural attenuation was on par with bioaugmentation. Hence, depending on the type of soil, natural attenuation might

outweigh bioaugmentation and a careful investigation using laboratory treatability studies are highly recommended before the upscale of a developed bioremediation strategy to field level.

Keywords: Manufactured gas plant (MGP)Soil bioremediation; Polycyclic aromatic hydrocarbons (PAHs)Heavy metals; Natural attenuation; Bacterial consortium; Bioaugmentation

Marco Andreolli, Nicola Albertarelli, Silvia Lampis, Pierlorenzo Brignoli, Nazaninalsadat Seyed Khoei, Giovanni Vallini. (Department of Biotechnology, University of Verona, Eurovix SpA). Bioremediation of diesel contamination at an underground storage tank site: a spatial analysis of the microbial community. World Journal of Microbiology and Biotechnology, Volume 32(2016): 6

The present study reports on a real case of contamination due to the chronic leakage of diesel fuel from an underground tank at a dismissed service station. Speciation of the microbial community according to both lateral and vertical gradients from the origin of the contaminant release was analyzed by means of the PCR–DGGE technique. Moreover, the effects of a landfarming treatment on both the microbial community structure and the abatement of contamination were analyzed. The concentration of total petrol hydrocarbons (TPHs) decreased along the horizontal gradient (from 7042.2 ± 521.9 to 112.2 ± 24.3 mg kg^{-1}), while increased downwards from the position of the tank (from 502.6 ± 43.7 to 4972.5 ± 275.3 mg kg^{-1}). PCR–DGGE analyses and further statistical treatment of the data indicated a correlation between structure of the bacterial communities and amount of diesel fuel contamination. On the other hand, level of contamination, soil texture and depth were shown to affect the fungal community. *Chloroflexi* and *Ascomycota* were the most abundant microbes ascertained through culture-independent procedures. Landfarming promoted 91.6 % reduction of TPHs in 75 days. Furthermore, PCR–DGGE analyses evidenced that both bacterial and fungal communities of the treated soil were restored to the pristine conditions of uncontaminated topsoil. The present study demonstrated that bacterial and fungal communities were affected differently by soil factors such as level of hydrocarbon contamination as well as soil depth and texture. This report shows that a well-planned landfarming treatment can drive the restoration of the soil in terms of both abatement of the contaminants and resilience of the microbial community structure.

Keywords: PCR–DGGE; Landfarming; Bioremediation; Hydrocarbons contaminated soil; Diesel leakage; Underground tank

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The purpose of this study was to assess the dissolution of Si, Fe, Cu and Zn from a smelter slag sample under acidic chemical and bacterial leaching conditions. The Cu-containing solid phases were Cu-sulfides (57% distribution), fayalite (18%) and metallic Cu (16%). Zn was mostly associated with fayalite, magnetite and Na-silicate phases (Σ94%). Two mixed cultures (HB1 and HB2) were enriched from samples taken from the slag lagoon site at the smelter location. Comparable results of metal dissolution were obtained with the two mixed cultures. The enrichment culture HB1 was characterized further by denaturing gradient gel electrophoresis (DGGE) of polymerase chain reaction amplified 16S rRNA genes. Based on the 16S rRNA gene sequences, culture HB1 contained at least *Acidithiobacillus ferrivorans* and *Alicyclobacillus*

cycloheptanicus, with sequences of three DGGE bands matching distantly with *Alicyclobacillus tolerans* and *Alicyclobacillus herbarium* in the database. *Alicyclobacillus* spp. have not been previously associated with slag lagoons or slag bioleaching. Approximately 80% Cu and 25% Zn were dissolved from the slag (10% pulp) in shake flasks when S^0 was provided for the bacteria to produce H_2SO_4. Bioleaching in stirred tanks was conducted at controlled pH values and was practiced at pH levels promoting metal dissolution and suppressing iron and silicate solubilization from fayalite and Na-silicate. Chemical leaching at pH 2.3–4.0 did not yield substantial dissolution of valuable metals.

Keywords: *Acidithiobacillus*; *Alicyclobacillus*; Bacterial leaching; Bioleaching; Chemical leaching; Smelter slag

Marco Andreolli, Silvia Lampis, Pierlorenzo Brignoli, Giovanni Vallini. (Department of Biotechnology, University of Verona, Eurovix SpA - Viale Enrico Mattei 17). *Trichoderma longibrachiatum* Evx1 is a fungal biocatalyst suitable for the remediation of soils contaminated with diesel fuel and polycyclic aromatic hydrocarbons. Environmental Science and Pollution Research, Volume 23(9) (2016): 9134-9143

Trichoderma sp. strain Evx1 was isolated from a semi-deciduous forest soil in Southern Italy. It decolorizes polynuclear organic dyes and tolerates high concentrations of phenanthrene, anthracene, fluoranthene, and pyrene. The ability of this ascomycete fungus to degrade polycyclic aromatic hydrocarbons was verified in vitro and confirmed by its strong phenoloxidase activity in the presence of gallic acid. Phylogenetic characterization of *Trichoderma* sp. Evx1 positioned this strain within the species *Trichoderma longibrachiatum*. The potential use of this species for the bioremediation of contaminated environmental matrices was tested by inoculating diesel-spiked soil with a dense mycelial suspension. The biodegradation percentage of the $C_{12\text{-}40}$ hydrocarbon fraction in the inoculated soil rose to 54.2 ± 1.6 %, much higher than that in non-inoculated soil or soil managed solely by a combination of watering and aeration. The survival and persistence of *T. longibrachiatum* Evx1 throughout the bioremediation trial was monitored by PCR-DGGE analysis. The fungal strain was still present in the soil 30 days after bioaugmentation. These findings indicate that *T. longibrachiatum* Evx1 may be a suitable inoculum in bioremediation protocols for the reclamation of soils contaminated by complex mixtures of hydrocarbons.

Keywords: Bioremediation; Diesel fuel; Hydrocarbon polluted soil; Polycyclic aromatic hydrocarbons; Polynuclear organic dye decolorization; *Trichoderma longibrachiatum* Evx1

A. C. Agnello, D. Huguenot, E. D. van Hullebusch, G. Esposito. (Université Paris-Est, Laboratoire Géomatériaux et Environnement (EA 4508), UPEMDipartimento di Ingegneria Civile e Meccanica, Università degli Studi di Cassino e del Lazio Meridionale, Université Paris-Est, Laboratoire Géomatériaux et Environnement (EA 4508), UPEM). Citric acid- and Tween® 80-assisted phytoremediation of a co-contaminated soil: alfalfa (*Medicago sativa* L.) performance and remediation potential. Environmental Science and Pollution Research, Volume 23(9) (2016): 9215-9226

A pot experiment was designed to assess the phytoremediation potential of alfalfa (*Medicago sativa* L.) in a co-contaminated (i.e., heavy metals and petroleum hydrocarbons) soil and the influence of citric acid and Tween® 80 (polyethylene glycol sorbitan monooleate), applied individually and combined together, for their possible use in chemically assisted

phytoremediation. The results showed that alfalfa plants could tolerate and grow in a co-contaminated soil. Over a 90-day experimental time, shoot and root biomass increased and negligible plant mortality occurred. Heavy metals were uptaken by alfalfa to a limited extent, mostly by plant roots, and their concentration in plant tissues were in the following order: Zn > Cu > Pb. Microbial population (alkane-degrading microorganisms) and activity (lipase enzyme) were enhanced in the presence of alfalfa with rhizosphere effects of 9.1 and 1.5, respectively, after 90 days. Soil amendments did not significantly enhance plant metal concentration or total uptake. In contrast, the combination of citric acid and Tween® 80 significantly improved alkane-degrading microorganisms (2.4-fold increase) and lipase activity (5.3-fold increase) in the rhizosphere of amended plants, after 30 days of experiment. This evidence supports a favorable response of alfalfa in terms of tolerance to a co-contaminated soil and improvement of rhizosphere microbial number and activity, additionally enhanced by the joint application of citric acid and Tween® 80, which could be promising for future phytoremediation applications.

Keywords: Soil remediation; Heavy metals; Hydrocarbons; Alfalfa (*Medicago sativa* L.); Citric acid; Tween® 80

Haiyan Pei, Yuanyuan Shao, Christopher Peter Chanway, Wenrong Hu, Panpan Meng, Zheng Li, Yang Chen, Guangxiang Ma. (School of Environmental Science and Engineering, Shandong University. Shandong Provincial Engineering Centre on Environmental Science and Technology). Bioaugmentation in a pilot-scale constructed wetland to treat domestic wastewater in summer and autumn. Environmental Science and Pollution Research, Volume 23(8) (2016): 7776-7785

In order to determine whether bioaugmentation is an effective technique in wetlands before the plants were harvested, the nitrogen (N) removal from a constructed wetland (CW) planted with *Phragmites* was evaluated after inoculating with *Paenibacillus* sp. XP1 in Northern China. The experiment was loaded with secondary effluent of rural domestic wastewater (RDW) using the batch-loaded method for over a 17-day period in summer and autumn. Chemical oxygen demand (CODcr), ammonia nitrogen (NH_3-N), and total nitrogen (TN) decreased significantly in the CW with *Phragmites* inoculated with *Paenibacillus* sp. XP1. Four days after treatments were set up, the removal efficiencies were found to be 76.2 % for CODcr, 83 % for NH_3-N, and 63.8 % for TN in summer and 69.5 % for CODcr, 76.9 % for NH_3-N, and 55.6 % for TN in autumn, which were higher than the control group without inoculation during the entire 17-day experiment. The inoculated bacteria did not have a noticeable effect on total phosphorus (TP) removal in autumn. However, bioaugmentation still keep a low P concentration in the whole CW. First-order kinetic model represented well the CODcr, TN, and TP decay in CWs with bioaugmentation, resulting in very good coefficients of determination, which ranged from 0.97 to 0.99. It indicated that bioaugmentation would be an effective treatment for pollutant removal from RDW in the CWs.

Keywords: Constructed wetlands; *Paenibacillus* sp. XP1; Nitrogen removal; Domestic wastewater; Hydraulic retention time; Bioaugmentation

Monica Ruffini Castiglione, Lucia Giorgetti, Simone Becarelli, Giovanna Siracusa, Roberto Lorenzi, Simona Di Gregorio. (Department of Biology, University of Pisa, National Research Council (CNR), Institute of Biology and Agricultural Biotechnology (IBBA), Research Unit of Pisa). Polycyclic aromatic hydrocarbon-contaminated soils: bioaugmentation of autochthonous bacteria and toxicological assessment of the bioremediation process by means of *Vicia faba* L. Environmental Science and Pollution Research, Volume 23(8) (2016): 7930-7941

Two bacterial strains, *Achromobacter* sp. (ACH01) and *Sphingomonas* sp. (SPH01), were isolated from a heavily polycyclic aromatic hydrocarbon (PAH)-contaminated soil (5431.3 ± 102.3 ppm) for their capacity to use a mixture of anthracene, pyrene, phenanthrene and fluorene as sole carbon sources for growth and for the capacity to produce biosurfactants. The two strains were exploited for bioaugmentation in a biopile pilot plant to increase the bioavailability and the degradation of the residual PAH contamination (99.5 ± 7.1 ppm) reached after 9 months of treatment. The denaturing gel gradient electrophoresis (DGGE) profile of the microbial ecology of the soil during the experimentation showed that the bioaugmentation approach was successful in terms of permanence of the two strains in the soil in treatment. The bioaugmentation of the two bacterial isolates positively correlated with the PAH depletion that reached 7.9 ± 2 ppm value in 2 months of treatment. The PAH depletion was assessed by the loss of the phyto-genotoxicity of soil elutriates on the model plant *Vicia faba* L., toxicological assessment adopted also to determine the minimum length of the decontamination process for obtaining both the depletion of the PAH contamination and the detoxification of the soil at the end of the process. The intermediate phases of the bioremediation process were the most significant in terms of toxicity, inducing genotoxic effects and selective DNA fragmentation in the stem cell niche of the root tip. The selective DNA fragmentation can be related to the selective induction of cell death of mutant stem cells that can compromise offsprings.

Keywords: *Achromobacter* sp.; Bioaugmentation; Biosurfactants; Genotoxicity; Phytotoxicity; Polycyclic aromatic hydrocarbons; *Sphingomonas* sp.; *Vicia faba* L.

Yu Shi, Zhanbin Huang, Xiujie Liu, Suheryani Imran, Licheng Peng, Rongji Dai, Yulin Deng. (School of Life Science, Beijing Institute of Technology, School of Chemical and Environmental Engineering, China University of Mining and Technology—Beijing). **Environmental materials for remediation of soils contaminated with lead and cadmium using maize (*Zea mays* L.) growth as a bioindicator. Environmental Science and Pollution Research, Volume 23(7) (2016): 6168-6178**

Heavy metal pollution is a severe environmental problem. Remediation of contaminated soils can be accomplished using environmental materials that are low cost and environmentally friendly. We evaluated the individual and combination effects of humic acid (HA), super absorbent polymer (SAP), zeolite (ZE), and fly ash composites (FC) on immobilization of lead (Pb) and cadmium (Cd) in contaminated soils. We also investigated long-term practical approaches for remediation of heavy metal pollution in soil. The biochemical and morphological properties of maize (*Zea mays* L.) were selected as biomarkers to assess the effects of environmental materials on heavy metal immobilization. The results showed that addition of test materials to soil effectively reduced heavy metal accumulation in maize foliage, improving chlorophyll levels, plant growth, and antioxidant enzyme activity. The test materials reduced heavy metal injury to maize throughout the growth period. A synergistic effect from combinations of different materials on immobilization of Pb and Cd was determined based on the reduction of morphological and biochemical injuries to maize. The combination of zeolite and humic acid was especially effective. Treatment with a combination of HA + SAP + ZE + FC was superior for remediation of soils contaminated with high levels of Pb and Cd.

Keywords: Environmental materials; Heavy metal; Lead; Cadmium; Injuries; Immobilization; Soil

Chen Chen, Wenrui Lei, Min Lu, Jianan Zhang, Zhou Zhang, Chunling Luo, Yahua Chen, Qing Hong, Zhenguo Shen. (College of Life Sciences, Nanjing Agricultural University, State Key Laboratory of Organic Geochemistry, Guangzhou Institute of Geochemistry, Chinese Academy of Sciences). Characterization of Cu(II) and Cd(II) resistance mechanisms in *Sphingobium* sp. PHE-SPH and *Ochrobactrum* sp. PHE-OCH and their potential application in the bioremediation of heavy metal-phenanthrene co-contaminated sites. Environmental Science and Pollution Research, Volume 23(7) (2016): 6861-6872

Soil that is co-contaminated with heavy metals (HMs) and polycyclic aromatic hydrocarbons (PAHs) is difficult to bioremediate due to the ability of toxic metals to inhibit PAH degradation by bacteria. We demonstrated the resistance mechanisms to Cu(II) and Cd(II) of two newly isolated strains of *Sphingobium* sp. PHE-SPH and *Ochrobactrum* sp. PHE-OCH and further tested their potential application in the bioremediation of HM-phenanthrene (PhA) co-contaminated sites. The PHE-SPH and PHE-OCH strains tolerated 4.63 and 4.34 mM Cu(II) and also showed tolerance to 0.48 and 1.52 mM Cd(II), respectively. Diverse resistance patterns were detected between the two strains. In PHE-OCH cells, the maximum accumulation of Cu(II) occurred in the cell wall, while the maximum accumulation was in the cytoplasm of PHE-SPH cells. This resulted in a sudden suppression of growth in PHE-OCH and a gradual inhibition in PHE-SPH as the concentration of Cu(II) increased. Organic acid production was markedly higher in PHE-OCH than in PHE-SPH, which may also have a role in the resistance mechanisms, and contributes to the higher Cd(II) tolerance of PHE-OCH. The factors involved in the absorption of Cu(II) or Cd(II) in PHE-SPH and PHE-OCH were identified as proteins and carbohydrates by Fourier transform infrared (FT-IR) spectroscopy. Furthermore, both strains showed the ability to efficiently degrade PhA and maintained this high degradation efficiency under HM stress. The high tolerance to HMs and the PhA degradation capacity make *Sphingobium* sp. PHE-SPH and *Ochrobactrum* sp. PHE-OCH excellent candidate organisms for the bioremediation of HM-PhA co-contaminated sites.

Keywords: Bioremediation; Co-contamination; Heavy metals; Ochrobactrum; Sphingobium; Phenanthrene

Lilian Marchand, Celestino-Quintela Sabaris, Dominic Desjardins, Nadège Oustrière, Eric Pesme, Damien Butin, Gaetan Wicart, Michel Mench. (INRA, UMR 1202 BIOGECOUniversity of Bordeaux, UMR 1202 BIOGECO, Bat B2, Allée Geoffroy St-HilaireMairie de BORDEAUX, Service Aménagements Paysagers, Direction des Parcs, des Jardins et des Rives, Departamento Biología Vegetal y Ecología, Facultad de Ciencia y Tecnologia, Universidad del País Vasco/EHU, Institut de Recherche en Biologie Végétale (IRBV), Université de Montréal–Jardin Botanique de Montréal, INRA, UMR 1202 BIOGECOUniversity of Bordeaux, UMR 1202 BIOGECO, Bat B2, Allée Geoffroy St-Hilaire). Plant responses to a phytomanaged urban technosol contaminated by trace elements and polycyclic aromatic hydrocarbons. Environmental Science and Pollution Research, Volume 23(4) (2016): 3120-3135

Medicago sativa was cultivated at a former harbor facility near Bordeaux (France) to phytomanage a soil contaminated by trace elements (TE) and polycyclic aromatic hydrocarbons (PAH). In parallel, a biotest with *Phaseolus vulgaris* was carried out on potted soils from 18 sub-sites to assess their phytotoxicity. Total soil TE and PAH concentrations, TE concentrations in the soil pore water, the foliar ionome of *M. sativa* (at the end of the first growth season) and of *Populus nigra* growing in situ, the root and shoot biomass and the foliar ionome of *P. vulgaris* were determined. Despite high total soil TE, soluble TE concentrations were generally low,

mainly due to alkaline soil pH (7.8–8.6). Shoot dry weight (DW) yield and foliar ionome of *P. vulgaris* did not reflect the soil contamination, but its root DW yield decreased at highest soil TE and/or PAH concentrations. Foliar ionomes of *M. sativa* and *P. nigra* growing in situ were generally similar to the ones at uncontaminated sites. *M. sativa* contributed to bioavailable TE stripping by shoot removal (in g ha^{-1} $harvest^{-1}$): As 0.9, Cd 0.3, Cr 0.4, Cu 16.1, Ni 2.6, Pb 4, and Zn 134. After 1 year, 72 plant species were identified in the plant community across three subsets: (I) plant community developed on bare soil sowed with *M. sativa*; (II) plant community developed in unharvested plots dominated by grasses; and (III) plant community developed on unsowed bare soil. The shoot DW yield (in mg ha^{-1} $harvest^{-1}$) varied from 1.1 (subset I) to 6.9 (subset II). For subset III, the specific richness was the lowest in plots with the highest phytotoxicity for *P. vulgaris.*

Keywords: Ecological restoration; Gentle remediation option; *Medicago sativa;* Plant community; Phytoremediation

Yeon-Jun Shin, Sang-Min Park, Jong-Chan Yoo, Chil-Sung Jeon, Seung-Woo Lee, Kitae Baek. (Department of Environmental Engineering, Chonbuk National University, Department of Environmental Engineering, Chonbuk National University, JIU EnE Co. Ltd.). A new approach for remediation of As-contaminated soil: ball mill-based technique. Environmental Science and Pollution Research, Volume 23(4) (2016): 3963-3970

In this study, a physical ball mill process instead of chemical extraction using toxic chemical agents was applied to remove arsenic (As) from contaminated soil. A statistical analysis was carried out to establish the optimal conditions for ball mill processing. As a result of the statistical analysis, approximately 70 % of As was removed from the soil at the following conditions: 5 min, 1.0 cm, 10 rpm, and 5 % of operating time, media size, rotational velocity, and soil loading conditions, respectively. A significant amount of As remained in the grinded fine soil after ball mill processing while more than 90 % of soil has the original properties to be reused or recycled. As a result, the ball mill process could remove the metals bound strongly to the surface of soil by the surface grinding, which could be applied as a pretreatment before application of chemical extraction to reduce the load.

Keywords: Arsenic; Ball mill; Wet grinding; Fractionation; Particle size; Remediation

Andrés Rodríguez-Seijo, Manoel Lago-Vila, María Luisa Andrade, Flora A. Vega. (Department of Plant Biology and Soil Science, Universidade de Vigo). Pb pollution in soils from a trap shooting range and the phytoremediation ability of *Agrostis capillaris* L. Environmental Science and Pollution Research, Volume 23(2) (2016): 1312-1323

Pb pollution caused by shooting sport activities is a serious environmental problem that has increased considerably in recent decades. The aims of this study were firstly to analyze Pb pollution in soils from a trap shooting range abandoned in 1999, secondly to study the effectiveness of different extractants [$CaCl_2$, DTPA, NH_4OAc, low molecular weight organic acids (LMWOA), and bidistilled water (BDW)] in order to determine Pb bioavailability in these soils, and finally to evaluate the phytoremediation ability of spontaneous vegetation (*Agrostis capillaris* L.). To this end, 13 soils from an old trap shooting range (Galicia, NW Spain) were studied. It was found that Pb levels in the soils were higher than 100 mg kg^{-1}, exceeding the generic reference levels, and three of these samples even exceeded the USEPA threshold level (400 mg kg^{-1}). In general, the reagent that best represents Pb bioavailability and has the greatest

extraction efficiency was $CaCl_2$, followed by DTPA, NH_4OAc, LMWOA, and BDW. *A. capillaris* Pb contents ranged between 9.82 and 1107.42 mg kg^{-1} (root) and between 6.43 and 135.23 mg kg^{-1} (shoot). Pb accumulation in roots, as well as the presence of secondary mineral phases of metallic Pb in the adjacent soil, showed the phytostabilization properties of *A. capillaris*.

Keywords: *Agrostis capillaris;* Lead; Pellets; Phytostabilization; Single extraction; Shooting range

Chirawee Sangthong, Kunchaya Setkit, Benjaphorn Prapagdee . (Faculty of Environment and Resource Studies, Mahidol University). Improvement of cadmium phytoremediation after soil inoculation with a cadmium-resistant *Micrococcus* sp. Environmental Science and Pollution Research, Volume 23(1) (2016): 756-764

Cadmium-resistant *Micrococcus* sp. TISTR2221, a plant growth-promoting bacterium, has stimulatory effects on the root lengths of *Zea mays* L. seedlings under toxic cadmium conditions compared to uninoculated seedlings. The performance of *Micrococcus* sp. TISTR2221 on promoting growth and cadmium accumulation in *Z. mays* L. was investigated in a pot experiment. The results indicated that *Micrococcus* sp. TISTR2221significantly promoted the root length, shoot length, and dry biomass of *Z. mays* L. transplanted in both uncontaminated and cadmium-contaminated soils. *Micrococcus* sp. TISTR2221 significantly increased cadmium accumulation in the roots and shoots of *Z. mays* L. compared to uninoculated plants. At the beginning of the planting period, cadmium accumulated mainly in the shoots. With a prolonged duration of cultivation, cadmium content increased in the roots. As expected, little cadmium was found in maize grains. Soil cadmium was significantly reduced with time, and the highest percentage of cadmium removal was found in the bacterial-inoculated *Z. mays* L. after transplantation for 6 weeks. We conclude that *Micrococcus* sp. TISTR2221 is a potent bioaugmenting agent, facilitating cadmium phytoextraction in *Z. mays* L.

Keywords: Cadmium; Phytoextraction; Indole-3-acetic acid; *Micrococcus* sp.; *Zea mays* L.

Zhiguo He, Yuting Hu, Zhen Yin, Yuehua Hu, Hui Zhong. (School of Minerals Processing and Bioengineering, Central South UniversityKey Laboratory of Biohydrometallurgy of Ministry of Education, Central South University). Microbial Diversity of Chromium-Contaminated Soils and Characterization of Six Chromium-Removing Bacteria. Environmental Management, Volume 57(6) (2016): 1319-1328

Three soil samples obtained from different sites adjacent to a chromium slag heap in a steel alloy factory were taken to examine the effect of chromium contamination on soil bacterial diversity as determined by construction of 16S rDNA clone libraries and sequencing of selected clones based on restriction fragment length polymorphism (RFLP) analysis. Results revealed that *Betaproteobacteria*, *Gammaproteobacteria*, *Firmicutes*, and *Alphaproteobacteria* occurred in all three soil samples, although the three samples differed in their total diversity. Sample 1 had the highest microbial diversity covering 12 different classes, while Sample 3 had the lowest microbial diversity. Strains of six different species were successfully isolated, one of which was identified as *Zobellella denitrificans*. To our knowledge, this is the first report of a strain belonging to the genus *Zobellella* able to resist and reduce chromium. Among all isolates studied, *Bacillus odysseyi* YH2 exhibited the highest Cr(VI)-reducing capability, with a total removal of 23.5 % of an initial Cr(VI) concentration of 350 mg L^{-1}.

Keywords: Bacterial diversity; 16S rRNA gene; Chromate-reducing bacteria; Chromate reduction

Shekoofeh Sadat Etemadzadeh, Giti Emtiazi, Zahra Etemadifar. (Department of Biology, Faculty of Science, University of Isfahan, email: emtiazi@sci.ui.ac.ir). Heterotrophic Bioleaching of Sulfur, Iron, and Silicon Impurities from Coal by *Fusarium oxysporum* FE and *Exophiala spinifera* FM with Growing and Resting Cells. Current Microbiology, Volume 72(6) (2016): 707-715

Coal is the most abundant fossil fuel containing sulfur and other elements which promote environmental pollution after burning. Also the silicon impurities make the transportation of coal expensive. In this research, two isolated fungi from oil contaminated soil with accessory number KF554100 (*Fusarium oxysporum* FE) and KC925672 (*Exophiala spinifera* FM) were used for heterotrophic biological leaching of coal. The leaching were detected by FTIR, CHNS, XRF analyzer and compared with iron and sulfate released in the supernatant. The results showed that *E. spinifera* FM produced more acidic metabolites in growing cells, promoting the iron and sulfate ions removal while resting cells of *F. oxysporum* FE enhanced the removal of aromatic sulfur. XRF analysis showed that the resting cells of *E. spinifera* FM proceeded maximum leaching for iron and silicon (48.8, 43.2 %, respectively). CHNS analysis demonstrated that 34.21 % of sulfur leaching was due to the activities of resting cells of *F. oxysporum* FE. Also *F. oxysporum* FE removed organic sulfur more than *E. spinifera* FM in both growing and resting cells. FTIR data showed that both fungi had the ability to remove pyrite and quartz from coal. These data indicated that inoculations of these fungi to the coal are cheap and impurity removals were faster than autotrophic bacteria. Also due to the removal of dibenzothiophene, pyrite, and quartz, we speculated that they are excellent candidates for bioleaching of coal, oil, and gas.

Anila Fariq, Ayesha Saeed. (Fatima Jinnah Women University. Email neelaahmad@gmail.com). Production and Biomedical Applications of Probiotic Biosurfactants. Current Microbiology, Volume 72(4) (2016): 489-495

Biosurfactants have been widely used for environmental and industrial applications. However, their use in medical field is still limited. Probiotic biosurfactants possess an immense antimicrobial, anti-adhesive, antitumor, and antibiofilm potential. Moreover, they have an additional advantage over conventional microbial surfactants because probiotics are an integral part of normal human microflora and their biosurfactants are innocuous to human. So, they can be effectively exploited for medicinal use. Present review is aimed to discourse the production and biomedical applications of probiotic biosurfactants.

Smiley Sharma, Piyush Malaviya. (Department of Environmental Sciences, University of Jammu, Jammu (J&K), India).Bioremediation of tannery wastewater by chromium resistant novel fungal consortium. Ecological Engineering, Volume 91(2016): 419–425

A consortium of four Cr-resistant ascomycetous fungi (*Cladosporeum perangustum* and *Penicillium commune* – isolated from tannery wastewater contaminated soil; *Paecilomyces lilacinus* and *Fusarium equiseti* – isolated from tannery sludge) was employed for tannery wastewater bioremediation. For construction of immobilized fungal consortium, various natural as well as synthetic support materials were screened. Nylon mesh was selected as the best support as it exhibited maximum immobilization of the fungal strains. The tannery wastewater treatment by nylon mesh immobilized fungal consortium in a stirred tank bioreactor showed good reduction in various pollution parameters [COD (82.52%), color (86.19%), Cr(VI) (100%), Total Cr (99.92%), Total Pb (95.91%)] after 120 h of treatment. A major part of reduction in these parameters occurred within first 24 h of the treatment. Moreover, toxicity assessment of

the tannery wastewater on *Triticum aestivum* revealed 49.33% germination in treated wastewater compared to complete inhibition of seed germination in untreated wastewater.

Keywords: Bioremediation; Fungi; Toxicity; Wastewater

Luiza Moraes, Gabriel Martins da Rosa, Bruna Barcelos Cardias, Lucielen Oliveira dos Santos, Jorge Alberto Vieira Costa. (Laboratory of Biochemical Engineering, College of Chemistry and Food Engineering, Federal University of Rio Grande, Rio Grande, RS, Brazil). Microalgal biotechnology for greenhouse gas control: Carbon dioxide fixation by *Spirulina* sp. at different diffusers. Ecological Engineering, Volume 91(2016): 426–431

The carbon dioxide (CO_2) emissions from fossil fuels contributes to global warming. This phenomenon became a major political issue in the fields of science, environment, and economy in current years. Microalgae can convert CO_2 into biomass and oxygen through the photosynthesis. The aim of this study was to evaluate the influence of diffusers configuration and CO_2 flow rate in mass transfer, CO_2 fixation efficiency by *Spirulina* and in the biomass composition produced. Two flow rates (0.05 and 0.3 vvm) and four diffusers (sintered stone (SS), porous curtain (PC), perforated ring (PR) and porous wood (PW)) were used in this study. The maximum CO_2 mass transfer coefficient (123.2 h^{-1}) in the CO_2–H_2O system corresponded to the higher flow rate (0.3 vvm) using the diffuser porous curtain (PC). The maximum biomass productivity (125.9 ± 5.3 mg L^{-1} d^{-1}) was observed for PC with a flow rate of 0.05 vvm. Increasing the flow rate (0.3 vvm) with PC resulted in a 26% increase in the carbohydrate content in biomass. The results showed a smaller flow rate with porous diffusers might promote an increase in CO_2 fixation efficiency by microalgae.

Keywords: Biomass; Flow rate; Global warming; Mass transfer; Microalgae

Chang-Ho Kang[a], Yoon-Jung Kwon[b], Jae-Seong So[a]. ([a] Department of Biological Engineering, Inha University, Incheon 22212, South Korea, [b] Department of Organic and Nano System Engineering, Konkuk University, Seoul 05029, Korea). Bioremediation of heavy metals by using bacterial mixtures. Ecological Engineering, Volume 89, April 2016, Pages 64–69

Environmental pollution by heavy and toxic metals because of mining, metallurgic processes, and other chemical industries is a worldwide problem affecting both human health and the environment. The aim of this study was to investigate the synergistic effect of bacterial mixtures on the bioremediation of a mixture of Pb, Cd, and Cu from contaminated soils. Compared to the single culture method, the bacterial mixtures showed higher growth rate, urease activity, and resistance to heavy metals. Four bacterial strains were isolated and identified from bacterial mixtures—*Viridibacillus arenosi* B-21, *Sporosarcina soli* B-22, *Enterobacter cloacae* KJ-46, and *E. cloacae* KJ-47, which obtained from an abandoned mine site in Korea and showed effective microbially induced calcite precipitation (MICP). The following parameters were monitored during the course of the experiment: optical density, pH, urease activity, calcite production, tolreance to heavy metals, and impermeability test. Synergistic effects on the remediation of various heavy metals via modification of the bacterial mixtures were observed and, after 48 h, remediation of 98.3% for Pb, 85.4% for Cd, and 5.6% for Cu were recorded. Compared with single strain cultures, the bacterial mixtures demonstrated greater resistance and efficiency for the remediation of heavy metals. Thus, our results show that the use of bacterial mixtures is useful in the bioremediation of heavy metals from the contaminated environment.

Keywords: MICP; Bioremediation; Bacterial mixtures; Urease; Heavy metal

M.S. Podder, C.B. Majumder. (Department of Chemical Engineering, Indian Institute of Technology, Roorkee, Roorkee 247667, India). Study of the kinetics of arsenic removal from wastewater using *Bacillus arsenicus* biofilms supported on a Neem leaves/$MnFe_2O_4$ composite. Ecological Engineering, Volume 88(2016): 195–216

The pollution caused by arsenic is major environmental problem, vital to be resolved. New technologies, easy for implementing and adapting to any system, require extraordinary consideration and are motivation of this research. The performance of a biofilm of *Bacillus arsenicus* MTCC 4380 supported on Neem leaves/$MnFe_2O_4$ composite on scavenging of As(III) and As(V) was evaluated. Optimum conditions of biosorption/bioaccumulation were determined as a function of contact time and temperature. The equilibrium was achieved after about 240 min at a temperature of 30 °C and biosorbent dose of 0.9 g/L. Non-linear regression analysis was done for determining the best-fit kinetic model based on three correlation coefficients and three error functions and also for predicting the parameters involved in kinetic models. The results showed that both Brouers–Weron–Sotolongo and Avrami models for both As(III) and As(V) were proficient to provide realistic description of biosorption/bioaccumulation kinetic. Applicability of mechanistic models in the current investigation exhibited that the rate governing step in the biosorption/bioaccumulation of both As(III) and As(V) was film diffusion rather than intraparticle diffusion. The evaluated thermodynamic parameters ΔG^0, ΔH^0 and ΔS^0 exposed that biosorption/bioaccumulation of both As(III) and As(V) was feasible, spontaneous and exothermic under investigated conditions. The activation energy (*Ea*) calculated from Arrhenius equation indicated the nature of biosorption/bioaccumulation being ion exchange type. Increasing concentration of As(III) and As(V) moreover improved the initial sorption rate *h*, from 3.86 to 694.03 mg/g min and 4.72–520.39 mg/g min, respectively. The outcomes attained are very favourable and inspire the usage of this biofilm in environmental applications.[1]

Keywords: Arsenic; Wastewater; Biosorption and bioaccumulation; Mechanistic; Thermodynamic

Elena Cervelli[a], Stefania Pindozzi[a], Alessandra Capolupo[a], Collins Okello[b], Marina Rigillo[c], Lorenzo Boccia[a]. ([a] Department of Agricultural Sciences, University of Naples Federico II, Portici (Na), Italy, [b] Department of Biosystems Engineering, Gulu University, P.O. Box 166, Gulu, Uganda, [c] Department of Architecture, University of Naples Federico II, Naples, Italy). Ecosystem services and bioremediation of polluted areas. Ecological Engineering, Volume 87(2016): 139–149

Contaminated areas represent a crucial concern in contemporary planning all over the world. The absence of shared value for such areas leads to abandonment and soil sealing specially if such areas have lost their agricultural potential. The European Project LIFE/ENV/IT/275 Ecoremed has implemented a protocol for the bioremediation of contaminated soils in Campania region. The cultivation of no food crops (Poplar and Giant reed) is proposed as buffer crops waiting for the characterization of the areas. This facilitates the uptake of the mineral contaminants and the biodegradation of organic compounds reducing the risk for leaching and the run off of harmful contaminants that would occur on bare soils.

The study discusses a new approach to land use change (LUC) assessment based on environmental and socio-economic factors, evaluated through GIS tool and decision support software (ArcGIS/ILWIS). Literature data have been used to assess the current value of the ecosystem services (ES) provided by such crops (€/ha/year) and the benefits that people obtained

from ecosystems. Three scenarios have sorted out and compared through multicriteria analysis. Moving from the deep knowledge of the environmental condition of the territory the study shows the alternative ES values of the land use change starting from no-change scenario to energy crops (Poplar and Giant reed), to abandonment. Results show that is possible to asses an increase of the ES value, both in case of a private and public action, also referring to the opportunities for farmers income in the short and medium-long period.

Keywords: LUC scenarios; Multicriteria-Spatial Decision Support Systems; Ecosystem services; Bioremediation

Shiladitya Ghosh, Ranjana Chowdhury, Pinaki Bhattacharya. (Chemical Engineering Department, Jadavpur University). Mixed consortia in bioprocesses: role of microbial interactions. Applied Microbiology and Biotechnology, Volume 100(10) (2016): 4283-4295

The utilization of mixed consortia or mixed culture has become a current research trend of applied microbiology, bioprocess engineering and biotechnology. The constituent microorganisms of such mixed cultures can jointly perform complex processes efficiently, yielding the desired product at an augmented rate, in comparison to monocultures. It is understandable that the interactions between the microbial partners in these mixed cultures are expected to have a significant impact on the combined performance of the microorganisms and the bioprocess as a whole. Prevalence of positive interactions (commensalism or mutualism) among microbial members of a mixed culture or consortia can significantly enhance the product outcome of the bioprocess, ensuring their industrial application and long-term stability. On the contrary, negative interaction (parasitism, predation or ammensalism) leads to elimination of microbial members from the consortia causing the destruction of community structure as well as disruption of cumulative performance. Therefore, a priori knowledge on the type of interaction between the microorganisms is also essential for the optimization of the performance of the designed consortia. This could only be achieved through the study of inter-microbial interaction prevailing in a mixed culture. In the present article, different bioprocess applications of mixed cultures, currently in practice along with types of positive microbial interactions involved, have been reviewed. Complexity of mixed cultures from the perspective of multiple types of intra-culture relationships has been explained in detail. Overall, the necessity for more in-depth research studies on “microbial interaction” in mixed culture bioprocesses has been stressed in the article.

Keywords: Microbial consortia; Bioprocessing; Microbial interaction; Commensalism; Mutualism; Strategic design

Chunshuang Liu, Kang Han, Duu-Jong Lee, Qilin Wang. (College of Chemical Engineering, China University of Petroleum, Department of Chemical Engineering, National Taiwan UniversityDepartment of Chemical Engineering, National Taiwan University of Science and Technology. Email: djlee@ntu.edu.tw , Advanced Water Management Centre (AWMC), The University of Queensland). Simultaneous biological removal of phenol, sulfide, and nitrate using expanded granular sludge bed reactor. Applied Microbiology and Biotechnology, Volume 100(9) (2016): 4211-4217

Biological removal of sulfide, nitrate, and phenol at loading rates of 600 g S/(m^3 day), 900 g N/(m^3 day), and 450 g C/(m^3 day), respectively, from synthetic wastewaters was achieved in an expanded granular sludge bed (EGSB) reactor, whose rates are much higher than literature works and are considered feasible for handling high-strength petrochemical wastewaters without dilution. Effects of C/S ratio (2–2.5:1) on EGSB performance were noted insignificantly. The strains *Bacillus* sp., *Thauera* sp., and *Pseudomonas* sp. were the heterotrophic denitrifiers and

the strains *Thiobacillus* sp., *Azoarcus* sp., and *Sulfurovum* sp. were the autotrophic denitrifiers in the EGSB granules. The EGSB reactor experienced biological breakdown at loadings higher than 1200 g S/(m^3 day), 1800 g N/(m^3 day), and 900 g C/(m^3 day) by the following mechanism: high sulfide first inhibits heterotrophic denitrifies (*Bacillus* sp. and *Pseudomonas* sp.), thereby accumulating nitrite in the system; then, the accumulated nitrite inhibits autotrophic denitrifiers (*Thiobacillus* sp., *Azoarcus* sp., and *Sulfurovum* sp.) to complete breakdown of the system.

Keywords: Sulfide; EGSB; Microbial community; Breakdown

Rong Zhang, Xingjian Xu, Wenli Chen, Qiaoyun Huang. (State Key Laboratory of Agricultural Microbiology, Huazhong Agricultural University, Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Laboratory of Arable Land Conservation (Middle and Lower Reaches of Yangtze River), Ministry of Agriculture, College of Resources and Environment, Huazhong Agricultural University. Email: qyhuang@mail.hzau.edu.cn). **Genetically engineered *Pseudomonas putida* X3 strain and its potential ability to bioremediate soil microcosms contaminated with methyl parathion and cadmium. Applied Microbiology and Biotechnology, Volume 100(4) (2016): 1987-1997**

A multifunctional *Pseudomonas putida* X3 strain was successfully engineered by introducing methyl parathion (MP)-degrading gene and enhanced green fluorescent protein (EGFP) gene in *P. putida* X4 (CCTCC: 209319). In liquid cultures, the engineered X3 strain utilized MP as sole carbon source for growth and degraded 100 mg L^{-1} of MP within 24 h; however, this strain did not further metabolize *p*-nitrophenol (PNP), an intermediate metabolite of MP. No discrepancy in minimum inhibitory concentrations (MICs) to cadmium (Cd), copper (Cu), zinc (Zn), and cobalt (Co) was observed between the engineered X3 strain and its host strain. The inoculated X3 strain accelerated MP degradation in different polluted soil microcosms with 100 mg MP kg^{-1} dry soil and/or 5 mg Cd kg^{-1} dry soil; MP was completely eliminated within 40 h. However, the presence of Cd in the early stage of remediation slightly delayed MP degradation. The application of X3 strain in Cd-contaminated soil strongly affected the distribution of Cd fractions and immobilized Cd by reducing bioavailable Cd concentrations with lower soluble/exchangeable Cd and organic-bound Cd. The inoculated X3 strain also colonized and proliferated in various contaminated microcosms. Our results suggested that the engineered X3 strain is a potential bioremediation agent showing competitive advantage in complex contaminated environments.

Keywords: Genetically engineered strain; Bioremediation; Methyl parathion; Cadmium

Rossana Liguori, Valeria Ventorino, Olimpia Pepe, Vincenza Faraco. (Department of Agriculture University of Naples Federico II, Department of Chemical Sciences University of Naples Federico II. Email: vfaraco@unina.it). **Bioreactors for lignocellulose conversion into fermentable sugars for production of high added value products. Applied Microbiology and Biotechnology, Volume 100(2) (2016): 597–611**

Lignocellulosic biomasses derived from dedicated crops and agro-industrial residual materials are promising renewable resources for the production of fuels and other added value bioproducts. Due to the tolerance to a wide range of environments, the dedicated crops can be cultivated on marginal lands, avoiding conflict with food production and having beneficial effects on the environment. Besides, the agro-industrial residual materials represent an abundant, available, and cheap source of bioproducts that completely cut out the economical and

environmental issues related to the cultivation of energy crops. Different processing steps like pretreatment, hydrolysis and microbial fermentation are needed to convert biomass into added value bioproducts. The reactor configuration, the operative conditions, and the operation mode of the conversion processes are crucial parameters for a high yield and productivity of the biomass bioconversion process. This review summarizes the last progresses in the bioreactor field, with main attention on the new configurations and the agitation systems, for conversion of dedicated energy crops (*Arundo donax*) and residual materials (corn stover, wheat straw, mesquite wood, agave bagasse, fruit and citrus peel wastes, sunflower seed hull, switchgrass, poplar sawdust, cogon grass, sugarcane bagasse, sunflower seed hull, and poplar wood) into sugars and ethanol. The main novelty of this review is its focus on reactor components and properties.

Keywords: Single and double helical ribbon impeller; Rushton impeller; S-shaped impeller; Anchor impeller; Pitched-blade impeller; Peg-mixer; Paddle blade magnetic impeller

Anindya Chanda, Phani M. Gummadidala, Ola M. Gomaa. (Department of Environmental Health Sciences, Arnold School of Public Health, University of South Carolina. Email: achanda@mailbox.sc.edu, Microbiology Department, National Center for Radiation Research and Technology). **Mycoremediation with mycotoxin producers: a critical perspective. Applied Microbiology and Biotechnology, Volume 100(1) (2016): 17-29**

Filamentous fungi that produce mycotoxins also demonstrate the ability to degrade a wide variety of naturally occurring and anthropogenically generated hazardous wastes. Hence, these are emerging as excellent candidates for bioremediation. Their mycelia exhibit the robustness of adapting to highly restrictive environmental conditions often experienced in the presence of persistent pollutants, which makes them more useful compared to other microbes. However, it now appears that several regulatory factors that govern mycotoxin synthesis in these toxigenic strains also regulate their bioremediation abilities. To this end, mycoremediation and mycotoxin synthesis have been thoroughly but independently investigated; hence, much less is understood about the overlaps between the two processes. This review aims to shed light on this critical knowledge gap and provide some useful insights into the future research that might overcome the challenges associated with these shared regulatory modules. This will enable the harnessing of the full potential of mycoremediation by minimizing mycotoxin contamination.

Keywords: Bioremediation; Mycoremediation; Filamentous fungi; Mycotoxin; Aflatoxin; Biosorption; Laccase; Oxidoreductases; Cytochrome P450 systems; Oxidative stressc; AMP signaling

Biotransformation

Fadime Kara Murdoch[a, b], F. Dilek Sanin[c.] ([a] Department of Biotechnology, Middle East Technical University, 06800 Ankara, Turkey, [b] Department of Biology, Selcuk University, 42030, Konya, Turkey, [c] Department of Environmental Engineering, Middle East Technical University, 06800 Ankara, Turkey). **Biotransformation of Nonylphenol Diethoxylate in anaerobic digesters: Accumulation of metabolites and their effects on digester performance. International Biodeterioration & Biodegradation, Volume 110(2016): 61–68**

Nonylphenol(poly)ethoxylates (NPnEOs) have caused great concern over the last few decades due to their lipophilic, hydrophobic, and toxic properties. NPnEOs can be degraded to a certain

extent in wastewater treatment plants; however since they accumulate in sludge, understanding their influence on digester performance and their fate become important, especially in regards to land application of biosolids. In this respect, the biotransformation of nonylphenol diethoxylate (NP2EO), an accumulative metabolite of NPnEOs, into degradation products was monitored in NP2EO-amended lab-scale semi-continuous anaerobic digesters. Determination and quantification of the degradation products, nonylphenol monoethoxylate (NP1EO), nonylphenol (NP) and nonylphenoxy acetic acid (NP1EC), was performed by gas chromatography-mass spectrometry (GC/MS). Results revealed that 90% of NP2EO was eliminated from the system within approximately 52 days following the spike. As biodegradation of NP2EO progressed, both NP1EO and NP accumulated in the sludge samples. NP1EC was not detected in any of the digesters. Methane production, solids reduction and COD removal were not affected by the spike of NP2EO or by the presence of biodegradation products (NP1EO and NP) in the digester system. The persistence and accumulation of NP and NP1EO verifies concerns about the potential danger for land application of biosolids.

Keywords: Anaerobic digestion; Biodegradation; Nonylphenol diethoxylate; Nonylphenol monoethoxylate; Nonylphenol; Sludge

Melissa Rodríguez-Delgado[a], Carolina Orona-Navar[a], Raúl García-Morales[a], Carlos Hernandez-Luna[b], Roberto Parra[a], Jürgen Mahlknecht[a], Nancy Ornelas-Soto[a]. ([a] Centro del Agua para América Latina y el Caribe, Tecnológico de Monterrey, Campus Monterrey, NL 64849, Mexico, [b] Laboratorio de Enzimología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León, Av. Universidad s/n, Ciudad Universitaria, San Nicolás de los Garza, NL, 64450, Mexico). **Biotransformation kinetics of pharmaceutical and industrial micropollutants in groundwaters by a laccase cocktail from *Pycnoporus sanguineus* CS43 fungi. International Biodeterioration & Biodegradation, Volume 108(2016): 34–41**

In this work, the biocatalytic ability of laccases from filtered culture supernatant of *Pycnoporus sanguineus* was evaluated without mediators and under mild reaction conditions. This 100 U L^{-1} laccase cocktail removed 50% Diclofenac, 97% β-Naphthol and 71% 2,4 Dichlorophenol within 8 h of reaction and 78% for 5,7-Diiodo-8-hydroxyquinoline within 3.5 h; at initial concentrations of 10 mg L^{-1} and at 25 °C. Furthermore, this enzyme cocktail also removed in excess of 53% all tested compounds in a real groundwater sample from northwestern Mexico. In comparison with purified laccases, the use of cocktail offers operational advantages since additional purification steps can be avoided.

Keywords: Laccase; *Pycnoporus sanguineus*; Micropollutants; Biotransformation; Groundwater

Sándor Gonda[a], Attila Kiss-Szikszai[b], Zsolt Szűcs[a], Borbála Balla[a], Gábor Vasas[a]. ([a]University of Debrecen, Department of Botany, Division of Pharmacognosy, Egyetem tér 1, H-4010 Debrecen, Hungary, [b] University of Debrecen, Department of Organic Chemistry, Egyetem tér 1, H-4010 Debrecen, Hungary). **Efficient biotransformation of non-steroid anti-inflammatory drugs by endophytic and epiphytic fungi from dried leaves of a medicinal plant, *Plantago lanceolata* L. International Biodeterioration & Biodegradation, Volume 108(2016): 115–121**

In the current study, decomposition of diclofenac, diflunisal, ibuprofen, mefenamic acid and piroxicam was tested using nine identified strains of endophytic and epiphytic fungi (from

Ascomycota) adapted to natural products resembling the pharmaceuticals. The strains were isolated from a medicinal plant, *Plantago lanceolata* leaves. Metabolites were tentatively identified by liquid chromatography – tandem mass spectrometry (LC-MS^3).

Eighteen of the 45 combinations resulted in significant decrease of the concentration of the NSAIDs in model solutions. The most active strains were *Aspergillus nidulans* and *Bipolaris tetramera*, while *Epicoccum nigrum* and *Aspergillus niger* showed somewhat less potency. Piroxicam and diclofenac were most resistant to biotransformation, while ibuprofen and mefenamic acid were efficiently metabolized by most strains. Ten metabolites could be tentatively identified, including hydroxy-metabolites of all tested NSAIDs, and a dihydroxy-metabolite of piroxicam. This biotransformation is likely to modify the toxicity and bioaccumulation potential of these pharmaceuticals.

The results highlight the applicability of polyphenol-rich dried medicinal plant materials as an excellent source of fungi with high biotransforming potential. The results also suggest more in-depth testing of these fungi for biodegradation processes.

Keywords: Biodegradation; Biotransformation; Non-steroid anti-inflammatory drugs; Epiphytic fungi; Phylloplane fungi; Endophytes

Anja Dallinger[1], Ilka Duldhardt[1], Jan Kabisch[1], Rabea Schlüter, Frieder Schauer. (Institute of Microbiology, Ernst Moritz Arndt University of Greifswald, Friedrich-Ludwig-Jahn-Str. 15, D-17487 Greifswald, Germany). **Biotransformation of cyclohexane and related alicyclic hydrocarbons by *Candida maltosa* and *Trichosporon* species. International Biodeterioration & Biodegradation, Volume 107(2016): 132–139**

The hydrocarbons of crude oil and oil products such as gasoline or diesel oil comprise an aliphatic, an aromatic, and an alicyclic fraction. The alicyclic fraction represents a group of substances which, along with polycyclic hydrocarbons and tar-like components, are among the most biodegradation resistant components of oil. The major part of the alicyclic oil fraction is made up of cyclohexane and its derivatives. Little is currently known about the microbial, especially fungal, degradation of alicyclic hydrocarbons. In this study, the ability of yeasts of the genera *Candida* and *Trichosporon* to use cyclohexane and some related alicyclic hydrocarbons as substrates was investigated. The anamorphic ascomycetous yeast *Candida maltosa* and different strains of the anamorphic basidiomycetous yeast genus *Trichosporon* are not able to utilize cyclohexane as carbon source when present at 0.005%–1.0% and at concentrations of over about 0.5% cyclohexane is toxic for them. However at concentrations of 0.25%–0.4% the yeasts can oxidize cyclohexane and transform it via cyclohexanol to cyclohexanone. Cyclohexanone seems to be a dead-end-product for these yeasts because no further conversion of cyclohexanone to ε-caprolactone could be demonstrated. Analysis of the cycloalkane oxidation after cell cultivation with different carbon sources revealed that non-specific enzymes were involved and no additional enzyme induction seems to occur in the presence of cycloalkanes.

Keywords: Hydrocarbons; Biodegradation; Transformation; Fungi; *Candida*; *Trichosporon*

Hua Yang, Zhaojun Li, Jian Long, Yongchao Liang, Jianming Xue, Murray Davis, Wenxiang He. (Institute of Agricultural Resources and Regional Planning, Key Laboratory of Plant Nutrition and Fertilizer, Ministry of Agriculture, Chinese Academy of Agricultural Sciences. Guizhou Key Laboratory of Mountain Environment, Guizhou Normal University, College of Natural Resources and Environment, Northwest A&F University). **Prediction models for transfer of arsenic from soil to corn grain (*Zea mays* L.). Environmental Science and Pollution Research, Volume 23(7) (2016): 6277-6285**

In this study, the transfer of arsenic (As) from soil to corn grain was investigated in 18 soils collected from throughout China. The soils were treated with three concentrations of As and the transfer characteristics were investigated in the corn grain cultivar Zhengdan 958 in a greenhouse experiment. Through stepwise multiple-linear regression analysis, prediction models were developed combining the As bioconcentration factor (BCF) of Zhengdan 958 and soil pH, organic matter (OM) content, and cation exchange capacity (CEC). The possibility of applying the Zhengdan 958 model to other cultivars was tested through a cross-cultivar extrapolation approach. The results showed that the As concentration in corn grain was positively correlated with soil pH. When the prediction model was applied to non-model cultivars, the ratio ranges between the predicted and measured BCF values were within a twofold interval between predicted and measured values. The ratios were close to a 1:1 relationship between predicted and measured values. It was also found that the prediction model (Log [BCF]=0.064 pH-2.297) could effectively reduce the measured BCF variability for all non-model corn cultivars. The novel model is firstly developed for As concentration in crop grain from soil, which will be very useful for understanding the As risk in soil environment.

Keywords: Arsenic; Soils; Corn grain; BCF; Prediction model; Cross-species extrapolation

Chen Liu, Jinxia Liu. (Department of Civil Engineering, McGill University, Montreal, Quebec, H3A 0C3, Canada). Aerobic biotransformation of polyfluoroalkyl phosphate esters (PAPs) in soil ☆. Environmental Pollution, Volume 212(2016): 230–237

Microbial transformation of polyfluoroalkyl phosphate esters (PAPs) into perfluorocarboxylic acids (PFCAs) has recently been confirmed to occur in activated sludge and soil. However, there lacks quantitative information about the half-lives of the PAPs and their significance as the precursors to PFCAs. In the present study, the biotransformation of 6:2 and 8:2 diPAP in aerobic soil was investigated in semi-dynamics reactors using improved sample preparation methods. To develop an efficient extraction method for PAPs, six different extraction solvents were compared, and the phenomenon of solvent-enhanced hydrolysis was investigated. It was found that adding acetic acid could enhance the recoveries of the diPAPs and inhibit undesirable hydrolysis during solvent extraction of soil. However 6:2 and 8:2 monoPAPs, which are the first breakdown products from diPAPs, were found to be unstable in the six solvents tested and quickly hydrolyzed to form fluorotelomer alcohols. Therefore reliable measurement of the monoPAPs from a live soil was not achievable. The apparent DT_{50} values of 6:2 diPAP and 8:2 diPAP biotransformation were estimated to be 12 and > 1000 days, respectively, using a double first-order in parallel model. At the end of incubation of day 112, the major degradation products of 6:2 diPAP were 5:3 fluorotelomer carboxylic acid (5:3 acid, 9.3% by mole), perfluoropentanoic acid (PFPeA, 6.4%) and perfluorohexanoic acid (PFHxA, 6.0%). The primary product of 8:2 diPAP was perfluorooctanoic acid (PFOA, 2.1%). The approximately linear relationship between the half-lives of eleven polyfluoroalkyl and perfluoroalkyl substances (PFASs, including 6:2 and 8:2 diPAPs) that biotransform in aerobic soils and their molecular weights suggested that the molecular weight is a good indicator of the general stability of low-molecular-weight PFAS-based compounds in aerobic soils.

Keywords: Polyfluoroalkyl and perfluoalkyl substances (PFAS); Polyfluoroalkyl phosphate esters (PAPs); Perfluorooctanoic acid (PFOA); Biotransformation; Soil; Hydrolysis

Pallavi T. Mohite, Ameeta Ravi Kumar, , Smita S. Zinjarde. (Institute of Bioinformatics and Biotechnology, Savitribai Phule Pune University). Biotransformation of hexavalent

chromium into extracellular chromium(III) oxide nanoparticles using*Schwanniomyces occidentalis.* Biotechnology Letters, Volume 38(3) (2016): 441-446

To demonstrate biotransformation of toxic Cr(VI) ions into Cr_2O_3 nanoparticles by the yeast *Schwanniomyces occidentalis.*

Reaction mixtures containing *S. occidentalis* NCIM 3459 and Cr(VI) ions that were initially yellow turned green after 48 h incubation. The coloration was due to the synthesis of chromium (III) oxide nanoparticles (Cr_2O_3NPs). UV–Visible spectra of the reaction mixtures showed peaks at 445 and 600 nm indicating $^4A_{2g} \rightarrow {}^4T_{1g}$ and $^4A_{2g} \rightarrow {}^4T_{2g}$ transitions in Cr_2O_3, respectively. FTIR profiles suggested the involvement of carboxyl and amide groups in nanoparticle synthesis and stabilization. The Cr_2O_3NPs ranged between 10 and 60 nm. Their crystalline nature was evident from the selective area electron diffraction and X-ray diffraction patterns. Energy dispersive spectra confirmed the chemical composition of the nanoparticles. These biogenic nanoparticles could find applications in different fields.

S. occidentalis mediated biotransformation of toxic Cr(VI) ions into crystalline extracellular Cr_2O_3NPs under benign conditions.

Keywords: Cr_2O_3; nanoparticles; Hexavalent chromium biotransformation; *Schwanniomyces occidentalis*

Fatima Benlboukht[a], Laurent Lemee[c], Soumia Amir[b], André Ambles[c], Mohamed Hafidi[a]. ([a] Laboratoire Ecologie et Environnement (Unité associée au CNRST, URAC 32, Unité associée au CNERS), Faculté des Sciences Semlalia, Cadi Ayyad University, BP: 2390 Marrakech, Morocco, [b] Département de Biologie, Faculté Polydisciplinaire, Beni Mellal, Morocco, [c] Université de Poitiers—CNRS, UMR 7285 (IC2MP), TSA 51106, 4 rue Michel Brunet, 86073 Poitiers Cedex 9, France). **Biotransformation of organic matter during composting of solid wastes from traditional tanneries by thermochemolysis coupled with gas chromatography and mass spectrometry. Ecological Engineering, Volume 90(2016): 87–95**

In the present paper, Thermochemolysis (or Thermally Assisted Hydrolysis/Methylation) is used as a way of following the biotransformation of organic matter during composting of solid wastes from traditional tanneries. The qualitative analysis of the pyrograms allowed us to discriminate between four main families of compounds: aromatic compounds, lipids, polysaccharides and nitrogen-containing substances. The quantitative data revealed some variations in the chemical composition of the macromolecular content.

Lipids are the most transformed fraction during the composting process. Animal and plant fatty acids showed a sensible decrease. Fungal fatty acids mainly increased during the thermophilic phase whereas bacterial fatty acids increased when the growth of fungi is repressed. During composting of solid wastes from traditional tanneries an adapted microbial community has been developed. Various lignin-derived units during composting showed a strong increase in *p*-hydroxyphenyl type-compounds in comparison with the other aromatic structures due to high decomposition of grass cuttings. Tannin derived compounds also increased throughout the composting. Lignin and condensed tannins polymers are partially degraded and stabilized by covalent linkage to more complex organic molecules such as humic substances.

Nitrogen containing compounds increased during composting as a consequence of the high rate of degradation of the other fractions and/or their combination with polyphenolic structure leading to the formation of humic substances. In our study a correlation was found between NTK and nitrogen containing substances.

Keywords: Tannery; Waste; Composting; Stability; Thermochemolysis

Lei Ren, Yang Jia, Nahurira Ruth, Yanhua Shi, Junhuan Wang, Cheng Qiao, Yanchun Yan. (Graduate School of Chinese Academy of Agricultural Sciences, Faculty of Life Science, Tangshan Normal University). Biotransformations of bisphenols mediated by a novel *Arthrobacter* sp. strain YC-RL1. Applied Microbiology and Biotechnology, Volume 100(4) (2016): 1967-1976

Arthrobacter sp. strain YC-RL1, capable of utilizing bisphenol A (BPA) as sole carbon source for growth, was isolated from petroleum contaminated soil. YC-RL1 could rapidly degrade BPA in a wide range of pH (5.0–9.0) and temperature (20–40 °C). Substrate analysis found that YC-RL1 could also degrade bisphenol F (BPF) and tetrabromobisphenol A (TBBPA). The maximum and minimum concentrations of BPA (0.2–600 mg/L), BPF (0.2–600 mg/L), and TBBPA (0.2–300 mg/L) for efficient biodegradation were detected. The released bromide ion and metabolic intermediates of BPF and BPA/TBBPA were detected, as well as the degradation pathways for BPF and BPA/TBBPA were deduced tentatively. The present study provides important information for the investigation of BPs degrading mechanism and the application of microbial remediation in BP-contaminated environment. This study is the first report about a genus *Arthrobacter* bacterium which could simultaneously degrade BPA, BPF, and TBBPA.

Keywords: Biodegradation; Bisphenols; *Arthrobacter* sp.; YC-RL1; Metabolites

Aurora M. Pat-Espadas, Elías Razo-Flores, J. Rene Rangel-Mendez, Juan A. Ascacio-Valdes, Cristobal N. Aguilar, Francisco J. Cervantes. (División de Ciencias Ambientales, Instituto Potosino de Investigación Científica y Tecnológica (IPICYT), Facultad de Ciencias Químicas, Departamento de Investigación en Alimentos (DIA-UAdeC), Universidad Autónoma de Coahuila). Immobilization of biogenic Pd(0) in anaerobic granular sludge for the biotransformation of recalcitrant halogenated pollutants in UASB reactors. Applied Microbiology and Biotechnology, Volume 100(3) (2016): 1427-1436

The capacity of anaerobic granular sludge to reduce Pd(II), using ethanol as electron donor, in an upflow anaerobic sludge blanket (UASB) reactor was demonstrated. Results confirmed complete reduction of Pd(II) and immobilization as Pd(0) in the granular sludge. The Pd-enriched sludge was further evaluated regarding biotransformation of two recalcitrant halogenated pollutants: 3-chloro-nitrobenzene (3-CNB) and iopromide (IOP) in batch and continuous operation in UASB reactors. The superior removal capacity of the Pd-enriched biomass when compared with the control (not exposed to Pd) was demonstrated in both cases. Results revealed 80 % of IOP removal efficiency after 100 h of incubation in batch experiments performed with Pd-enriched biomass whereas only 28 % of removal efficiency was achieved in incubations with biomass lacking Pd. The UASB reactor operated with the Pd-enriched biomass achieved 81 ± 9.5 % removal efficiency of IOP and only 61 ± 8.3 % occurred in the control reactor lacking Pd. Regarding 3-CNB, it was demonstrated that biogenic Pd(0) promoted both nitro-reduction and dehalogenation resulting in the complete conversion of 3-CNB to aniline while in the control experiment only nitro-reduction was documented. The complete biotransformation pathway of both contaminants was proposed by high-performance liquid chromatography–mass spectrometry (HPLC-MS) analysis evidencing a higher degree of nitro-reduction and dehalogenation of both contaminants in the experiments with Pd-enriched anaerobic sludge as compared with the control. A biotechnological process is proposed to recover Pd(II) from industrial streams and to immobilize it in anaerobic granular sludge. The Pd-enriched biomass is

also proposed as a biocatalyst to achieve the biotransformation of recalcitrant compounds in UASB reactors.

Keywords: Anaerobic granular sludge; Pd catalyst; Immobilized; UASB reactor; Recalcitrant pollutant

Biomarker

Ibtissem Louiz[a, c], Oum Kalthoum Ben Hassine[a], Olivier Palluel[b], Mossadok Ben-Attia[c], Sélim Aït-Aïssa[b]. ([a] Université de Tunis-El-Manar, Faculté des Sciences de Tunis, UR11ES08 Biologie Intégrative et Écologie Évolutive et Fonctionnelle des Milieux Aquatiques, 2092 El Manar, Tunisia, [b] Institut National de l'Environnement Industriel et des Risques (INERIS), Unité d'Écotoxicologie in vitro et in vivo, f-60550 Verneuil-en-Halatte, France, [c] Université de Carthage, Faculté des Sciences de Bizerte, UR, Laboratoire de Biosurveillance de l'Environnement, 7021 Zarzouna, Tunisia). **Spatial and temporal variation of biochemical biomarkers in*Gobius niger* (Gobiidae) from a southern Mediterranean lagoon (Bizerta lagoon, Tunisia): Influence of biotic and abiotic factors. Marine Pollution Bulletin, Volume 107(1) (2016): 305–314**

This study aims at evaluating both the influence of natural and some anthropogenic pressures on spatio-temporal variations on biomarker responses in sedentary benthic fish *Gobius niger*. For this purpose, variability of biotransformation enzymes and oxidative stress parameters response were studied in six stations from Bizerta lagoon as well as a reference station located in Ghar El Melh lagoon. Biomarker responses were shown to vary according to both physico-chemical parameters and anthropogenic pressures, but no influence of sex was reported. Based on multivariate analyses, the responses of biomarkers, obtained after covariate analysis in order to weigh the effect of physico-chemical parameters, allowed us to discriminate all stations, with a good classification rate for those that are highly contaminated. Altogether, this study shows the usefulness of *G. niger* as a sentinel species and stresses the necessity of integrating natural variables for data interpretation.

Keywords: *Gobius niger*; Bizerta lagoon; Biomarkers; Environmental factors; Pollution; Sentinel organism

Yongqin Lv[a], Yating Qin[a], Frantisek Svec[b], Tianwei Tan[a.] ([a] Beijing Key Laboratory of Bioprocess, College of Life Science and Technology, Beijing University of Chemical Technology, Beijing 100029, China, [b] International Research Center for Soft Matter, Beijing University of Chemical Technology, Beijing 100029, China). **Molecularly imprinted plasmonic nanosensor for selective SERS detection of protein biomarkers. Biosensors and Bioelectronics, Volume 80(2016): 433–441**

Molecularly imprinted plasmonic nanosensor has been prepared via the rational design of an ultrathin polymer layer on the surface of gold nanorods imprinted with the target protein. This nanosensor enabled selective fishing-out of the target protein biomarker even from a complex real sample such as human serum. Sensitive SERS detection of the protein biomarkers with a strong Raman enhancement was achieved by formation of protein imprinted gold nanorods aggregates, stacking of protein imprinted gold nanorods onto a glass plate, or self-assembly of protein imprinted gold nanorods into close-packed array. High specificity and sensitivity of this method were demonstrated with a detection limit of at least 10^{-8} mol/L for the target protein. This could provide a promising alternative for the currently used immunoassays and

fluorescence detection, and offer an ultrasensitive, non-destructive, and label-free technique for clinical diagnosis applications.

Keywords: Molecular imprinting; Gold nanorods; Nanosensor; Surface-enhanced Raman scattering; Protein biomarker

Biofertilizer

Jing Li, Juan Wang, Jinxin Li, Dahui Liu, Hongfa Li, Wenyuan Gao, Jianli Li, Shujie Liu. (Tianjin Key Laboratory for Modern Drug Delivery and High Efficiency, School of Pharmaceutical Science and Technology, Tianjin University. State Key Laboratory Breeding Base of Dao-di Herbs, China Academy of Chinese Medical Sciences, Institute of Medicinal Plants, Yunnan Academy of Agricultural Sciences, Key Laboratory of Industrial Fermentation Microbiology, Ministry of Education, Tianjin University of Science and Technology). *Aspergillus niger* Enhance Bioactive Compounds Biosynthesis As Well As Expression of Functional Genes in Adventitious Roots of *Glycyrrhiza uralensis* Fisch. Applied Biochemistry and Biotechnology, Volume 178(3) (2016): 576-593

In the present study, the culture conditions for the accumulation of *Glycyrrhiza uralensis* adventitious root metabolites in balloon-type bubble bioreactors (BTBBs) have been optimized. The results of the culture showed that the best culture conditions were a cone angle of 90° bioreactor and 0.4–0.6–0.4-vvm aeration volume. *Aspergillus niger* can be used as a fungal elicitor to enhance the production of defense compounds in plants. With the addition of a fungal elicitor (derived from *Aspergillus niger*), the maximum accumulation of total flavonoids (16.12 mg g^{-1}) and glycyrrhetinic acid (0.18 mg g^{-1}) occurred at a dose of 400 mg L^{-1} of *Aspergillus niger* resulting in a 3.47-fold and 1.8-fold increase over control roots. However, the highest concentration of polysaccharide (106.06 mg g^{-1}) was achieved with a mixture of elicitors (*Aspergillus niger* and salicylic acid) added to the medium, resulting in a 1.09-fold increase over *Aspergillus niger* treatment alone. Electrospray ionization tandem mass spectrometry (ESI-MS^n) analysis was performed, showing that seven compounds were present after treatment with the elicitors, including uralsaponin B, licorice saponin B_2, liquiritin, and (3R)-vestitol, only identified in the mixed elicitor treatment group. It has also been found that elicitors (*Aspergillus niger* and salicylic acid) significantly upregulated the expression of the cinnamate 4-hydroxylase (C4H), β-amyrin synthase (β-AS), squalene epoxidase (SE) and a cytochrome P450 monooxygenase (CYP72A154) genes, which are involved in the biosynthesis of bioactive compounds, and increased superoxide dismutase (SOD), catalase (CAT), and peroxidase (POD) activity.

Keywords: *Glycyrrhiza uralensis* Fisch; Adventitious root; *Aspergillus niger;* HPLC-ESI-$MS^{n;}$ Anti-oxidant enzymes; Gene

Biocomposting

Dan Xie, Weibing Wu, Xiaoxia Hao, Dongmei Jiang, Xuewei Li, Lin Bai. (College of Animal Science and Technology, Sichuan Agricultural University, Institute of Animal Genetics and Breeding, College of Animal Science and Technology, Sichuan Agricultural University). Vermicomposting of sludge from animal wastewater treatment plant mixed

with cow dung or swine manure using *Eisenia fetida.* Environmental Science and Pollution Research, Volume 23(8) (2016): 7767-7775

Vermicomposting of animal wastewater treatment plant sludge (S) mixed with cow dung (CD) or swine manure (SM) employing *Eisenia fetida* was tested. The numbers, weights, clitellum development, and cocoon production were monitored for 60 days at a detecting interval of 15 days. The results indicated that 100 % of the sludge can be the suitable food for growth and fecundity of *E. fetida*, while addition of CD or SM in sludge significantly ($P < 0.05$) increased the worm biomass and reproduction. The sludge amended with 40 % SM can be a great medium for the growth of *E. fetida*, and the sludge amended with 40 % CD can be a suitable medium for the fecundity of *E. fetida*. The addition of CD in sludge provided a better environment for the fecundity of earthworm than SM did. Moreover, vermicomposts obtained in the study had lower pH value, lower total organic carbon (TOC), lower NH_4^+-N, lower C/N ratio, higher total available phosphorous (TAP) contents, optimal stability, and maturity. NH_4^+-N, pH and TAP of the initial mixtures explained high earthworm growth. The results provided the theory basic both for management of animal wastes and the production of earthworm proteins using *E. fetida*.

Keywords: Vermicomposting; Earthworm; Animal wastewater treatment plant; Sludge; Cow dung; Swine manure

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Fusarium circinatum is a quarantine pathogen in numerous countries that causes important economic losses in forest nurseries and mature pine trees. Alternatives to chemical control of plant diseases such as suppressive composts and the use of biological control agents in growth media can reduce the incidence and spread of disease. In this work, four gorse composts obtained from forest cleaning green wastes and reference compost prepared from the organic fraction of solid urban waste were studied as environmentally sustainable peat substitutes. Their ability to suppress the effects of mating types M1 and M2 of the pathogen *F. circinatum* on *Pinus radiata* was evaluated in the presence or absence of the biocontrol agent *Trichoderma asperellum* strain T34. One of the gorse composts was more suppressive than the reference compost (15% and 55% of disease incidence, respectively). The former had a low EC, moderate amounts of P, Ca, Mg and K, and high levels of NH_4^+, as well as moderate levels of Ca, B and oligotrophic actinomycetes, the highest levels of total fungi, moderate levels of *Trichoderma* spp. and the lowest levels of *Fusarium* spp. Adding T34 to the moderately suppressive and non-suppressive composts decreased pre- and post-emergence incidence of the disease by up to 50%.

In conclusion, one gorse compost decreased the incidence of *F. circinatum* disease when used as a growth medium for *P. radiata* seedlings. *T. asperellum* strain T34 further reduced the incidence of disease and improved the health of pine seedlings grown in moderately non-suppressive composts.

Keywords: Cattle slurry; *Gibberella circinata*; Gorse; Pine; Poultry manure

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Brzeźnicka 60a, 42-200 Częstochowa, Poland, [b] GIRO Unit, Research and Technology, Food and Agriculture (IRTA), Carretera de Cabrils km 2, 08348 Cabrils, Barcelona, SpainThe effect of precomposted sewage sludge mixture amended with biochar on the growth and reproduction of *Eisenia fetida* during laboratory vermicomposting. Ecological Engineering, Volume 90(2016): 35–41

The obtained results showed that the addition of biochar to the mixture of sewage sludge and wheat straw prior to composting facilitated the growth and reproduction of *Eisenia fetida* during laboratory vermicomposting of this mixture. After 4 weeks of vermicomposting the average number of produced cocoons in the mixtures amended with biochar increased by 13% for SS + ST + 4%B and 66% for SS + ST + 8%B. Also, the number of juvenile earthworms was higher in the mixtures amended with biochar. However, the total weight of earthworms declined with the depletion of organic matter after 18 weeks of the experiment. Amending sewage sludge mixtures with biochar for vermicomposting resulted in higher reproduction rates, and thus could allow faster and more efficient conversion of sewage sludge into vermicompost.

Keywords: Vermicomposting; Sewage sludge; Biochar; *Eisenia fetida*; Reproduction rate; Growth

D. Dasa, P. Bhattacharyyab, B.C. Ghoshc, P. Banika. (a Agricultural and Ecological Research Unit, Indian Statistical Institute, 203 Barrackpore Trunk Road, Kolkata 700108, India, b Agricultural and Ecological Research Unit, Indian Statistical Institute, Giridih, 815301, Jharkhand, India, c Department of Agricultural and Food Engineering, Indian Institute of Technology, Kharagpur, IndiaBioconversion and biodynamics of *Eisenia foetida* in different organic wastes through microbially enriched vermiconversion technologies. Ecological Engineering, Volume 86(2016): 154–161

The present investigation is an attempt to convert organic wastes like water hyacinth, paddy straw and sawdust to organic manure through vermicomposting by *Eisenia foetida* together with the help of some beneficial microbes such as *Trichoderma viride* (cellulolytic), *Azotobacter chroococcum* (nitrogen fixing), *Bacillus polymixa* (phosphate solubilizing) and *Bacillus firmus* (potassium solubilizing). Chemical and biochemical properties of vermicompost prepared from the aforementioned organic wastes were studied. Earthworm biomass, growth performance, and cocoon production were higher in vermicompost prepared from water hyacinth and paddy straw as compared to vermicompost prepared from sawdust. All vermibeds showed significant reduction in pH, organic carbon, cellulose content and C/N ratio and substantial increase in humic acid, total N, available P and exchangeable K. Vermistabilization also increased the microbial population and enzyme activities of all organic wastes. Inoculation of *A. chroococcum*, *B. polymixa* and *B. firmus* alone or in combination with *T. viride* significantly increased nitrogen, available P and K content. Significant increases in microbial population and enzyme activities in vermicomposts were recorded with inoculation of *T. viride* either alone or in consortia. The best quality compost was prepared when the substrate was treated with all the four microorganisms together followed by vermicomposting. Results indicated that the combination of earthworms and microorganisms reduced the overall time required for composting besides producing a nutrient-enriched compost product.

Keywords: Vermicomposting; *Eisenia foetida*; Microorganisms; Organic wastes; Nutrients

Biopesticides

Noé Medina-Córdova, Raúl López-Aguilar, Felipe Ascencio, Thelma Castellanos, Angel I. Campa-Córdova, Carlos Angulo. (Centro de Investigaciones Biológicas del Noroeste, S.C., Instituto Politécnico Nacional #195, Col. Playa Palo de Santa Rita, La Paz C.P. 23090, BCS, Mexico). Biocontrol activity of the marine yeast *Debaryomyces hansenii* against phytopathogenic fungi and its ability to inhibit mycotoxins production in maize grain (*Zea mays* L.). Biological Control, Volume 97(2016): 70–79

Debaryomyces hansenii is an antagonistic yeast that has been shown high effectiveness against different phytopathogenic fungi in diverse habitats. Both, the antagonistic activity of *D. hansenii* BCS003 and its mechanism against four pathogenic fungi (*Mucor circinelloides*, *Aspergillus* sp., *Fusarium proliferatum* and *Fusarium subglutinans*) in maize grains (*Zea mays* L.) were evaluated. Results indicated an almost entirely decrease (97.2–98.3%) of mycelial growth in a radial inhibition assay against four strains of pathogenic fungi by the *D. hansenii* action. In diffusible and volatile compounds as well cell-free supernatants *in vitro* assays *D. hansenii* showed significant inhibitory activity ($p < 0.05$) against *Aspergillus* sp., *F. proliferatum* and *F. subglutinans*. The four isolated fungi were used to infect maize grains and results showed a partial inhibition of the mycelial growth and a 24 h delay in the disease appearance when compared to control (not *D. hansenii* treated maize grain). Moreover, the application of *D. hansenii* reduced the production of *F. subglutinans* fumonisins by 59.8% after seven days of co-incubation without affecting the chemical and mineral composition of maize grain. According to these results, *D. hansenii* BCS003 could be considered a potential biocontrol agent against toxigenic molds in maize grains, probably due to the synergistic effects of the factors such as the competition for nutrients and space, as well as the production of extracellular soluble and volatile compounds. The potential of marine *D. hansenii* as biocontrol agent merits further research to improve its efficacy.

Keywords: Marine *Debaryomyces hansenii*; Biocontrol; Phytopathogenic fungi; Fumonisin production; Maize

Carlos Alberto Tuão Gava, José Maria Pinto. (Embrapa Tropical Semi-Arid, Cx Postal 23, Petrolina, PE CEP 56302-970, Brazil). Biocontrol of melon wilt caused by *Fusarium oxysporum* Schlect f. sp. *melonis* using seed treatment with *Trichoderma* spp. and liquid compost. Biological Control, Volume 97(2016): 13–20

The control of melon wilt caused *Fusarium oxysporum* f. sp. *melonis* (*Fom*) has become a complex problem for melon (*Cucumis melo* L.) growers worldwide. In this study, we evaluated the ability of *Trichoderma* spp. to control melon wilt under field conditions, and the application of liquid compost as a food-based strategy to improve the biocontrol efficiency of the selected strain. In a first experiment, we evaluated the use of *Trichoderma harzianum* LCB47, *Trichoderma viride* LCB48, *Trichoderma koningii* LCB49, and *Trichoderma polysporum* LCB50 to control melon wilt in a naturally infested soil. The treatment with *T. polysporum* LCB50 (*Tp*) showed the highest efficiency to control melon wilt (44.85%), increasing the fruit yield in 43%. In the second experiment, *Tp* was applied as seed treatment, and repeated once at 15 days after transplanting. Two doses of liquid compost: 25 (LC25) and 50 mL pL^{-1} (LC50), were applied by fertigation on a weekly basis along the crop development. In this experiment, *T. polysporum* LCB50 applied alone resulted in a significant ($P < 0.05$) control of wilt (32.2%), and 27% increase in fruit production. Single application of both doses of LC did not significantly reduced disease incidence. However, a strong synergistic effect was observed applying *Tp* and

LC25 and LC50, resulting in a highly significant wilt control (68 and 72%, respectively) and an increase in productivity. The use of *Tp* + LC50 treatment increased in 100% the production of commercial fruits. From the results, a strategy based on the use of *T. polysporum* LCB50 and an organic matter source is proposed for the integrated management for melon wilt.

Keywords: Biological control; *Fusarium* wilt; *Cucumis melo*; Fertigation

Shivika Datta, Joginder Singh, Sharanpreet Singh, Jaswinder Singh. (School of Biotechnology and Biosciences, Lovely Professional University, Department of Zoology, Khalsa College Amritsar). Earthworms, pesticides and sustainable agriculture: a review. Environmental Science and Pollution Research, Volume 23(9) (2016): 8227-8243

The aim of this review is to generate awareness and understand the importance of earthworms in sustainable agriculture and effect of pesticides on their action. The natural resources are finite and highly prone to degradation by the misuse of land and mismanagement of soil. The world is in utter need of a healthy ecosystem that provides with fertile soil, clean water, food and other natural resources. Anthropogenic activities have led to an increased contamination of land. The intensification of industrial and agricultural practices chiefly the utilization of pesticides has in almost every way made our natural resources concave. Earthworms help in a number of tasks that support many ecosystem services that favor agrosystem sustainability but are degraded by exhaustive practices such as the use of pesticides. The present review assesses the response of earthworm toward the pesticides and also evaluates the relationship between earthworm activity and plant growth. We strictly need to refresh and rethink on the policies and norms devised by us on sustainable ecology. In an equivalent way, the natural resources should be utilized and further, essential ways for betterment of present and future livelihood should be sought.

Keywords: Bioremediation; Earthworms; Pesticides; Sustainable agriculture; Vermicompost

Megha Pant[1], Satyawati Sharma[1], Saurabh Dubey[1], Satya Narayan Naik[1], Phool Kumar Patanjali[2]. ([1] Centre for Rural Development and Technology (CRDT), Indian Institute of Technology (IIT), 110016 Delhi, India, [2] Formulation Division, Institute of Pesticide and Formulation Technology, Gurgaon, 122016 Haryana, India). Utilization of biodiesel by-products for mosquito control. Journal of Bioscience and Bioengineering, Volume 121(3) (2016): 2016, Pages 299–302

The current paper has elaborated the efficient utilization of non-edible oil seed cakes (NEOC), by-products of the bio-diesel extraction process to develop a herbal and novel mosquitocidal composition against the *Aedes aegypti* larvae. The composition consisted of botanical active ingredients, inerts, burning agents and preservatives; where the botanical active ingredients were karanja (*Pongamia glabra*) cake powder and jatropha (*Jatropha curcas*) cake powder, products left after the extraction of oil from karanja and jatropha seed. The percentage mortality value recorded for the combination with concentration, karanja cake powder (20%) and jatropha cake powder (20%), 1:1 was 96%. The coil formulations developed from these biodiesel by-products are of low cost, environmentally friendly and are less toxic than the synthetic active ingredients.

Keywords: Biodiesel; By-products; Biopesticides; Phorbol esters; Mosquito-coil; Karanja; Jatropha; *Aedes aegypti*; Knockdown

Sabah A. A. Jassim, Richard G. Limoges, Hassan El-Cheikh. (Applied Bio Research Inc.). Bacteriophage biocontrol in wastewater treatment. World Journal of Microbiology and Biotechnology, Volume 32 (2016): 70

Waterborne bacterial pathogens in wastewater remains an important public health concern, not only because of the environmental damage, morbidity and mortality that they cause, but also due to the high cost of disinfecting wastewater by using physical and chemical methods in treatment plants. Bacteriophages are proposed as bacterial pathogen indicators and as an alternative biological method for wastewater treatment. Phage biocontrol in large scale treatment requires adaptive and aggressive phages that are able to overcome the environmental forces that interfere with phage–host interactions while targeting unwanted bacterial pathogens and preventing biofilms and foaming. This review will shed light on aspects of using bacteriophage programming technology in wastewater plants to rapidly target and reduce undesirable bacteria without harming the useful bacteria needed for biodegradation.

Keywords: Bacteriophage; Phage reprogramming technology; Biocontrol; Water; Wastewater treatment; Sewage; Activated sludge process

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Species of the genus *Trichoderma* are economically important as biocontrol agents, serving as a potential alternative to chemical control. The applicability of *Trichoderma* isolates to different ecozones will depend on the behavior of the strains selected from each zone. The present study was undertaken to isolate biocontrol populations of *Trichoderma* spp. from the Argentine wheat regions and to select and characterize the best strains of *Trichoderma harzianum* by means of molecular techniques. A total of 84 out of the 240 strains of *Trichoderma* were able to reduce the disease severity of the leaf blotch of wheat. Thirty-seven strains were selected for the reduction equal to or greater than 50 % of the severity, compared with the control. The percentage values of reduction of the pycnidial coverage ranged between 45 and 80 %. The same last strains were confirmed as *T. harzianum* by polymerase chain reaction amplification of internal transcribed spacers, followed by sequencing. Inter-simple sequence repeat was used to examine the genetic variability among isolates. This resulted in a total of 132 bands. Further numerical analysis revealed 19 haplotypes, grouped in three clusters (I, II, III). Shared strains, with different geographical origins and isolated in different years, were observed within each cluster. The origin of the isolates and the genetic group were partially related. All isolates from Paraná were in cluster I, all isolates from Lobería were in cluster II, and all isolates from Pergamino and Santa Fe were in cluster III. Our results suggest that the 37 native strains of *T. harzianum* are important in biocontrol programs and could be advantageous for the preparation of biopesticides adapted to the agroecological conditions of wheat culture.

Keywords: Biological control; *Trichoderma harzianum;* Septoria leaf blotch; ISSR

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UR13AGR09 – Integrated Horticultural Production in the Tunisian Centre-East, Regional Center of Research on Horticulture and Organic Agriculture, University of Sousse, 4042, Chott-Mariem, Tunisia). Biocontrol of Fusarium wilt and growth promotion of tomato plants using endophytic bacteria isolated from *Nicotiana glauca* organs. Biological Control, Volume 97(2016): 80–88

Seven bacterial isolates, recovered from native *Nicotiana glauca* plants of the Tunisian Centre-East, and successfully colonizing the internal stem tissues of tomato cv. Rio Grande were screened for their ability to suppress tomato Fusarium wilt, caused by *Fusaium oxysporum* f. sp. *lycopersici*, and to enhance plant growth. S18 and S42 isolates were found to be the most effective in decreasing yellowing and wilt symptoms by 94 and 88% and the vascular browning extent by 95–97.5%, respectively, as compared to FOL-inoculated and untreated control. A significant enhancement in growth parameters of tomato plants inoculated with pathogen and treated with S18 and S42 isolates. These two bioactive isolates were characterized and identified using 16S rDNA sequencing genes as *Alcaligenes faecalis* S18 and *Bacillus cereus* S42, respectively. Pathogen mycelial growth was inhibited by 44.1 and 42.1% with S42 and S18 isolates, respectively. Using the disc diffusion method, S42 and S18 formed an inhibition zone against FOL of about 11.87–12.37 mm, respectively. The isolate S42 of *B. cereus* showed a proteolytic and chitinolytic activity. *A. faecalis* S18 exhibited only chitinolytic activity in chitin-agar medium. This isolate was also able to produce the volatile metabolite hydrogen cyanide. Indole-3-acetic acid production, phosphate solubilizing, and pectinase activity were assessed for these two bioactive isolates for elucidating their plant growth promoting traits and their endophytic colonization ability. This study clearly demonstrated that *N. glauca* is a potential source for the isolation of potent endophytic bacteria exhibiting Fusarium wilt-suppressive and plant growth-promoting effects on tomato.

Keywords: Biocontrol; Endophytic bacteria; *Fusarium oxysporum* f. sp. *lycopersici*; *Nicotiana glauca*; Tomato growth

Ranjan Ghosh, Soma Barman, Jesmina Khatun, Narayan C. Mandal. (Mycology and Plant Pathology Laboratory, Department of Botany, Visva-Bharati, Santiniketan 731235, West Bengal, India). Biological control of *Alternaria alternata* causing leaf spot disease of *Aloe vera* using two strains of rhizobacteria. Biological Control, Volume 97(2016): 102–108

Fungal pathogens causing the leaf spot disease of *Aloe vera* have been isolated from 40 randomly selected infected leaves, collected from different locations of Birbhum and Burdwan districts of West Bengal. All of the isolates showed similar morphological characteristics and the strain VBAV007, isolated from a severely infected *Aloe* leaf was identified as *Alternaria alternata* by D1/D2 region of 28S rRNA gene sequence homology. In addition to the destruction of leaf mesophyll tissues the pathogen also decreases the antimicrobial potential of *A. vera* gel. The commercially available fungicide mancozeb was effective at low concentration (100 µg/ml) to control the pathogen whereas it can tolerate 1000 µg/ml or more concentrations of bavistin. Two plant growth promoting rhizobacterial strains, viz. *Burkholderia cenocepacia* VBC7 and *Pseudomonas poae* VBK1 were able to produce prominent zones of inhibition against the pathogen in dual culture overlay plates. 89.3 ± 1.22% and 81.5 ± 2.67% inhibitions of conidial germination of the pathogen were noticed in the presence of cell free supernatant of VBK1 and VBC7 respectively. Radial growth assay also suggested prominent growth inhibition of VBAV007 by biocontrol strains. They induce mycelial breakage of pathogen as evidenced by

scanning electron micrographs. Greenhouse challenge experiments also suggested excellent capabilities of biocontrol agents to reduce disease severity in good measure even after exposure to high concentration (3.1×10^4 conidia/ml) of pathogenic spores. During *in vivo* field experiments 54.25 ± 3.55% disease severity was observed for untreated plants, whereas only 11.69 ± 1.25% and 15.22 ± 2.64% disease severities were noticed in plants treated with VBK1 and VBC7 respectively. Since biocontrol organisms have the potential to decrease the disease severity, they also help to maintain the good health as well as antimicrobial potential of *A. vera* plants.

Keywords: Leaf spot disease; *Alternaria alternata*; Rhizobacteria; Biological control; Antifungal potential; Challenge experiment

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Root rot disease, caused by the fungus *Fusarium solani* is an important soil-borne disease reducing common bean (*Phaseolus vulgaris* L.) production yields at up to 84%. The present study aimed at investigating the promotion of common bean seed germination and plant growth, and the biocontrol potential of two endophytic *Trichoderma* spp. against *F. solani*. The antagonistic and promotion effects of the endophytic fungi were evaluated by means of *in vitro* and *in vivo* experiments. The results achieved showed that the two *Trichoderma* spp. could exert over 86% and 27% inhibition of *F. solani* growth and spore germination respectively. The culture filtrate of *Trichoderma atroviridae* at 50% (v/v) also highly reduced *F. solani* mycelia growth and spore germination up to 80% and 100% respectively. The ethyl acetate extract of *T. atroviridae* showed a Minimum Inhibitory Concentration (MIC) of 0.66 mg/mL against *F. solani* germination. *T. atroviridae* showed high potential in promoting bean seed germination (100%) at 2×10^5 conidia/mL and in protecting bean seed from the deleterious effects caused by *F. solani*. In addition, *T. atroviridae* boosted the germination of bean seed by 20% when treated with 4×10^5 conidia/mL of *F. solani*, emphasizing its significant biocontrol potential *in vitro*. It was also less susceptible to resistance development by *F. solani*. Finally, *T. atroviridae* significantly reduced the disease severity and incidence by 11.42% and 40% respectively, and also improved growth parameters of bean plant. The results achieved in this study suggest further feasibility studies into using *T. atroviridae* to express growth promotion in plants for enhanced crop productivity, and to manage root rot disease.

Keywords: *Trichoderma atroviridae*; Seed germination; Plant growth promotion; *Phaseolus vulgaris* L.; *Fusarium solani*; *Terminalia catappa*

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Multiple formulations of known biocontrol agent (BCA) *Candida sake*, containing different coating-forming polymers and surfactants were tested at different polymer:BCA ratios, in order to improve control of *Botrytis cinerea* on grapes. The BCA cell viability on the grape surface was analyzed and reduction in disease incidence and severity was determined. Coating-forming solids improved the survival and efficacy of *C. sake* as a BCA against *B. cinerea*, depending on the polymer type and ratio. The incorporation of surfactants did not improve survival or disease control, although they promoted a better cell dispersion on the grape surface. Cell growth of the antagonist during incubation led to the formation of aggregates, even when surfactants were present. Sodium caseinate and starch were the most suitable polymers to formulate *C. sake* preparations to obtain coating-forming systems with this BCA and to increase its survival and efficacy at the minimum economic cost of the ingredients.

Keywords: Biological control; *Candida sake*; Grapes; Biopolymer; Edible coating; Microstructural analysis

Freda E. Anderson[a], Silvina P. Santos López[a], Romina M. Sánchez[a], Cintia G. Reinoso Fuentealba[a], Jane Barton[b]. ([a] CERZOS-CONICET, Camino La Carrindanga km 7, B8000FWB Bahía Blanca, Argentina, [b] Contractor to Landcare Research New Zealand, 14 Amber Lane, RD 1, Hamilton 3281, New Zealand). **_Puccinia araujiae_, a promising classical biocontrol agent for moth plant in New Zealand: Biology, host range and hyperparasitism by _Cladosporium uredinicola._ Biological Control, Volume 95(2016) : 23–30**

The rust fungus *Puccinia araujiae* is proposed as a biological control agent for moth plant (*Araujia hortorum*) in New Zealand. This pathogen completes its life cycle on this host, it has the capacity of damaging it by producing premature foliage senescence and defoliation, and, it is only known from members of the Oxypetalinae (Apocynaceae). *P. araujiae* was found to be heavily hyperparasitised by the fungus *Cladosporium uredinicola* in the field in Argentina. The mode of action of this hyperparasite was investigated and efforts are currently being made to completely eliminate it from a culture of the rust through a combination of superficial disinfection and multiple sequential inoculations. A protocol was developed for long term storage of teliospores of the rust at very low temperatures. Stored spores were shown to maintain their ability to germinate and produce infective basidiospores for up to 12 months. The possible effect of the hyperparasite on the performance of the rust as a biological control agent, should it be introduced into New Zealand, is discussed.

Keywords: Moth plant; *Puccinia araujiae*; *Cladosporium uredinicola*; Hyperparasitisim; Microcyclic rusts; Cryopreservation

Juan M. Palazzini[a], Enrique Alberione[b], Adriana Torres[a], Christina Donat[c], Jürgen Köhl[d], Sofia Chulze[a]. ([a] Departamento de Microbiología e Inmunología, Facultad de Ciencias Exactas Físico Químicas y Naturales, Universidad Nacional de Río Cuarto, Ruta Nacional 36 Km. 601, Río Cuarto, Córdoba, Argentina, [b] EEA INTA Marcos Juárez, Ruta Nacional 12, Marcos Juárez, Córdoba, Argentina, [c] Bio-ferm GmbH, Tulln, Austria, [d] Wageningen UR – Plant Research International, Wageningen, The Netherlands). **Biological control of _Fusarium graminearum sensu stricto,_ causal agent of Fusarium head blight of wheat, using formulated antagonists under field conditions in Argentina. Biological Control, Volume 94(2016): 56–61**

Fusarium head blight (FHB) mainly caused by *Fusarium graminearum* is a devastating disease that causes extensive yield and quality losses to wheat in humid and semi-humid regions of the world. The biocontrol effect of two bacterial strains on FHB incidence, severity and deoxynivalenol (DON) accumulation in wheat was evaluated in field trials during 2010 and 2011 at Marcos Juarez, Córdoba province, Argentina. *Bacillus subtilis* RC 218 and *Brevibacillus* sp. RC 263 applied at anthesis period were evaluated through several combinations of cell type, strains, inoculum density (10^4 and 10^6 cfu/ml) and physiological modification. A significant and consistent biocontrol effect on FHB severity and DON contamination was observed in all the evaluated treatments during both 2010 and 2011 field trials. Reduction in FHB severity ranged 62–76% and 42–58% for 2010 and 2011 field trials, respectively. When evaluating the effect of the combined strains ($10^4 + 10^4$ and $10^6 + 10^6$ cfu/ml), a better biocontrol effect was observed in 2010 field trial. After biocontrol treatments, no DON accumulation was observed in wheat heads; meanwhile in control plots an average of 1372 µg/kg DON was detected during the two trials. FHB incidence was significantly reduced by biocontrol treatments during the 2010 field trial but not during the 2011 field trial. The results showed the effectiveness of the two formulated biological control agents in reducing both FHB severity and DON accumulation by *F. graminearum* under semi controlled field conditions.

Keywords: Biological control; *Fusarium graminearum*; Fusarium head blight; *Bacillus subtilis* RC 218; *Brevibacillus* sp. RC 263

Endophytes from wheat as biocontrol agents against tan spot disease. Biological Control, Volume 92(2016): 17–23

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Endophytes from wheat cultivars isolated in Buenos Aires province, Argentina, were assessed for their potential as biocontrol agents against *Pyrenophora tritici-repentis* (Died.) Drechsler (anamorph *Drechslera tritici-repentis*) (Died.) Shoem (*Dtr*), the causal agent of tan spot of wheat. Endophytes were screened using dual culture techniques and examining the effect on growth, sporulation and the antifungal activity in greenhouse assays. The most of endophytes tested significantly reduced *Dtr* growth compared to the control except *Rhodotorula rubra* from 11 to 15 days post inoculation. *Trichoderma hamatum*, *Penicillium* sp., *Bacillus* sp. and *Paecilomyces lilacinus* significantly reduced the colony diameter of the pathogen. Most of the endophytes evaluated showed morphological changes in the conidia and/or the mycelia of *D. tritici-repentis*. In addition, two endophytes, *Bacillus* sp. and *Fusarium* sp., reduced significantly the percent spore germination of *Dtr* compared to the control by 82% and 52% respectively. In greenhouse experiment *T. hamatum*, *Chaetomium globosum* and *Fusarium* sp. significantly ($P \leqslant 0.05$) reduced the average disease severity on all three leaves compared to the control. However, the best antagonistic effect was shown with *T. hamatum* as it resulted in the greatest suppression in the greenhouse and in the dual-plate assays. Likewise, *Bacillus* sp. was other highlighted

microorganism that antagonized the pathogen in *in vitro* assays. From our promising results, we conclude that endophytes have potential in the biological control of tan spot of wheat caused by *D. tritici-repentis*, particularly *T. hamatum* and *Bacillus* sp.

Keywords: Endophytic fungi; Endophytes; *Triticum aestivum*; *Pyrenophora tritici-repentis*; Tan spot

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Trichoderma species are well-known biological control agents. In this study, metabolites from 128 *Trichoderma* isolates were extracted from liquid cultures using ethyl acetate and tested for their activities against seven *Phytophthora* isolates. Following preliminary analysis, eight *Trichoderma* isolates were selected for further tests. Among them, the metabolites from *Trichoderma atroviride*/*petersenii* (KACC, Korea Agricultural Culture Collection, 40557) and *Trichoderma virens* (KACC 40929) showed the strongest inhibitory activities against *Phytophthora* isolates. Treatment with KACC 40557 extract inhibited *Phytophthora* growth, induced defense-related genes, and caused plant hormonal changes during *Phytophthora* infection in the detached leaves of pepper and tomato plants. Our results showed the potential for use of *Trichoderma* metabolites as biological control agents against *Phytophthora* pathogens.

Keywords *Trichoderma*; *Phytophthora*; Metabolites; Ethyl acetate extract; Biological control

Saifei Yuan[a], Meiyun Li[a], Zhiying Fang[a], Yan Liu[a], Wen Shi[a], Bing Pan[a], Kai Wu[c], Junxiong Shi[b], Biao Shen[a], Qirong Shena. (a Jiangsu Key Laboratory for Organic Solid Waste Utilization, Nanjing Agricultural University, Nanjing 210095, China, b Institute of Tobacco Science Research, Guiyang 550081, China, c Solar Energy Research Institute of Yunnan Normal University, Yunnan 650500, China).**Biological control of tobacco bacterial wilt using *Trichoderma harzianum* amended bioorganic fertilizer and the arbuscular mycorrhizal fungi *Glomus mosseae*. Biological Control, Volume 92(2016): 164–171**

Tobacco bacterial wilt (TBW) caused by *Ralstonia solanacearum* (RS) is one of the most serious tobacco diseases worldwide and no effective control measures are available to date. This study investigated the potential of *Trichoderma harzianum* SQR-T037 amended bioorganic fertilizer (BOF) and the arbuscular mycorrhizal fungi (AMF) *Glomus mosseae* 171 (Gm) on the control of TBW and promotion of plant growth in pot experiments. The results showed that the disease incidence in plants treated with integrated application of *G. mosseae* 171 and *T. harzianum* SQR-T037 amended bioorganic fertilizer (Gm + BOF) was the lowest, with a control efficacy of

68.2%, which is greater than that of BOF or Gm alone (26.8% and 14.7%, respectively). The application of BOF or Gm alone significantly reduced the abundance of RS in rhizosphere soil, but the integrated treatment (Gm + BOF) showed the strongest inhibitory effect (with a 21.3% increase in inhibition). The root colonization of *G. mosseae* 171 in samples treated with Gm + BOF was higher than that in samples with solely Gm treatment, indicating that the BOF significantly promoted *G. mosseae* mycorrhizal colonization. The results showed that the *G. mosseae* also had a positive effect on SQR-T037 rhizospheric colonization. Denaturing gradient gel electrophoresis (DGGE) results showed that application of BOF and Gm alone or in combination changed the diversity of the rhizospheric microbial community. The integrated application of Gm + BOF to tobacco plants significantly increases the activity of polyphenol oxidase (PPO), phenylalanine ammonia lyase (PAL), and peroxidase (POD), enzymes associated to systemic resistance. Additionally, the integrated application of Gm with BOF increased the tobacco plant height, shoot dry weight, and root dry weight. In conclusion, a synergistic biological approach integrating application of Gm and BOF for TBW protection seems promising.

Keywords: Biological control; *Ralstonia solanacearum*; Bioorganic fertilizer; *Trichoderma harzianum*; *Glomus mosseae*

Sara Neuville, Anne Le Ralec, Yannick Outreman, Bruno Jaloux. (Département d'Ecologie, Agrocampus Ouest Centre d'Angers, UMR1349 IGEPP, Agrocampus Ouest, UMR1349 IGEPP). The delay in arrival of the parasitoid *Diaeretiella rapae* influences the efficiency of cabbage aphid biological control. BioControl, Volume 61(2) (2016): 115-126

The efficiency of the biological control strategies based on parasitoids, either as a release or a conservative measure, depends on the timely arrival or release of the parasitoids after colonization of the field by the pest. In this study, the effects of the delay between the cabbage aphid *Brevicoryne brassicae* (Hemiptera: Aphididae) infestation and the release of its parasitoid *Diaeretiella rapae* (Hymenoptera: Braconidae) and of the number of parasitoid releases on aphid population dynamics and host plant growth were investigated. When the parasitoids were released at the start of the infestation, 89.6 % of the aphids were parasitized one month later, and the damage to cabbage was low. The identical number of parasitoids released two weeks after the start of the infestation partially controlled the aphid population, but the growth of the cabbage was altered. The earliest introduction of the parasitoid to the crop led to an efficient host regulation, and the release in three times rather than in one time did not improve the control efficiency at this release delay. The implications for biological control strategies that use parasitoids of aphids are discussed.

Keywords: Biological control; Release delay; Functional response; Hymenoptera; Braconidae

Fernanda Colombari, Andrea Battisti. (Department of Agronomy Food Natural Resources Animals and Environment (DAFNAE), University of Padova – Agripolis). Spread of the introduced biocontrol agent *Torymus sinensis* in north-eastern Italy: dispersal through active flight or assisted by wind? BioControl, Volume 61(2) (2016): 127-139

In successful classical biological control, natural enemies can provide enduring pest suppression if they reproduce and disperse without continued human management. To explain the efficient control exerted on the Asian chestnut gall wasp *Dryocosmus kuriphilus* Yasumatsu (Hymenoptera: Cynipidae) by the parasitoid *Torymus sinensis* Kamijo (Hymenoptera: Torymidae), it is required that the latter has the capacity to track the range expansion of its host. In the present study, we hypothesized that the distribution of infested patches and the prevailing wind directions would interactively influence and accelerate the spread of the parasitoid. It

emerged that the spread capability of *T. sinensis* is high and likely affected by a combination of short- and long-distance flights (stratified dispersal). In particular, the ability to disperse long distances represents a successful trait of the parasitoid because the natural dispersal of its host is high and frequently aided by unintentional human-mediated transportation.

Keywords: Hymenoptera; *Torymus sinensis;* Torymidae; *Dryocosmus kuriphilus;* Cynipidae; Wind

J. Christopher Bergh, Jon W. Stallings. (Virginia Tech, Alson H. Smith Jr. Agricultural Research and Extension Center, Virginia Tech, Alson H. Smith Jr. Agricultural Research and Extension CenterStatistics Department, North Carolina State University). Field evaluations of the contribution of predators and the parasitoid, *Aphelinus mali*, to biological control of woolly apple aphid, *Eriosoma lanigerum*, in Virginia, USA. BioControl, Volume 61(2) (2016): 155-165

A series of experiments in Virginia, USA apple orchards evaluated the temporal effects of natural enemies on *Eriosoma lanigerum* (Hausmann) (Hemiptera: Aphididae) colonies on potted and mature apple trees. Exclusion cage studies using potted trees resulted in increasing colony numbers on fully caged trees and declining colony numbers or colony extinction on trees exposed to natural enemies. Closer examination of the fate of individual colonies on potted trees produced a similar result and revealed that syrphids oviposited in colonies within two days of tree deployment. *Heringia calcarata* (Loew) (Diptera: Syrphidae) was the predominant predator and had a greater and more rapid impact on colonies than did the parasitoid *Aphelinus mali* (Haldeman) (Hymenoptera: Aphelinidae). The fate of cohorts of naturally-occurring *E. lanigerum* colonies on mature trees was examined over two seasons and confirmed that *H. calcarata* and *A. mali* were most strongly associated with colony demise.

Keywords: Hemiptera; Aphididae; Diptera; Syrphidae; *Malus domestica*

Christopher D. Harvey, Christine T. Griffin. (Department of Biology, Maynooth UniversitySchool of Human and Life Sciences, Canterbury Christ Church University, Department of Biology, Maynooth University). Local host-dependent persistence of the entomopathogenic nematode *Steinernema carpocapsae* used to control the large pine weevil *Hylobius abietis.* BioControl, Volume 61(2) (2016): 185-193

Entomopathogenic nematodes (EPN) applied inundatively to suppress insect pests are more likely to persist and establish in stable agroecosystems than in annual crops. We investigated a system of intermediate stability: three stumps harbouring the large pine weevil (*Hylobius abietis* L.; Coleoptera: Curculionidae), a major European forestry pest. We tested whether persistence of EPN *Steinernema carpocapsae* Weiser (Rhabditida: Steinernematidae) applied around stumps is maintained by recycling of EPN through pine weevils developing within stumps. *Steinernema carpocapsae* was detected in soil around and under the bark of treated tree stumps up to two years, but not 4–5 years after application. Differences in nematode presence between sites were better explained by tree species (pine or spruce) than soil type (mineral or peat). Presence of *S. carpocapsae* in soil was positively correlated with the number of *H. abietis* emerging from untreated stumps the previous year, which was greater for pine stumps than spruce stumps.

Keywords: *Steinernema;* Hylobius; Entomopathogenic nematodes; Pine weevil; Persistence; Bark

T. Han, C. You, L. Zhang, C. Feng, C. Zhang, J. Wang, F. Kong. (Pest Integrated Management Key Laboratory of China Tobacco, Tobacco Research Institute of Chinese Academy of Agricultural Sciences, Tobacco Research Institute of Yuxi). Biocontrol potential of antagonist *Bacillus subtilis* Tpb55 against tobacco black shank. BioControl, Volume 61(2) (2016): 195-205

Tobacco black shank caused by *Phytophthora nicotianae* is a very important oomycete disease of tobacco, and it is widely distributed around the world. In order to develop effective prevention techniques, this study examined the effects of an antagonistic bacterium, *Bacillus subtilis* Tpb55 strain, on the prevention of tobacco black shank in vitro and in vivo. Dual culture test results showed *B. subtilis* Tpb55 strain have a strong antagonism to *P. nicotianae*, inhibit the growth of its hyphae, and produce significant inhibition zones. Scanning electron microscopy showed that the Tpb55 strain can damage the structure of *P. nicotianae* hyphae, cause hyphae deformity, hyphae rupture, and protoplasm leakage. Control effects of Tpb55 strains on tobacco black shank in pot and field experiment can reach up to 70.66 and 59.34 %, respectively. In this study, Tpb55 strain was also labeled with green fluorescent protein (GFP) in order to monitor their rhizosphere colonization of tobacco. The Tpb55 strain's colonization on tobacco roots showed a diffused distribution, largely in the root meristem and elongation zone areas. They can gather focally into microcolonies, forming a biofilm like structure. A small number of these bacteria can colonize at the intercellular space and among vascular bundles. After inoculation, Tpb55-GFP was found to colonize tobacco roots for 30 days or more. The number of bacteria peaked on the 4th day at 1.51×10^7 cfu g^{-1}. By the 12th day, it had dropped to 1.1×10^6 cfu g^{-1}. This study shows that the effect of Tpb55 strains on controlling of tobacco black shank is correlated to their ability to inhibit mycelia growth and ability to successfully colonize tobacco roots.

Keywords: Antagonistic bacteria; Colonization; Tobacco black shank; *Bacillus subtilis*

Min A. Hahn, Urs Schaffner, Patrick Häfliger, Andreas Lüscher. (Agroscope, Institute for Sustainability SciencesDepartment of Botany, University of British Columbia, CABI, Agroscope, Institute for Sustainability Sciences). Establishment and early impact of the native biological control candidate *Pyropteron chrysidiforme* on the native weed *Rumex obtusifolius* in Europe. BioControl, Volume 61(2) (2016): 221-232

Rumex obtusifolius (Caryophyllales: Polygonaceae) is one of the most troublesome weeds in European grasslands and non-chemical control options are largely lacking. In this study, we assessed the potential of the native root-feeding specialist insect *Pyropteron chrysidiforme* (Lepidoptera: Sesiidae) for inundative biological control of *R. obtusifolius*. At multiple grassland sites, we applied *P. chrysidiforme* varying in developmental stage and level of protection onto *R. obtusifolius* to be examined in the subsequent autumn and spring. We consistently found the highest infestation resulting from the application of eggs (71 % of plants infested in autumn) with concomitantly elevated root decay and fewer rosettes compared to control plants. Moreover, in spring we found trends for associated decreases in biomass and number of shoots. Our findings support *P. chrysidiforme* as a promising biological control candidate of *R. obtusifolius*, but further investigations will be required to assess the consistency and long-term impacts of this novel approach.

Keywords: Polygonaceae; Sesiidae; Biological control; Weed; Root herbivory; Native control agent

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7254 Institut Sophia AgrobiotechCNRS, UMR 7254 Institut Sophia AgrobiotechINRA, UEFM Laboratoire BioContrôle). BioControl, Volume 61(1) (2016): 13-22

High-density rearing conditions for the mass-production of biological control agents are known to affect individual quality and performance. However, complex phenotypic traits like dispersal behaviour and their response to rearing conditions are rarely investigated, although they are likely to affect directly biocontrol efficiency in the field. In this study, we develop an original experimental design to evaluate two complementary components of dispersal behaviour in *Trichogramma*. Then, we investigate how these components respond to variations in rearing density, and their correlation with traits related to parasitoid fitness. We find that under high-density conditions, a large proportion of individuals display reduced mobility and fecundity, indicative of a lower-quality phenotype. These interactive effects between dispersal performance and individual fitness highlight the need to develop integrative experimental designs to easily quantify complex phenotypic traits related to the field performance of biological control agents.

Keywords: Phenotypic plasticity; Condition-dependence; Industrial rearing; Ambulatory dispersal; Aerial dispersal; *Trichogramma*

Antonio Biondi, Lucia Zappalà, Angelo Di Mauro, Giovanna Tropea Garzia, Agatino Russo, Nicolas Desneux, Gaetano Siscaro. (Department of Agriculture, Food and Environment, University of Catania. Department of Environmental Science, Policy and Management, University of California Berkeley, French National Institute for Agricultural Research (INRA), UMR 1355-7254 Institut Sophia Agrobiotech, Univ. Nice Sophia Antipolis, CNRS, Department of Agriculture, Food and Environment, University of Catania). Can alternative host plant and prey affect phytophagy and biological control by the zoophytophagous mirid *Nesidiocoris tenuis*? BioControl, Volume 61(1) (2016): 79-90

Nesidiocoristenuis (Reuter) (Hemiptera: Miridae) is an important natural enemy of several key arthropod pests. However, in tomato crop this predator can cause economic damage owing to its zoophytophagous behavior. We investigated in laboratory conditions the influence of two alternative plants, *Dittrichiaviscosa* L. (Asteraceae) and *Sesamumindicum* (L.) (Pedaliaceae), with or without prey, on *N. tenuis* damage and its biological control services on *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) eggs. Both *D. viscosa* and *S. indicum*, as companion plants in dual-choice bioassays, significantly reduced the damage of the mirid on tomato. *S. indicum* was more attractive than *D. viscosa* for feeding and oviposition and its presence did not interfere with the predation on *T. absoluta* eggs. We also studied the potential of the three plants as preyless rearing substrate for the mirid, and only *S. indicum* showed to be a suitable host plant for *N. tenuis* development and oviposition. The potential applications of *S. indicum* in *N. tenuis* field management and mass rearing are discussed.

Keywords: *Tuta absoluta; Sesamum indicum; Dittrichia viscosa;* Omnivory; Miridae; Banker plant

Caterina Rotolo, Rita Milvia De Miccolis Angelini, Stefania Pollastro, Francesco Faretra. (Department of Soil, Plant and Food Sciences – Plant Pathology Section, University of Bari ALDO MORO). A Taq Man-based qPCR assay for quantitative detection of the biocontrol agents *Bacillus subtilis* strain QST713 and *Bacillus amyloliquefaciens* subsp. *plantarum* strain D747. BioControl, Volume 61(1) (2016): 91-101

Biological control agents (BCAs) play an important role in crop protection. They can improve sustainability, prevent resistance to fungicides in target pathogens and reduce fungicide residues on produce. *Bacillus subtilis* strain QST713 (Serenade Max; Bayer CropScience, Leverkusen, Germany) and *Bacillus amyloliquefaciens* subsp. *plantarum* strain D747 [Amylo-X; CBC Europe S.r.l.—Biogard Division, Nova Milanese (MB), Italy] are two commercially available BCAs that are used against grey mould on table grape and other crops. TaqMan-based quantitative (q)PCR assays were developed and validated for quantitative and specific detection of the two BCAs on grape bunches following field sprays. Specific molecular markers were developed for each BCA, and TaqMan probes were designed and tested in qPCR on DNA extracted from washing water of grape berries. The assay proved specific and sensitive for both BCAs allowing detection at density as low as three colony-forming units (CFU) per gram of berries. The method will be useful to investigate the population dynamics of the two BCAs following their applications in vineyards.

Keywords: Grapevine; Grey mould; Biological control; Bacillaceae; qPCR; Molecular markers

Jörg G. Stephan, Johannes Albertsson, Liying Wang, Mario Porcel. (Department of Ecology, Swedish University of Agricultural Sciences, Department of Plant Breeding, Swedish University of Agricultural Sciences, Southern Swedish Forest Research Centre, Swedish University of Agricultural Sciences, Department of Plant Protection Biology, Swedish University of Agricultural Sciences). **Weeds within willow short-rotation coppices alter the arthropod community and improve biological control of the blue willow beetle. BioControl, Volume 61(1) (2016): 103-114**

Outbreaks of the blue willow beetle *Phratora vulgatissima* (L.) (Coleoptera: Chrysomelidae) threaten the yield of willow plantations that rely on biological control by natural enemies. Here we show that weed presence increases herbivore and predator/parasitoid diversity on willow shoots and causes increased predation on *P. vulgatissima* eggs compared to shoots within plots without weeds. We argue that, in addition to higher abundance, the community shift in favour of egg consumers and additive predator effects causes the higher predation pressure. This increase (~35 %) was apparent despite more alternative prey. Neither the willow genotype on which the predator–prey interaction occurred nor the clutch size affected egg predation levels. Our results support root's enemy hypothesis and suggest that intensive weed control might counteract biological control in willow plantations. However, at least during the establishing phase of the plantation, increased biocontrol probably does not compensate for yield losses caused by competing weeds.

Keywords: Arthropod community composition; Habitat diversity; Clutch size; Egg predation; Chrysomelidae; Salicaceae

Cai You, Chengsheng Zhang, Fanyu Kong, Chao Feng, Jing Wang. (Pest Integrated Management Key Laboratory of China Tobacco, Tobacco Research Institute of Chinese Academy of Agricultural Sciences (CAAS), 11 Keyuan Road four, Qingdao 266101, China). **Comparison of the effects of biocontrol agent *Bacillus subtilis* and fungicide metalaxyl–mancozeb on bacterial communities in tobacco rhizospheric soil. Ecological Engineering, Volume 91(2016): 119–125**

Bacillus subtilis Tpb55 is a biocontrol agent isolated from the tobacco phyllosphere that has significant inhibitory effect on tobacco black shank pathogen *Phytophthora parasitica* var. *nicotianae*. However, its potential ecological risk remains unknown. In this study, we investigated the impact of *B. subtilis* Tpb55 and the fungicide metalaxyl–mancozeb on bacterial communities in tobacco rhizospheric soil using amplified ribosomal DNA restriction analysis

and clone library analyses of 16S rRNA genes. Our results demonstrate that the treatments affected the bacterial communities in different ways. The dominant phyla *Acidobacteria* and *Proteobacteria* comprised 27.11% and 26.51%, respectively, of control soil; 29.61% and 37.99%, respectively, of Tpb55-treated soil; and 20.00% and 39.44%, respectively, of fungicide-treated soil. The most abundant class of *Proteobacteria* in control soil was *Betaproteobacteria* (11.45%); in contrast, Alphaproteobacteria (15.08%) and Gammaproteobacteria (16.67%) were the most abundant classes in Tpb55- and fungicide-treated soils, respectively. Bacteria that typically show plant-growth-promoting activity belonging to the genera *Bradyrhizobium*, *Rhizobium* and *Dyella* were enriched in Tpb55 treatment whereas genera known as pesticide-degrading bacteria such as *Rhodopseudomonas* and *Phenylobacterium* appeared in fungicide treatment. Tpb55 treatment increased soil bacterial diversity relative to control and fungicide treatment.

Keywords: *Bacillus subtilis*; Fungicide; Bacterial communities; Amplified ribosomal DNA restriction analysis; 16S rRNA genes

Biodegradation

Simone Cappello[a], Anna Volta[a, b], Santina Santisi[a, c], Claudia Morici[d], Giuseppe Mancini[b], Paola Quatrini[e], Maria Genovese[a], Michail M. Yakimov[a], Michele Torregrossa[d]. ([a] Institute for Coastal Marine Environment (IAMC)-CNR of Messina, Messina, Italy, [b] Dep. of Industrial Engineering, Faculty of Engineering, University of Catania, Catania, Italy, [c] Faculty of Science MM. FF. NN. Ph.D School in "Biology and Cellular Biotechnology", University of Messina, Italy, [d] Dep, of Civil, Environmental, Aerospatial, Material Engineering, Faculty of Engineering, University of Palermo, Palermo, Italy, [e] Dept. of "Scienze e Tecnologie Biologiche, Chimiche e Farmaceutiche" (STEBICEF), University of Palermo, Italy). **Oil-degrading bacteria from a membrane bioreactor (BF-MBR) system for treatment of saline oily waste: Isolation, identification and characterization of the biotechnological potential. International Biodeterioration & Biodegradation, Volume 110(2016): 235–244**

A collection of forty-two (42) strains was obtained during microbiological screening of a Membrane Bioreactor (MBR) system developed for the treatment of saline oily waste originated from marine transportation. The diversity of the bacterial collection was analyzed by amplification and sequencing of the 16S rRNA gene. Taxonomic analysis showed high level of identity with recognized sequences of seven (7) distinct bacterial genera *(Alcanivorax, Erythrobacter, Marinobacter, Microbacterium, Muricauda, Rhodococcus* and *Rheinheimera*). The biotechnological potential of the isolates was screened considering an important factor such as the biosurfactant production. In particular fourteen (14) biosurfactant producing bacteria were selected and further tested, for growth on crude oil and hydrocarbon degradation. Data obtained from this study confirmed the high activity of bacteria related to genera *Alcanivorax* (isolates MBR-B11 and MBR-G10), *Rheinheimera* (isolates MBR-H02 and MBR-H05), *Rhodococcus* (isolates MBR-F04 and MBR-G05) and *Muricauda* (isolate MBR-G04) and underline the possible application of these bacteria in remediation of saline oily waste water.

Keywords: Alcanivorax; Oil-degrading bacteria; Membrane bioreactor (MBR) system; Saline oily waste; Oil pollution

Fucai Deng[a], Changjun Liao[a, b], Chen Yang[a, c], Chuling Guo[a, c], Zhi Dang[a, c]. ([a] College of Environment and Energy, South China University of Technology, Guangzhou 510006, China, [b] Department of Environmental Engineering, Guangdong Vocational College of Environmental Protection Engineering, Foshan, 528216, China, [c] The Key Laboratory of Pollution Control and Ecosystem Restoration in Industry Clusters, Ministry of Education, China). **Enhanced biodegradation of pyrene by immobilized bacteria on modified biomass materials. International Biodeterioration & Biodegradation, Volume 110(2016): 46–52**

The degradation of pyrene (PYR) by *Mycobacterium gilvum* immobilized on peanut shell powder (PSP) was improved by chemically modifying the PSP. The physicochemical properties of the modified biomass (M-PSP) were characterized with surface area analysis, X-ray diffraction, Fourier transform infrared and solid-state CP/MAS ^{13}C NMR spectra. The results showed that the chemical modification decreased the crystallinity of the biomass and destroyed the benzene rings in the cellulose, which improved the porosity of PSP. Fluorescein diacetate activity (FDA) of cells immobilized on the M-PSP decreased more slowly than cells immobilized on PSP. The PYR degradation efficiencies achieved by bacteria immobilized on M-PSP was higher than that achieved by immobilized bacteria on PSP after 7 d. It revealed that chemical modification of biomass could further improve bacterial activity and enhance the degradation ability of the cells compared with the raw one, as we expected.

In summary, this study shows that M-PSP is a good immobilizing bio-mass for supporting pollutant-degrading bacteria and could be employed as an effective material for PYR biodegradation.

Keywords: Pyrene; Biodegradation; Bacteria immobilization; Biomass; Chemical modification; ^{13}C NMR

Marcela Moreira de Souza[a], Tatiana Simonetto Colla[a], Francielle Bücker[a], Marco Flores Ferrão[b], Chun Te Huang[b], Robson Andreazza[c], Flávio Anastácio de Oliveira Camargo[d, 1], Fátima Menezes Bento[a, 2]. ([a] Institute of Basic Health Sciences, Department of Microbiology, Immunology and Parasitology, Federal University of Rio Grande do Sul, 500 Sarmento Leite, 90050170 Porto Alegre, RS, Brazil, [b] Chemistry Institute, Department of Inorganic Chemistry, Federal University of Rio Grande do Sul, Av. Bento Gonçalves, 9500 Porto Alegre, RS, Brazil, [c] Center of Engineering, Federal University of Pelotas, 1734 Almirante Barroso, 96010-280 Pelotas, RS, Brazil, [d] Agronomy Faculty, Soil Department, Federal University of Rio Grande do Sul, 7712 Av. Bento Gonçalves, Porto Alegre, RS, Brazil). **Biodegradation potential of *Serratiamarcescens* for diesel/biodiesel blends. International Biodeterioration & Biodegradation, Volume 110(2016): 141–146**

Biodiesel is considered to be a natural substitute for petroleum. Moreover, its low toxicity and susceptibility to microbial biodegradation as compared to fossil diesel could reduce the impact on ecosystems in the event of an accidental spill. However, there is a paucity of studies in this field. Thus in the present study, the diesel/biodiesel biodegradation potential of the *Serratia marcescens* strain 110 UFRGS, isolated from a harbor in southern Brazil, was investigated, using a mineral medium containing the following diesel/biodiesel blends: B5, B10, B25 or B100. The isolate exhibited the lowest increase in CFU mL^{-1} and cell hydrophobicity in the treatment of B100. Infrared spectroscopy showed high percentages of biodegradation of the biodiesel blends, and B100 showed good biodegradability by the isolate under test. *S. marcescens* strain 110 UFRGS also displayed the presence of alkB gene. In summary, *S. marcescens* showed a high diesel/biodiesel degradation rate and is potentially useful for the bioremediation of environments contaminated with diesel/biodiesel.

Keywords: Biodiesel; Diesel; Biodegradation; *Serratia marcescens*; Bioremediation; Biotechnology

Ghasemali Mohebali[a], Andrew S. Ball[b]. ([a] Microbiology and Biotechnology Research Group, Research Institute of Petroleum Industry, Tehran, Iran, [b] Centre for Environmental Sustainability and Remediation School of Science, RMIT University, Australia). **Biodesulfurization of diesel fuels – Past, present and future perspectives. International Biodeterioration & Biodegradation, Volume 110(2016): 163–180**

The world focus on environmentally friendly fuels requires refiners to convert the increasingly poor-quality crude oil into high-quality finished products. Refineries are facing many challenges including heavier crude oils and increased fuel quality standards. Global society is moving towards zero-sulfur fuel and hydrodesulfurization (HDS) is the most common technology used by refineries to remove sulfur from intermediate streams. However, HDS has several disadvantages and therefore recent research has focused on improving HDS catalysts and processes and also on the development of alternative technologies. Among the alternative technologies one possible approach is biodesulfurization (BDS). BDS is a process that is based around bacterial potential. In this process, bacteria remove organosulfur from oil fractions without degrading the carbon skeleton of the compounds. BDS operates at ambient temperature and pressure with high selectivity, resulting in decreased energy costs, low emission and no generation of undesirable side-products. For assessing the potential of BDS as a biorefining process, pilot plants have been operated. The results obtained for BDS may be generally applicable to other areas of biorefining. In this review the history, current status and future challenges of BDS will be discussed. The integration use of BDS systems with existing HDS technology is discussed as a future approach by the oil industry, providing an efficient and environmentally friendly approach to desulphurization.

Keywords: Biodesulfurization; Diesel fuels; Dibenzothiophene; Bacteria

Stephanie L. Mathews[a, b], Amy M. Grunden[b], Joel Pawlak[a]. ([a] Department of Forest Biomaterials, Biltmore Hall, Campus Box 8005, North Carolina State University, Raleigh, NC 27695, USA, [b] Department of Plant and Microbial Biology, 4550A Thomas Hall Box 7612, North Carolina State University, Raleigh, NC 27695, USA). **Degradation of lignocellulose and lignin by *Paenibacillus glucanolyticus.* International Biodeterioration & Biodegradation, Volume 110(2016) : 79–86**

Lignocellulose is an abundant renewable carbon source that has been used for fuel and chemical production. Lignocellulose refers to the plant cell wall and is composed of cellulose, hemicellulose, and lignin. Lignin is a recalcitrant amorphous aromatic compound. *Paenibacillus glucanolyticus* SLM1, a facultative anaerobe that grows optimally at pH 9, was isolated from pulp mill waste. Initial characterization showed that this bacterium could degrade cellulose and hemicellulose and also suggested that it may be able to degrade lignin. This work examines the ability of *P. glucanolyticus* SLM1 and the type strain *P. glucanolyticus* 5162 to degrade lignocellulose, lignin, and aromatic lignin-related compounds using growth studies, dye degradation assays, GC–MS, and GPC. Our results show that both strains of *P. glucanolyticus* can degrade aromatic lignin-related compounds under aerobic and anaerobic conditions. These strains can also degrade polymeric lignin under anaerobic conditions. However, only *P. glucanolyticus* SLM1 can also degrade polymeric lignin under aerobic conditions.

Keywords: Lignin degradation; Lignocellulose degradation; *Paenibacillus glucanolyticus*; Bioproducts

Dalel Daâssi[a, b], Alicia Prieto[c], Héla Zouari-Mechichi[a], María Jesús Martínez[c], Moncef Nasri[a], Tahar Mechichi[a]. ([a] Laboratory of Enzyme Engineering and Microbiology, Ecole Nationale d'Ingénieurs de Sfax, University of Sfax, Route de Soukra Km 4,5, BP 1173, 3038 Sfax, Tunisia, [b] Department of Biology, Faculty of Sciences and Arts, Khulais, University of Jeddah, Jeddah, Saudi Arabia, [c] Centro de Investigaciones Biológicas (CIB-CSIC), Ramiro de Maeztu 9, E-28040 Madrid, Spain). **Degradation of bisphenol A by different fungal laccases and identification of its degradation products. International Biodeterioration & Biodegradation, Volume 110(2016): 181–188**

Different fungal laccases were used as biocatalysts for the biotransformation of bisphenol A (BPA). The quantitative analysis by gas chromatography-mass spectrometry (GC–MS) showed that BPA is more rapidly oxidized by *Coriolopsis gallica* laccase among the different fungal laccases tested. Carboxylic acid derivatives such as tartaric acid was found as BPA degradation products resulting from reactions catalyzed by 1 U ml^{-1} of laccase from *C. gallica* in the presence of 1 mM of the laccase-mediator 1-hydroxybenzotriazole (HBT), while β-hydroxybutyric acid resulted from oxidative reactions without HBT. BPA was completely removed within 3 h and pyroglutamic acid was found as a supplementary oxidative degradation product from HBT when identified by GC–MS. Laccase played a critical role in BPA biodegradation and catalyzed a cross-coupling reaction.

Keywords: Bisphenol A; Laccases; Biodegradation; Identification; Intermediates; Pathway

Kathirvel Thirunavukarasu[a], Subramanian Purushothaman[a], Janardhanam Sridevi[b], Mayilvahanan Aarthy[a], Marichetti Kuppuswami Gowthaman[a], Toshiaki Nakajima-Kambe[c], Numbi Ramudu Kamini[a]. ([a] Department of Biotechnology, CSIR-Central Leather Research Institute, Adyar, Chennai 600 020, India, [b] Chemical Physics Laboratory, CSIR-Central Leather Research Institute, Adyar, Chennai 600 020, India, [c] Bioindustrial Sciences, Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan). **Degradation of poly(butylene succinate) and poly(butylene succinate-co-butylene adipate) by a lipase from yeast *Cryptococcus* sp. grown on agro-industrial residues. International Biodeterioration & Biodegradation, Volume 110(2016): 99–107**

The yeast, *Cryptococcus* sp. MTCC 5455 was grown on various agro-industrial residues for the production of lipase. A maximum lipase activity of 753 ± 19 U g dry substrate^{-1} (U gds^{-1}) and a biomass of 103 ± 5 mg gds^{-1} was obtained at 25 °C and 120 h using cottonseed oil cake with 71% moisture content and 30% (v/w) inoculum. The recovery of the enzyme was increased by 14.1%, when the fermented substrate was extracted in 2 mM $CaCl_2.2H_2O$ solution. The crude enzyme partially purified by $(NH_4)_2SO_4$ precipitation showed a major 22 kDa protein on SDS-PAGE. The enzyme has good potential for hydrolysis of poly(butylene succinate) (PBS) and poly(butylene succinate-co-butylene adipate) (PBSA) and complete degradation of the polymeric films were observed at 72 h and 16 h respectively. The degradation was evaluated by Fourier transform infrared (FTIR) and ^1H NMR spectroscopy. The complete hydrolysis of polymers by *Cryptococcus* sp. lipase makes the process ideal and also serves as a baseline for its exploitation in polymer degradation.

Keywords: *Cryptococcus* sp.; Lipase; Cottonseed oil cake; Poly(butylene succinate); Poly(butylene succinate-co-butylene adipate); Degradation

Kashif Rasool[a], Dae Sung Lee[b]. ([a] Qatar Environment and Energy Research Institute, Hamad Bin Khalifa University, Qatar Foundation, PO BOX 5825, Doha, Qatar, [b] Department of Environmental Engineering, Kyungpook National University, 80 Daehak-ro, Buk-gu, Daegu 41566, Republic of Korea). Effect of ZnO nanoparticles on biodegradation and biotransformation of co-substrate and sulphonated azo dye in anaerobic biological sulfate reduction processes. International Biodeterioration & Biodegradation, Volume 109(2016): 150–156

In recent years, rapid increase of nanomaterial applications exposed the wastewater treatment plants to the new challenges. Potential effects of nanoparticles (NPs) on biological sulfate reduction and dyes biodegradation in biological wastewater treatment systems still need to be investigated. This study explored the effects of zinc oxide nanoparticles (ZnO-NPs) on sulfate reducing bacteria (SRB) culture treating textile wastewater. Batch reactor studies were performed by exposing the mixed SRB culture to different initial ZnO-NPs concentrations. Increasing ZnO-NPs concentrations from 0 to 200 mg l^{-1} inhibited the reactor performance by decreasing COD, sulfate, and color removal efficiencies from 54.4%, 78.1%, and 95.4% to 30.1%. 44.0%, and 80.0%, respectively. Moreover, dye biotransformation was also adversely affected in the presence of ZnO-NPs as revealed by the increase in total aromatic amines formation and the decrease in activities of various oxido-reductive enzymes such as veratryl alcohol oxidase, lignin peroxidase, and azo reductase.

Keywords: Zinc oxide nanoparticles; Direct red 80; Biological sulfate reduction; Wastewater; Biotransformation

Shiying Sun, Zhen Zhang, Yuancai Chen, Yongyou Hu. (The Key Lab of Pollution Control and Ecosystem Restoration in Industry Clusters, Ministry of Education, State Key Laboratory of Pulp and Paper Engineering, College of Environment and Energy, South China University of Technology, Guangzhou Higher Education Mega Centre, Guangzhou 510006, PR China). Biosorption and biodegradation of BDE-47 by *Pseudomonas stutzier*. International Biodeterioration & Biodegradation, Volume 108(2016): 16–23

The biosorption and biodegradation in the removal process of 2, 2, 4, 4-tetrabromodiphenyl ether (BDE-47) by *Pseudomonas stutzier KS0013* (*Ps*) were investigated to elucidate the bio-dissipation mechanism with the influences of glucose and rhamnolipids. The sorption capacity of live *Ps* (1.163 mg g^{-1}) was significantly larger than that of heat-killed *Ps* (0.845 mg g^{-1}), indicating biosorption of BDE-47 was metabolically mediated. The BDE-47 was rapidly adsorbed by *Ps* at the initial stage, and degradation was observed only after 4 h. Based on the *Kp* values, the BDE-47 was more likely to dissolve in water rather than adsorb on the *Ps*. Furthermore, cell surface hydrophobicity of *Ps* was significantly enhanced with additional rhamnolipids. Meanwhile, rhamnolipids was adsorbed on BDE-47 binding sites and subsequently blocked BDE-47 biosorption, therefore posed an adverse effect on biodegradation.

Keywords: Biosorption; Biodegradation; 2,2,4,4-Tetrabromodiphenyl ether (BDE-47); Hydrophobicity; Rhamnolipids

Péter Harkai, István Szabó' , Mátyás Cserháti, Csilla Krifaton, Anita Risa, Júlia Radó, Adrienn Balázs, Kinga Berta, Balázs Kriszt. (Department of Environmental Safety and Ecotoxicology, Institute of Aquaculture and Environmental Safety, Szent István University, 1 Páter Károly St Gödöllő 2100, Hungary). Biodegradation of aflatoxin-B1 and

zearalenone by *Streptomyces* sp. Collection. International Biodeterioration & Biodegradation, Volume 108, March 2016, Pages 48–56

Aflatoxin B1 (AFB1) and zearalenone (ZON) are hazardous mycotoxins. AFB1 has cytotoxic, mutagenic and carcinogenic effects, whereas ZON can disrupt the endocrine system. Biodegradation by microbes is an effective method to eliminate these hazardous toxins. The aim of this work was to screen AFB1 and ZON biodegrading potential of one hundred and twenty-four *Streptomyces* strains deposited in the *Actinomycetes* strain collection of the Department of Environmental Safety and Ecotoxicology. Two different biotests were used for screening purposes: SOS-Chromotest was used to monitor genotoxicity and select microorganisms with the best AFB1 degrading potential. Estrogenic effect of ZON was measured with a yeast based bioluminescent test including human estrogen receptors Bioluminescent Yeast Estrogen System (BLYES). Biodegradation experiments were conducted with 1 mg l^{-1} AFB1 and 1 mg l^{-1} ZON concentration. On the base of the results, ten strains were selected for biodegradation experiments and Enzyme-linked Immunosorbent Assay tests (ELISA). The results of these tests *Streptomyces cacaoi subsp. asoensis* (K234) strain degraded AFB1 over 88 per cent and totally eliminated genotoxicity. Two strains of *Streptomyces rimosus* (K145, K189) degraded almost total amount of ZON and estrogenicity was not detected besides that.

Keywords: Mycotoxin; Aflatoxin B1; Zearalenone; *Streptomyces*; Biodegradation

Travers H. Ching[a, b], Brandon A. Yoza[a], Ruijin Wang[a, b], Stephen Masutani[a], Stuart Donachie[c], Lloyd Hihara[d], Qing X. Li[b]. ([a] Hawaii Natural Energy Institute, 1680 East West Rd. POST #109, University of Hawai‘i at Mānoa, HI 96822, USA, [b] Department of Molecular Biosciences and Bioengineering, 1955 East West Rd. Ag. Science #218, University of Hawai‘i at Mānoa, HI 96822, USA, [c] Department of Microbiology, 2538 McCarthy Mall, Snyder Hall 207, University of Hawai‘i at Mānoa, HI 96822, USA, [d] Department of Mechanical Engineering, 2540 Dole St. #302, University of Hawai‘i at Mānoa, HI 96822, USA). **Biodegradation of biodiesel and microbiologically induced corrosion of 1018 steel by *Moniliella wahieum* Y12. International Biodeterioration & Biodegradation, Volume 108(2016): 122–126**

A putatively novel basidiomycetous fungus termed *Moniliella wahieum* $Y12^T$ was isolated from a 20% biodiesel blend. The strain maximally degraded biodiesel at a rate of 3.56×10^{-2} mg/h during log phase growth. Induction of metal corrosion by the strain in a mass loss procedure using 1018 metal coupons showed total mass reduction exceeded that in controls by 70% through 30 days. Enhanced corrosion was observed at the pellicle and due to medium acidification. This is the first investigation of a *Moniliella* sp. and its impact on biodiesel stability and 1018 steel corrosion. (*M. wahieum* $Y12^T$ = ATCC MYA-4962).

Keywords: Microbiologically influenced corrosion; Biodiesel; Biodegradation; Corrosion; *Moniliella wahieum* Y12; MIC

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tolerant to diverse physical settings – Assessments in liquid- and slurry-phase systems. International Biodeterioration & Biodegradation, Volume 108(2016): 149–157

Field-scale bioremediation of PAHs contaminated soils have proved to be difficult and challenging due to inhibited growth of PAH degrading microbes. In this study, for the first time mixed bacterial cultures designated as consortia-A and N were developed using elite metal or acid tolerant, N-fixing, P-solubilizing and biosurfactant producing PAH degraders enriched from manufactured gas plant sites. The two consortia could degrade both LMW and HMW PAHs. Kinetic studies of PAH degradation by the consortia showed the highest biodegradation rate constants (k = 0.027–0.61 day^{-1}) and lowest half-life time (*t1/2* = 1–26 days) values reported to date in liquid cultures and highlighted the use of consortium-A for the remediation of acidic soils due to its tolerance up to pH 5. Furthermore, bioaugmentation of these consortia has proven to be effective in degradation of LMW (>95%) and HMW (90%) PAHs from spiked soil slurries. Amendment of consortia-A and N exhibited 10.7 and 44.3% more total PAHs degradation, respectively than natural attenuation in 60 days even from the real long-term mixed contaminated soils. Thus the results of this study demonstrate the great potential of these novel bacterial consortia, particularly consortium-N for use in field-scale bioremediation of PAHs in long-term mixed contaminated neutral soils.

Keywords: PAHs; Heavy metals; Bacterial consortia; PGPR; MGP soil; Bioremediation

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Exploring the capacity for anaerobic biodegradation of polycyclic aromatic hydrocarbons and naphthenic acids by microbes from oil-sands-process-affected waters. International Biodeterioration & Biodegradation, Volume 108(2016): 214–221

Both polycyclic aromatic hydrocarbons (PAHs) and naphthenic acids (NAs) are natural components of fossil fuels, but they are also widespread toxic and environmentally persistent pollutants. They are the major cause of environmental toxicity in oil-sands-process waters (OSPW). This study aimed to investigate the anaerobic biodegradation of the PAHs pyrene and 2-methylnaphthalene, and the NAs adamantane-1-carboxylic acid and a “natural” NA mixture (i.e., acid-extractable NAs from OSPW) under sulfate-reducing and methanogenic conditions by a microbial community derived from an oil sands tailings pond. Using gas-chromatography mass spectrometry (GC–MS), the rate of biodegradation was measured in relation to changes in bacterial community composition. Only 2-methylnaphthalene was significantly degraded after 260 days, with significantly more degradation under sulfate-reducing (40%) than methanogenic conditions (25%). During 2-methylnaphthalene biodegradation, a major metabolite was produced and tentatively identified as 2-naphthoic acid. Denaturing gradient gel electrophoresis (DGGE) demonstrated an increase in intensity of bands during the anaerobic biodegradation of 2-methylnaphalene, which derived from species of the genera *Fusibacter*, *Alkaliphilus*, *Desulfobacterium*, *Variovorax*, *Thaurea*, and *Hydrogenophaga*. Despite the biodegradation of 2-methylnaphthalene, this study demonstrates that, under anaerobic conditions, NAs and high-molecular-weight PAHs are the predominant molecules likely to persist in OSPW. Therefore alternative remediation strategies are required.

Keywords: Polycyclic aromatic hydrocarbon; Naphthenic acids; Oil sands process waters; Anaerobic biodegradation

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Microbial degradation is a promising soil remediation strategy for polycyclic aromatic hydrocarbons (PAHs) frequently polluting some post-industrial environments. Thirteen PAH-degrading bacterial strains were isolated from bare or ryegrass-vegetated aged-contaminated soil, based on their potential for phenanthrene biodegradation. 16S rRNA gene phylogeny showed that all isolates were affiliated with three closely related taxonomic subgroups within the *Pseudomonas* genus. Two of these subgroups were exclusively retrieved from planted soil. Genes encoding PAH-ring hydroxylating dioxygenases were detected in all strains and matched known sequences in other *Pseudomonas* strains from polluted environments. Genes for protocatechuate-3,4-dioxygenases (*pca*H) and catechol-2,3-dioxygenases were also detected in all strains, whereas the catechol-1,2-dioxygenase gene was absent. The presence of *pca*H genes, the utilization of protocatechuate, the strong inhibitory effect of salicylate and the detection of phthalate during phenanthrene biodegradation suggest that these isolates preferentially catabolize PAHs *via* the protocatechuate pathway. Metabolic profiling was further performed for three representative isolates on a large range of 61 organic substrates. Although closely related phylogenetically, they were able to use different sets of labile carbon compounds (e.g. sugars, amino acids), PAHs and their metabolites, and released different degradation products from phenanthrene. These contrasted metabolic capabilities might reflect differential adaptation to their respective environment.

Keywords: Phenanthrene; *Pseudomonas*; Dioxygenase; Bioremediation; Ryegrass

Sandra Ricci[a], Federica Antonelli[a], Carlotta Sacco Perasso[a], Domenico Poggi[b], Edoardo Casoli[c]. ([a] ISCR, Superior Institute for Conservation and Restoration, Biology Laboratory, Via di San Michele, 23, 00153 Rome, Italy, [b] Artelab S.r.l., ISCR, via Federico Nansen, 102, 00154 Roma, Italy, [c] Sapienza University of Rome, Department of Environmental Biology, Piazzale Aldo Moro, 5, 00185 Rome, Italy). **Bioerosion of submerged lapideous artefacts: Role of endolithic rhizoids of *Acetabularia acetabulum* (Dasycladales, Chlorophyta). International Biodeterioration & Biodegradation, Volume 107(2016): 10–16**

The endolithic activity of the green alga *Acetabularia acetabulum* (Linnaeus) P.C. Silva, 1952 (Ulvophyceae, Dasycladales, Polyphysaceae) was documented on different lithotypes recovered in the Underwater Archaeological Park of Baiae (Naples). The results show that rhizoids of *A. acetabulum* penetrate several micrometres deep into marble and limestone creating characteristic ramified boreholes, while they colonized only the surface of brick.

Resin casts of tunnels bored by rhizoids, known as the ichnospecies *Fascichnus grandis* Radtke, 1991, were described in detail.

The study reports for the first time the significant role of *A. acetabulum* in the bioerosion process of underwater archaeological artefacts.

Keywords: Bioerosion; *Acetabularia acetabulum*; Endolithic rhizoids; *Fascichnus grandis*; Ichnospecies; Cultural heritage; Baiae (Naples, Italy)

Yuhua Liu[a, b], Xiaoke Hu[a], Hui Liu[c]. ([a] Key Laboratory of Coastal Biology and Bioresource Utilization, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, China, [b] University of Chinese Academy of Sciences, Beijing, China, [c] Diyuan Biological Technology Co., Ltd., Yantai, China). **Industrial-scale culturing of the crude oil-degrading marine *Acinetobacter* sp. strain HC8-3S. International Biodeterioration & Biodegradation, Volume 107(2016): 56–61**

The marine bacterium *Acinetobacter* sp. strain HC8-3S, capable of degrading petroleum hydrocarbons, was previously shown to be applicable for bioremediation. Here, we evaluated the performance of the strain during industrial-scale fermentation, long-term storage, and biodegradation processes. Fermentation parameters were optimized for industrial-scale culturing using lower salinity and fewer inorganic salts in the culture medium. The shelf-life of the fermentation broth was evaluated in different storage conditions. Biodegradation efficiency of the strain was evaluated using gas chromatography. Results indicated that the optimum conditions for one-ton scale fermentation were 30 °C, pH 7.4–7.8, and rotation speed 90 rpm; the cell density reached $3.6 \pm 1.9 \times 10^{10}$ CFU ml^{-1} after 12 h. The low temperature can preserved fermentation broth for longer time. When the storage temperature was down to 4 °C from room temperature, half-life of strain HC8-3S extended from 9 days to 34 days. The biodegradation rate of the saturated hydrocarbon fraction of crude oil was 94% after treatment with the strain for 5 days. The results indicate that *Acinetobacter* sp. strain HC8-3S can be enriched efficiently on a large scale, making it a potentially useful industrial strain. This crude oil degradative capability of the strain HC8-3S provides possible application for the clean-up of crude oil-contaminated environment.

Keywords: *Acinetobacter* sp.; Industrial-scale fermentation; Long-term storage; Crude oil-degrading bacterium

Haiyan Zhou, Hui Wang, Yong Huang, Tingting Fang. (State Key Joint Laboratory on Environmental Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing 100084, China). **Characterization of pyrene degradation by halophilic *Thalassospira* sp. strain TSL5-1 isolated from the coastal soil of Yellow Sea, China. International Biodeterioration & Biodegradation, Volume 107(2016): 62–69**

High molecular weight polycyclic aromatic hydrocarbons (HMW-PAHs) are more persistent and less bioavailable because of their poorer solubility in saline environments. In this study, a new halophilic bacterium capable of degrading various HMW-PAHs was isolated from the coastal soil of Yellow Sea, China. It was identified as *Thalassospira* sp. strain TSL5-1 based on 16S rRNA gene sequence analysis and biochemical tests. Influences of salinity, pH and additional nutrients on pyrene degradation by TSL5-1 were investigated. The pyrene degradation could occur at salinity ranging from 0.5% to 19.5%, with optimal value kept between 3.5% and 5%. The degradation activity was affected greatly by pH fluctuation. Yeast could efficiently promote pyrene removal while peptone had the opposite effect. GC–MS analysis revealed that the pyrene was degraded to generate a series of intermediates such as phenanthrene-4-carboxylic acid methyl ester, 2-hydroxy-2-H-benzo[h]chromene-2-carboxylic acid, 2-carboxylbenzaldehyde, phthalic acid and salicylic acid. Particularly, identification of phthalic acid and salicylic acid showed that phthalate and salicylic acid routes were simultaneously contained in the pyrene

degradation, which was remarkably different from those for other pyrene-degraders. To our knowledge, it was the first time to propose a metabolic pathway of pyrene degradation by *Thalassospira* strains.

Keywords: Pyrene; Halophile; *Thalassospira* sp.; Metabolic pathway; Salicylic acid route

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Tributyltin (TBT) is one of the most deleterious compounds introduced into natural environment by humans. The ability of *Cunninghamella echinulata* to degrade tributyltin (TBT) (5 mg l^{-1}) as well as the effect of the xenobiotic on fungal amino acids composition and proteins profile were examined. *C. echinulata* removed 91% of the initial biocide concentration and formed less hazardous compounds dibutyltin (DBT) and monobutyltin (MBT). Moreover, the fungus produced a hydroxylated metabolite (TBTOH), in which the hydroxyl group was bound directly to the tin atom. Proteomics analysis showed that in the presence of TBT, the abundances of 22 protein bands were changed and the unique overexpressions of peroxiredoxin and nuclease enzymes were observed. Determination of free amino acids showed significant changes in the amounts of 19 from 23 detected metabolites. A parallel increase in the level of selected amino acids such as betaine, alanine, aminoisobutyrate or proline and peroxiredoxin enzyme in TBT-containing cultures revealed that TBT induced oxidative stress in the examined fungus.

Keywords: Fungi; Tributyltin; Biodegradation; LC-MS/MS; Proteomics; Oxidative stress

S. Sasso[a], A.Z. Miller[b], M.A. Rogerio-Candelera[b], B. Cubero[b], M.L. Coutinho[c], L. Scrano[d], S.A. Bufo[a]. ([a] Department of Sciences, University of Basilicata, Via dell'Ateneo Lucano 10, 85100, Potenza, Italy, [b] Instituto de Recursos Naturales y Agrobiologia de Sevilla (IRNAS-CSIC), Av. Reina Mercedes 10, 41012 Seville, Spain, [c] Vicarte, Departamento de Conservação e Restauro, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Monte de Caparica, 2829-516 Caparica, Portugal, [d] Department of European Cultures (DICEM), University of Basilicata, Via dell'Ateneo Lucano 10, 85100, Potenza, Italy). **Potential of natural biocides for biocontrolling phototrophic colonization on limestone. International Biodeterioration & Biodegradation, Volume 107(2016): 102–110**

Rocks, either in natural geological outcrops or in stone monuments, are common habitats for a wide variety of microorganisms which colonize both rock surfaces and cracks. Physical properties such as porosity and surface roughness make limestone susceptible to biological colonization, which may induces aesthetic and/or physical and chemical damages. Organisms causing biodeterioration on monuments have usually been controlled by chemical products (biocides). In order to overcome the impact of these substances on the environment, human health and stone substrates, alternative tools such as natural products from plants or microorganisms can be used as an innovative approach for stone conservation.

In this work, the efficiency of natural biocides (cells free culture filtrates of *Trichoderna harzianum* and *Burkholderia gladioli*, as well as glycoalkaloids from spontaneous *Solanaceae*) was tested under laboratory conditions against a multi-species phototrophic culture developing on Hontoria limestone. Their efficiency was assessed by digital image analysis, *in vitro* chlorophyll *a* quantification and confocal laser scanning microscopy. These techniques showed a

good correlation, revealing that cells free filtrate of *Trichoderma harzianum* had an antagonistic action against the multi-species phototrophic culture tested in this work.

Keywords: Stone; Biodeterioration; Biocide; Phototrophic colonization; Digital image analysis

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Phenol is a toxic aromatic compound produced as a by-product of industrial activities. Biological treatment of highly saline wastewaters containing phenol can be performed through halophilic microorganisms. In this study, the ability of halophilic archaeal isolates to degrade phenol was investigated. Among 103 tested isolates, the strain designated A235 was identified as having the highest phenol degradation capacity on solid and liquid media containing 20% (w/v) NaCl and phenol as the sole carbon and energy source. The strain was adapted sequentially to increasing phenol concentrations. The removal of phenol via cross-toluene adaptation was increased by 14% in the medium. The growth kinetics of strain A235 during growth on phenol was found to fit the Monod model. The values of μmax and Ks were calculated to be 0.015 h^{-1} and 71.4 g l^{-1}, respectively. For an initial phenol concentration of 100 ppm, the biodegradation by A235 was found to be optimal at pH 7.5, 37 °C and 200 rpm when the culture contained 20% (w/v) NaCl, 0.025% yeast extract and the inoculum size was set at 10%. A preliminary enzyme screening indicated that the degradation of phenol was achieved through a *meta*-cleavage pathway involving a catechol 2,3-dioxygenase. Catechol 2,3-dioxygenase displayed its highest catalytic activity at 42 °C, 2 M KCl, and pH 8. To the best of our knowledge, this is the first report showing the ability an extremely halophilic archaeon to metabolize phenol at higher salt concentrations.

Keywords: Halophilic archaea; Phenol biodegradation; Adaptation; Catechol 2,3-dioxygenase

Laura Levin[a, 1], Maira Carabajal[a, 1], Martin Hofrichter[b], René Ullrich[b]. ([a] University of Buenos Aires, Faculty of Exact and Natural Sciences, Department of Biodiversity and Experimental Biology, Intendente Güiraldes 2160 – Ciudad Universitaria – C1428EGA, Argentina, [b] Technical University of Dresden – International Institute Zittau, Department of Bio- and Environmental Science, Markt 23, Zittau 02763, Germany). **Degradation of 4-nitrophenol by the white-rot polypore *Trametes versicolor.* International Biodeterioration & Biodegradation, Volume 107(2016): 174–179**

The ability of *Trametes versicolor* strain BAFC 2234 to degrade 4-nitrophenol *in vivo* and *in vitro* was evaluated. *T. versicolor* grew in the presence of 0.5 mM 4-nitrophenol and degraded 98.4% of this toxic compound in less than 96 h. The strain secreted different ligninolytic oxidoreductases such as laccase, Mn-peroxidase and versatile peroxidase. Substantial conversion of nitrophenol, a typical high-redox potential phenolic substrate, is reported for versatile peroxidase for the first time; 2,4-dinitrophenol and a dimer were identified as products. *T. versicolor* immobilized on natural sponge-like material from *Luffa aegyptiaca* removed 97% of 4-nitrophenol (1 mM) over a period of 72 h. 4-Nitrophenol phytotoxicity decreased noticeably after fungal treatment.

Keywords: 4-Nitrophenol transformation; *Trametes versicolor*; Versatile peroxidase; Immobilization

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Bisphenol A (BPA) has been described as a estrogenic compound. However, it is used in the production of polycarbonate, epoxy resins and other plastics. Mixed microbial cultures, such as activated sludge, have been proposed as a feasible methodology to achieve the decontamination of wastewater containing BPA. Several studies on the biodegradation of BPA have demonstrated the presence of 4-hydroxyacetophenone (4HAP), 4-hydroxybenzaldehyde (4HB) and 4-hydroxybenzoic acid (A4HB) as the main metabolic intermediates. The objective of the present work was to study the kinetics and stoichiometric characteristics of the aerobic degradation of BPA and its metabolic intermediates by activated sludge. The effect of the sludge age (SA), and the concentration of each compound was analyzed. The biodegradation of the compounds was analyzed by an open respirometer. The kinetics of the biodegradation of all the tested compounds was influenced by the SA, the acclimation process, and the concentration of the tested compound. The stoichiometry of the reactions was not affected by the studied conditions. The oxidation coefficient ($Y_{O/S}$) was 10.0 ± 0.5, 5.2 ± 0.2, 3.7 ± 0.2, and 3.0 ± 0.1 $molO_2\ molS^{-1}$ for BPA, 4HAP, 4HB, and 4HBA, respectively. Based on the obtained $Y_{O/S}$ values, the aerobic biodegradation pathway of the tested compounds by BPA-acclimated activated sludge is discussed.

Keywords: Activated sludge; Bisphenol A; Kinetics; Stoichiometry

Cristina González-Fernández[a], Ahmed Mahdy[a, b], Ignacio Ballesteros[a, c], Mercedes Ballesteros[a, c]. ([a] Biotechnological Processes for Energy Production Unit – IMDEA Energy, 28935 Móstoles, Madrid, Spain, [b] Department of Agricultural Microbiology, Faculty of Agriculture, Zagazig University, 44511 Zagazig, Egypt, [c] Biofuels Unit – Research Center for Energy, Environment and Technology (CIEMAT), 28040 Madrid, Spain). Impact of temperature and photoperiod on anaerobic biodegradability of microalgae grown in urban wastewater. International Biodeterioration & Biodegradation, Volume 106(2016): 16–23

This study was designed to elucidate how temperature and photoperiod, two of the principal parameters affecting microalgae culture conditions influenced the anaerobic digestion of harvested biomass when grown in wastewater under different scenarios (I: 23°C/14 h illumination, II: 15 °C/14 h and III: 15 °C, 11 h). With respect to biomass cultivation, temperature affected biomass productivity but not final biomass concentration. Scenario I mediated faster ammonium and phosphate removal (100% for all the evaluated scenarios) and greater organic matter removal (80.5% compared to 56.5% and 70.8% obtained for Scenario II and III, respectively). Biomass grown under unfavorable conditions of light and temperature (Scenario III) evidenced the highest nitrogen assimilation due to the lowest ammonia stripping (6%). Different cultivation scenarios resulted in a different macromolecular profile of the harvested biomass. Carbohydrates accumulation prevailed under Scenario I while low temperature (Scenario II) and short photoperiod (Scenario III) increased lipid and protein

content. Harvested biomass was subjected to anaerobic digestion. Anaerobic biodegradability of the three types of biomass remained in the narrow range of 36–42%, however different hydrolysis constant rates were calculated. Comparison between the theoretically calculated and experimentally obtained methane yield values showed that biomass collected at Scenario III only reached 36.1% of the theoretical methane yield achievable compared to 46.5% attained with the biomass collected at Scenario I. Further research on microalgae communities and cell wall composition is required to understand the methane yield mismatch.

Keywords: Microalgae; Wastewater; Nutrients; Recovery; Methane

Hao Zhang[a, 1], Yamei Zhang[b, 1], Zhiguang Hou[a], Xiaomei Wang[c], Jing Wang[a], Zhongbin Lu[a], Xiaofeng Zhao[a], Fengjie Sun[d], Hongyu Pan[b]. ([a] College of Resource and Environment, Jilin Agricultural University, Changchun, PR China, [b] College of Plant Sciences, Jilin University, Changchun, PR China, [c] College of Agriculture, Jilin Agricultural University, Changchun, PR China, [d] School of Science and Technology, Georgia Gwinnett College, Lawrenceville, GA, USA). **Biodegradation potential of deltamethrin by the *Bacillus cereus* strain Y1 in both culture and contaminated soil. International Biodeterioration & Biodegradation, Volume 106(2016): 53–59**

Pesticide residues in soil are closely related to food safety. Microbial degradation is one of the effective ways to remove the pesticide residues. We isolated a potentially deltamethrin degrading bacterium *Bacillus cereus* strain Y1 and characterized its dissipation capability in both culture and contaminated soil. In liquid medium, the optimal temperature, pH value, and inoculum of dissipation were 30 °C, 7.0, and 7.0% (v/v), respectively. The dissipation rates were 99.4% and 22.8% in 96 h when the initial concentration of deltamethrin were 10 and 100 mg l^{-1}, respectively. Dissipation of deltamethrin followed the pesticide degradation kinetic equation at initial concentrations between 5 and 100 mg l^{-1}. Soil sample was contaminated by deltamethrin with a concentration of 10 mg kg^{-1}, inoculation of 10^{10} CFU g^{-1} dry soil, and cultured at 30 °C. The dissipation rate of deltamethrin was 74.9% in 25 days and was only 45.1% in control lacking strain Y1. Results in greenhouse and open field experiments demonstrate that strain Y1 increases the dissipation rate of deltamethrin in both soil and Chinese cabbage. This study provides scientific evidence and support for the agricultural applications of *B. cereus* strain Y1 in bioremediation to reduce pesticide residues.

Keywords: *Bacillus cereus*; Biodegradation; Bioremediation; Deltamethrin; Dissipation; Y1

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Wheat bran was tested as the solid substrate for the tray-type solid-state fermentation (SSF) production of polygalacturonase (PG) enzyme by *A. sojae* mutant strain – a high-PG activity producer. PG production of *A. sojae* was found to reduce as the thickness of the substrate increase from 8 mm to 14 mm at 90% relative humidity. An interaction between the thickness of the bed and relative humidity of the environment was determined with the help of experimental design and statistical analysis tools. As a result, the PG activity could be enhanced by 31% as the process conditions optimized. Additionally, 11 mm thickness and 70% relative humidity were

selected as the PG production favoring conditions with the maximum PG activity of 298 U/g substrate in tray type of SSF without the addition of any nutritive or inducing supplements into wheat bran. The kinetic study conducted in the trays revealed the presence of reduction in the water activity on the 4th day of the SSF process under stated conditions. The productivity of the process conducted under optimized conditions was 3.41 U/g substrate^{-1} h^{-1} for the 4th day of the SSF.

Keywords: Wheat bran; Solid-state fermentation; *Aspergillus sojae*; Tray type fermentation

Federica Marano[a], Federico Di Rita[b], Maria Rita Palombo[a], Neil Thomas William Ellwood[c], Laura Bruno[d]. ([a] Dipartimento di Scienze della Terra – Sapienza, Università di Roma, Piazzale Aldo Moro, 5, 00185 Roma, Italy, [b] Dipartimento di Biologia Ambientale – Sapienza, Università di Roma, Piazzale Aldo Moro, 5, 00185 Roma, Italy, [c] Dipartimento di Scienze, Università Roma Tre, Viale G. Marconi 446, 00146 Roma, Italy, [d] Dipartimento di Biologia, Università di Roma 'Tor Vergata', Via della Ricerca Scientifica snc, 00133 Roma, Italy). **A first report of biodeterioration caused by cyanobacterial biofilms of exposed fossil bones: A case study of the middle Pleistocene site of La Polledrara di Cecanibbio (Rome, Italy). International Biodeterioration & Biodegradation, Volume 106, January 2016, Pages 67–74**

La Polledrara di Cecanibbio is a Pleistocene fossiliferous deposit near Rome (Italy) where large quantities of bones, belonging mainly to elephants, have been discovered and 'musealized' under an enclosing structure. The prevailing environmental conditions inside the museum and the exposition *in situ* of the fossilized remains have resulted in the development of phototrophic biofilms on the bones and the nearby sediments. Samples of bones and sediment were investigated with different microscopy techniques (light, confocal laser scanning, scanning electron and petrographic microscopes) that allowed the identification of the cyanobacterium *Leptolyngbya* sp. as the almost entirely dominant organism of the biofilms. The present study identifies for the first time endolithic activity of this cyanobacterium on exposed fossilized bones. There was some indication that this species was euendolithic but this remains to be elucidated. The development of these phototrophic biofilms greatly reduces the aesthetic value of the site and evidence suggests that they may cause extensive structural damage to the bones, threatening the scientific and cultural assets of one of the richest fossiliferous deposits in Italy. This study on the biodeterioration of fossil remains gives useful insights for the conservation of this spectacular site.

Keywords: *Leptolyngbya* sp.; Endolithic activity; Fossil bones; Conservation of Cultural Heritage; Microscopy

Yongrui Pi[a, b], Long Meng[a, b], Mutai Bao[a, b], Peiyan Sun[c], Jinren Lu[b]. ([a] Key Laboratory of Marine Chemistry Theory and Technology, Ministry of Education, Ocean University of China, Qingdao 266100, China, [b] College of Chemistry & Chemical Engineering, Ocean University of China, Qingdao 266100, China, [c] Key Laboratory of Marine Spill Oil Identification and Damage Assessment Technology, North China Sea Environmental Monitoring Center, State Oceanic Administration, Qingdao 266033, China). **Degradation of crude oil and relationship with bacteria and enzymatic activities in laboratory testing ☆. International Biodeterioration & Biodegradation, Volume 106(2016): 106–116**

The biodegradation of petroleum hydrocarbons is one of the most important processes involved in the weathering and eventual removal of petroleum hydrocarbons from the marine environment. The effect of four variables—$(NH_4)_2SO_4$, K_2HPO_4, temperature and inoculation—

on crude oil biodegradation (BDR) were evaluated using response surface methodology to confirm the nutrients effect on the biodegradation and explore the relationships between BDR and bacterial biomass, dehydrogenase activity and peroxidase activity. These variables were optimized to allow the highest removal of crude oil, and the results indicated that crude oil removal could increase to even higher levels if the temperature and the concentrations of $(NH_4)_2SO_4$ and K_2HPO_4 were increased. Following biodegradation, the enzymatic activities were evaluated using a modified spectrophotometric method; the results showed that an increase in the temperature and inoculation quantity resulted in a higher dehydrogenase activity (mg TPF $(l{\cdot}h)^{-1}$) and that the highest peroxidase activity (18.50 U) occurred at 2.01 $g{\cdot}l^{-1}$ $(NH_4)_2SO_4$, 1.10 $g{\cdot}l^{-1}$ K_2HPO_4, 25 °C and 1.0% inoculation. The crude oil BDR increased substantially with bacterial biomass and decreased slightly with dehydrogenase activity or peroxidase activity, which was consistent with the coefficients in the fitted equation. The correlation between microbial degradation of crude oil and bacterial biomass and enzymatic activities can be used in simulations of biodegradation processes with petroleum hydrocarbons, PAHs and other hydrocarbon compounds and provides a more thorough understanding of the microbial community's function in contaminated soil.

Keywords: Crude oil; Biodegradation; Response surface methodology; The relationship; Enzymatic activities; Bacterial biomass

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Bioremediation is one of the milestones achieved by the biotechnological innovations. It is generating superior results in waste management such as removal of textile dyes, which are considered xenobiotic compounds and recalcitrant to biodegradation. In the present bioremedial approach, *Brevibacillus laterosporus* was used as an effective microbial tool to decolorize disperse dye Disperse Red 54 (DR54). Under optimized conditions (pH 7, 40°C), *B. laterosporus* led to 100% decolorization of DR54 (at 50 mg L^{-1}) within 48 h. Yeast extract and peptone, supplemented in medium enhanced the decolorization efficiency of the bacterium. During the decolorization process, activities of enzymes responsible for decolorization, such as tyrosinase, veratryl alcohol oxidase and NADH–-DCIP reductase were induced by 1.32-, 1.51- and 4.37-fold, respectively. The completely different chromatographic/spectroscopic spectrum of metabolites obtained after decolorization confirmed the biodegradation of DR54 as showed by High pressure liquid chromatography, High pressure thin layer chromatography and Fourier transform infrared spectroscopy. Gas chromatography–Mass spectroscopy studies suggested the parent dye was biodegraded into simple final product, *N*-(1λ^3-chlorinin-2-yl)acetamide. Phytotoxicity study suggested that the metabolites obtained after biodegradation of DR54 were non-toxic as compared to the untreated dye signifying the detoxification of the DR54 by *B. laterosporus*.

Keywords: Biodegradation; Bioremediation; Decolorization; Detoxification; High pressure thin layer chromatography

John E. Aston, , William A. Apel, , Brady D. Lee, , David N. Thompson, Jeffrey A. Lacey, Deborah T. Newby, David. W. Reed, Vicki S. Thompson. (Biological and Chemical Processing Department, Idaho National Laboratory, Biological and Chemical Processing Department, Idaho National Laboratory, Energy and Environment Directorate, Pacific Northwest National Laboratory). Degradation of phenolic compounds by the lignocellulose deconstructing thermoacidophilic bacterium *Alicyclobacillus Acidocaldarius.* Journal of Industrial Microbiology & Biotechnology, Volume 43(1) (2016): 13-23

Alicyclobacillus acidocaldarius, a thermoacidophilic bacterium, has a repertoire of thermo- and acid-stable enzymes that deconstruct lignocellulosic compounds. The work presented here describes the ability of *A. acidocaldarius* to reduce the concentration of the phenolic compounds: phenol, ferulic acid, ρ-coumaric acid and sinapinic acid during growth conditions. The extent and rate of the removal of these compounds were significantly increased by the presence of micro-molar copper concentrations, suggesting activity by copper oxidases that have been identified in the genome of *A. acidocaldarius*. Substrate removal kinetics was first order for phenol, ferulic acid, ρ-coumaric acid and sinapinic acid in the presence of 50 µM copper sulfate. In addition, laccase enzyme assays of cellular protein fractions suggested significant activity on a lignin analog between the temperatures of 45 and 90 °C. This work shows the potential for *A. acidocaldarius* to degrade phenolic compounds, demonstrating potential relevance to biofuel production and other industrial processes.

Keywords: *Alicyclobacillus acidocaldarius*, Thermophiles, Phenolics, Bioremoval

Jianfeng Hou[1], Feixia Liu[1, 3], Nan Wu[1, 2], Jiansong Ju[2] and Bo Yu[1]. ([1]CAS Key Laboratory of Microbial Physiological and Metabolic Engineering, Institute of Microbiology, Chinese Academy of Sciences. [2]University of Chinese Academy of Sciences). Efficient biodegradation of chlorophenols in aqueous phase by magnetically immobilized aniline-degrading *Rhodococcus rhodochrous* strain. Journal of Nanobiotechnology,14(2016): 5

Chlorophenols are environmental contaminants, which are highly toxic to living beings due to their carcinogenic, mutagenic and cytotoxic properties. Bacterial degradation has been considered a cost-effective and eco-friendly method of removing chlorophenols, compared to the traditional physical–chemical processes.

In this study, we first developed an efficient process for the biodegradation of chlorophenols by magnetically immobilized *Rhodococcus rhodochrous* cells. *R. rhodochrous* DSM6263 degrades chlorophenols following the first step of hydroxylation at the *ortho*-positions of chlorophenolic rings. The cells immobilized by *k*-carrageenan with 9 g/L Fe_3O_4 nanoparticles could efficiently degrade 2-chlorophenol, 4-chlorophenol, 2,3-dichlorophenol and their mixture, which were even higher than those by free cells. The magnetically nanoparticle-immobilized cells could be used at least for six cycles.

Given the much easier separation by an external magnetic field and high degradation efficiency, this study provides a promising technique for improving biocatalysts used in the bioremediation process for chlorophenols in wastewater.

Keywords: Chlorophenols; *Rhodococcus rhodochrous;* Magnetic immobilization; Bioremediation

Rifat Zubair Ahmed, Nuzhat Ahmed. (Centre for Molecular Genetics, University of Karachi. Department of Postgraduate Studies and Research, National Institute of Blood Disease and Bone Marrow Transplantatio, Centre for Molecular Genetics, University of Karachi). Isolation of *Rhodococcus* sp. CMGCZ Capable to Degrade High Concentration of Fluoranthene. Water, Air, & Soil Pollution, 227(2016):162

A bacterial strain CMGCZ was isolated from an abandoned oil field soil sample and identified as *Rhodococcus* sp. by 16S rRNA sequencing. *Rhodococcus* sp. CMGCZ was investigated for the degradation of model polycyclic aromatic hydrocarbons (PAHs) and Iranian light crude oil (ILCO) as a sole carbon source in minimal medium. Biodegradation enhancement was attained by supplementing the minimal medium with yeast extract (YE). *Rhodococcus* sp. CMGCZ was capable to degrade 13.2 % naphthalene (Nap), 13.1 % phenanthrene (Phe), and 99.3 % fluoranthene (Fla) in 1 week and 11 % aliphatic fraction of ILCO in 2 weeks as a sole carbon and energy source. Effect of YE supplementation on degradation potential of *Rhodococcus* sp. CMGCZ depended upon the added hydrocarbon in the medium. YE completely inhibited Nap degradation, slightly enhanced degradation of Phe (14.8 %) and ILCO aliphatics (13.2 %), and promoted a more rapid degradation of Fla (100 %). YE addition promoted rapid degradation of Fla and eliminated delay of 24 h in Fla degradation that was observed in minimal medium. *Rhodococcus* sp. CMGCZ was capable to degrade high concentrations of Fla (1000 mg l^{-1}). Rieske [Fe_2-S_2] center was amplified in *Rhodococcus* sp. CMGCZ that exhibited homology with Rieske [Fe_2-S_2] domain protein of *Mycobacterium* species and *pahAC* gene of uncultured bacterium clones.

Keywords: Biodegradation; Dioxygenase; Fluoranthene; *Rhodococcus;* Yeast extract

Shuyu Liu, Xiaohui Hu, Wenjun Jiang, Liyan Ma, Min Cai, Hong Xu, minghong Wu, Fang Ma. (School of Environment and Chemical Engineering, Shanghai UniversityState Key Laboratory of Urban Water Resource and Environment, Harbin Institute of Technology. (School of Environment and Chemical Engineering, Shanghai University, Department of Chemistry and Biochemistry, Florida International University, Key Laboratory of East China Sea and Oceanic Fishery Resources Exploitation, Ministry of Agriculture, Chinese Academy of Fishery Sciences, Department of Chemistry and Biochemistry, University of South Carolina, School of Environment and Chemical Engineering, Shanghai University, School of Environment and Chemical Engineering, Shanghai University, State Key Laboratory of Urban Water Resource and Environment, Harbin Institute of Technology). Degradation of Microcystins from *Microcystis aeruginosa* by 185-nm UV Irradiation. Water, Air, & Soil Pollution, 227(2016): 129

Microcystins (MCs) are toxic compounds produced by cyanobacteria in eutrophicate water environment and threaten the drinking water quality which often leads to serious sicknesses. MCs are difficult to be removed in water treatment when the concentration is very low but still harmful. When the MC concentration is low (μg/L), filter or some conventional chemical does not work, but UV can keep removing it to a lower level by some active groups. Herein, 185-nm UV irradiation in an immersing mode was used to remove MCs. Compared with the normal radiation mode, the immersing mode showed a remarkable degradation rate of MCs and a greater removal efficiency than the direct radiation. Radicals of ·H and ·OH were produced and strengthened the removal rate, after H_2O absorbed 185 nm photons. Three important factors of pH value, initial concentration, and aeration capacity were investigated. When pH was less than

7, a better removal rate by ·H was found, due to the main path of MC degradation and Adda strain removal. When the initial concentration increased, the MC removal ratio decreased because HO· formed near the lamp surface and degraded MC molecules fast. When the aeration capacity improved, the MC removal ratio for the presence of air enforced reaction of dissolved oxygen with hydrated electrons and hydrogen atoms produced in the radiolysis.

Keywords: Microcystins; Immersion; Irradiation185 nm UV; Degradation

Hongxia Xu, Xiaohui Li, Yuanyuan Sun, Xiaoqing Shi, Jichun Wu. (Key Laboratory of Surficial Geochemistry, Ministry of Education, School of Earth Sciences and Engineering, Hydrosciences Department, Nanjing University, Key Laboratory of Surficial Geochemistry, Ministry of Education, School of Earth Sciences and Engineering, Hydrosciences Department, Nanjing University, Key Laboratory of Surficial Geochemistry, Ministry of Education, Key Laboratory of Surficial Geochemistry, Ministry of Education, School of Earth Sciences and Engineering, Hydrosciences Department, Nanjing University). Biodegradation of Pyrene by Free and Immobilized Cells of *Herbaspirillum chlorophenolicum* Strain FA1. Water, Air, & Soil Pollution, 227 (2016): 120

Herbaspirillum chlorophenolicum strain FA1, a gram-negative bacterium isolated from activated sludge, was found to be able to use pyrene as sole carbon and energy sources. During biodegradation, the contribution of biosorption to the whole pyrene removal mattered in the early reaction stage, and biodegradation was the predominant process. Pyrene biodegradation was significantly enhanced with the presence of a typical carboxylated aromatic metabolite (phthalic acid) at concentrations of 30–50 mg l^{-1}, and the metabolite itself could also be efficiently biodegraded. For the purpose of practical application, immobilization of strain FA1 was carried out, and polyvinyl alcohol (PVA)-diatomite carrier by chemical method was proved to be the most efficient, with a PYR biodegradation of 92.8 % in 10 days. Investigation on the pyrene biodegradation kinetics by both free and immobilized cells showed that the experimental data fitted well to the first-order kinetic model. Besides, the PVA-diatomite carrier (chemical method) could be reused in at least eight consecutive biodegradation processes of PYR without any significant decrease in biodegradation efficiency. Further storage stability tests revealed that the ability to degrade pyrene using immobilized cells remained stable after storage at 4 °C for 45 days. Moreover, strain FA1 exhibited a relative broad substrate profile, including naphthalene, fluorene, phenanthrene, anthracene, fluoranthene, benzo[b]fluoranthene, benzene, toluene, and Tween 80. Taken together, results indicate that strain FA1 might be high potential in the development of treatment technologies for PAHs contamination.

Keywords: Pyrene; *Herbaspirillum chlorophenolicum;* Biodegradation; Biosorption; Immobilization

Sumaiya Al-Kindi, Raeid M. M. Abed. (Biology Department, College of Science, Sultan Qaboos University). Comparing Oil Degradation Efficiency and Bacterial Communities in Contaminated Soils Subjected to Biostimulation Using Different Organic Wastes. Water, Air, & Soil Pollution, 227(2016): 36

The use of organic wastes in bioremediation of oil-contaminated desert soils has received little attention, although their use is cost-effective. We evaluated the use of spent mushroom compost (SMC), poultry manure (PM), and urea in the stimulation of respiration activities and oil degradation in a polluted desert soil. Moreover, we followed post treatment shifts in bacterial community structure using MiSeq sequencing. The addition of SMC and PM resulted in a significant increase in the evolved CO_2 from 8.7 ± 1.9 to 25.7 ± 1.6 and to 23.4 ± 1.2 mg CO_2 g^{-1} soil after 96 days of incubation, respectively. In contrast, changes in respiration activities after

the addition of urea were insignificant. Gas chromatography–mass spectrometry (GC-MS) analysis revealed that most of the alkanes (C_{14}-C_{30}) were degraded in all biostimulated soils at a rate of 0.12–0.19 mg g^{-1} soil day^{-1}, which was significantly higher than in the untreated soil ($P < 0.05$). Bacterial community analysis showed that 87–94 % of total sequences in the original soil belonged to *Firmicutes*, *Actinobacteria*, and *Proteobacteria*. While the relative abundance of *Firmicutes* remained unchanged after the addition of PM (37–48 % of total sequences), it increased in the urea treatment (44–87 %) and dramatically decreased in the SMC treatment (0.5–4.5 %). The remaining bacterial groups were still detectable after the treatments, although no clear treatment-related shifts could be observed, due to the large difference in the relative abundance of the same bacterial groups among the same replicates. We conclude that the use of organic wastes could be one of the ways of combating petroleum pollution in desert soils.

Keywords: Organic wastes; Biostimulation; MiSeq; GC-MS; Desert soils

Alba Blánquez, Francisco Guillén, Juana Rodríguez, M. Enriqueta Arias, Manuel Hernández. (Department of Biomedicine and Biotechnology, University of Alcalá). The degradation of two fluoroquinolone based antimicrobials by SilA, an alkaline laccase from *Streptomyces ipomoeae.* World Journal of Microbiology and Biotechnology, 32(2016) : 52

The presence of fluoroquinolone based antimicrobials in natural waters represents a significant emerging environmental problem. In this study the suitability of a novel alkaline bacterial laccase, SilA, from *Streptomyces ipomoeae* to degrade two key antimicrobials, Ciprofloxacin and Norfloxacin under alkaline conditions in the presence of natural mediators was assessed. Results showed that only the selected SilA-acetosyringone system was able to degrade more than 90 % of both fluoroquinolones. HPLC analysis of the degradation products obtained after enzyme treatment confirmed the disappearance of the antimicrobials and the mediator after 24 h. The time course of the degradation showed that during the first 4 h a 75 % of degradation of fluoroquinolones was detected while the mediator remained stable. A concomitant appearance of new chromatographic peaks derived from the fluoroquinolones and/or the mediator was detected. Moreover, toxicity assays demonstrated that the SilA-acetosyringone system was able to reduce the toxicity of Ciprofloxacin and Norfloxacin by 90 and 70 %, respectively. In conclusion, these findings support the suitability of a low cost and environmentally friendly strategy based on the SilA-acetosyringone system for a primary treatment of contaminated alkaline wastewaters with this type of emerging pollutants.

Keywords: Biodegradation; Detoxification; Fluoroquinolones; Laccase-mediator system; *Streptomyces*

Qian Liu[a], Hong-ying Yang[a], Lin-lin Tong[a], Zhe-nan Jin[a], Wolfgang Sand[b]. ([a] School of Metallurgy, Northeastern University, 110819 Shenyang, China, [b] Aquatische Biotechnologie, Biofilm Centre, Universität Duisburg—Essen, 45141 Essen, Germany). Fungal degradation of elemental carbon in Carbonaceous gold ore. Hydrometallurgy, Volume 160(2016): 90–97

Phanerochaete chrysosporium was used to decompose elemental carbon in Carbonaceous gold ore and enhance cyanide recovery of gold. The degradation of elemental carbon amounted to 34% due to fungal treatment for 14 days. A positive correlation between the fungal degradation of elemental carbon and the activity of degradation enzymes was noted. Organic acids and nitrogenous bases, which are generated by the fungi, caused the degradation of elemental carbon

indirectly. *P. chrysosporium* caused a surface exfoliation of elemental carbon in the form of layers and the destruction of the microcrystalline and pore structure. The amount of oxygen-containing groups and of aliphatic groups was increased. The amount of aromatic rings, the specific surface area, the pore volume and the condensation index of aromatic rings were decreased. Also the thermal properties of elemental carbon changed significantly, whereas the amount of the low-stability compounds was increased. *P. chrysosporium* can reduce the interference of elemental carbon with the cyanide recovery of gold. The amount of gold recovery increased from 44% to 62%. This improvement is ascribed to the combined effect of degradation and passivation of elemental carbon by *P. chrysosporium*.

Keywords: *Phanerochaete chrysosporium*; Carbonaceous gold ore; Elemental carbon; Degradation; Cyanidation

Francisco Ríos, Alejandro Fernández-Arteaga, Manuela Lechuga, Encarnación Jurado, Mercedes Fernández-Serrano. (Department of Chemical Engineering, Faculty of Sciences, University of Granada). Kinetic study of the anaerobic biodegradation of alkyl polyglucosides and the influence of their structural parameters. Environmental Science and Pollution Research, Volume 23(9) (2016): 8286-8293

This paper reports a study of the anaerobic biodegradation of non-ionic surfactants alkyl polyglucosides applying the method by measurement of the biogas production in digested sludge. Three alkyl polyglucosides with different length alkyl chain and degree of polymerization of the glucose units were tested. The influence of their structural parameters was evaluated, and the characteristics parameters of the anaerobic biodegradation were determined. Results show that alkyl polyglucosides, at the standard initial concentration of 100 mgC L^{-1}, are not completely biodegradable in anaerobic conditions because they inhibit the biogas production. The alkyl polyglucoside having the shortest alkyl chain showed the fastest biodegradability and reached the higher percentage of final mineralization. The anaerobic process was well adjusted to a pseudo first-order equation using the carbon produced as gas during the test; also, kinetics parameters and a global rate constant for all the involved metabolic process were determined. This modeling is helpful to evaluate the biodegradation or the persistence of alkyl polyglucosides under anaerobic conditions in the environment and in the wastewater treatment.

Keywords: Alkyl polyglucosides; Anaerobic biodegradation; Digested sludge; Kinetics of biodegradation; Method of biogas production; Non-ionic surfactants

Yeonjung Lee, Bomi Lee, Jin Hur, Jun-Oh Min, Sun-Yong Ha, Kongtae Ra, Kyung-Tae Kim, Kyung-Hoon Shin. (Department of Marine Sciences and Convergent Technology, Hanyang University, Department of Environment and Energy, Sejong University, Division of Polar Ocean Environment Research, Korea Polar Research Institute, Marine Environment and Conservation Research Division, Korea Institute of Ocean Science and Technology). Biodegradability of algal-derived organic matter in a large artificial lake by using stable isotope tracers. Environmental Science and Pollution Research, Volume 23(9) (2016); 8358-8366

In order to understand the biodegradability of algal-derived organic matter, biodegradation experiments were conducted with ^{13}C and ^{15}N-labeled natural phytoplankton and periphytic algal populations in experimental conditions for 60 days. Qualitative changes in the dissolved organic matter were also determined using parallel factor analysis and the stable carbon isotopic composition of the hydrophobic dissolved organic matter through the experimental period. Although algal-derived organic matter is considered to be easily biodegradable, the initial amounts of total organic carbon newly produced by phytoplankton and periphytic algae

remained approximately 16 and 44 % after 60 days, respectively, and about 22 and 43 % of newly produced particulate nitrogen remained. Further, the dissolved organic carbon derived from both algal populations increased significantly after 60 days. Although the dissolved organic matter gradually became refractory, the contributions of the algal-derived organic matter to the dissolved organic matter and hydrophobic dissolved organic matter increased. Our laboratory experimental results suggest that algal-derived organic matter produced by phytoplankton and periphytic algae could contribute significantly to the non-biodegradable organic matter through microbial transformations.

Keywords Non-biodegradable organic matter; Stable isotope labeling; Phytoplankton; Periphytic algae; Biodegradability; PARAFAC

Chunyan Li, Hailian Zang, Qi Yu, Tongyang Lv, Yi Cheng, Xiaosong Cheng, Keran Liu, Wanjun Liu, Pianpian Xu. (College of Resource and Environment, Northeast Agricultural University, College of First Clinical Medicine, Harbin Medical University). Biodegradation of chlorimuron-ethyl and the associated degradation pathway by *Rhodococcus* sp. D310-1. Environmental Science and Pollution Research, Volume 23(9) (2016): 8794-8805

Chlorimuron-ethyl is a typical long-term residual sulfonylurea herbicide, and strategies for its removal have attracted increasing attention. Microbial degradation is considered the most acceptable dissipation method. In this study, we optimized the cultivation conditions (substrate concentration, pH, inoculum concentration, and temperature) of the chlorimuron-ethyl-degrading bacterium *Rhodococcus* sp. D310-1 using response surface methodology (RSM) to improve the biodegradation efficiency. A maximum biodegradation rate of 88.95 % was obtained. The Andrews model was used to describe the changes in the specific degradation rate as the substrate concentration increased. Chlorimuron-ethyl could be transformed with a maximum specific degradation rate (q_{max}), half-saturation constant (K_S), and inhibition constant (K_i) of 0.4327 day^{-1}, 63.50045 mg L^{-1}, and 156.76666 mg L^{-1}, respectively. Eight biodegradation products (2-amino-4-chloro-6-methoxypyrimidine, ethyl 2-sulfamoyl benzoate, 2-sulfamoyl benzoic acid, *o*-benzoic sulfimide, 2-[[(4-chloro-6-methoxy-2-pyrimidinyl) carbamoyl] sulfamoyl] benzoic acid, ethyl 2-carbonyl sulfamoyl benzoate, ethyl 2-benzenesulfonyl isocyanate benzoate, and *N*,*N*-2(ethyl formate)benzene sulfonylurea) were identified, and three possible degradation pathways were proposed based on the results of high performance liquid chromatography HPLC, liquid chromatography tandem mass spectroscopy (LC-MS/MS), and Fourier transform infrared spectroscopy (FTIR) analyses and the relevant literature. This systematic study is the first to examine the chlorimuron-ethyl degradation pathways of the genus *Rhodococcus*.

Keywords: Chlorimuron-ethyl; *Rhodococcus* sp. D310-1; Response surface methodology; Kinetics; LC-MS

Aleksandra Felczak, Przemysław Bernat, Sylwia Różalska, Katarzyna Lisowska. (Department of Industrial Microbiology and Biotechnology, Faculty of Biology and Environmental Protection University of Lodz). Quinoline biodegradation by filamentous fungus *Cunninghamella elegans* and adaptive modifications of the fungal membrane composition. Environmental Science and Pollution Research, Volume 23(9) (2016): 8872–8880

Quinoline, which belongs to N-heterocyclic compounds, occurs naturally in the environment and is used in numerous industrial processes. The structures of various chemicals, such as dyes and

medicines, are based on this compound. Due to that fact, quinoline and its derivatives are widely distributed in environment and can exert toxic effects on organisms from different trophic levels. The ability of the filamentous fungus *Cunninghamella elegans* IM 1785/21Gp to degrade quinoline and modulate the membrane composition in response to the pollutant was studied. *C. elegans* IM 1785/21Gp removes quinoline with high efficiency and transforms the pollutant into two novel hydroxylated derivatives, 2-hydroxyquinoline and 3-hydroxyquinoline. Moreover, due to the disruption in the membrane stability by quinoline, *C. elegans* IM 1785/21Gp modulates the fatty acid composition and phospholipid profile.

Keywords: Quinoline; Degradation; Fungi; Phospholipid profile

Xiaobin Liao, Bingxin Li, Rusen Zou, Yu Dai, Shuguang Xie, Baoling Yuan. (Institute of Municipal and Environmental Engineering, College of Civil Engineering, Huaqiao University, State Key Joint Laboratory of Environmental Simulation and Pollution Control, College of Environmental Sciences and Engineering, Peking University). **Biodegradation of antibiotic ciprofloxacin: pathways, influential factors, and bacterial community structure. Environmental Science and Pollution Research, Volume 23(8) (2016): 7911-7918**

Antibiotic ciprofloxacin is ubiquitous in the environment. However, little is known about ciprofloxacin dissipation by microbial community. The present study investigated the biodegradation potential of ciprofloxacin by mixed culture and the influential factors and depicted the structure of ciprofloxacin-degrading microbial community. Both the original microbiota from drinking water biofilter and the microbiota previously acclimated to high levels of ciprofloxacin could utilize ciprofloxacin as sole carbon and nitrogen sources, while the acclimated microbiota had a much stronger removal capacity. Temperature rise and the presence of carbon or nitrogen sources favored ciprofloxacin biodegradation. Many novel biotransformation products were identified, and four different metabolic pathways for ciprofloxacin were proposed. Bacterial community structure illustrated a profound shift with ciprofloxacin biodegradation. The ciprofloxacin-degrading bacterial community was mainly composed of classes *Gammaproteobacteria*, *Bacteroidia*, and *Betaproteobacteria*. Microorganisms from genera *Pseudoxanthomonas*, *Stenotrophomonas*, *Phenylobacterium*, and *Leucobacter* might have links with the dissipation of ciprofloxacin. This work can provide some new insights towards ciprofloxacin biodegradation.

Keywords: Antibiotic; Biofilter; *Bacteroidetes; Proteobacteria;* High-throughput sequencing

Ya Zhang, Jianhua Li, Lei Zhou, Guoqing Wang, Yanhong Feng, Zunyao Wang, Xi Yang. (State Environmental Protection Key Laboratory of Soil Environmental Management and Pollution Control, Nanjing Institute of Environmental Sciences, Chinese Ministry of Environmental Protection. State Key Laboratory of Pollution Control and Resource Reuse, School of the Environment, Nanjing University, Université Lyon 1, UMR CNRS 5256, Institut de recherches sur la catalyse et l'environnement de Lyon (IRCELYON), State Environmental Protection Key Laboratory of Soil Environmental Management and Pollution Control, Nanjing Institute of Environmental Sciences, Chinese Ministry of Environmental Protection). **Aqueous photodegradation of antibiotic florfenicol: kinetics and degradation pathway studies. Environmental Science and Pollution Research, Volume 23(7) (2016): 6982-6989**

The occurrence of antibacterial agents in natural environment was of scientific concern in recent years. As endocrine disrupting chemicals, they had potential risk on ecology system and human beings. In the present study, the photodegradation kinetics and pathways of florfenicol were

investigated under solar and xenon lamp irradiation in aquatic systems. Direct photolysis half-lives of florfenicol were determined as 187.29 h under solar irradiation and 22.43 h under xenon lamp irradiation, respectively. Reactive oxygen species (ROS), such as hydroxyl radical (·OH) and singlet oxygen ($^1O_2$) were found to play an important role in indirect photolysis process. The presence of nitrate and dissolved organic matters (DOMs) could affect photolysis of florfenicol in solutions through light screening effect, quenching effect, and photoinduced oxidization process. Photoproducts of florfenicol in DOMs solutions were identified by solid phase extraction-liquid chromatography-mass spectrometry (SPE-LC-MS) analysis techniques, and degradation pathways were proposed, including photoinduced hydrolysis, oxidation by $^1O_2$ and ·OH, dechlorination, and cleavage of the side chain.

Keywords: Florfenicol; Photodegradation; Antibacterial agent; Reactive oxygen species; Pathways; Photochemistry; Dissolved organic matter

Linlin Wang, Litao Tang, Ran Wang, Xiaoya Wang, Jinshao Ye, Yan Long. (Research Center of Environmental Pollution Control and Remediation of Guangdong Province, Key Laboratory of Environmental Exposure and Health of Guangzhou City, School of Environment, Jinan University). Biosorption and degradation of decabromodiphenyl ether by *Brevibacillus brevis* and the influence of decabromodiphenyl ether on cellular metabolic responses. Environmental Science and Pollution Research, Volume 23(6) (2016): 5166-5178

There is global concern about the effects of decabromodiphenyl ether (BDE209) on environmental and public health. The molecular properties, biosorption, degradation, accumulation, and cellular metabolic effects of BDE209 were investigated in this study to identify the mechanisms involved in the aerobic biodegradation of BDE209. BDE209 is initially absorbed by wall teichoic acid and N-acetylglucosamine side chains in peptidoglycan, and then, BDE209 is transported and debrominated through three pathways, giving tri-, hepta-, octa-, and nona-bromodiphenyl ethers. The C–C bond energies decrease as the number of bromine atoms on the diphenyl decreases. Polybrominated diphenyl ethers (PBDEs) inhibit protein expression or accelerate protein degradation and increase membrane permeability and the release of Cl^-, Na^+, NH_4^+, arabinose, proteins, acetic acid, and oxalic acid. However, PBDEs increase the amounts of K^+, Mg^{2+}, PO_4^{3-}, SO_4^{2-}, and NO_3^- assimilated. The biosorption, degradation, accumulation, and removal efficiencies when *Brevibacillus brevis* (1 g L^{-1}) was exposed to BDE209 (0.5 mg L^{-1}) for 7 days were 7.4, 69.5, 16.3, and 94.6 %, respectively.

Keywords: Bioaccumulation; Biotransformation; Metabolism; Polybrominated diphenyl ether; Cell wall; Chem; Office

Tatiana Volova, Natalia Zhila, Olga Vinogradova, Anna Shumilova, Svetlana Prudnikova, Ekaterina Shishatskaya. (Institute of Biophysics SB RAS, 50/50 Akademgorodok). Characterization of biodegradable poly-3-hydroxybutyrate films and pellets loaded with the fungicide tebuconazole. Environmental Science and Pollution Research, Volume 23(6) (2016): 5243-5254

Biodegradable polymer poly(3-hydroxybutyrate) (P3HB) has been used as a matrix to construct slow-release formulations of the fungicide tebuconazole (TEB). P3HB/TEB systems constructed as films and pellets have been studied using differential scanning calorimetry, X-ray structure analysis, and Fourier transform infrared spectroscopy. TEB release from the experimental formulations has been studied in aqueous and soil laboratory systems. In the soil with known

composition of microbial community, polymer was degraded, and TEB release after 35 days reached 60 and 36 % from films and pellets, respectively. That was 1.23 and 1.8 times more than the amount released to the water after 60 days in a sterile aqueous system. Incubation of P3HB/TEB films and pellets in the soil stimulated development of P3HB-degrading microorganisms of the genera *Pseudomonas*, *Stenotrophomonas*, *Variovorax*, and *Streptomyces*. Experiments with phytopathogenic fungi *F. moniliforme* and *F. solani* showed that the experimental P3HB/TEB formulations had antifungal activity comparable with that of free TEB.

Keywords: Poly(3-hydroxybutyrate); Tebuconazole; Slow-release formulations; Controlled release; Antifungal activity

Hsi-Ling Chou, Mei-Yin Hwa, Yao-Chuan Lee, Yu-Jie Chang, Yi-Tang Chang. (Department of Microbiology, Soochow University, Department of Environmental Engineering, TunNang University, Department of Earth and Life Science, University of Taipei). Microbial degradation of decabromodiphenyl ether (DBDE) in soil slurry microcosms. Environmental Science and Pollution Research, Volume 23(6) (2016): 5255-5267

Decabromodiphenyl ether (DBDE), which has been identified as an endocrine disrupting compound, is used as brominated flame retardant, and this can result in serious bioaccumulation within ecological systems. The objective of this study was to explore DBDE bioremediation (25 mg/kg) using laboratory scale soil slurry microcosms. It was found that effective biodegradation of DBDE occurred in all microcosms. Various biometabolites were identified, namely polybrominated diphenyl ethers congeners and hydroxylated brominated diphenyl ether. Reductive debrominated products such as tri-BDE to hepta-BDE congeners were also detected, and their total concentrations ranged from 77.83 to 91.07 ng/g. The mechanism of DBDE biodegradation in soil slurry microcosms is proposed to consist of a series of biological reactions involving hydroxylation and debromination. Catechol 2,3-oxygenase genes, which are able to bring about meta-cleavage at specific unbrominated locations in carbon backbones, were identified as present during the DBDE biodegradation. No obvious effect on the ecological functional potential based on community-level physiological profiling was observed during DBDE biodegradation, and one major facultative *Pseudomonas* sp. (99 % similarity) was identified in the various soil slurry microcosms. These findings provide an important basis that should help environmental engineers to design future DBDE bioremediation systems that use a practical microcosm system. A bacterial-mixed culture can be selected as part of the bioaugmentation process for in situ DBDE bioremediation. A soil/water microcosm system can be successfully applied to carry out ex situ DBDE bioremediation.

Keywords: Decabromodiphenyl ether; Soil slurry microcosm; Catechol 2,3-oxygenaseCommunity-level physiological profiling; *Pseudomonas* sp.

Chunli Liao, Xiaobo Liu. (College of Life Science and Engineering, Henan University of Urban Construction, The Key Laboratory of Industrial Biotechnology, Ministry of Education, School of Biotechnology, Jiangnan University). Prevent the degradation of algicidal ability in *Scenedesmus*-lysing bacteria using optimized cryopreservation. Environmental Science and Pollution Research, Volume 23(6) (2016): 5925-5930

With the anthropogenic nutrient loading increasing, the frequency and impacts of harmful algal blooms (HABs) have intensified in recent years. To biocontrol HABs, many corresponding algal-lysing bacteria have been exploited successively. However, there are few studies on an effective algal-lysing culture collection to prevent cells from death and particularly the degradation of algicidal ability to their hosts. An optimized cryopreservation was developed and

experiments on the validation of this method on preventing algicidal degradation and effects of this optimized cryopreservation on the survival rate of *Scenedesmus*-lysing bacterium, *Enterobacter* NP23, isolated from *Scenedesmus* sp. community, China, on the algicidal dynamic of *Scenedesmus wuhanensis* was investigated. The optimized cryoprotectant composition consists of 30.0 g/L gelatin, 48.5 g/L sucrose, and 28.4 g/L glycerol, respectively. Using this approach, the survival rate of NP23 cells can still maintain above 90 % and the algal-lysing rate only decline 4 % after the 18-month cryoprotection. Moreover, the 16 generations' passage experiment showed a significant ($p < 0.05$) genetic stability of algicidal capacity after 18 months. The growth dynamic of *S. wuhanensis* was investigated in a 5-L bioreactor during 132 h in the absence or presence of NP23. As a result, NP23 has a significant ($p < 0.05$) inhibition to *S. wuhanensis* growth when injected into algal culture in the exponential phase at 60th hour. In addition, *S. wuhanensis* culture initially with NP23 exhibited a slow growth, performing a prolonged lag phase without a clear stationary phase and then rapidly decreased. Our findings, combined with the capacity of preventing the degradation of algicidal ability collectively suggest that the use of this opitimized cryopreservation may be a promising strategy for maintaining algicidal cells.

Keywords: Harmful algal blooms; Algal-lysing bacterium; *Scenedesmus wuhanensis;* Degradation; Cryopreservation

Małgorzata P. Oksińska, Elżbieta G. Magnucka, Krzysztof Lejcuś, Stanisław J. Pietr. (Laboratory of Agricultural Microbiology, Department of Plant Protection, Wrocław University of Environmental and Life Sciences, Institute of Environmental Engineering, Wrocław University of Environmental and Life Sciences). **Biodegradation of the cross-linked copolymer of acrylamide and potassium acrylate by soil bacteria. Environmental Science and Pollution Research, Volume 23(6) (2016): 5969-5977**

Chemical cross-linking and the high molecular weight of superabsorbent copolymers (SAPs) are the two main causes of their resistance to biodegradation. However, SAP particles are colonized by microorganisms. For the purposes of this study, the dry technical copolymer of acrylamide and potassium acrylate containing 5.28 % of unpolymerized monomers was wrapped in a geotextile and incubated in unsterile Haplic Luvisol soil as a water absorbing geocomposite. The highest number of soil bacteria that colonized the hydrated SAP and utilized it as the sole carbon and energy source was found after the first month of incubation in soil. It was equal to 7.21–7.49 $\log_{10}$ cfu g^{-1} of water absorbed by the SAP and decreased by 1.35–1.61 $\log_{10}$ units within the next 8 months. During this time, the initial SAP water holding capacity of 1665.8 g has decreased by 24.40 %. Moreover, the 5 g of SAP dry mass has declined by 31.70 %. Two bacteria, *Rhizobium radiobacter* 28SG and *Bacillus aryabhattai* 31SG isolated from the watered SAP were found to be able to biodegrade this SAP in pure cultures. They destroyed 25.07 and 41.85 mg of 300 mg of the technical SAP during the 60-day growth in mineral Burk's salt medium, and biodegradation activity was equal to 2.95 and 6.72 μg of SAP μg^{-1} of protein, respectively. *B. aryabhattai* 31SG and *R. radiobacter* 28SG were also able to degrade 9.99 and 29.70 mg of 82 mg of the ultra-pure SAP in synthetic root exudate medium during the 30-day growth, respectively.

Keywords: Superabsorbent copolymers; Geocomposite; Agriculture; Cross-linked copolymer of acrylamide and potassium acrylate; *Bacillus aryabhattai; Rhizobium radiobacter*

Lata Kumari, Dhanesh Tiwary, Pradeep Kumar Mishra. (Department of Chemistry, Indian Institute of Technology, Banaras Hindu University, Department of Chemical Engineering and Technology, Indian Institute of Technology, Banaras Hindu University). Biodegradation of C.I. Acid Red 1 by indigenous bacteria *Stenotrophomonas* sp. BHUSSp X2 isolated from dye contaminated soil. Environmental Science and Pollution Research, Volume 23(5) (2016): 4054-4062

A significant proportion of xenobiotic recalcitrant azo dyes are being released in environment during carpet dyeing. The bacterial strain *Stenotrophomonas* sp. BHUSSp X2 was isolated from dye contaminated soil of carpet industry, Bhadohi, India. The isolated bacterial strain was identified morphologically, biochemically, and on the basis of 16S rRNA gene sequence. The isolate decolorized 97 % of C.I. Acid Red 1 (Acid RED G) at the concentration of 200 mg/l within 6 h under optimum static conditions (temperature −35 °C, pH 8, and initial cell concentration 7×10^7 cell/ml). Drastic reduction in dye degradation rate was observed beyond initial dye concentration from 500 mg/l (90 %), and it reaches to 25 % at 1000 mg/l under same set of conditions. The analysis related to decolorization and degradation was done using UV-Vis spectrophotometer, HPLC, and FTIR, whereas the GC-MS technique was utilized for the identification of degradation products. Phytotoxicity analysis revealed that degradation products are less toxic as compared to the original dye.

Keywords: Xenobiotic; *Stenotrophomonas* sp. BHUSSp X2; C.I. Acid Red 1; DecolorizationToxicity; Biotransformation; Biodegradation

M. Gopinath, C. Mohanapriya, K. Sivakumar, G. Baskar, C. Muthukumaran, R. Dhanasekar. (Department of Biotechnology, Karpaga Vinayaga College of Engineering and Technology, Department of Biotechnology, St Joseph's College of Engineering, Department of Industrial Biotechnology, Government College of Technology, Department of Chemical Engineering, Annamalai University). Biodegradation of toluene vapor in coir based upflow packed bed reactor by *Trichoderma asperellum* isolate. Environmental Science and Pollution Research, Volume 23(5) (2016): 4129-4137

In the present study, a new biofiltration system involving a selective microbial strain isolated from aerated municipal sewage water attached with coir as packing material was developed for toluene degradation. The selected fungal isolate was identified as *Trichoderma asperellum* by 16S ribosomal RNA (16S rRNA) sequencing method, and pylogenetic tree was constructed using BLASTn search. Effect of various factors on growth and toluene degradation by newly isolated *T. asperellum* was studied in batch studies, and the optimum conditions were found to be pH 7.0, temperature 30 °C, and initial toluene concentration 1.5 (*v*/*v*)%. Continuous removal of gaseous toluene was monitored in upflow packed bed reactor (UFPBR) using *T. asperellum*. Effect of various parameters like column height, flow rate, and the inlet toluene concentration were studied to evaluate the performance of the biofilter. The maximum elimination capacity (257 g m^{-3} h^{-1}) was obtained with the packing height of 100 cm with the empty bed residence time of 5 min. Under these optimum conditions, the *T. asperellum* showed better toluene removal efficiency. Kinetic models have been developed for toluene degradation by *T. asperellum* using macrokinetic approach of the plug flow model incorporated with Monod model.

Keywords: Biofilter; *Trichoderma asperellum;* UFPBR; Plug flow model; Kinetics; Removal efficiency; Toluene

Sana Romdhane, Marion Devers-Lamrani, Fabrice Martin-Laurent, Christophe Calvayrac, Emilie Rocaboy-Faquet, David Riboul, Jean-François Cooper, Lise

Barthelmebs. (Biocapteurs Analyses Environnement (BAE), University of Perpignan Via DomitiaLaboratoire de Chimie des Biomolécules et de l'Environnement–CRIOBE–USR 3278 CNRS EPHE, University of Perpignan Via DomitiaINRA, UMR 1347 Agroécologie, Pole Ecoldur, INRA, UMR 1347 Agroécologie, Pole Ecoldur, Laboratoire de Chimie des Biomolécules et de l'Environnement–CRIOBE–USR 3278 CNRS EPHE, University of Perpignan Via Domitia, INPT, ENSIACET, Université de ToulouseLaboratoire de Génie Chimique (LGC UMR 5503), CNRS). Isolation and characterization of *Bradyrhizobium* sp. SR1 degrading two β-triketone herbicides. Environmental Science and Pollution Research, Volume 23(5) (2016): 4138-4148

In this study, a bacterial strain able to use sulcotrione, a β-triketone herbicide, as sole source of carbon and energy was isolated from soil samples previously treated with this herbicide. Phylogenetic study based on16S rRNA gene sequence showed that the isolate has 100 % of similarity with several *Bradyrhizobium* and was accordingly designated as *Bradyrhizobium* sp. SR1. Plasmid profiling revealed the presence of a large plasmid (>50 kb) in SR1 not cured under nonselective conditions. Its transfer to *Escherichia coli* by electroporation failed to induce β-triketone degrading capacity, suggesting that degrading genes possibly located on this plasmid cannot be expressed in *E. coli* or that they are not plasmid borne. The evaluation of the SR1 ability to degrade various synthetic (mesotrione and tembotrione) and natural (leptospermone) triketones showed that this strain was also able to degrade mesotrione. Although SR1 was able to entirely dissipate both herbicides, degradation rate of sulcotrione was ten times higher than that of mesotrione, showing a greater affinity of degrading-enzyme system to sulcotrione. Degradation pathway of sulcotrione involved the formation of 2-chloro-4-mesylbenzoic acid (CMBA), previously identified in sulcotrione degradation, and of a new metabolite identified as hydroxy-sulcotrione. Mesotrione degradation pathway leads to the accumulation of 4-methylsulfonyl-2-nitrobenzoic acid (MNBA) and 2-amino-4 methylsulfonylbenzoic acid (AMBA), two well-known metabolites of this herbicide. Along with the dissipation of β-triketones, one could observe the decrease in 4-hydroxyphenylpyruvate dioxygenase (HPPD) inhibition, indicating that toxicity was due to parent molecules, and not to the formed metabolites. This is the first report of the isolation of bacterial strain able to transform two β-triketones.

Keywords: β-Triketone; Sulcotrione; Mesotrione; Biodegradation; *Bradyrhizobium* sp. SR1

Martha Patricia García de Llasera, José de Jesús Olmos-Espejel, Gabriel Díaz-Flores, Adriana Montaño-Montiel. (Facultad de Química, Departamento de Química Analítica, Universidad Nacional Autónoma de México). Biodegradation of benzo(a)pyrene by two freshwater microalgae *Selenastrum capricornutum* and *Scenedesmus acutus*: a comparative study useful for bioremediation. Environmental Science and Pollution Research, Volume 23(4) (2016): 3365-3375

A comparative evaluation of the removal of benzo(a)pyrene (BaP) by sorption and degradation by two microalgal species, *Selenastrum capricornutum* and *Scenedesmus acutus* was performed. The monitoring of the amount of BaP remaining in the liquid culture media and the biomass along with the appearance of three metabolites (4,5 dihydrodiol-BaP; 7,8-dihydrodiol-BaP; and 9,10 dihydrodiol-BaP) at short time periods (from 0.25 to 72 h) in cultures exposed to BaP was made by high-performance liquid chromatography (HPLC) with fluorescence and UV detection. Complete removal of BaP was achieved by the two live microalgal species: *S. capricornutum* at

15 h of exposure (99 %) and *S. acutus* at 72 h of exposure (95 %). Sorption is an important phenomenon for BaP removal by *S. capricornutum* but biodegradation is the principal means of removing BaP in live cells. The formation of metabolites by *S. capricornutum* is rapid and seems to be proportional to the amount of the BaP added to cultures. In contrast, in these bioassays, most of the BaP removal of *S. acutus* is due to sorption rather than degradation. The appearance of metabolites in the cultures is very slow and at a low amount compared to cultures of *S. capricornutum*. The similarities and differences existing between the two microalgae are important for the establishment of the conditions for bioremediation.

Keywords: Benzo(a)pyrene; Biodegradation; Removal; Microalgae; Metabolites; Bioremediation; *Selenastrum capricornutum; Scenedesmus acutus*

M. Homolková, P. Hrabák, M. Kolář, M. Černík. (Faculty of Mechatronics, Informatics and Interdisciplinary Studies & Institute for Nanomaterials, Advanced Technologies and Innovations, Technical University of Liberec, Regional Centre of Advanced Technologies and Materials, Palacký University in Olomouc). Degradability of chlorophenols using ferrate(VI) in contaminated groundwater. Environmental Science and Pollution Research, Volume 23(2) (2016): 1408-1413

The production and use of chlorophenolic compounds in industry has led to the introduction of many xenobiotics, among them chlorophenols (CPs), into the environment. Five CPs are listed in the priority pollutant list of the U.S. EPA, with pentachlorophenol (PCP) even being proposed for listing under the Stockholm Convention as a persistent organic pollutant (POP). A green procedure for degrading such pollutants is greatly needed. The use of ferrate could be such a process. This paper studies the degradation of CPs (with an emphasis on PCP) in the presence of ferrate both in a spiked demineralized water system as well as in real contaminated groundwater. Results proved that ferrate was able to completely remove PCP from both water systems. Investigation of the effect of ferrate purity showed that even less pure and thus much cheaper ferrate was applicable. However, with decreasing ferrate purity, the degradability of CPs may be lower.

Keywords: Degradability; Ferrate; Fe(VI); Pentachlorophenol; Chlorophenols; Complex contaminated water

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The presence of pharmaceuticals in the environment has triggered concern among the general population and received considerable attention from the scientific community in recent years. However, only a few publications have focused on anticancer drugs, a class of pharmaceuticals that can exhibit cytotoxic, genotoxic, mutagenic, carcinogenic and teratogenic effects. The present study investigated the photodegradation, biodegradation, bacterial toxicity, mutagenicity and genotoxicity of cyclophosphamide (CP) and 5-fluorouracil (5-FU). The photodegradation experiments were performed at a neutral to slight pH range (7–7.8) using two different lamps

(medium-pressure mercury lamp and a xenon lamp). The primary elimination of the parent compounds was monitored by means of liquid chromatography tandem mass spectrometry (LC-IT-MS/MS). NPOC (non-purgeable organic carbon) analyses were carried out in order to assess mineralization rates. The Closed Bottle Test (CBT) was used to assess ready biodegradability. A new method using *Vibrio fischeri* was adopted to evaluate toxicity. CP was not degraded by any lamp, whereas 5-FU was completely eliminated by irradiation with the mercury lamp but only partially by the Xe lamp. No mineralization was observed for the experiments performed with the Xe lamp, and a NPOC removal of only 18% was registered for 5-FU after 256 min using the UV lamp. Not one of the parent compounds was readily biodegradable in the CBT. Photo transformation products (PTPs) resulting from photolysis were neither better biodegradable nor less toxic than the parent compound 5-FU. In contrast, the results of the tests carried out with the UV lamp indicated that more biodegradable and non-toxic PTPs of 5-FU were generated. Three PTPs were formed during the photodegradation experiments and were identified. The results of the *in silico* QSAR predictions showed positive mutagenic and genotoxic alerts for 5-FU, whereas only one of the formed PTPs presented positive alerts for the genotoxicity endpoint.

Keywords: Cyclophosphamide; 5-Fluorouracil; Photodegradation; Biodegradation; Toxicity

Víctor M Luque-Almagro, Conrado Moreno-Vivián, María Dolores Roldán. (Departamento de Bioquímica y Biología Molecular, Edificio Severo Ochoa, 1ª Planta, Campus de Rabanales, Universidad de Córdoba, 14071 Córdoba, Spain). **Biodegradation of cyanide wastes from mining and jewellery industries. Current Opinion in Biotechnology, Volume 38(2016): 9–13**

Cyanide, one of the known most toxic chemicals, is widely used in mining and jewellery industries for gold extraction and recovery from crushed ores or electroplating residues. Cyanide toxicity occurs because this compound strongly binds to metals, inactivating metalloenzymes such as cytochrome *c* oxidase. Despite the toxicity of cyanide, cyanotrophic microorganisms such as the alkaliphilic bacterium *Pseudomonas pseudoalcaligenes* CECT5344 may use cyanide and its derivatives as a nitrogen source for growth, making biodegradation of cyanurated industrial waste possible. Genomic, transcriptomic and proteomic techniques applied to cyanide biodegradation ('cyan-omics') provide a holistic view that increases the global insights into the genetic background of cyanotrophic microorganisms that could be used for biodegradation of industrial cyanurated wastes and other biotechnological applications.

Susanne L Waaijers[1], John R Parsons[2]. ([1] National Institute for Public Health and the Environment (RIVM), Center for Safety of Substances and Products, P.O. Box 1, 3720 BA Bilthoven, The Netherlands, [2] Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, P.O. Box 94240, 1092 GE Amsterdam, The Netherlands). **Biodegradation of brominated and organophosphorus flame retardants. Current Opinion in Biotechnology, Volume 38(2016): 14–23**

Brominated flame retardants account for about 21% of the total production of flame retardants and many of these have been identified as persistent, bioaccumulative and toxic. Nevertheless, debromination of these chemicals under anaerobic conditions is well established, although this can increase their toxicity. Consequently, the production and use of these chemicals has been restricted and alternative products have been developed. Many of these are brominated compounds and share some of the disadvantages of the chemicals they are meant to replace. Therefore, other, nonbrominated, flame retardants such as organophosphorus compounds are

also being used in increasing quantities, despite the fact that knowledge of their biodegradation and environmental fate is often lacking.

Chu-Wen Yang, Wei-Zhi Chen, Bea-Ven Chang. (Department of Microbiology, Soochow University, Taipei, Taiwan). Biodegradation of tetrabromobisphenol-A in sludge-amended soil. Ecological Engineering, Volume 91(2016): 143–147

This study investigated the degradation of tetrabromobisphenol-A (TBBPA) and changes in the bacterial community in sludge-amended soil. The results indicated that TBBPA degradation was enhanced by spent mushroom compost (SMC), enzyme extract (EE) and extract-containing microcapsule (MC) in soil–sludge mixtures, with SMC showing a greater TBBPA degradation rate than the other additives. The TBBPA degradation rates were enhanced with SMC at the second and third additions. The bacterial composition differed in the soil–sludge mixtures with and without SMC. *Bacillus, Flavobacterium, Geobacter, Mycobacterium, Pseudomonas, Rhodococcus, Sphingomonas* and *Streptococcus* were major bacterial communities in TBBPA degradation in the soil–sludge mixtures.

Keywords: Tetrabromobisphenol-A; Degradation; Bacterial community; Spent mushroom compost; Sludge; Soil

Sofija S. Poguberović[a], Dejan M. Krčmar[a], Snežana P. Maletić- Zoltán Kónya[b, c], Dragana D. Tomašević Pilipović[a], Djurdja V. Kerkez[a], Srdjan D. Rončević[a]. ([a] University of Novi Sad, Faculty of Sciences, Department of Chemistry, Biochemistry and Environmental Protection, Trg Dositeja Obradovica 3, Novi Sad 21000, Serbia, [b] Department of Applied and Environmental Chemistry, University of Szeged, Rerrich Bélatér 1, Szeged H-6720, Hungary, c MTA-SZTE Reaction Kinetics and Surface Chemistry Research Group, Rerrich Bélatér 1, Szeged H-6720, Hungary).Removal of As(III) and Cr(VI) from aqueous solutions using "green" zero-valent iron nanoparticles produced by oak, mulberry and cherry leaf extracts. Ecological Engineering, Volume 90(2016): 42–49

The production of nano zero-valent iron nanoparticles, using the extract from natural products, increased in recent years as it represents green and environmentally friendly method. Synthesis of green zero-valent iron nanoparticles (nZVI) using oak, mulberry and cherry leaf extracts (OL-nZVI, ML-nZVI and CH-nZVI) proved to be a promising approach for As(III) and Cr(VI) removal from aqueous solutions. The oak, mulberry and cherry leaves were chosen because of their high oxidant capacity as an important property for the production of the nZVIs. Also, oak, mulberry and cherry trees are widely distributed and easy to find in Vojvodina, the north province of Serbia. Characterization of produced green nZVI materials confirmed the formation of nanosize zero-valent iron particles within the size of 10–30 nm. Nanoparticles were spherical in shape and represented stable material with minimum agglomeration observed by TEM and SEM morphology measurements. Batch experiments revealed that the adsorption kinetics followed pseudo-second order rate equation. The obtained adsorption isotherm data could be well described by the Freundlich model. In addition, investigated pH effect showed that varying the initial pH value had a great effect on As(III) and Cr(VI) removal. This study indicated that nZVI could be produced by low cost and non toxic method with oak, mulberry and cherry leaf extracts and potentially be used as a new green material for remediation of water matrices contaminated with As(III) and Cr(VI).

Keywords: As(III) and Cr(VI) removal; Zero-valent iron nanoparticles; Green adsorbent; Leaves

Giuseppe Di Girolamoa, Marco Grigattia, Lorenzo Bertinb, Claudio Ciavattaa, Lorenzo Barbantia. ([a] Department of Agricultural Sciences, University of Bologna, Viale Fanìn 44, 40127 Bologna, Italy, [b] Department of Civil, Environmental, and Materials Engineering, University of Bologna, Via Terracini 28, 40131 Bologna, Italy). Enhanced substrate degradation and methane yield with maleic acid pre-treatments in biomass crops and residues. Biomass and Bioenergy, Volume 85(2016): 306–312

Organic acids are envisaged as alternative catalysts to strong mineral acids, in pre-treatment of ligno-cellulosic biomass for anaerobic digestion (AD). To evaluate this hypothesis, an untreated control and four pre-treatments (25 °C for 24 h) involving two levels of maleic acid (34.8 and 69.6 kg m^{-3}), alone and combined with sulphuric acid (4 kg m^{-3}), were studied in three agricultural substrates: Arundo (aka giant reed), Barley straw and B133 fibre sorghum. Methane production was assessed in a batch AD assay (35 °C for 51 days) with 4 g L^{-1} of volatile solid (VS) load. Fibre composition and structure were investigated through chemical analysis and Fourier transform infrared (FTIR) spectrometry. Arundo and B133 that were the most and least recalcitrant substrate, respectively, staged the highest and lowest increase in methane with high maleic acid: +62% over 218 cm^3 g^{-1} of VS in untreated Arundo; +36% over 284 cm^3 g^{-1} of VS in untreated B133. Barley straw showed an intermediate behaviour (+41% over 269 cm^3 g^{-1} of VS). H_2SO_4 addition to maleic acid did not improve CH_4 output. The large increase in methane yield determined by pre-treatments was reflected in the concurrent decrease of fibre (between 14 and 39% depending on fibrous component). Based on FTIR spectra, bands assigned to hemicellulose and cellulose displayed lower absorbance after pre-treatment, supporting the hypothesis of solubilisation of structural carbohydrates and change in fibre structure. Hence, maleic acid was shown a suitable catalyst to improve biodegradability of ligno-cellulosic biomass, especially in recalcitrant substrates as Arundo.

Keywords: Maleic acid; Ligno-cellulosic biomass; Anaerobic digestion; FTIR analysis; Methane

Fengmei Li, Shuhai Guo, Niels Hartog, Ye Yuan, Xuelian Yang. (Institute of Applied Ecology, Chinese Academy of Sciences, KWR Watercycle Research Institute, Shenyang University). Isolation and characterization of heavy polycyclic aromatic hydrocarbon-degrading bacteria adapted to electrokinetic conditions. Biodegradation, Volume 27(1) (2016): 1-13

Polycyclic aromatic hydrocarbon (PAH)-degrading bacteria capable of growing under electrokinetic conditions were isolated using an adjusted acclimation and enrichment procedure based on soil contaminated with heavy PAHs in the presence of an electric field. Their ability to degrade heavy PAHs under an electric field was individually investigated in artificially contaminated soils. The results showed that strains PB4 (*Pseudomonas fluorescens*) and FB6 (*Kocuria* sp.) were the most efficient heavy PAH degraders under electrokinetic conditions. They were re-inoculated into a polluted soil from an industrial site with a PAH concentration of 184.95 mg kg^{-1}. Compared to the experiments without an electric field, the degradation capability of *Pseudomonas fluorescens* and *Kocuria* sp. was enhanced in the industrially polluted soil under electrokinetic conditions. The degradation extents of total PAHs were increased by 15.4 and 14.0 % in the electrokinetic PB4 and FB6 experiments (PB4 + EK and FB6 + EK) relative to the PB4 and FB6 experiments without electrokinetic conditions (PB4 and FB6), respectively. These results indicated that *P. fluorescens* and *Kocuria* sp. could efficiently

degrade heavy PAHs under electrokinetic conditions and have the potential to be used for the electro-bioremediation of PAH-contaminated soil, especially if the soil is contaminated with heavy PAHs.

Keywords: Heavy polycyclic aromatic hydrocarbons; Degrading bacteria; Electric field; Industrially polluted soil

Olivier Chapleur, Céline Madigou, Raphaël Civade, Yohan Rodolphe, Laurent Mazéas, Théodore Bouchez. (Hydrosystems and Bioprocesses Research Unit, Irstea). Increasing concentrations of phenol progressively affect anaerobic digestion of cellulose and associated microbial communities. Biodegradation, Volume 27(1) (2016): 15-27

Performance stability is a key issue when managing anaerobic digesters. However it can be affected by external disturbances caused by micropollutants. In this study the influence of phenol on the methanization of cellulose was evaluated through batch toxicity assays. Special attention was given to the dynamics of microbial communities by means of automated ribosomal intergenic spacer analysis. We observed that, as phenol concentrations increased, the different steps of anaerobic cellulose digestion were unevenly and progressively affected, methanogenesis being the most sensitive: specific methanogenic activity was half-inhibited at 1.40 g/L of phenol, whereas hydrolysis of cellulose and its fermentation to VFA were observed at up to 2.00 g/L. Depending on the level of phenol, microbial communities resisted either through physiological or structural adaptation. Thus, performances at 0.50 g/L were maintained in spite of the microbial community's shift. However, the communities' ability to adapt was limited and performances decreased drastically beyond 2.00 g/L of phenol.

Keywords: ARISAE; C50; Inhibition; Micropollutants; Phenol degradation

Udonna Ndu, Tamar Barkay, Amina Traore Schartup, Robert P. Mason, John R. Reinfelder. (Marine Sciences Department, University of Connecticut. Department of Environmental Sciences, Rutgers University, Department of Biochemistry and Microbiology, Rutgers University, Department of Environmental Health, Harvard School of Public Health, Marine Sciences Department, University of Connecticut). The effect of aqueous speciation and cellular ligand binding on the biotransformation and bioavailability of methylmercury in mercury-resistant bacteria. Biodegradation, Volume 27(1) (2016): 29-36

Mercury resistant bacteria play a critical role in mercury biogeochemical cycling in that they convert methylmercury (MeHg) and inorganic mercury to elemental mercury, Hg(0). To date there are very few studies on the effects of speciation and bioavailability of MeHg in these organisms, and even fewer studies on the role that binding to cellular ligands plays on MeHg uptake. The objective of this study was to investigate the effects of thiol complexation on the uptake of MeHg by measuring the intracellular demethylation-reduction (transformation) of MeHg to Hg(0) in Hg-resistant bacteria. Short-term intracellular transformation of MeHg was quantified by monitoring the loss of volatile Hg(0) generated during incubations of bacteria containing the complete *mer* operon (including genes from putative mercury transporters) exposed to MeHg in minimal media compared to negative controls with non-*mer* or heat-killed cells. The results indicate that the complexes MeHgOH, MeHg-cysteine, and MeHg-glutathione are all bioavailable in these bacteria, and without the *mer* operon there is very little biological degradation of MeHg. In both *Pseudomonas stutzeri* and *Escherichia coli*, there was a pool of MeHg that was not transformed to elemental Hg(0), which was likely rendered unavailable to Mer enzymes by non-specific binding to cellular ligands. Since the rates of MeHg accumulation and transformation varied more between the two species of bacteria examined than among

MeHg complexes, microbial bioavailability, and therefore microbial demethylation, of MeHg in aquatic systems likely depends more on the species of microorganism than on the types and relative concentrations of thiols or other MeHg ligands present.

Keywords: Methylmercury; Bioavailability; Cysteine; Glutathione; Broad spectrum mercury resistance

YuYang Zhou, Huanlin Huang, Dongsheng Shen. (School of Environmental Science and Engineering, Zhejiang Gongshang University Zhejiang Provincial Key Laboratory of Solid Waste Treatment and Recycling, Zhejiang Gongshang University). Multi-substrate biodegradation interaction of 1, 4-dioxane and BTEX mixtures by *Acinetobacter baumannii* DD1. Biodegradation, Volume 27(1) (2016): 37-46

This study evaluated substrate interactions during the aerobic biodegradation of 1, 4-dioxane and BTEX mixtures by a pure culture, *Acinetobacter baumannii* DD1, which is capable of utilizing 1, 4-dioxane for growth. *A. baumannii* DD1 could utilize BTEX as a sole carbon source, but could not utilize *m*-xylene and *p*-xylene. In binary mixtures, there was a lag of about 14 h before the degradation of BTE, and 1, 4-dioxane only started to be utilized when BTE was completely degraded by 1, 4-dioxane-grown DD1. Furthermore, the biodegradation rate of 1, 4-dioxane decreased from 73.33 to 40.74 mg/(h g dry weight) after the biodegradation of benzene. 1, 4-dioxane could not be degraded after the biodegradation of *o*-xylene in 80 h. DD1 could also not degrade *m*-xylene and *p*-xylene coexisting with 1, 4-dioxane. The ability of DD1 to degrade BTEX occurred in the following order: benzene > ethylbenzene > toluene > *o*-xylene > *m*-xylene = *p*-xylene. The biodegradation of 1, 4-dioxane was not activated in the mixture with *o*-xylene, primarily because of the accumulation of the specific toxic intermediate, 2, 3-dimethylphenol. The lag in BTE degradation was presumably because of the induction of enzymes necessary for BTE degradation. Additionally, SDS-PAGE analysis demonstrated that there were different proteins during the degradation of benzene and 1, 4-dioxane.

Keywords: Biodegradation; 1, 4-dioxane; BTEX; Enzyme; Substrate inhibition

Jiaxiu Song, Wenbing Wang, Rongjie Li, Jun Zhu, Yongming Zhang, Rui Liu, Bruce E. Rittmann. (Department of Environmental Science and Engineering, College of Life and Environmental Science, Shanghai Normal University, Zhejiang Provincial Key Laboratory of Water Science and Technology, Department of Environmental Technology and Ecology, Yangtze Delta Region Institute of Tsinghua University, Swette Center for Environmental Biotechnology, Biodesign Institute, Arizona State University). UV photolysis for enhanced phenol biodegradation in the presence of 2,4,6-trichlorophenol (TCP). Biodegradation, Volume 27(1) (2016): 59-67

A bacterial strain isolated from activated sludge and identified as *Bacillus amyloliquefaciens* could biodegrade phenol, but 2,4,6-trichlorophenol (TCP) inhibited phenol biodegradation and biomass growth. UV photolysis converted TCP into dichlorocatechol, monochlorophenol, and dichlorophenol, and this relieved inhibition by TCP. Phenol-removal and biomass-growth rates were significantly accelerated after UV photolysis: the monod maximum specific growth rate (μ_{max}) increased by 9 % after TCP photolysis, and the half-maximum-rate concentration (K_S) decreased by 36 %. Thus, the major benefit of UV photolysis in this case was to transform TCP into a set of much-less-inhibitory products.

Keywords: 2,4,6-trichlorophenol; Biodegradation; Kinetics; Phenol; Photolysis

Firouz Abbasian, Robin Lockington, Mallavarapu Megharaj, Ravi Naidu. (Global Centre for Environmental Remediation (GCER), Faculty of Science and Information Technology, The University of NewcastleCooperative Research Centre for Environmental Risk Assessment and Remediation of the Environment (CRC-CARE), University of Newcastle, Future Industry Institute (FFI), University of South Australia, Global Centre for Environmental Remediation (GCER), Faculty of Science and Information Technology, The University of NewcastleCooperative Research Centre for Environmental Risk Assessment and Remediation of the Environment (CRC-CARE), University of Newcastle). A Review on the Genetics of Aliphatic and Aromatic Hydrocarbon Degradation. Applied Biochemistry and Biotechnology, Volume 178(2) (2016): 224-250

Because of the high diversity of hydrocarbons, degradation of each class of these compounds is activated by a specific enzyme. However, most of other downstream enzymes necessary for complete degradation of hydrocarbons maybe common between different hydrocarbons. The genes encoding proteins for degradation of hydrocarbons, including the proteins required for the uptake of these molecules, the specific enzyme used for the initial activation of the molecules and other necessary degrading enzymes are usually arranged as an operon. Although the corresponding genes in many phylogenetic groups of microbial species show different levels of diversity in terms of the gene sequence, the organisation of the genes in the genome or on plasmids and the activation mode (inductive or constitutive), some organisms show identical hydrocarbon-degrading genes, probably as a result of horizontal gene transfer between microorganisms.

Keywords: Genetics; Hydrocarbons; Alkanes; Aromatics

Munamato Mabhegedhe, Karl Rumbold, Monde Ntwasa. (Gary Magadzire School of Agriculture and Natural Sciences, Great Zimbabwe University, Off Great Zimbabwe Road, P. O. Box 1235, Masvingo, Zimbabwe, School of Molecular and Cell Biology, Faculty of Science, University of the Witwatersrand, 1 Jan Smuts Avenue, Braamfontein 2000, Johannesburg, South Africa). Cellulose degradation capabilities of dung beetle, Euoniticellus intermedius, larva gut consortia. African Journal of Biotechnology, Volume15(9)(2016): 315-319

This study assessed the capabilities of the dung beetle, *Euoniticellus intermedius* (Coleoptera: Scarabaeida), larva gut consortia in degrading cellulose that can serve as glucose source for biofuels production. A total of 144 live dung beetles were randomly collected from a dairy farm and bred in a temperature controlled insect rearing room. On reaching the late second to third instar stage, dung beetle larvae were harvested, dissected and the gut micro-flora were cultured in medium containing cellulose as sole carbon source. Microbial growth (total protein concentration) and cellulose degradation activity (reducing sugars concentration) in the cellulose cultures were monitored successively for 15 days. Statistical analysis showed that there was significant microbial growth, but no significant increase in reducing sugar levels. Despite the lack of increase in reducing sugar levels, it was concluded that the dung beetle larva gut has micro-flora with cellulose degrading capabilities that allowed it to grow and survive in the cellulose minimal medium.

Key words: Dung beetle, *Euoniticellus intermedius*, cellulose, biofuels.

Cormac D. Murphy. (UCD School of Biomolecular and Biomedical Science, University College Dublin). Microbial degradation of fluorinated drugs: biochemical pathways, impacts on the environment and potential applications. Applied Microbiology and Biotechnology, Volume 100(6) (2016): 2617-2627

Since the discovery over 60 years ago of fluorocortisone's biological properties (9-α-Fluoro derivatives of cortisone and hydrocortisone; Fried J and Sabo EF, J Am Chem Soc 76: 1455–1456, 1954), the number of fluorinated drugs has steadily increased. With the improvement in synthetic methodologies, this trend is likely to continue and will lead to the introduction of new fluorinated substituents into pharmaceutical compounds. Although the biotransformation of organofluorine compounds by microorganisms has been well studied, specific investigations on fluorinated drugs are relatively few, despite the increase in the number and variety of fluorinated drugs that are available. The strength of the carbon-fluorine bond conveys stability to fluorinated drugs; thus, they are likely to be recalcitrant in the environment or may be partially metabolized to a more toxic metabolite. This review examines the research done on microbial biotransformation and biodegradation of fluorinated drugs and highlights the importance of understanding how microorganisms interact with this class of compound from environmental, clinical and biotechnological perspectives.

Keywords: Organofluorine; Biotransformation; Fluorometabolite; Pollutant

Lene Lange, Yuhong Huang, Peter Kamp Busk. (Department of Chemical and Biochemical EngineeringTechnical University of Denmark). Microbial decomposition of keratin in nature—a new hypothesis of industrial relevance. Applied Microbiology and Biotechnology, Volume 100(5) (2016): 2083–2096

Discovery of keratin-degrading enzymes from fungi and bacteria has primarily focused on finding one protease with efficient keratinase activity. Recently, an investigation was conducted of all keratinases secreted from a fungus known to grow on keratinaceous materials, such as feather, horn, and hooves. The study demonstrated that a minimum of three keratinases is needed to break down keratin, an endo-acting, an exo-acting, and an oligopeptide-acting keratinase. Further, several studies have documented that disruption of sulfur bridges of the keratin structure acts synergistically with the keratinases to loosen the molecular structure, thus giving the enzymes access to their substrate, the protein structure. With such complexity, it is relevant to compare microbial keratin decomposition with the microbial decomposition of well-studied polymers such as cellulose and chitin. Interestingly, it was recently shown that the specialized enzymes, lytic polysaccharide monoxygenases (LPMOs), shown to be important for breaking the recalcitrance of cellulose and chitin, are also found in keratin-degrading fungi. A holistic view of the complex molecular self-assembling structure of keratin and knowledge about enzymatic and boosting factors needed for keratin breakdown have been used to formulate a hypothesis for mode of action of the LPMOs in keratin decomposition and for a model for degradation of keratin in nature. Testing such hypotheses and models still needs to be done. Even now, the hypothesis can serve as an inspiration for designing industrial processes for keratin decomposition for conversion of unexploited waste streams, chicken feather, and pig bristles into bioaccessible animal feed.

Keywords: Fungal and bacterial keratinases; Endo-, exo-, and oligoacting keratinases; Synergistic enzymes; Chemical boosters; Lytic polysaccharide monooxygenases; Keratin decomposition model

Xiaobin Liao, Bingxin Li, Rusen Zou, Shuguang Xie, Baoling Yuan. (Institute of Municipal and Environmental Engineering, College of Civil Engineering, Huaqiao University, State Key Joint Laboratory of Environmental Simulation and Pollution Control, College of Environmental Sciences and Engineering, Peking University, State Key Joint Laboratory

of Environmental Simulation and Pollution Control, College of Environmental Sciences and Engineering, Peking University). Antibiotic sulfanilamide biodegradation by acclimated microbial populations. Applied Microbiology and Biotechnology, Volume 100(5) (2016): 2439-2447

Sulfonamide antibiotics are commonly detected in the environment. Microbial degradation can play an important role in the dissipation of sulfonamide antibiotics. However, many aspects regarding the influential factor and biodegradation pathway remain essentially unclear. Moreover, phylogenetic information on the sulfonamide-degrading microbial community is still very limited. The present study investigated the biodegradation of sulfonamide antibiotic sulfanilamide by acclimated mixed culture and its influential factors, and the sulfanilamide-degrading microbial community. At the initial sulfanilamide concentration of 100 μg/L, nearly half of the antibiotic could be removed by acclimated microbial populations after 1 week of incubation, and an average removal rate of 78.3 % could be achieved in 4 weeks. *p*-Phenylenediamine, benzene sulfonamide, and hydroxylamine benzene sulfonamide were identified as the potential intermediates. Sulfanilamide biodegradation could be enhanced by a temperature rise and the presence of external carbon or nitrogen sources. The richness, diversity, and structure of the bacterial community showed a remarkable change with sulfanilamide biodegradation. Firmicutes and Bacteroidetes (mainly represented by classes Bacilli and Flavobacteriia) dominated the sulfanilamide-degrading bacterial community.

Keywords: Antibiotic; Acclimation; Biodegradation; Bacterial community; High-throughput sequencing

Yu Jiang, Yu Shang, Kai Yang, Hongyu Wang. (School of Civil Engineering, Wuhan University). Phenol degradation by halophilic fungal isolate JS4 and evaluation of its tolerance of heavy metals. Applied Microbiology and Biotechnology, Volume 100(4) (2016): 1883-1890

Phenol is one of the most common pollutants in many kinds of industrial wastewater, some of which are in high salinity, resulting in more difficulties of biodegradation. In this work, a halophilic strain capable of utilizing phenol as sole source of carbon and energy in both hypersaline and no-salt media was isolated and identified as genus *Debaryomyces.* The optimization of environmental parameters including phenol concentration, pH, dissolved oxygen as well as salinity was carried out and tolerance of heavy metals by the strain was evaluated. The strain *Debaryomyces* sp. was able to grow in culture when initial phenol concentration, pH, agitation and salinity were at wide ranges (0–1200 mg L^{-1}, 4.0–10.0, 50–200 rpm, 0 %-15 %, respectively). High removal efficiency was hardly affected in the presence of 5 mM of Zn (II) and Mn (II). Under optimal conditions (pH 6.0, 200 rpm, 1 % of salinity without heavy metals), 500 mg L^{-1} of phenol could be completely degraded within 32 h. The high removal efficiency of phenol by the strain with significant variations of process parameters might contribute to the bioremediation of phenol-polluted environments under hypersaline or no-salt conditions.

Keywords: Phenol; Hypersaline condition; *Debaryomyces* sp.*;* Bioremediation; Heavy metals

S. Ghosh Ray, M. M. Ghangrekar. (P. K. Sinha Centre for Bioenergy, ATDC, Indian Institute of Technology, Department of Civil Engineering, Indian Institute of Technology). Biodegradation kinetics of thin-stillage treatment by *Aspergillus awamori* and characterization of recovered chitosan. Applied Microbiology and Biotechnology, Volume 100(4) (2016): 1955-1965

An attempt has been made to provide solution for distillery wastewater using fungal pretreatment followed by an anaerobic process to achieve higher organic matter removal, which is a challenge at present with currently adopted technologies. Submerged growth kinetics of distillery wastewater supernatant by *Aspergillus awamori* was also evaluated. The proposed kinetic models using a logistic equation for fungal growth and the Leudeking–Piret equation for product formation were validated experimentally, and substrate consumption equation was derived using estimated kinetic coefficients. Up to 59.6 % chemical oxygen demand (COD) and 70 % total organic carbon (TOC) removals were observed in 96 h of fungal incubation. Maximum specific growth rate of fungi, coefficient of biomass yield on substrate and growth-associated product formation coefficient were estimated to be 0.07 ± 0.01 h^{-1}, 0.614 kg biomass/kg utilized COD and 0.215 kg CO_2/kg utilized TOC, respectively. The chitosan recovery of 0.072–0.078 kg/kg of dry mycelium was obtained using dilute sulphuric acid extraction, showing high purity and characteristic chitosan properties according to FTIR and XRD analyses. After anaerobic treatment of the fungal pretreated effluent with COD concentration of 7.920 ± 0.120 kg COD/m^3 (organic loading rate of 3.28 kg COD/m^3 day), overall COD reduction of 91.07 % was achieved from distillery wastewater.

Keywords: *Aspergillus awamori;* Chitosan extraction; Distillery wastewater treatment; Fungal treatment; Kinetics of fungal degradation

Biosensor

Timothy Hamerly, Brian Bothner. (Department of Chemistry and Biochemistry, Montana State University). Investigations into the Use of a Protein Sensor Assay for Metabolite Analysis. Applied Biochemistry and Biotechnology, Volume 178(1) (2016): 101-113

Rapid and definitive classification of biological samples has application in industrial, agricultural, and clinical settings. Considerable effort has been given to analytical methods to address such applications over the past 50 years, with the majority of successful solutions focusing on a single molecular target. However, in many cases, a single or even a few features are insufficient for accurate characterization or classification. Serum albumin (SA) proteins are a class of cargo-carrying proteins in blood that have evolved to transport a wide variety of metabolites and peptides in mammals. These proteins have up to seven binding sites which communicate allosterically to orchestrate a complex pick-up and delivery system involving a large number of different molecules at any time. The ability of SA proteins to bind multiple molecular species in a sophisticated manner inspired the development of assays to differentiate complex biological solutions. The combination of SA and high-resolution liquid chromatography mass spectrometry (LC-MS) is showing exciting promise as a protein sensor assay (PSA) for classification of complex biological samples. In this study, the PSA has been applied to cells undergoing and recovering from mild oxidative stress. Analysis using traditional LC-MS-based metabolomics failed to differentiate samples into treatment or temporal groups, whereas samples first treated with the PSA were cleanly classified into both correct treatment and temporal groups. The success of the PSA could be attributed to selective binding of metabolites, leading to a reduction in sample complexity and a general reduction in chemical noise. Metabolites important to successful sample classification were often enriched by 100-fold or more yet displayed a wide range of affinities for SA. The end result of PSA treatment is better

classification of samples with a reduction in the number of features seen overall. Together, these results demonstrate how the use of a protein-based assay before LC-MS analysis can greatly improve separation and lead to more accurate and successful tracking of the metabolic state in an organism, suggesting potential application in a wide range of fields.

Keywords: Bovine serum albumin; Protein sensor; Oxidative stress; Metabolomics; LC-MS; Biomarker

Hiroaki Sakamoto, Yuma Minpou, Takayuki Sawai, Yasufumi Enami, Shin-ichiro Suye. (Tenure-Track Program for Innovation Research, University of FukuiResearch and Education Program for Life Science, University of Fukui, Department of Applied Chemistry and Biotechnology, Graduate School of Engineering, University of Fukui, Department of Frontier Fiber Technology and Science, Graduate School of Engineering, University of Fukui. Research and Education Program for Life Science, University of Fukui, Optoelectonic Engineering, School of Systems Engineering, Kochi University of Technology). A Novel Optical Biosensing System Using Mach–Zehnder-Type Optical Waveguide for Influenza Virus Detection. Applied Biochemistry and Biotechnology, Volume 178(4) (2016): 687-694

In order to minimize the damage from viral epidemics, early detection of the causative agent of a viral epidemic and prevention of its immediate spread are urgent social demands. Therefore, in this study, we evaluated the utility of a Mach–Zehnder-type optical waveguide as a sensing device for influenza virus detection. However, it is impossible to detect a 100-nm-size virus using a sol-gel optical biosensor because sol-gel glass has a pore size of only a few nanometers, which makes it impossible for the virus to diffuse into the silica thin film. In order to construct the influenza-specific Mach–Zehnder optical biosensor for influenza detection, a stable antibody immobilization method with resulting high density on the sol-gel surface is strongly required. In this study, the sol-gel glass surface was modified with amino and carboxyl groups, and an anti-H1N1/HA1 antibody was covalently immobilized using a cross-linking agent. We successfully prepared a carboxyl-modified sol-gel surface, using NHS/EDC as the cross-linker, for antibody immobilization, and confirmed the detection of influenza virus using the antibody-immobilized sol-gel glass. After treatment with a 100 μg/mL influenza virus solution for 15 min, a peak wavelength shift (~24 nm) was observed in the output light spectrum.

Keywords: Molecular immobilization; Optical biosensing; Influenza virus detection

Wei He, Sheng Yuan, Wen-Hui Zhong, Md. Ashaduzzaman Siddikee, Chuan-Chao Dai. (College of Life Sciences, Nanjing Normal University, College of Geography Sciences, Nanjing Normal University, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University). Application of genetically engineered microbial whole-cell biosensors for combined chemosensing. Applied Microbiology and Biotechnology, Volume 100(3) (2016): 1109-1119

The progress of genetically engineered microbial whole-cell biosensors for chemosensing and monitoring has been developed in the last 20 years. Those biosensors respond to target chemicals and produce output signals, which offer a simple and alternative way of assessment approaches. As actual pollution caused by human activities usually contains a combination of different chemical substances, how to employ those biosensors to accurately detect real contaminant samples and evaluate biological effects of the combined chemicals has become a realistic object of environmental researches. In this review, we outlined different types of the recent method of genetically engineered microbial whole-cell biosensors for combined chemical evaluation, epitomized their detection performance, threshold, specificity, and application progress that have

been achieved up to now. We also discussed the applicability and limitations of this biosensor technology and analyzed the optimum conditions for their environmental assessment in a combined way.

Keywords: Engineered microbial whole-cell biosensor; Bioavailability; Combined chemicals

Bioengineering

Qing Meng, Tao Zhang, Bo Jiang, Wanmeng Mu, Ming Miao. (State Key Laboratory of Food Science and Technology, Jiangnan University). Advances in applications, metabolism, and biotechnological production of L-xylulose. Applied Microbiology and Biotechnology, Volume 100(2) (2016): 535-540

L-Xylulose is an intermediate in certain metabolic pathways and is classified as a rare sugar. It shows important physiological effects such as acting as an inhibitor of α-glucosidase and decreasing blood glucose, and it can be employed to produce other significant rare sugars, such as L-ribose and L-xylose which contribute to the production of antiviral drugs. Chemical synthesis of L-xylulose was performed, but it is difficult and low yielding. The biotransformation from xylitol to L-xylulose by xylitol 4-dehydrogenase was studied intensively. This review describes the occurrence of L-xylulose in certain metabolic pathways, its bioproduction, and application potential.

Keywords: L-Xylulose; Rare sugar; Metabolic pathways; Bioproduction; Application potential

Pollen Biotechnology

Hongsheng Zhou, Hao Yin, Jianqing Chen, Xing Liu, Yongbin Gao, Juyou Wu, Shaoling Zhang (Center of Pear Engineering Technology Research, State Key Laboratory of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing 210095, China). Gene-expression profile of developing pollen tube of *Pyrus bretschneideri*. Gene Expression Patterns, Volume 20(1) (2016): 11–21

Pollen is an ideal model system for investigation of cell growth. In order to better understand the molecular biology mechanisms of the process of pear pollen tube development, RNA sequencing (RNA-Seq) technology was used to characterize the expression of genes during four development stages of pear pollen, including mature pollen grains (MP), hydrated pollen grains (HP), growing pollen tubes (PT) and stopped-growth pollen tubes (SPT). The four libraries generated a total of 47,072,151 clean reads that were mapped and assembled into 21,394 genes. Transcripts from the four stages were classified into 38 functional subcategories. Between MP and HP, 305 genes were differentially expressed, and 502 genes were differentially expressed between HP and PT. More importantly, we have observed that 2208 genes were differentially expressed between PT and SPT, and this is the first report of the gene expression comparison between the two development stages. Eight of the differentially expressed genes were randomly selected to confirm the RNA-Seq results by quantitative real-time PCR (qRT-PCR). Taken together, this research provides a platform for future research on pear pollen tube growth and growth cessation.

Keywords: Pear; Pollen tube; Development; Gene expression profile

Katrin Süring, Sabine Bach, Katrin Bossmann, Eike Wolter, Anett Neumann, Wolfgang Straff, Conny Höflich. (Environmental Medicine and Health Effects Assessment, Federal Environment Agency, Corrensplatz 1, 14195 Berlin, Germany). **PM10 contains particle-bound allergens: Dust analysis by Flow Cytometry. Environmental Technology & Innovation, Volume 5(2016): 60–66**

Exposure to inhalable particulate matter (PM10, particle size $\leq 10\ \mu m$ in diameter) can be associated with a number of adverse health effects such as airway inflammation and aggravation of asthma. Asthma can be triggered amongst others by birch pollen allergens like Bet v 1, but due to their size whole birch pollen cannot enter the lower respiratory tract. However, PM10 may act as carrier of adsorbed allergens and we speculated that Flow Cytometry, a method widely used to characterize suspended solids >0.5 µm in diameter, can be used to quantify these allergen-loaded particles. We show here, that the major birch pollen antigen Bet v 1 is bound to PM10 particles and that PM10 samples from high pollen season contain significantly higher proportions of Bet v 1 positive PM10>0.5 µm particles than PM10 samples from low pollen season. This difference may be of biological relevance as PM10 from high pollen season but not from low pollen season induced basophil activation in a pollen allergic proband. These findings indicate that ambient particles can transport adsorbed allergens into the lower respiratory airways where they could cause allergic sensitizations or trigger allergic reactions. Furthermore, Flow Cytometry adds to the list of tools for PM10 characterization.

Keywords: Basophil activation; Bet v 1; Birch pollen antigen; Flow Cytometry; Particulate matter; PM10

Biotechnology Policy Issue

Mogens Lund [a], mogens.lund@nibio.no, Jørgen Dejgård Jensen [b]. ([a]Norwegian Institute of Bioeconomic Research, Ås, Norway, [b]Department of Food and Resource Economics, University of Copenhagen, Denmark). **A real options approach to biotechnology investment policy—the case of developing a Campylobacter vaccine to poultry .Preventive Veterinary Medicine, Volume 128(2016): 58-69**

The aim of the article is to identify and analyse public-private incentives for the development and marketing of new animal vaccines within a real options methodological framework, and to investigate how real options methodology can be utilized to support economic incentives for vaccine development in a cost-effective way. The development of a vaccine against *Campylobacter jejuni* in poultry is applied as a case study. Employing the real options methodology, the net present value of the vaccine R&D project becomes larger than a purely probabilistic expected present value throughout the different stages of the project − and the net present value becomes larger, when more types of real options are taken into consideration. The insight from the real options analysis reveals opportunities for new policies to promote the development of animal vaccines. One such approach might be to develop schemes combining stage-by-stage optimized subsidies in the individual development stages, with proper account taken of investors'/developers' economic incentives to proceed, sell or cancel the project in the respective stages. Another way of using the real options approach to support the development of desirable animal vaccines could be to issue put options for the vaccine candidate, enabling vaccine developers to hedge against the economic risk from market volatility.

Keywords: Biotechnology; Campylobacter-vaccine; Real-Options-Valuation; Investment-policies

Evan Fraser[a], Alexander Legwegoh[a], Krishna KC[a], Mike CoDyre[a], Goretty Dias[b], Shelley Hazen[a], Rylea Johnson[a], Ralph Martin[c], Lisa Ohberg[a], Sri Sethuratnam[a], Lauren Sneyd[e], John Smithers[a], Rene Van Acker[c], Jennifer Vansteenkiste[a], Hannah Wittman[d], Rickey Yada[d]. ([a] Dept. of Geography, University of Guelph, Canada, [b] School of Environment, Enterprise and Development, University of Waterloo, Canada, [c] Ontario Agriculture College, University of Guelph, Canada, [d] Faculty of Land and Food Systems, University of British Columbia, Canada, [e] Department of Development Studies, St. Francis Xavier University, Canada). **Biotechnology or organic? Extensive or intensive? Global or local? A critical review of potential pathways to resolve the global food crisis. Trends in Food Science & Technology, Volume 48(2016): 78–87**

While experts agree that poverty, population, energy prices, climate change, and socio-political dynamics undermine global food security, there is no agreement on effective strategies to meet this challenge. For example, some promote “high tech” solutions (e.g. biotechnology) designed to boost yield while others prefer local food systems. To better understand these debates, this article explores four perspectives from the literature: (1) technology to increase food production; (2) equitable food distribution; (3) policies to reduce pollution and waste; and (4) community action to promote sovereign food systems. The paper concludes with recommendations on how food scientists can navigate these controversies to help research and policy making.

Keywords: Food security; Food sovereignty; Agricultural production; Poverty; Farming systems; Technology; GMOs; Biotechnology

Agricultural Biotechnology

M.E. Kragt[a, b], D.J. Pannell[a], A. McVittie[c], A.W. Stott[c], B. Vosough Ahmadi[c], P. Wilson[d]. ([a] Centre for Environmental Economics & Policy, School of Agricultural & Resource Economics, University of Western Australia, Crawley, WA 6009, Australia, [b] CSIRO Agriculture Flagship, Floreat, WA 6014, Australia, [c] Scotland's Rural College (SRUC), Kings Buildings, West Mains Rd, Edinburgh, Midlothian EH9 3JG, UK, [d] Rural Business Research Unit, Agricultural and Environmental Science, School of Biosciences, University of Nottingham, Leicestershire LE12 5RD, UK). **Improving interdisciplinary collaboration in bio-economic modelling for agricultural systems. Agricultural Systems, Volume 143(2016): 217–224**

Interest in models that integrate biophysical and economic components of agri-environmental systems has increased, largely in recognition of the multiple services provided by agri-environmental systems and reflecting the complexity of ‘multi-functional’ agriculture. We discuss the challenges of bio-economic modelling projects where biophysical and social-science research is integrated. Specific interdisciplinary challenges arise from, for example, differences in language and system understanding between disciplines, limited rewards for interdisciplinary research in the current academic merit system, and the time demands of interdisciplinary projects. Drawing on the authors' collective experiences in developing and applying bio-

economic models, we discuss ways to overcome these challenges. Important lessons for future integrated modelling projects are to invest enough time at the start of the project to align research expectations, recognising the central role of communication, and training research 'integrators' who can facilitate collaboration within interdisciplinary teams.

Keywords: Interdisciplinary research; Integrated modelling; Bioeconomics; Agricultural economics; Farm systems

Bioenergy

Saprativ P. Das[1], Ashutosh Gupta, Debasish Das, Arun Goyal. (Department of Biotechnology, Indian Institute of Technology Guwahati, Guwahati 781039, Assam, India). **Enhanced bioethanol production from water hyacinth (*Eichhornia crassipes*) by statistical optimization of fermentation process parameters using Taguchi orthogonal array design. International Biodeterioration & Biodegradation, Volume 109(2016): 174–184**

Water hyacinth (*Eichhornia crassipes*), a fast growing aquatic weed and a potential lignocellulosic substrate with high hemicellulosic (44.68 ± 0.39%, w w^{-1}) content was used for bioethanol production. The commercial fungal enzymes are expensive in nature. Taguchi orthogonal array design was employed for optimization of simultaneous saccharification and fermentation (SSF) process parameters involving recombinant *Clostridium thermocellum* hydrolytic enzymes and fermentative microbes for enhanced bioethanol production from mixed, microwave-assisted alkali and organosolv pretreated substrate. The factors optimized in 100 mL SSF medium were (%, v v^{-1}): GH5 cellulase (5.6 U mg^{-1}, 0.44 mg mL^{-1}), 0.5; GH43 hemicellulase (3.8 U mg^{-1}, 0.33 mg mL^{-1}), 2.0; *Saccharomyces cerevisiae* (~3.8 × 10^9 cells mL^{-1}), 0.5; *Candida shehatae* (~2.9 × 10^8 cells mL^{-1}), 2.0; pH, 5.4 and 35 °C, temperature. GH43 hemicellulase volume, pH and temperature were the three significant factors. The optimized flask SSF with 1% (w v^{-1}) substrate contributed ~2-fold upturn in ethanol titre and yield (1.84 g L^{-1}, 0.310 g of ethanol g of substrate^{-1}) as compared with unoptimized conditions (1.0 g L^{-1}, 0.160 gg^{-1}). 5% (w v^{-1}) substrate in shake flask and bioreactor contributed ethanol titre and yield of 9.78 g L^{-1}, 0.329 gg^{-1} and 13.7 g L^{-1}, 0.462 gg^{-1} respectively.

Keywords: Bioethanol; Taguchi orthogonal array; GH5 cellulase; GH43 hemicellulase; SSF; Bioreactor

Naga Raju Maddela[a], Ricardo Burgos[a], Venkateswarlu Kadiyala[b], Andrea Riofrio Carrion[c], Manjunatha Bangeppagari[d]. ([a] Department of Life Sciences, Universidad Estatal Amazónica, Puyo, Ecuador, [b] Faculty of Life Sciences, Sri Krishnadevaraya University, Anantapur, India, [c] Laboratory of Biology, Universidad Estatal Amazónica, Puyo, Ecuador, [d] Department of Life Sciences, Universidad de las Fuerzas Armadas-ESPE, Quito, Ecuador). **Removal of petroleum hydrocarbons from crude oil in solid and slurry phase by mixed soil microorganisms isolated from Ecuadorian oil fields. International Biodeterioration & Biodegradation, Volume 108(2016): 85–90**

Soil collected from oil fields of the Ecuadorian Amazon rainforest contained microorganisms capable of removing total petroleum hydrocarbons (TPHs) from crude oil. Following 16/18S rDNA sequence analysis, soil microorganisms efficient in the removal of TPHs were identified as *Bacillus cereus*, *Bacillus thuringiensis*, *Geomyces pannorum*, and *Geomyces* sp. A mixed culture of the above two isolates of bacteria and two of fungi were tested for its ability to remove TPHs from crude oil in solid phase (SOP) or slurry phase (SLP) of soil. The capability of the

mixed culture in removing TPHs after 30 d incubation was higher in SLP than in SOP. Results of ecotoxicity studies using *Artemia salina* corroborated with those of TPHs removal from crude oil in SOP and SLP by the mixed culture of the selected bacteria and fungi.

Keywords: Crude oil pollution; Soil bacteria and fungi; TPHs removal; Solid or slurry phase; Ecotoxicity

E. Lobakova[a], S. Vasilieva[a], P. Kashcheeva[b], E. Ivanova[b], G. Dolnikova[a], K. Chekanov[a], R. Idiatulov[b], M. Kirpichnikov[a], V. Buznik[b], A. Dedov[b]. ([a] Biological Faculty of M.V. Lomonosov Moscow State University, Moscow, 119234, Russia, [b] Gubkin Russian State University of Oil and Gas, Moscow, 119991, Russia). **New bio-hybrid materials for bioremoval of crude oil spills from marine waters. International Biodeterioration & Biodegradation, Volume 108(2016): 99–107**

We report, for the first time, on the successful use of the new type of bio-hybrid materials (BHM) on the basis of polymeric nonwoven material made from methyl methacrylate-acrylonitrile (MA) which is an efficient oil-absorbent. The biomass and biomass-derived cell-structured support materials of duckweed plants (*Wolffia arrhiza, Lemna minuscula*) were incorporated into polymeric fibers and association of oil-degrading bacteria was immobilized. The bacteria immobilized on BHM with duckweeds structures (BHM + AD) degraded 93–97% of n-alkanes in artificial sea water after 25 days of incubation and removed the adsorbed oil from the polymer fibers almost completely whereas the oil-degrading efficiency of the bacteria immobilized on the additive-free MA was ca. twice lower. It is suggested that, in oligotrophic sea water, the plant-derived structures might furnish biogenic elements for the immobilized microorganisms increasing their oil degrading activity. The possibilities of the use of the new type of BHM for bioremoval of crude oil spills from marine waters are discussed.

Keywords: Water treatment; Oil biodegradation; Oil-degrading bacteria; Oil sorbents; Polymeric materials; Immobilization

Bo Wang, Yongzhen Peng, Yuanyuan Guo, Shuying Wang. (Key Laboratory of Beijing for Water Quality Science and Water Environment Recovery Engineering, Engineering Research Center of Beijing, Beijing University of Technology, Beijing 100124, PR China). **Bioproduction of volatile fatty acid from the fermentation of waste activated sludge for *in situ* denitritation. Journal of Bioscience and Bioengineering, Volume 121(4) (2016): 431 – 434**

Waste activated sludge (WAS) fermentation integrated with denitritation (the reduction of nitrite to dinitrogen gas) at different pHs was investigated in batch-mode reactors over a 24-day period. The results showed that in comparison with controlled pHs, the volatile fatty acid (VFA) bioproduction for *in situ* denitritation was significantly improved at uncontrolled pH. VFA fermented from WAS was quickly consumed by denitritation at uncontrolled pH, which accelerated sludge degradation. On the other hand, sludge digestion was benefited from the alkalinity produced from denitritation, while methanogenesis was prohibited by alkalinity and nitrite. The integrated sludge fermentation and denitritation can be cost-effectively applied to wastewater treatment plants, so that organic substrates (e.g., VFAs) are produced for denitritation via simultaneous sludge fermentation, which enables WAS reutilization and enhances nitrogen removal efficiency without the need of external carbon sources.

Key words: Waste activated sludge; Fermentation; Denitritation; pH; Volatile fatty acid

Wouter Van Hecke, Pieter Vandezande, Marjorie Dubreuil, Maarten Uyttebroek, Herman Beckers, Heleen De Wever. (Flemish Institute for Technological Research (VITO), Business Unit Separation and Conversion Technology). Biobutanol production from C5/C6 carbohydrates integrated with pervaporation: experimental results and conceptual plant design. Journal of Industrial Microbiology & Biotechnology, Volume 43(1) (2016): 25-36

In this study, a simulated lignocellulosic hydrolyzate was used in a continuous two-stage fermentor setup for production of acetone, butanol and ethanol. An organophilic pervaporation unit was coupled to the second fermentor. The dilution rate in the first fermentor was kept constant at 0.109 h^{-1}, while the dilution rate in the second fermentor was gradually decreased from 0.056 to 0.020 h^{-1}. Glucose was completely consumed, while 61 % of the xylose was consumed at the lowest dilution rate, leading to an overall solvent productivity of 0.65 g L^{-1} h^{-1} and a high concentration of 185 g kg^{-1} solvents in the permeate in the last fermentation zone during 192 h. Based on the experimental results, a process integrated with organophilic pervaporation was conceptually designed and compared with a base-case. Chemcad simulations indicate an energy reduction of ~50 % when organophilic pervaporation is used. This study also demonstrates significant reductions in process flows and energy consumption by the use of organophilic pervaporation as in situ product recovery technology.

Keywords: Bioprocess design; Biobutanol; Process integration; Product inhibitionIn situ product recovery; Pervaporation

Willy Yee. (Department of Applied Sciences, Faculty of Science and Technology, Nilai University). Microalgae from the Selenastraceae as emerging candidates for biodiesel production: a mini review. World Journal of Microbiology and Biotechnology, Volume 32(2016): 64

Over the years, microalgae have been identified to be a potential source of commercially important products such as pigments, polysaccharides, polyunsaturated fatty acids and in particular, biofuels. Current demands for sustainable fuel sources and bioproducts has led to an extensive search for promising strains of microalgae for large scale cultivation. Prospective strains identified for these purposes were among others, mainly from the genera *Hematococcus*, *Dunaliella*, *Botryococcus*, *Chlorella*, *Scenedesmus* and *Nannochloropsis*. Recently, microalgae from the Selenastraceae emerged as potential candidates for biodiesel production. Strains from the Selenastraceae such as *Monoraphidium* sp. FXY-10, *M. contortum* SAG 47.80, *Ankistrodesmus* sp. SP2-15 and *M. minutum* were high biomass and lipid producers when cultivated under optimal conditions. A number of Selenastraceae strains were also reported to be suitable for cultivation in wastewater. This review highlights recent reports on potential strains from the Selenastraceae for biodiesel production and contrasts their biomass productivity, lipid productivity as well as fatty acid profile. Cultivation strategies employed to enhance their biomass and lipid productivity as well as to reduce feedstock cost are also discussed in this paper.

Keywords: *Ankistrodesmus;* Biodiesel; Biomass; Lipid; Microalgae; *Monoraphidium;* Selenastraceae

Ankisha Vijay, Monika Vaishnava, Meenu Chhabra. (Department of Biology, Indian Institute of Technology–Jodhpur). Microbial fuel cell assisted nitrate nitrogen removal using cow manure and soil. Environmental Science and Pollution Research, Volume 23(8) (2016): 7744-7756

Microbial fuel cells (MFCs) are emerging wastewater treatment systems with a proven potential for denitrification. In this study, we have developed a high-rate denitrifying MFC. The anode consisted of cow manure and fruit waste and the cathode consisted of cow manure and soil. The initial chemical oxygen demand (COD)/nitrate nitrogen (NO_3^--N) was varied from 2 to 40 at the cathode while keeping the anode ratio fixed at 100. NO_3^--N removal rate of 7.1 ± 0.9 kg NO_3^--N/m^3 net cathodic compartment (NCC)/day was achieved at cathode COD/NO_3^--N ratio 7.31 with the current density of 190 ± 9.1 mA/m^2 and power density of 31.92 ± 4 mW/m^2 of electrode surface area. We achieved an open-circuit voltage (OCV) of 410 ± 20 mV at initial cathodic NO_3^--N of 0.345 g/l. The cathode COD/NO_3^--N ratio had a significant influence on MFC's OCV and nitrate removal rate. Lower OCV (<150 mV) and NO_3^--N removal rates were observed at COD/NO_3^--N ratio >12 and <7. Experiments done at different cathode pH values indicated that the optimum pH for denitrification was 7. Under optimized biochemical conditions, nitrate removal rate of 6.5 kg NO_3^--N/m^3 net cathodic compartment (NCC)/day and power density of 210 mW/m^2 were achieved in a low resistance MFC. The present study thus demonstrates the utility of MFCs for the treatment of high nitrate wastes.

Keywords: Microbial fuel cell; Biocathode; Heterotrophic denitrification; Cow manure; Soil; Wastewater treatment

Rachel Chen, Jennifer Dou. (School of Chemical and Biomolecular Engineering, Georgia Institute of Technology, Department of Biochemistry and Cell Biology, Rice University). **Biofuels and bio-based chemicals from lignocellulose: metabolic engineering strategies in strain development. Biotechnology Letters, Volume 38(2) (2016): 213-221**

Interest in developing a sustainable technology for fuels and chemicals has unleashed tremendous creativity in metabolic engineering for strain development over the last few years. This is driven by the exceptionally recalcitrant substrate, lignocellulose, and the necessity to keep the costs down for commodity products. Traditional methods of gene expression and evolutionary engineering are more effectively used with the help of synthetic biology and -omics techniques. Compared to the last biomass research peak during the 1980s oil crisis, a more diverse range of microorganisms are being engineered for a greater variety of products, reflecting the broad applicability and effectiveness of today's gene technology. We review here several prominent and successful metabolic engineering strategies with emphasis on the following four areas: xylose catabolism, inhibitor tolerance, synthetic microbial consortium, and cellulosic oligomer assimilation.

Keywords: Catabolite repression; Inhibitor tolerance ; Laboratory evolution; Lignocellulose biomass; Metabolic engineering ; Microbial consortium; Strain development; Xylose metabolism

Zhanying Zhang[1], Ian M O'Hara[1], Sagadevan Mundree[1], Baoyu Gao[2], Andrew S Ball[3], Nanwen Zhu[4], Zhihui Bai[5], Bo Jin[6]. ([1] Centre for Tropical Crops and Biocommodities, Queensland University of Technology, Brisbane, QLD 4001, Australia, [2] School of Environmental Science and Engineering, Shandong University, Jinan, China, [3] School of Applied Sciences, RMIT University, Bundoora, VIC 3083, Australia, [4] School of Environmental Science and Engineering, Shanghai Jiao Tong University, Shanghai 200240, China, [5] Research Centre for Eco-Environ. Sciences, Shuangqing Road, Beijing 100085, China, [6] School of Chemical Engineering, The University of Adelaide, Adelaide, SA 5005,

Australia). Biofuels from food processing wastes, Current Opinion in Biotechnology, Volume 38(2016): 97–105

Food processing industry generates substantial high organic wastes along with high energy uses. The recovery of food processing wastes as renewable energy sources represents a sustainable option for the substitution of fossil energy, contributing to the transition of food sector towards a low-carbon economy. This article reviews the latest research progress on biofuel production using food processing wastes. While extensive work on laboratory and pilot-scale biosystems for energy production has been reported, this work presents a review of advances in metabolic pathways, key technical issues and bioengineering outcomes in biofuel production from food processing wastes. Research challenges and further prospects associated with the knowledge advances and technology development of biofuel production are discussed.

Kirsten Heimann. (Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University, Townsville, QLD 4811, Australia). Novel approaches to microalgal and cyanobacterial cultivation for bioenergy and biofuel production. Current Opinion in Biotechnology, Volume 38(2016): 183–189

Growing demand for energy and food by the global population mandates finding water-efficient renewable resources. Microalgae/cyanobacteria have shown demonstrated capacity to contribute to global energy and food security. Yet, despite proven process technology and established net energy-effectiveness and cost-effectiveness through co-product generation, microalgal biofuels are not a reality. This review outlines novel biofilm cultivation strategies that are water-smart, the opportunity for direct energy conversion via anaerobic digestion of N_2-fixing cyanobacterial biomass and integrative strategies for microalgal biodiesel and/or biocrude production via supercritical methanol-direct transesterification and hydrothermal liquefaction, respectively. Additionally, fermentation of cyanobacterial biofilms could supply bioethanol to feed wet transesterification to biodiesel conversion for on-site use in remote locations.

Xin Zhou, Yong Xu, Shiyuan Yu. (College of Chemical Engineering, Nanjing Forestry University. Jiangsu Province Key Laboratory of Green Biomass Based Fuel Chemical). Simultaneous Bioconversion of Xylose and Glycerol to Xylonic Acid and 1,3-Dihydroxyacetone from the Mixture of Pre-Hydrolysates and Ethanol-Fermented Waste Liquid by *Gluconobacter oxydans.* Applied Biochemistry and Biotechnology, Volume 178(10 (2016): 1-8

Simultaneous bioconversion of xylose and glycerol to xylonic acid and 1,3-dihydroxyacetone (DHA) was realized by using *Gluconobacter oxydans* (*G. oxydans*). Currently, the enzymatic hydrolysate to ethanol-fermented waste liquid and the inorganic acid pre-hydrolysate that contain abundant glycerol and xylose were difficult to be utilized or disposed. Based on the method of compressed oxygen supply-sealed and stirred tank reactor system (COS-SSTR), the xylonic acid and 1,3-dihydroxyacetone could be co-produced rapidly with the mixture of the dilute sulfuric acid pre-hydrolysate and ethanol-fermented waste liquid of enzymatic hydrolysate (MPEW) as material. By means of the system, we finally produced 102.3 ± 3.2 g/L xylonic acid and 40.6 ± 1.8 g/L 1,3-dihydroxyacetone at yield of 92.4 ± 2.8 % and 80.6 ± 3.5 % directly and simultaneously from the mixed solution. The central features of this bioprocess application would enable cost-competitive bacterial xylonic acid and 1,3-dihydroxyacetone production from lignocellulosic materials.

Keywords: Xylonic acid (XA); 1,3-Dihydroxyacetone (DHA); XyloseGlycerol; Compressed oxygen supply; *Gluconobacter oxydans*

Jing-Rong Cheng, Xue-Ming Liu, Zhi-Yi Chen. (Sericultural & Agri-Food Research Institute, Guangdong Academy of Agricultural Sciences, Key Laboratory of Functional Foods, Ministry of Agriculture, Guangdong Key Laboratory of Agricultural Products Processing. Guangzhou Institute of Energy Conversion, Chinese Academy of Sciences, Sericultural & Agri-Food Research Institute, Guangdong Academy of Agricultural Sciences, Key Laboratory of Functional Foods, Ministry of Agriculture, Guangdong Key Laboratory of Agricultural Products Processing). Methane Production from Rice Straw Hydrolysate Treated with Dilute Acid by Anaerobic Granular Sludge. Applied Biochemistry and Biotechnology, Volume 178(1) (2016): 9-20

The traditional anaerobic digestion process of straw to biogas faces bottlenecks of long anaerobic digestion time, low digestion rate, less gas production, etc., while straw hydrolysate has the potential to overcome these drawbacks. In this study, the dilute sulphuric acid–treated hydrolysate of rice straw (DSARSH) containing high sulfate was firstly proved to be a feasible substrate for methane production under mesophilic digestion by granular sludge within a short digestion time. Batch anaerobic digestion process was operated under different initial chemical oxygen demand (COD) values at temperature of 37 °C with the pH of 8.5. Among the initial COD values ranging from 3000 to 11,000 mg/L, 5000 mg/L was proved to be the most appropriate considering high COD removal efficiency (94.17 ± 1.67 %), CH_4 content (65.52 ± 3.12 %), and CH_4 yield (0.346 ± 0.008 L_{CH4}/g COD $_{removed}$) within 120 h. Furthermore, when the studied system operated at the initial COD of 5000 mg/L, the sulfate removal ratio could reach 56.28 %.

Keywords: Methane production; Granular sludge; DSARSH; Sulfate; Anaerobic digestion

Tigressa Helena S. Rodrigues, Emanuel Meneses de Barros, Jeferson de Sá Brígido, Winne M. da Silva, Maria Valderez P. Rocha, Luciana Rocha B. Gonçalves. (Departamento de Engenharia Química, Universidade Federal do Ceará). The Bioconversion of Pretreated Cashew Apple Bagasse into Ethanol by SHF and SSF Processes. Applied Biochemistry and Biotechnology, Volume 178(6) (2016): 1167-1183

Ethanol production from acidic-alkaline pretreated cashew apple bagasse (CAB-OH) was investigated using separated hydrolysis and fermentation (SHF) and simultaneous saccharification and fermentation (SSF) processes. First, a screening of *Kluyveromyces* strains was conducted by SHF and a maximum ethanol concentration of 24.1 g L^{-1} was obtained using *Kluyveromyces marxianus* ATCC36907, which presented similar profiles when compared to results obtained by a *Saccharomyces* strain. The effect of temperature on ethanol production conducted by SHF using *K. marxianus* ATCC36907 was investigated, and the maximum ethanol yield ($Y_{E/G}$) was obtained at 40 °C (0.46 g g^{-1}) using a synthetic medium. In the SHF using CAB-OH hydrolysate, the maximum ethanol concentration obtained was 24.9 g L^{-1}, 5.92 g L^{-1} h^{-1} of productivity, and ethanol yield of 0.43 g g^{-1} at 40 °C. Afterwards, *K. marxianus* ATCC36907 was used in the bioconversion of CAB-OH by SSF, and an ethanol concentration of 41.41 ± 0.2 g L^{-1} was obtained using 10 % CAB-OH at 40 °C, 150 rpm and 24 h, resulting in a $Y'_{E/G}$ of 0.50 $g_E\, g_G^{-1}$ and an efficiency of 98.4 %, in the process conducted with cellobiase supplementation. SHF and SSF processes using CAB-OH and *K. marxianus* ATCC36907 can be used to ethanol production, but the SSF process required only one step to achieve the same production.

Keywords: Cashew apple bagasse; Second-generation ethanol; Enzymatic hydrolysis; *Kluyveromyces; Saccharomyces;* Simultaneous saccharification and fermentation

Alemayehu Gashaw. (Department of Chemistry, Faculty of Natural and Computational Sciences, Bule Hora University, Bule Hora, Ethiopia.Corresponding Author Email: alexgashaw@gmail.com). Co-digestion of municipal organic wastes with night soil and cow dung for biogas production: A Review. African Journal of Biotechnology, Volume 15(2)(2016): 32-44

Currently, biogas production is one of the most promising renewable energy sources and it represents a very promising way to overcome the problem of waste treatment. Biogas, which is principally composed of methane and carbon dioxide, can be obtained by anaerobic fermentation of biomass such as manure, night soil, sewage sludge and municipal solid wastes. Furthermore, the solid residuals of fermentation (the digested slurry) might be reused as fertilizer, to enhance the fertility of the soil. The huge amount of waste generates in the urban areas especially organic fraction of municipal solid waste or simply municipal bio-waste, which is used as feedstock for biogas production; represents an environmentally sustainable energy source since it improves solid waste management while simultaneously providing an alternative clean energy source. The primary advantages of biogas technology is the use of organic wastes with a low nutrient content to degrade by co-digesting with different substrates in the anaerobic bioreactors, and the process simultaneously leads to low cost production of biogas, which could be vital for meeting future energy needs. This review clearly indicates that co-digestion of municipal organic waste with night soil and cow dung is one of the most effective biological processes to treat a wide variety of solid organic wastes and the use of these wastes for biogas production. In addition, this review briefly discussed the factors affecting biogas production and analytical methods.

Key words: Biogas, anaerobic digestion, municipal solid waste, pretreatment.

Chansom Keo-oudone, Sukanya Nitiyon, Phonepasith Sotitham, Akio Tani, Noppon Lertwattanasakul, Napatchanok Yuangsaard, Somchanh Bounphanmy, Savitree Limtong, Mamoru Yamada*. (Department of Biology, Faculty of Science, National University of Laos, Lao PDR, Laos, Applied Molecular Bioscience, Graduate School of Medicine, Yamaguchi University, Ube, Yamaguchi 755-8505, Japan, Department of Microbiology, Faculty of Science, Kasetsart University, Thailand, Institute of Plant Science and Resources, Okayama University, Kurashiki, Okayama 710-0046, Japan, Applied Molecular Bioscience, Graduate School of Medicine, Yamaguchi University, Ube, Yamaguchi 755-8505, Japan.,Department of Biological Chemistry, Faculty of Agriculture, Yamaguchi University, Yamaguchi 753-8515, Japan.,Research Center for Thermotolerant Microbial Resources, Yamaguchi University, Yamaguchi 753-8315, Japan). Isolation and characterization of thermotolerant ethanol-fermenting yeasts from Laos and application of whole-cell matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS) analysis for their quick identification. African Journal of Biotechnology, Volume 15(6)(2016): 153-164

Thermotolerant yeasts, which are expected to be applicable for high-temperature fermentation as an economical process, were isolated from four provinces in Laos. Of these yeasts, five isolates exhibited stronger fermentation abilities in a 16% sugars-containing medium of glucose, sucrose, sugarcane or molasses at 40°C than that of Kluyveromyces marxianus DMKU 3-1042, one of the most thermotolerant and efficient yeasts isolated previously in Thailand. One of the five strains, BUNL-17, exhibited the highest ethanol fermentation performance at 45°C. Yeast identification was achieved by whole-cell matrix-assisted laser desorption/ionization time-of-flight mass

spectrometry (MALDI-TOF/MS) analysis as well as by nucleotide sequencing of the D1/D2 domain of the large subunit rRNA gene, revealing that the isolated strains can be categorized into Pichia kudriavzevii, Cyberlindnera rhodanensis and K. marxianus and that all of the five strains are K. marxianus. The results of this study showed that the former analysis is much faster than the latter and reliable and equivalent to the latter.

Keywords: Ethanol fermentation, thermotolerant yeast, Kluyveromyces marxianus.

Jeonghee Yun, Sang Don Lee, Kyung-Suk Cho. (Department of Environmental Science and Engineering, Ewha Womans University). Biomethane production and microbial community response according to influent concentration of molasses wastewater in a UASB reactor. Applied Microbiology and Biotechnology, Volume 100(10) (2016): 4675-4683

This study aimed to investigate the interaction between methane production performance and active microbial community dynamics at different loading rates by increasing influent substrate concentration. The model system was an upflow anaerobic sludge blanket (UASB) reactor using molasses wastewater. The active microbial community was analyzed using a ribosomal RNA-based approach in order to reflect active members in the UASB system. The methane production rate (MPR) increased with an increase in organic loading rate (OLR) from 3.6 to 5.5 g $COD \cdot L^{-1} \cdot day^{-1}$ and then it decreased with further OLR addition until 9.7 g $COD \cdot L^{-1} \cdot day^{-1}$. The UASB reactor achieved a maximum methane production rate of 0.48 $L \cdot L^{-1} \cdot day^{-1}$ with a chemical oxygen demand (COD) removal efficiency of 91.2 % at an influent molasses concentration of 16 g $COD \cdot L^{-1}$ (OLR of 5.5 g $COD \cdot L^{-1} \cdot day^{-1}$). In the archaeal community, *Methanosarcina* was predominant irrespective of loading rate, and the relative abundance of *Methanosaeta* increased with loading rate. In the bacterial community, *Firmicutes* and *Eubacteriaceae* were relatively abundant in the loading conditions tested. The network analysis between operation parameters and microbial community indicated that MPR was positively associated with most methanogenic archaea, including the relatively abundant *Methanosarcina* and *Methanosaeta*, except *Methanofollis*. The most abundant *Methanosarcina* was negatively associated with *Bifidobacterium* and *Methanosaeta*, whereas *Methanosaeta* was positively associated with *Bifidobacterium*.

Keywords: Methane; Molasses wastewater; Substrate concentration; Upflow anaerobic sludge blanket; Microbial community

Ánxela Fernández-Naveira, Haris Nalakath Abubackar, María C. Veiga, Christian Kennes. (Chemical Engineering Laboratory, Faculty of Sciences, University of La Coruña). Carbon monoxide bioconversion to butanol-ethanol by *Clostridium carboxidivorans*: kinetics and toxicity of alcohols. Applied Microbiology and Biotechnology, Volume 100(9) (2016): 4231-4240

Butanol production from carbon monoxide-rich waste gases or syngas is an attractive novel alternative to the conventional acetone-butanol-ethanol (ABE) fermentation. Solvent toxicity is a key factor reported in ABE fermentation with carbohydrates as substrates. However, in the gas-fermentation process, kinetic aspects and the inhibition effect of solvents have not thoroughly been studied. Therefore, different batch bottle experiments were carried out with the bacterial species *Clostridium carboxidivorans* using CO as carbon source for butanol-ethanol fermentation. A maximum specific growth rate of $0.086 \pm 0.004\ h^{-1}$ and a biomass yield of 0.011

$g_{biomass}/g_{CO}$ were found, which is significantly lower than in other clostridia grown on sugars. Besides, three assays were carried out to check the inhibitory effect of butanol, ethanol, and their mixtures. Butanol had a higher inhibitory effect on the cells than ethanol and showed a lower IC_{50}, reduced growth rate, and slower CO consumption with increasing alcohol concentrations. A concentration of 14–14.50 g/L butanol caused 50 % growth inhibition in *C. carboxidivorans*, and 20 g/L butanol resulted in complete inhibition, with a growth rate of 0 h^{-1}. Conversely, 35 g/L ethanol decreased by 50 % the final biomass concentration respect to the control and yielded the lowest growth rate of 0.024 h^{-1}. The inhibitory effect of mixtures of both alcohols was also checked adding similar, near identical, concentrations of each one. Growth decreased by 50 % in the presence of a total concentration of alcohols of 16.22 g/L, consisting of similar amounts of each alcohol. Occasional differences in initially added concentrations of alcohols were minimal. The lowest growth rate (0.014 h^{-1}) was observed at the highest concentration assayed (25 g/L).

Keywords: *Clostridium carboxidivorans;* Butanol; Ethanol; Inhibitory effect; Batch experiment; IC_{50}

Alessandra Adessi, Margherita Concato, Andrea Sanchini, Federico Rossi, Roberto De Philippis. (Department of Agrifood Production and Environmental Sciences, University of FlorenceInstitute of Chemistry of Organometallic Compounds (ICCOM), CNR, Department of Agrifood Production and Environmental Sciences, University of Florence. Institute of Chemistry of Organometallic Compounds (ICCOM), CNR).). Hydrogen production under salt stress conditions by a freshwater *Rhodopseudomonas palustris* strain. Applied Microbiology and Biotechnology, Volume 100(6) (2016): 2917-2926

Hydrogen represents a possible alternative energy carrier to face the growing request for energy and the shortage of fossil fuels. Photofermentation for the production of H_2 constitutes a promising way for integrating the production of energy with waste treatments. Many wastes are characterized by high salinity, and polluted seawater can as well be considered as a substrate. Moreover, the application of seawater for bacterial culturing is considered cost-effective. The aims of this study were to assess the capability of the metabolically versatile freshwater *Rhodopseudomonas palustris* 42OL of producing hydrogen on salt-containing substrates and to investigate its salt stress response strategy, never described before. *R. palustris* 42OL was able to produce hydrogen in media containing up to 3 % added salt concentration and to grow in media containing up to 4.5 % salinity without the addition of exogenous osmoprotectants. While the hydrogen production performances in absence of sea salts were higher than in their presence, there was no significant difference in performances between 1 and 2 % of added sea salts. Nitrogenase expression levels indicated that the enzyme was not directly inhibited during salt stress, but a regulation of its expression may have occurred in response to salt concentration increase. During cell growth and hydrogen production in the presence of salts, trehalose was accumulated as a compatible solute; it protected the enzymatic functionality against salt stress, thus allowing hydrogen production. The possibility of producing hydrogen on salt-containing substrates widens the range of wastes that can be efficiently used in production processes.

Keywords: Biological hydrogen production; Photofermentation; *Rhodopseudomonas palustris;* Salt stress; Trehalose

Alper Bayrakdar, Ebrahim Tilahun, Baris Calli. (Department of Environmental Engineering, Marmara University). Biogas desulfurization using autotrophic denitrification process. Applied Microbiology and Biotechnology, Volume 100(2) (2016): 939-948

The aim of this study was to evaluate the performance of an autotrophic denitrification process for desulfurization of biogas produced from a chicken manure digester. A laboratory scale upflow fixed bed reactor (UFBR) was operated for 105 days and fed with sodium sulfide or H_2S scrubbed from the biogas and nitrate as electron donor and acceptor, respectively. The S/N ratio (2.5 mol/mol) of the feed solution was kept constant throughout the study. When the UFBR was fed with sodium sulfide solution with an influent pH of 7.7, about 95 % sulfide and 90 % nitrate removal efficiencies were achieved. However, the inlet of the UFBR was clogged several times due to the accumulation of biologically produced elemental sulfur particles and the clogging resulted in operational problems. When the UFBR was fed with the H_2S absorbed from the biogas and operated with an influent pH of 8–9, around 98 % sulfide and 97 % nitrate removal efficiencies were obtained. In this way, above 95 % of the H_2S in the biogas was removed as elemental sulfur and the reactor effluent was reused as scrubbing liquid without any clogging problem.

Keywords: Clogging; Elemental sulfur; Nitrate; Scrubbing; Sulfide oxidation

Dominik Montag, Bernhard Schink. (Department of Biology, University of Konstanz). Biogas process parameters-energetics and kinetics of secondary fermentations in methanogenic biomass degradation. Applied Microbiology and Biotechnology, Volume 100(2) (2010): 1019-1026

Pool sizes of short-chain fatty acids (formate, acetate, propionate, and butyrate), hydrogen, and carbon monoxide were assayed in digesting sludge from four different methanogenic reactors degrading either sewage sludge or agricultural products and wastes at pH 8.0 and 40 or 47 °C. Free reaction energies were calculated for the respective degradation reactions involved, indicating that acetate, propionate, and butyrate degradation all supplied sufficient energy (−10 to −30 kJ per mol reaction) to sustain the microbial communities involved in the respective processes. Pools of formate and hydrogen were energetically equivalent as electron carriers. In the sewage sludge reactor, homoacetogenic acetate formation from H_2 and CO_2 was energetically feasible whereas syntrophic acetate oxidation appeared to be possible in two biogas reactors, one operating at enhanced ammonia content (4.5 g NH_4^+-N per l) and the other one at enhanced temperature (47 °C). Maximum capacities for production of methanogenic substrates did not exceed the consumption capacities by hydrogenotrophic and aceticlastic methanogens. Nonetheless, the capacity for acetate degradation appeared to be a limiting factor especially in the reactor operating at enhanced ammonia concentration.

Keywords: Methanogenesis; Energetics; Pool sizes; Fatty acids; Syntrophy; Secondary fermentations

Nano Biotechnology

Janine Moll[1, 2], Alexander Gogos[1], Thomas D. Bucheli[1], Franco Widmer[1] and Marcel G. A. van der Heijden[1, 2, 3.] . ([1]Agroscope, Institute for Sustainability Sciences ISS, [2]Plant-Microbe-Interactions, Department of Biology, Utrecht University, [3]Institute of Evolutionary Biology and Environmental Studies, University of Zurich). Effect of nanoparticles on red clover and its symbiotic microorganisms. Journal of Nanobiotechnology, Volume 14(2016): 36

Nanoparticles are produced and used worldwide and are released to the environment, e.g., into soil systems. Titanium dioxide (TiO_2) nanoparticles (NPs), carbon nanotubes (CNTs) and cerium dioxide (CeO_2) NPs are among the ten most produced NPs and it is therefore important to test, whether these NPs affect plants and symbiotic microorganisms that help plants to acquire nutrients. In this part of a joint companion study, we spiked an agricultural soil with TiO_2 NPs, multi walled CNTs (MWCNTs), and CeO_2 NPs and we examined effects of these NP on red clover, biological nitrogen fixation by rhizobia and on root colonization of arbuscular mycorrhizal fungi (AMF). We also tested whether effects depended on the concentrations of the applied NPs.

Plant biomass and AMF root colonization were not negatively affected by NP exposure. The number of flowers was statistically lower in pots treated with 3 mg kg^{-1} MWCNT, and nitrogen fixation slightly increased at 3000 mg kg^{-1} MWCNT.

This study revealed that red clover was more sensitive to MWCNTs than TiO_2 and CeO_2 NPs. Further studies are necessary for finding general patterns and investigating mechanisms behind the effects of NPs on plants and plant symbionts.

Keywords: Nanomaterials; Agriculture; Crop; Beneficial soil microbes; Ecosystem services

N. Dasgupta-Schubert[1], D. K. Tiwari[2] and L. M. Villaseñor Cendejas[3]. ([1]Instituto de Investigaciones Químico Biológicas (IIQB), University of Michoacan (UMSNH), [2]Colegio de Michoacán, Jardines del Cerro Grande, [3]Instituto de Física y Matemáticas (IFM), University of Michoacan (UMSNH)). **Comment on 'Carbon and fullerene nanomaterials in plant system'. Journal of Nanobiotechnology, Volume 14 (2016)** :**28**

A recent review article entitled "Carbon and fullerene nanomaterials in plant system" published in this journal, misinterprets a component of our (published) work on the interactions of carbon nanotubes with plants. In this comment, we provide the rationale to counter this misconstruction.

Keywords: Carbon nanotubes; Fe(II); Fe(III); Iron oxidation

Bipinchandra K. Salunke, Shailesh S. Sawant, Sang-Ill Lee, Beom Soo Kim. (Department of Chemical Engineering, Chungbuk National University, Department of Environmental Engineering, Chungbuk National University, Department of Chemical Engineering, Chungbuk National University). **Microorganisms as efficient biosystem for the synthesis of metal nanoparticles: current scenario and future possibilities. World Journal of Microbiology and Biotechnology,Volume : 32(5)(2016) : 88**

Nanoparticles, the elementary structures of nanotechnology, are important materials for fundamental studies and variety of applications. The different sizes and shapes of these materials exhibit unique physical and chemical properties than their bulk materials. There is a great interest in obtaining well-dispersed, ultrafine, and uniform nanoparticles to delineate and utilize their distinct properties. Nanoparticle synthesis can be achieved through a wide range of materials utilizing a number of methods including physical, chemical, and biological processes with various precursors from liquids and solids. There is a growing need to prepare environmentally friendly nanoparticles that do not produce toxic wastes in their process synthesis protocol. This kind of synthesis can be achieved by green environment benign processes, which happen to be mostly of a biological nature. Microorganisms are one of the most attractive and simple sources for the synthesis of different types of nanoparticles. This review is an attempt to provide the up-to-date information on current status of nanoparticle synthesis by different types of microorganisms such as fungi, yeast, bacteria, cyanobacteria, actinomycete, and algae. The probable biosynthesis mechanism and conditions for size/shape control are

described. Various applications of microbially synthesized nanoparticles are summarized. They include antibacterial, antifungal, anticancer, larvicidal, medical imaging, biosensor, and catalytic applications. Finally, limitations and future prospects for specific research are discussed.

Keywords: Biosynthesis; Nanoparticles; Microorganisms; Mechanism; Applications

Radek Zouzelka, Pavlina Cihakova, Jana Rihova Ambrozova, Jiri Rathousky. (J. Heyrovsky Institute of Physical Chemistry Academy of Sciences of the Czech Republic, Department of Physical Chemistry, University of Chemistry and Technology Prague, Department of Water Technology and Environmental Engineering, University of Chemistry and Technology Prague, J. Heyrovsky Institute of Physical Chemistry Academy of Sciences of the Czech Republic). Combined biocidal action of silver nanoparticles and ions against Chlorococcales (S*cenedesmus quadricauda, Chlorella vulgaris)* and filamentous algae (*Klebsormidium sp.*). Environmental Science and Pollution Research, Volume 23(9) (2016): 8317-8326

Despite the extensive research, the mechanism of the antimicrobial and biocidal performance of silver nanoparticles has not been unequivocally elucidated yet. Our study was aimed at the investigation of the ability of silver nanoparticles to suppress the growth of three types of algae colonizing the wetted surfaces or submerged objects and the mechanism of their action. Silver nanoparticles exhibited a substantial toxicity towards Chlorococcales *Scenedesmus quadricauda*, *Chlorella vulgaris*, and filamentous algae *Klebsormidium sp.*, which correlated with their particle size. The particles had very good stability against agglomeration even in the presence of multivalent cations. The concentration of silver ions in equilibrium with nanoparticles markedly depended on the particle size, achieving about 6 % and as low as about 0.1 % or even less for the particles 5 nm in size and for larger ones (40–70 nm), respectively. Even very limited proportion of small particles together with larger ones could substantially increase concentration of Ag ions in solution. The highest toxicity was found for the 5-nm-sized particles, being the smallest ones in this study. Their toxicity was even higher than that of silver ions at the same silver concentration. When compared as a function of the Ag^+ concentration in equilibrium with 5-nm particles, the toxicity of ions was at least 17 times higher than that obtained by dissolving silver nitrite (if not taking into account the effect of nanoparticles themselves). The mechanism of the toxicity of silver nanoparticles was found complex with an important role played by the adsorption of silver nanoparticles and the ions released from the particles on the cell surface. This mechanism could be described as some sort of synergy between nanoparticles and ions. While our study clearly showed the presence of this synergy, its detailed explanation is experimentally highly demanding, requiring a close cooperation between materials scientists, physical chemists, and biologists.

Keywords: Silver nanoparticles; Silver ions; Concentration of silver ions in equilibrium with silver nanoparticles; Algae; Toxicity; Uptake of silver by algae

Lina Sun, Shijun Zhu, Zhengzhong Yang, Qing Chen, Hongming Liu, Jun Zhang, Gang Hu, Shunpeng Li, Qing Hong. (College of Resources and Environmental Sciences, Nanjing Agricultural University, Key Laboratory of Agricultural Environmental Microbiology, Ministry of Agriculture, College of Life Sciences, Nanjing Agricultural University). Degradation of monocrotophos by *Starkeya novella* YW6 isolated from paddy soil. Environmental Science and Pollution Research, Volume 23(4) (2016): 3727-3735

A bacteria strain, YW6, capable of utilizing monocrotophos (MCP) as the sole carbon and nitrogen sources for growth was isolated from paddy soil and identified as *Starkeya novella*. Strain YW6 completely degraded 0.2 mM MCP within 36 h without any lag period. Addition of carbon source resulted in slowing down of the initial rate of degradation of MCP, while the presence of a more favorable source of nitrogen enhanced the degradation of MCP. In addition to the degradation of MCP, strain YW6 was also able to degrade a wide range of organophosphorus pesticides (OPs) containing P–O–C bond, but not dimethoate, which has P–S–C bond. A MCP degradation pathway was proposed on the basis of metabolite production patterns and identification of the metabolites. MCP is hydrolyzed at the P–O–C bond to form *N*-methylacetoacetamide and dimethyl phosphate; *N*-methylacetoacetamide is transformed to *N*-methyl-4-oxo-pentanamide, which was subsequently converted to 5-(methylamino)-5-oxo-pentanoic acid, and 5-(methylamino)-5-oxo-pentanoic acid is cleaved to glutaric acid and methylamine. These findings provide new insights into the microbial metabolism of MCP. To the best of our knowledge, this is the first report on the degradation of MCP by *Starkeya* bacteria.

Keywords: Monocrotophos; MCP; *Starkeya novella* YW6; Degradation pathway; Organophosphorus pesticide; Metabolite

Xiao Ze[1,†], Mingyu Su[2,†], Xiaoyang Zhao[1,†], Hao Jiang[1,†], Jie Hong[1], Xiaohong Yu[1], Dong Liu[1], Bingqing Xu[1], Lei Sheng[1], Qiuping Zhou[1], Junling Zhou[1], Jingwen Cui[1], Kai Li[1], Ling Wang[3], Yuguan Ze[1,*] and Fashui Hong[1,*]. ([1]Medical College of Soochow University, Suzhou, China, [2]Suzhou Environmental Monitor Center, Suzhou, China, [3]Library of Soochow University, Suzhou, China. [*]Correspondence to: Y. Ze; e-mail: zeyuguan@suda.edu.cn or F. Hong; e-mail: hongfsh_cn@sina.com). **TiO_2 nanoparticle-induced neurotoxicity may be involved in dysfunction of glutamate metabolism and its receptor expression in mice. Environmental Toxicology, Volume 31(6) (2016): 655–662**

Titanium dioxide nanoparticles (TiO_2 NPs) have been used in environmental management, food, medicine, and industry. But TiO_2 NPs have been demonstrated to cross the blood–brain barrier and store up in the brain organization, leading to glutamate-mediated neurotoxicity. However, the neurotoxicity in the brain is not well understood. In this study, mice were exposed to 1.25, 2.5, or 5 mg/kg body weight TiO_2 NPs for 9 months, and the glutamate–glutamine cyclic pathway and expressions of glutamate receptors associated with the hippocampal neurotoxicity were investigated. Our findings showed elevations of glutamate release and phosphate-activated glutaminase activity, and reductions in glutamine and glutamine synthetase in the hippocampus following exposure to TiO_2 NPs. Furthermore, TiO_2 NPs significantly inhibited the expression of *N*-methyl-D-aspartate receptor subunits (including NR1, NR2A, and NR2B) and metabotropic glutamate receptor 2 in mouse hippocampus. These findings suggest that the imbalance of glutamate metabolism triggered inhibitions of glutamate receptor expression in the TiO_2 NP-exposed hippocampus.

Keywords: titanium dioxide nanoparticles; mice; hippocampus; glutamate–glutamine cyclic pathway; glutamate receptors

Maysaa Chasib Al-Moahmmedawi. (Scholar Rescue Fund- Institute of International Education (IIE) USA. Corresponding Author Email: dr.maysaa78@yahoo.com). **Nanoformulation and antibiotic releasing property of cefotaxime nanoparticles. African Journal of Biotechnology, Volume 15(14)(2016): 539-548**

The objective of this study was to design nano-antibiotic to enhance their release from biomaterial agents. Cefotaxime was used as a model antibiotic substance in this carrier system.

These nanoparticles were preformulated using different concentrations of polycaprolactone (PCL) and poly (vinyl alcohol) as coating material and prepared using double emulsion solvent evaporation method. The physiochemical properties of cefotaxime nano-antibiotic (Cefo-NPs) stability were determined. Results showed that the encapsulation efficiency of nanoparticles increased with increase in polymer concentration. In addition, dynamic light scattering (DLS) and atomic force microscope (AFM) indicated that the particles size were in the range of 189 to 219 nm. The drug release profile of Cefo-NPs shows rapidly the release behaviour under acidic environment. And thus make it a promising tool for control bacterial infection.

Keywords: Polycaprolactone, poly (vinyl alcohol), cefotaxime, nanoparticle.

Sweety A. Wadhwani, Utkarsha U. Shedbalkar, Richa Singh, Balu A. Chopade. (Department of Microbiology, Savitribai Phule Pune University, University Department of Biochemistry, The Institute of Science, Dr. Babasaheb Ambedkar Marathwada University). Biogenic selenium nanoparticles: current status and future prospects. Applied Microbiology and Biotechnology, Volume 100(6) (2016): 2555-2566

Selenium nanoparticles (SeNPs) are gaining importance in the field of medicine owing to their antibacterial and anticancer properties. SeNPs are biocompatible and non-toxic compared to the counterparts, selenite (SeO_3^{-2}) and selenate (SeO_4^{-2}). They can be synthesized by physical, chemical, and biological methods and have distinct bright orange-red color. Biogenic SeNPs are stable and do not aggregate owing to natural coating of the biomolecules. Various hypotheses have been proposed to describe the mechanism of microbial synthesis of SeNPs. It is primarily a two-step reduction process from SeO_4^{-2} to SeO_3^{-2} to insoluble elemental selenium (Se^0) catalyzed by selenate and selenite reductases. Phenazine-1-carboxylic acid and glutathione are involved in selenite reduction. Se factor A (SefA) and metalloid reductase Rar A present on the surface of SeNPs confer stability to the nanoparticles. SeNPs act as potent chemopreventive and chemotherapeutic agents. Conjugation with antibiotics enhances their anticancer efficacy. These also have applications in nanobiosensors and environmental remediation.

Keywords: Selenium nanoparticles; Selenate reduction; Mechanism; Antibacterial activity; Anticancer

Divya Arora, Nisha Sharma , Vishal Sharma, Vidushi Abrol, Ravi Shankar, Sundeep Jaglan. (Quality Control & Quality Assurance Division, CSIR-Indian Institute of Integrative MedicineCSIR-Academy of Scientific & Innovative Research, Govt. of India, Quality Control & Quality Assurance Division, CSIR-Indian Institute of Integrative Medicine). An update on polysaccharide-based nanomaterials for antimicrobial applications. Applied Microbiology and Biotechnology, Volume 100(6) (2016): 2603-2615

Scientific community has made a lot of efforts to combat the infectious diseases using antimicrobial agents, but these are associated with problems of development of multi-drug resistance and their adverse side effects. To tackle these challenges, nanocarrier-based drug delivery system using polysaccharides has received enormous attention in the past few years. These antimicrobial agents can become more efficacious when adsorbed, entrapped, or linked to polysaccharides. In addition, these nanocarrier-based systems provide an increase in the surface area of the drug and are able to achieve the targeted drug delivery as well as used for the synthesis of packaging materials with improved mechanical strength, barrier, and antimicrobial

properties. This review focuses on potential therapeutic applications of nanocarrier-based drug delivery systems using polysaccharides for antimicrobial applications.

Keywords: Polysaccharide; Nanoparticle; Chitosan; Hyaluronic acid; Dextran; Antimicrobial

Gunabalan Madhumitha, Ganesh Elango, Selvaraj Mohana Roopan. (Chemistry of Heterocycles and Natural Products Research Laboratory, Organic Chemistry Division, School of Advanced Sciences, VIT University). Biotechnological aspects of ZnO nanoparticles: overview on synthesis and its applications. Applied Microbiology and Biotechnology, Volume 100(2) (2016): 571-581

The physicochemical methods of the synthesis of zinc nanoparticles (ZnO NPs) and some detailed studies on ZnO toxicity mechanism and biokinetics have been reported. However, some of these physical and chemical methods of synthesis are expensive and can also have toxic substances absorbed onto them. Hence, eco-friendly synthesis of nanoparticles due to their easier process, cheaper availability, and high stability is dominating new research. In particular, ZnO NPs which are now being synthesized through major biological systems involved in this are bacteria, fungi, and plant extracts; this has increased studies in various applications in the biological field. In this review, we have elaborated on various natural source-mediated syntheses of ZnO NPs and their role in various biological activities like antimicrobial, anticandidal, larvicidal, cytotoxic, and photocatalytic activities. Apart from these applications, ZnO NPs are also reported to help to prevent dust formation, for several years, on oil paintings.

Keywords: ZnO NPs; Natural sources; Biosynthesis; Application studies; Historical preservations

Biomimicry

Moheb Sabry Aziz, Amr Y. El sheriff. (Alexandria University, Faculty of Engineering, Architectural Engineering Department, Egypt). Biomimicry as an approach for bio-inspired structure with the aid of computation. Alexandria Engineering Journal, Volume 55(1) (2016): 707–714

Biomimicry is the study of emulating and mimicking nature, where it has been used by designers to help in solving human problems. From centuries ago designers and architects looked at nature as a huge source of inspiration. Biomimicry argues that nature is the best, most influencing and the guaranteed source of innovation for the designers as a result of nature's 3.85 billion years of evolution, as it holds a gigantic experience of solving problems of the environment and its inhabitants. The biomimicry emerging field deals with new technologies honed from bio-inspired engineering at the micro and macro scale levels. Architects have been searching for answers from nature to their complex questions about different kinds of structures, and they have mimicked a lot of forms from nature to create better and more efficient structures for different architectural purposes. Without computers these complex ways and forms of structures couldn't been mimicked and thus using computers had risen the way of mimicking and taking inspiration from nature because it is considered a very sophisticated and accurate tool for simulation and computing, as a result designers can imitate different nature's models in spite of its complexity.

Keywords: Biomimicry; Structure; Computation; Bio-inspired design

Yung-Jeh CHU. (Department of Civil Engineering, Faculty of Engineering, University of Malaya, Kuala Lumpur 50603, Malaysia. Email: chujeh2022@gmail.com). A new

biomimicry marine current turbine: Study of hydrodynamic performance and wake using software OpenFOAM. Journal of Hydrodynamics, Ser. B, Volume 28(1) (2016): 125-141

Inspired by Dryobalanops aromatica seed, a new biomimicry marine current turbine is proposed. Hydrodynamic performance and wake properties are two key factors determining whether a new marine current turbine design is practical or not. Thus, a study of hydrodynamic performance and wake of the proposed biomimicry turbine is conducted. The computational fluid dynamics (CFD) software, OpenFOAM is used to generate the required results for the mentioned study. The hydrodynamic performance and wake properties of the proposed biomimicry turbine is compared to two conventional turbines of Bahaj et al. and Pinon et al. respectively. The simulation results showed that the proposed biomimicry marine current turbine gives optimum power output with its power coefficient, $C_p \approx 0.376$ at the tip speed ratio (TSR) of 1.5. Under the same boundary conditions, the maximum torque pro- duced by the proposed biomimicry turbine at zero rotational speed is 38.71 Nm which is 1110% greater than the torque generated by the turbine of Bahaj et al.. The recovery distance for the wake of the biomimicry turbine is predicted to be 10.6% shorter than that of IFREMER-LOMC turbine. The above-mentioned results confirm the potential application of the proposed biomimicry marine curre- nt turbine in the renewable energy industry.

Keywords: marine current turbine; wake; biomimicry; computational fluid dynamics (CFD); OpenFOAM

C.W. Letchford[a], D.C. Lander[a], P. Case[b], A. Dyson[c], M. Amitay[d]. ([a] Department of Civil and Environmental Engineering, Rensselaer Polytechnic Institute, Troy, NY, USA, [b] The Alan G. Davenport Wind Engineering Group, University of Western Ontario, London, ON, Canada, [c] Center for Architecture, Science and Ecology, Rensselaer Polytechnic Institute, Troy, NY, USA, [d] Center for Flow Physics and Control, Department of Mechanical, Nuclear and Aerospace Engineering, Rensselaer Polytechnic Institute, Troy, NY, USA). **Bio-mimicry inspired tall buildings: The response of cactus-like buildings to wind action at Reynolds Number of 10^4. Journal of Wind Engineering and Industrial Aerodynamics, Volume 150(2016): 22–30**

Applying bio-mimicry intelligence to the aerodynamic performance of tall slender buildings has potential to lead to not only improved response to wind loading, but generate savings in material and construction costs, affect energy consumption by providing self-shading and controlling local air flow to promote local wind energy generation and ventilation strategies. To this end, the alongwind and crosswind responses of high aspect ratio (15:1) cylinders, (smooth, roughened and grooved) were obtained from wind tunnel tests in simulated smooth and rough atmospheric boundary layer flows. The influence of top, flat or domed was also studied. The *Saguaro* cactus-inspired cylinder with 24 circumferential grooves was seen to have large reductions (~20%) for mean and fluctuating alongwind base shear (drag) and overturning moments in comparison with smooth cylinders and is in agreement with 2D studies in uniform low turbulence flow. Domed tops also led to reduced drag over flat tops. Differences in fluctuating crosswind base shear (lift) and overturning moment were much less marked. In spectral terms the amplitudes of response near the pronounced vortex shedding frequency were almost unchanged, however the cactus-shape had a higher Strouhal Number indicating a shift to a higher frequency as might be attributed to a narrowing of the wake.

Keywords: Bio-mimicry; Tall building geometry; Wind loads

Name of Journals

1. Acta Biotechnologica
2. Aerobiologia
3. Annual Review-Plant Pathology
4. Annual Review- Ecology and Systematics
5. Annual Review-Biochemistry
6. Annual Review-Biomedical Engineering
7. Annual Review-Biophysics and Biomolecular Structure
8. Annual Review-Microbiology
9. Annual Review-Pharmacology and Toxicology
10. Annual Review-Phytopathology
11. Annual Review-Physiology
12. Annual Review-Plant Physiology
13. Annual Review-Public Health
14. African Journal of Biotechnology
15. Applied and Environmental Microbiology
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36. Biotechnology and Applied Biochemistry
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67. Indian Journal of Ecology
68. Indian Journal of Experimental Biology
69. Indian Journal of Environmental Toxicology
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71. Indian Journal of Plant Physiology
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73. International Journal of Biotechnology
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75. Journal of Applied Sciences and Environmental Management
76. Journal of Agriculture and Environmental Ethics
77. Journal Biological Control

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