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ENVIS CENTRE

On

ENVIRONMENTAL BIOTECHNOLOGY

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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 biannually Abstract Volume on our thematic area Environmental Biotechnology under fifteen sub-heads. The volume contains abstracts of scientific articles from relevant 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 36th 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 2020. 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 15 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 variety 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 indicates 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 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 worm. 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 variety of environments. These specific substances may include sugars, proteins, or humas and variety 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 broad-based engineering disciplines 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 allergenicity 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 was non-polluting bioenergy sources or energy generation from organic wastes and biomass. These are all ecofriendly solutions. Biomass energy supply-demand balances have become a component of energy sector analysis and planning and is propelled huge importance in the countries. Biomasses, 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	Biotechnology(s)	Endocrinol	Endocrinological
Biotechno	Biotechnology	Engg	Engineering
Biotechnol	Biotechnological	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	Immunological	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

Mengchen Lv^a, Xuexi Tang^{ab}, Yirong Zhao^a, Jun Li^a, Bihan Zhang^a, Luying Li^a, Yongshun Jiang^c, Yan Zhao^{ab} (a. Department of Marine Ecology, Ocean University of China, Qingdao 266003, China, b. Laboratory for Marine Ecology and Environmental Science, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266071, China, c. College of Marine Science and Technology, Qingdao Agricultural University, No.17 Wenhai Road, Qingdao 266000, China) **The toxicity, bioaccumulation and debromination of BDE-47 and BDE-209 in *Chlorella* sp. under multiple exposure modes, Science of The Total Environment, Volume 723 (2020), 138086**

Polybrominated diphenyl ethers (PBDEs) are a series of important persistent organic pollutants (POPs) in marine environments. Microalgae are the start of PBDEs bioaccumulated and bioconcentrated along the marine food web. In order to investigate the variations of PBDEs bioaccumulation by microalgae and its influencing factors, we set up a series of experiments with *Chlorella* sp. under different BDE-47 or BDE-209 exposure modes to measure their toxicity, bioaccumulation and degradation patterns. The inhibition effect on cell growth was much more obvious in BDE-47 than BDE-209, with the EC₅₀ values at 96 h calculated as 64.7 µg L⁻¹ and 4070 µg L⁻¹, respectively. Microalgal uptake rates showed BDE-209 diffused less into cells than BDE-47, with highest measured uptake rates of 0.145×10^{-7} µg h⁻¹ cell⁻¹ and 0.45×10^{-7} µg h⁻¹ cell⁻¹, respectively. The bioaccumulation amount by unit microalgal cell varied with PBDE concentrations and culture time, which appeared to be related to the changes of extracellular polymeric substances (EPS) and cellular neutral lipids under the toxicity of PBDEs. Finally, we found *Chlorella* sp. delayed the debromination patterns of BDE-209 compared to seawater. This study linked the toxicity, microalgal bioaccumulation and metabolism of PBDEs, provided new insights in the research of POPs by microalgae and marine food webs.

Keywords: PBDEs, *Chlorella* sp., Toxicity, Bioaccumulation, EPS, Lipids, Debromination

Santu Ghosh, Mukul Mal, Sudipto Mandal (Ecology and Environmental Modelling Laboratory, Department of Environmental Science, The University of Burdwan, Burdwan, 713104, India) **A dynamic model of cadmium bioaccumulation in *Lamellidens marginalis*, an edible shellfish in India, Ecological Modelling, Volume 419 (2020), 108957**

Mussels, as food is widely accepted by people around the world as it possesses good nutritive value. Along with the local fishes, a gradual increase in the market demand of the *Lamellidens marginalis* is observed in the eastern part of India. These mussels are collected from reservoirs by the local people for their daily requirements and usual business. The reservoirs receive the wastewater or sewage from the nearby tanneries and households. Consequently, people are prone to a high risk of cadmium pollution through the consumption of mussels. Thus, the study of the bioaccumulation of cadmium in the organs of mussel is felt be need of the hour.

A dynamic model was constructed to observe the daily accumulation of cadmium in the different organs of mussel. The model was constructed in the STELLA 6.0 software, and a sensitivity analysis was performed followed by calibration and validation.

The scenario analysis revealed that the bioaccumulation of cadmium in the gills was sensitive to the input rate of cadmium to the system. The retention of cadmium in the alimentary canal and the kidney was dependent on the excretion rate of mussels. Cadmium deposition in the muscles and hepatopancreas was strongly regulated by the transfer rate of cadmium from the alimentary canal and the depuration rate respectively. However, the cadmium bioaccumulation in the foot was dependent on the surface area of foot. The sensitivity analysis showed that the input rate of cadmium into the system was the system sensitive parameter. If the cadmium is checked at the entry point of the reservoir, then the mussels could be easily harvested by the local people, and there would be less risk of cadmium pollution to the human.

Keywords: Adsorption, Bioaccumulation, Cadmium transport, Depuration, Simulation model

Julia Martín^a, Felix Hidalgo^b, Esteban Alonso^a, María Teres^a García-Corcoles^c, Jose Luis Vilchez^c, Alberto Zafra-Gómez^c (a. Department of Analytical Chemistry, Escuela Politécnica Superior, University of Seville, C/ Virgen de África 7, E-41011 Seville, Spain, b. Department of Zoology, University of Granada, Campus of Fuentenueva, E-18071 Granada, Spain, c. Research Group of Analytical Chemistry and Life Sciences, Department of Analytical Chemistry, University of Granada, Campus of Fuentenueva, E-18071 Granada, Spain) **Assessing bioaccumulation potential of personal care, household and industrial products in a marine echinoderm (*Holothuria tubulosa*), Science of The Total Environment, Volume 720 (2020), 137668**

A bioaccumulation study of 16 emerging contaminants including preservatives, UV-filters, biocides, alkylphenols, anionic surfactants and plasticizers, in *Holothuria tubulosa* Gmelin, 1791 specimens was developed. Water and sediments from their coastal habitat were also analyzed. Sediment-water distribution coefficients (log K_d) were in the range 0.78 to 2.95. A rapid uptake and bioaccumulation of pollutants was found. Compounds were detected in intestine and gonads of *H. tubulosa* after only eight days of exposure. Field-based bioconcentration (BCF) and biota-sediment accumulation factors (BSAF) were calculated. Log BCF > 1 were obtained for most of the compounds studied, indicating their tendency to accumulate in tissue of *H. Tubulosa*. BCF values decrease as follow: Triclocarban > anionic surfactants > benzophenone 3 > non-ionic surfactants > bisphenol A > parabens. These data provide a detailed accounting of the distribution patterns of some emerging contaminants in organisms at the lower trophic level, representing a potential source of contaminants for organisms in higher levels of the food chain.

Keywords: Personal care products, Household and industrial chemicals, *Holothuria tubulosa*, Environmental partitioning, Bioaccumulation studies, Marine pollution

Weiyan Que, Bihe Wang, Feili Li, Xiujuan Chen, Hui Jin, Zangfang Jin (College of Environment, Zhejiang University of Technology, Hangzhou 310032, China) **Mechanism of lead bioaccumulation by freshwater algae in the presence of organic acids, Chemical Geology, Volume 540 (2020), 119565**

The accumulation of heavy metals by freshwater algae becomes more complex in the presence of dissolved organic matter but it is unclear how and to what extent. In this study, we

comparatively assessed the effects of malic acid and citric acid on the bioaccumulation of Pb by *Chlorella pyrenoidosa*. A 6 h exposure experiment showed that adding organic acid (OA) to an algae–Pb binary system prolonged the adsorption equilibrium time and that the extended time was related to the concentration and number of carboxyl groups of the OA. A pseudo-second-order model fit the kinetic data well in the presence of OAs. The normality of carboxyl groups was negatively correlated with the bioaccumulation rate, k_2 , but positively correlated with the maximum bioaccumulation capacity, q_{max} , of Pb following a linear equation, $Y = 121.3x + 52.2$, $R^2 = 0.9877$. Neither the Freundlich model nor the Langmuir model could fit the isotherm data in the presence of OA, suggesting that a new mechanism might exist. The quantitative relationship between bioaccumulated Pb and carboxyl group of OA indicated a stoichiometric relationship, which seemed to support the theory of a ternary complex of Pb, OA, and algal surface. Our results have added clarity to the current understanding of the accumulation of heavy metals by algae in freshwater ecosystems.

Keywords: Freshwater algae, Lead, Bioaccumulation, Organic acid, Ternary complex, Hydrogen phosphate ion

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MerP/MerT-mediated mechanism: A different approach to mercury resistance and bioaccumulation by marine bacteria, Journal of Hazardous Materials, Volume 388 (2020), 122062

Currently, mechanism underlying mercury resistance and bioaccumulation of marine bacteria remains little understood. A marine bacterium *Pseudomonas pseudoalcaligenes* S1 is resistant to 120 mg/L Hg²⁺ with bioaccumulation capacity of 133.33 mg/g. Accordingly, Hg²⁺ resistance and bioaccumulation mechanism of S1 was investigated at molecular and cellular level. Annotation of S1 transcriptome reveals 772 differentially expressed genes, including Hg²⁺-relevant genes merT, merP and merA. Both merT and merP gene have three complete copies in S1 genome, while merA gene has only one. In order to evaluate the function of these Hg²⁺-relevant genes, three recombinant strains were constructed to express MerA (named as A), MerT/MerP (TP) and MerT/MerP/MerA (TPA), respectively. The results show that Hg²⁺ resistance of strain TP, TPA, and A are improved with minimum inhibition concentration (MIC) being 60 mg/L, 40 mg/L, and 20 mg/L, respectively compared to 2 mg/L of host strain. Strain TP and TPA exhibit enhanced Hg²⁺ bioaccumulation capacity, while strain A does not differ from the control. Their equilibrium Hg²⁺ bioaccumulation capacities are 110.48 mg/g, 94.49 mg/g, 83.76 mg/g and 82.29 mg/g, respectively. Summarily, different from most microorganisms that exhibit Hg²⁺ resistance by MerA-mediated mechanism, marine bacterium S1 achieves Hg²⁺ resistance and bioaccumulation capability via MerT/MerP-mediated strategy.

Keywords: Marine bacteria, Mercury, MerT/MerP, MerA, Bioaccumulation

Lesly Paradina Fernández^{ab}, Romina Brasca^{abc}, Andrés M. Attademo^{bd}, Paola M. Peltzer^{bd}, Rafael C. Lajmanovich^{bd}, María J. Culzoni^{ab} (a. Laboratorio de Desarrollo Analítico y

Quimiometría (LADAQ), Cátedra de Química Analítica I, Facultad de Bioquímica y Ciencias Biológicas, Universidad Nacional del Litoral, Ciudad Universitaria, 3000, Santa Fe, Argentina, b. Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Godoy Cruz 2290, 1425, Buenos Aires, Argentina, c. Programa de Investigación y Análisis de Residuos y Contaminantes Químicos (PRINARC), Facultad de Ingeniería Química, Universidad Nacional del Litoral, Santiago del Estero 2654, 3000, Santa Fe, Argentina, d. Laboratorio de Ecotoxicología, Facultad de Bioquímica y Ciencias Biológicas, Universidad Nacional del Litoral, Ciudad Universitaria, 3000, Santa Fe, Argentina) Bioaccumulation and glutathione S-transferase activity on *Rhinella arenarum* tadpoles after short-term exposure to antiretrovirals, *Chemosphere*, Volume 246 (2020), 125830

The aim of the present study was to investigate the bioaccumulation and toxicological effects of four antiretrovirals (lamivudine, stavudine, zidovudine and nevirapine) on *Rhinella arenarum* tadpoles, after short-term (48 h) exposure to these drugs at sublethal concentrations. The analytical procedure involved a simple extraction method followed by ultra-high performance liquid chromatography with diode array detection and chemometric analysis for data processing. Under the conditions studied, the analytes investigated, particularly nevirapine, showed possible bioaccumulation in tadpoles. Besides, an increase in the bioaccumulation was observed when increasing the exposure concentration. In addition, the enzymatic biomarkers measured to evaluate the toxicological effects showed that acetylcholinesterase activity was similar to that of the control group, while glutathione S-transferase activity was increased, indicating potential oxidative stress damage. Our results also allowed demonstrating the usefulness of chemometric algorithms to quantitate analytes in complex matrices, such as those absorbed by tadpoles in aquatic ecosystems. The results also evidenced the short-term antiretroviral bioaccumulation in tadpoles and the alteration of antioxidant systems, highlighting the need of environmental studies to elucidate the ecotoxicological risk of antiretrovirals in humans and wildlife.

Keywords: Antiretrovirals, Bioaccumulation, Toxicological biomarkers, Tadpoles, UHPLC-DAD

Haohan Yang^a, Guanghua Lu^{ab}, Zhenhua Yan^a, Jianchao Liu^a, Huike Dong^a, Xuhui Bao^a, Xiadong Zhang^a, Yu Sun^a (a. Key Laboratory for Integrated Regulation and Resources Development on Shallow Lakes of Ministry of Education, College of Environment, Hohai University, Nanjing 210098, China, b. Water Conservancy Project & Civil Engineering College, Tibet Agriculture & Animal Husbandry University, Linzhi 860000, China) Residues, bioaccumulation, and trophic transfer of pharmaceuticals and personal care products in highly urbanized rivers affected by water diversion, *Journal of Hazardous Materials*, Volume 391 (2020), 122245

Little information is available on the bioaccumulation and trophic transfer of pharmaceuticals and personal care products (PPCPs) in urban rivers system, particularly for those affected by water transfer. Herein, a comprehensive study was conducted to investigate the biological residues, bioaccumulation and trophic transfer of 45 PPCPs in the Nanjing Qinhuai River system under the background of water diversion projects. A total of 30 compounds were detected with a descending order of overall concentration as plankton > benthic mollusc > fish (except grass carp). Higher biological residues were observed in the downstream than those in the upstream, with the largest increase for fish (136.4 %) and the lowest increase for phytoplankton (5.4 %). However, the bioaccumulation classifications of most PPCPs were unchanged among the three

different water-diversion regions. Trophic magnification factors (TMFs) of organic UV filters (homosalate, oxybenzone, ethylhexyl methoxycinnamate and octocrylene) ranged from 1.23 to 2.04, suggesting trophic magnification potential, while trophic dilution for pharmaceuticals (sertraline, citalopram, caffeine and roxithromycin) with TMFs of 0.42 to 0.50 were observed. A notable positive correlation was observed between the pH-dependent distribution coefficient (logDow) and the TMFs of the PPCPs ($P < 0.05$). Although the human health hazard assessment indicated no immediate health risk via the consumption of freshwater food, attention should be paid to the joint effects of PPCPs.

Keywords: PPCPs, Bioaccumulation, Trophic transfer, Urbanized rivers, Water transfer

Zhi Lin^a, Xingting Fan^a, Junlin Huang^a, Rong Chen^{ab}, Qiao-Guo Tan^{ab} (a. Fujian Provincial Key Laboratory for Coastal Ecology and Environmental Studies, College of the Environment and Ecology, Xiamen University, Xiamen, Fujian, 361102, China, b. Center for Marine Environmental Chemistry and Toxicology, Xiamen University, Xiamen, Fujian, 361102, China) **Intertidal mussels do not stop metal bioaccumulation even when out of water: Cadmium toxicokinetics in *Xenostrobus atratus* under influences of simulated tidal exposure, Environmental Pollution, Volume 261 (2020), 114192**

Intertidal bivalves are periodically exposed in air. It is tempting to speculate that the organisms would temporarily escape from contaminants when they are out of water and thus have lower risks. In this study, we tested this speculation by investigating cadmium (Cd) toxicokinetics in an intertidal mussel, *Xenostrobus atratus*, under the effects of tidal exposure using simulated tidal regimes. The uptake rate constant (k_u) of Cd ranged from 0.045 L g⁻¹ d⁻¹ to 0.109 L g⁻¹ d⁻¹, whereas the elimination rate constant (k_e) of Cd ranged from 0.029 d⁻¹ to 0.091 d⁻¹. Cd bioaccumulation was slightly higher in the continuously immersed mussels than the alternately immersed mussels, but much lower than what would be expected if assuming bioaccumulation being proportional to immersion duration. Cd uptake was observed even when mussels were exposed in air, due to uptake of Cd dissolved in mantle cavity fluid and internalization of Cd adsorbed on mussel tissues. Overall, tidal height showed limited effects on Cd bioaccumulation, consistent with the trend of Cd concentrations found in *X. atratus* collected from different tidal heights. The mantle cavity uptake mechanism is expected to be applicable to other contaminants and bivalves, and should have important implications in risk assessments for intertidal environment.

Keywords: Toxicokinetics, Cadmium, Intertidal, Tidal height, Mussel

Bioremediation

S. Mary Celin, Sandeep Sahai Anchita Kalsi, Pallvi Bhanot (Centre for Fire Explosives and Environment Safety (CFEES), DRDO, Delhi, India) **Environmental monitoring approaches used during bioremediation of soils contaminated with hazardous explosive chemicals, Trends in Environmental Analytical Chemistry, Volume 26 (2020), e00088**

Defense sites are contaminated with explosives, which are released during manufacturing, firing, testing and training operations; loading, assembly and packing activities; and demilitarization

operations. Explosive chemicals are hazardous in nature. Contamination of the soil and the underlying groundwater by explosives pose serious threat to human and animal health and the eco-system. Bioremediation is an eco-friendly technology as it exploits nature's own agents- the microbes in degrading the contaminant of interest. This waste treatment technology has been extensively studied for degrading the explosive pollutant. Environmental monitoring, a process of systematic collection of data and analysis is essential in performance evaluation of any waste treatment system. This paper gives a comprehensive overview on the environmental monitoring approaches used during bioremediation of explosives contaminated soil. Biogeochemical factors viz., presence and survivability of microbes, bioavailability of the contaminant, pH, temperature, moisture content, redox conditions, presence/addition of substrate and nutrients and presence of intermediates/co-contaminants in the soil environment that are reported to affect the bioremediation of explosives are highlighted. Details on physical, chemical and biological parameters monitored during bioremediation are included. Advancements in instrumental techniques are evolving rapidly and its application in bioremediation approaches promise an enhanced understanding of the mineralization of explosive in the soil environment. Recent developments in application of advanced analytical instrumentation techniques, future research insights with recommendations, which will illuminate the selection of appropriate monitoring tool for evaluating bioremediation are also summarized.

Keywords: Explosive, Soil bioremediation, Biogeo-chemical factors, Monitoring, Molecular tools, Instrumental techniques

Ponniah Anusha, Devarajan Natarajan (Natural Drug Research Laboratory, Department of Biotechnology, Periyar University, Salem, Tamilnadu, India) Bioremediation potency of multi metal tolerant native bacteria *Bacillus cereus* isolated from bauxite mines, kolli hills, Tamilnadu- A lab to land approach, Biocatalysis and Agricultural Biotechnology, Volume 25 (2020), 101581

Bioremediation approaches by native microorganisms are an effective and best resolution for treating metal contaminated area. The aim of the study was to determine the metal remediation efficiency of native bacteria *B.cereus* in lab and field remediation study. Minimum inhibitory concentration of metals show, the isolate was highly resistant to lead ions followed by other test metals and also highly resistant to multiple antibiotics. The optimum pH (pH 7) and temperature (35 °C) for bacterial growth was determined. Bioremediation efficiency of batch culture method by the strain was found to be 91.98% (Cu), 79.9% (Cr), 97.17% (Pb), 77.44% (Zn), 81.6% (Fe), 62.8% (Mn) and 60.92% (Mg) respectively. FT-IR analysis, resulted N–H primary amine, C–C stretch and N–O aliphatic nitro compounds present in the lead treated by *B. cereus*. We noticed some functional groups may be altered in the treated sample than control (–C triple bond C–alkyne and C–N amine groups). The novelty of the work is the simplest trail for field based metal remediation by the multi metal tolerant bacteria in bauxite mined waste soil. The strain shows notable percentage of in-situ remediation over eight weeks of experiments i.e 71.8% (Pb), 53% (Cu) and 41.4% (Cr). The outcome of In-situ remediation results suggest that *B.cereus* have a noticeable remediation capacity to all the metals particularly lead, so it could be served as a potential strain for In-situ field based bioremediation and in future it can be used for soil reclamation of toxic soil into nontoxic soil.

Keywords: *Bacillus cereus*, 16s rRNA, FT-IR, MIC, In-situ bioremediation

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Five heavy metals namely, arsenic (As), cadmium (Cd), chromium (Cr), lead (Pb) and mercury (Hg) are carcinogenic and show toxicity even at trace amounts, posing threats to environmental ecology and human health. There is an emerging trend of employing microalgae in phycoremediation of heavy metals, due to several benefits including abundant availability, inexpensive, excellent metal removal efficiency and eco-friendly nature. This review presents the recent advances and mechanisms involved in bioremediation and biosorption of these toxic heavy metals utilizing microalgae. Tolerance and response of different microalgae strains to heavy metals and their bioaccumulation capability with value-added by-products formation as well as utilization of non-living biomass as biosorbents are discussed. Furthermore, challenges and future prospects in bioremediation of heavy metals by microalgae are also explored. This review aims to provide useful insights to help future development of efficient and commercially viable technology for microalgae-based heavy metal bioremediation.

Keywords: Microalgae, Bioremediation, Biosorption, Heavy metals, Mechanism

Parminder Kaur, Chandrajit Balomajumder (Department of Chemical Engineering, Indian Institute of Technology Roorkee, Roorkee, 247667, Uttarakhand, India) **Bioremediation process optimization and effective reclamation of mixed carbamate-contaminated soil by newly isolated Acremonium sp., Chemosphere, Volume 249, June (2020), 125982**

Global pollution from excessive pesticide use has become a serious environmental and public health problem. The aim of the study was to optimize the fungal mediated simultaneous removal of carbofuran and carbaryl from soil. Carb-PV5 strain was isolated from contaminated soil following enrichment culture technique; based on 18S rRNA sequencing, strain was identified as Acremonium sp. (MK514615); Field Emission Scanning Electron Microscopic analysis reflected its morphology. Towards the development of bioaugmentation strategy for the bioremediation of carbamate-contaminated soil, the process parameters were optimized employing Central Composite Rotatable Method. The experimental studies were performed in the range of biomass (0.2–0.6 g kg⁻¹), temperature (23–33 °C), pH (6–9) and moisture (10–30%). The degradation rate parameters, k and t_{1/2} were determined to as 0.475, 0.325 d⁻¹ and 5.39, 2.1 d with the corresponding r² of 0.9491, 0.9964 for zero and first order, respectively. The cube root growth kinetic constant k of Acremonium sp. varied from 0.0469 to 0.0512 (g^{1/3} L^{-1/3} h⁻¹) and 0.0378 to 0.0415 (g^{1/3} L^{-1/3} h⁻¹) for carbofuran and carbaryl, respectively. To confirm the model appropriacy and sustainability of the optimization procedure, bioremediation experiments were conducted onto real carbamate-contaminated soils. UPLC and GCMS analysis confirmed the successful removal of carbamates. The current study presents the first report on the bioaugmentation studies carried out on the mixed carbamate contaminated soil using newly isolated Acremonium sp.

Keywords: Acremonium, Bioremediation, Carbofuran, Carbaryl, Soil

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Lindane is a toxic and persistent organochlorine pesticide, whose extensive use generated its accumulation in different environmental matrices. Bioremediation is a promising technology that can be used combining bioaugmentation and biostimulation processes to soil restoration. The aim of the present work was to determine the conditions of maximum lindane removal by bioaugmentation with an actinobacteria consortium and biostimulation with sugarcane filter cake (SCFC). The assays were carried out on lindane-contaminated silty loam (SLS), clayey (CS), and sandy (SS) soils. Through complete factorial designs, the effects of three abiotic factors (moisture content, proportion and size of SCFC particles) were evaluated on lindane removal. In addition, a response optimizer determined the optimal conditions for pesticide removal in bioaugmented and biostimulated soils, in the range of levels studied for each factor. In these conditions, bioaugmentation of biostimulated soils increased the pesticide removal (SLS: 61.4%, CS: 70.8%, SS: 86.3%), heterotrophic microbial counts, and soil enzymatic activities, and decreased lindane T1/2, regarding the non-bioaugmented biostimulated controls, after 14 days of assay. The values of these parameters confirmed the efficiency of the bioremediation process. Finally, the viability of the four strains was demonstrated at the end of the assay. The results indicate that the simultaneous application of bioaugmentation with the actinobacteria consortium and biostimulation with SCFC constitutes a promising tool for restoring soils contaminated with lindane, by using the optimal conditions obtained through the factorial designs.

Keywords: Lindane, Bioaugmentation, Actinobacteria, Biostimulation, Sugarcane filter cake

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A novel biological approach using ark shell bivalves as potential species for remediation of effluents was studied to determine the microbial community interspecies interaction and nutrient cycling in a restoration system of mariculture effluents. A field study showed that *Scapharca subcrenata* was the main driver of the microbial community's interspecies-interaction (PERMANOVA, $R = 0.0572$, $P = 0.005$) in the treatment zone (TZ). Analysis of co-occurrence networks based on random matrix theory (RMT) indicated that the network's complexity

parameters were enhanced in the TZ and disrupted in the control zone (CZ) due to eutrophic disturbances. Concurrently, the TZ was correlated with more profound network modifications (i.e., higher modularity, total nodes (n), cohesion, and proportion of positive links), suggesting that *S. subcrenata* influenced microbial interspecies interactions in the system. Similarly, the co-occurring networks of generalists Proteobacteria (OTU2037) at genus Anaerospira and Actinobacteria (OTU9660) at genus Candidatus aquiluna for anaerobic ammonia-oxidation (ANAMMOX) were highly significant in the TZ. The top-down and bottom-up forces of *S. subcrenata* influenced the removal efficiency of nitrogenous compounds by reducing 81.51% of nitrite (NO₂-N), 84.61% of total ammonium nitrogen (TAN) and 72.78% of nitrate (NO₃-N). Generally, the introduction of ark shell bivalve (*S. subcrenata*) to the system as a biofilter provides a very low-cost bioremediation technology that could be one of the best restorations and remediation tools for mariculture effluents.

Keywords: Bioremediation, Nutrient cycling, Microbial interaction, Mariculture effluents, Bivalve grazer, Keystone taxa

Shivani Kumari, Amit Rahul Jamwal, Neha Mishra, Dileep Kumar Singh (Soil Microbial Ecology and Environmental Toxicology Laboratory, Department of Zoology, University of Delhi, New Delhi, Delhi, 110007, India) Recent developments in environmental mercury bioremediation and its toxicity: A review, Environmental Nanotechnology, Monitoring & Management, Volume 13 (2020), 100283

Mercury (Hg), a global pollutant produced by anthropogenic and natural means acts as a bioaccumulative toxin that severely affects our environment and human lives. Besides being a potent neurotoxin, mercury has several adverse effects on all the major body systems. Mercury changes its chemical forms in the environment and travels from place to place and finally it gets deposited deep down into soil and sediments. As mercury remediation through conventional approaches is costly and technically difficult, bioremediation is a more cost-effective, eco-friendly method and accepted by regulatory authorities. This paper emphasizes on the recent developments in the biochemical mechanism of mer operon and its utilization in mercury bioremediation. This review also focuses on the use of mercury resistant bacteria (MRB) for the remediation of mercury-contaminated sites. Furthermore, the role of yeast in mercury bioremediation has also been listed. Moreover, we have focused on the detailed application of whole-cell biosensor, nanotechnology, phytoremediation, plant-assisted microbial remediation and significance of modern biotechnological techniques such as transposon-mediated In-situ molecular breeding (ISMb) for effective removal of mercury. Conclusively, this review enhances the detailed understanding of mercury bioremediation scenarios on a global scale in recent times.

Keywords: Bioremediation, Mercury, Mercury resistant bacteria, mer operon, Phytoremediation, Toxicity

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Bioremediation of oily sludge polluted soil employing a novel strain of *Pseudomonas aeruginosa* and phytotoxicity of petroleum hydrocarbons for seed germination, Science of The Total Environment, Volume 737 (2020) 139766

Agricultural land pollution is key a problem globally, which is linked with growth of industries. Petroleum industrial sector is one of the major industrial sectors and the activities of petroleum industry lead to the agricultural land pollution. Oily sludge is a type of solid and hazardous waste generated from petroleum industrial activities. Hence, there is an urgent need to find remediation methods of the oily sludge contaminated agricultural land. Thus, the aim of this work was to study bioremediation of oily sludge polluted soil employing a novel strain of *Pseudomonas aeruginosa* and evaluation of phytotoxicity on germination of *Vigna radiata* seed in pots. Five different approaches were adopted for the bioremediation studies, which included Bioaugmentation + Biostimulation, bioaugmentation, biostimulation, natural attenuation and abiotic factors. Simultaneous application of *P. aeruginosa* NCIM 5514 and nutrients in microcosm showed $92.97 \pm 0.92\%$ decrease in oily sludge with good hydrocarbon utilizing bacterial count and decreased nutrient level in 56 days. Pot experiments on seed germination of mung beans (*Vigna radiata*) seeds was performed by pot experiments. 80.95% germination in five days in treated soil. From the results it was concluded that simultaneous use of oily sludge degraders and nutrient supplement could revive seed germination ability of oily sludge polluted soil effectively. This is first report of comparing five techniques to bioremediate oily sludge polluted soil using *Pseudomonas aeruginosa*, followed by pot study using *V. radiata* seeds, showing that *P. aeruginosa* can be an efficient bioremediation agent and can be effectively used for remediation of oily sludge contaminated soil.

Keywords: Agricultural soil, Seed germination rate, Oily sludge, Pot study, Mung beans

Biotransformation

Ondřej Ženata^a, Aneta Vrzalová^a, Petr Bachled^{ab}, Jana Janečková^b, Aleš Panáček^c, Libor Kvítek^c, Radim Vrzal^a (a. Department of Cell Biology and Genetics, Faculty of Science, Palacky University in Olomouc, Slechtitelu 27, Olomouc, CZ-783 71, Czech Republic, b. Department of Surgery, University Hospital, I.P. Pavlova 6, 775 15, Olomouc, Czech Republic, c. Regional Centre of Advanced Technologies and Materials, Department of Physical Chemistry, Faculty of Science, Palacky University in Olomouc, 17. listopadu 12, 771 46, Olomouc, Czech Republic) **The effect of graphene oxide on signalling of xenobiotic receptors involved in biotransformation, Chemosphere, Volume 253 (2020), 126753**

Graphene oxide (GO) is an engineered nanomaterial which was demonstrated to have outstanding capacity for adsorption of organic pollutants such as polycyclic aromatic hydrocarbons (PAHs) and polychlorinated biphenyls (PCBs), the ligands and activators of the aryl hydrocarbon receptor (AhR). Due to the partially overlapping ligand capacity of AhR and pregnane X receptor (PXR), we tested the impact of GO particles on their signalling. While reporter gene assay revealed potentiating effect of GO on ligand-activated AhR-dependent luciferase activity, there was no effect for PXR. However, inducible target genes for AhR (CYP1A1) or PXR (ABCB1) were decreased at mRNA as well as protein levels by the presence of GO in HepG2 (for AhR), LS180 (for PXR) or primary human hepatocytes (both receptors). Moreover, the presence of GO diminished PXR and AhR protein levels in primary cultures of human hepatocytes. This was partially reversed by proteasome inhibitor MG132 for AhR but not

for PXR. In conclusion, GO decreases ligand-stimulated activities of AhR and PXR in human cells.

Keywords: PXR, AhR, Graphene oxide, Human hepatocytes, CYP3A4, MG132

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Microbial treatment of heavy metal-polluted sites is considered an environmentally friendly bioremediation technology with high potential. This study shows that *Pseudomonas chengduensis* strain MBR, a bacterium that can potentially be applied in the treatment of heavy metal pollution, is most affected by Cd(II) stress at the beginning of its growth. Up to 100% of total Cd(II) adsorption occurs in the first 48 h after treatment of stationary phase cells with Cd(II). A biofilm forms on the cell surface, Cd(II) adsorbs, and is reduced to Cd (0) in the form of nanoscale particles. The genome of strain MBR was sequenced, annotated and analyzed. We identified various genes potentially related to cadmium resistance, transport and metabolism. Analysis of the strain MBR genome is helpful to explore the mechanism of Cd(II) resistance, and can provide new ideas for cadmium pollution control.

Keywords: Cadmium, Biosorption, Biotransformation, *Pseudomonas chengduensis*, MBR, Genomics

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This chapter reviews the current understanding of chemical and biochemical mechanisms of metabolism of warfare nerve agents describing the role of the enzymes involved in this process. Among enzymes participating in metabolism of nerve agents, the roles of A-esterases, serum cholinesterase, carboxylesterase, prolidase, and lipase are discussed. This chapter also discusses other aspects of metabolism of the agents, such as protein binding and the role of tissue depots for these compounds.

Keywords: Organophosphorus compounds, A-esterase, PON1, carboxylesterase, acetylcholinesterase, cholinesterase, metabolism, warfare nerve agents, soman, sarin, tabun, VX, cyclosarin, prolidase, lipase

Chuanqi Zhou, Jung-Chen Huang, Lixin Zheng, Shengbing He, Weil iZhou (School of Environmental Science and Engineering, Shanghai Jiao Tong University, 800 Dongchuan Rd, Minhang District, Shanghai 200240, China) Trophic transfer and biotransformation of selenium in the mosquito (*Aedes albopictus*) and interactive effects with hexavalent chromium, *Environmental Pollution*, Volume 262 (2020), 114288

As an essential micronutrient for animals with a narrow range between essentiality and toxicity, selenium (Se) usually coexists with chromium (Cr) in contaminated aquatic environments. This study investigated effects of three diets (*Microcystis aeruginosa*, *Chlorella vulgaris* and biofilms) exposed to Se or/and Cr on *Aedes albopictus* as a vector for the aquatic-terrestrial transfer of Se and Cr. Se(IV)-exposed mosquitoes concentrated Se up to 66-fold faster than Se(VI)-exposed ones, corresponding to the greater Se enrichment in Se(IV)-treated diets. Analysis using synchrotron-based X-ray absorption spectroscopy (XAS) showed that Se(0) (61.9–74.6%) dominated Se(VI)-exposed mosquitoes except for the *C. vulgaris*-fed larvae (organo-Se, 94.0%), while organo-Se accounted for 93.3–100.0% in Se(IV)-exposed mosquitoes. Cr accumulation in larvae (56.40–87.24 µg Cr/g DW) or adults (19.41–50.77 µg Cr/g DW) was not significantly different among all Cr(VI) treatments, despite varying diet Cr levels. With Cr(0) being dominant (57.7–94.0%), Cr(VI)-exposed mosquitoes posed little threat to predators. Although mosquitoes exposed to Se or Cr had shorter wings, adults supplied with *C. vulgaris* or biofilms co-exposed to Se(VI) and Cr(VI) had wings significantly (1.1–1.2 fold) longer than Se(VI) only exposed ones. Overall, our study reveals the role of *Ae. albopictus* in transferring waterborne Se and Cr from the contaminated aquatic ecosystem to the terrestrial ecosystem with the resulting eco-risks to wildlife in both ecosystems.

Keywords: Selenium, Hexavalent chromium, Asian tiger mosquito, Bioaccumulation, Speciation

Xi Wang^a, Qingzhu Liab^c, Qi Liao^{ab}, Yuchen Yan^a, Juan Xia^a, Qiuhong Lin^a, Qingwei Wang^{abc}, Yanjie Liang^{ab} (a. School of Metallurgy and Environment, Central South University, Changsha, 410083, China, b. Chinese National Engineering Research Center for Control & Treatment of Heavy Metal Pollution, Changsha, 410083, China, c. Water Pollution Control Technology Key Lab of Hunan Province, Changsha, 410083, China) Arsenic(III) biotransformation to tooeleite associated with the oxidation of Fe(II) via *Acidithiobacillus ferrooxidans*, *Chemosphere*, Volume 248 (2020), 126080

Tooeleite ($\text{Fe}_6(\text{AsO}_3)_4(\text{SO}_4)(\text{OH})_4 \cdot 4\text{H}_2\text{O}$), the only known ferric arsenite sulfate bearing mineral, has great potential for arsenic remediation due to its structure favoring incorporation of As(III). Based on the natural attenuation of removing As(III) directly by the formation of tooeleite via microorganisms, an iron-oxidizing bacterial strain *Acidithiobacillus ferrooxidans* ATCC 23270 (*At.ferrooxidans*) was selected to facilitate the formation of tooeleite. The optimized condition for the biogenic tooeleite was obtained at pH of 2.0, 30 °C and an initial arsenic of 500 mg/L. The process of biological mineralization is accompanied by the removal of 95.4% arsenic. What's more, biosynthetic tooeleite crystallization via a three-stage process was revealed using a combination of liquid and solid analyses (ICP-OES, XRD, XPS, FT-IR, SEM,

STEM, particle distribution). The three stages included Fe²⁺ oxidation by At.ferrooxidans, Fe³⁺ hydrolysis and an initial Fe–As amorphous precursors formation, and finally transforming to tooeleite crystal. Moreover, RT-qPCR was used to reveal the relationship between functional gene expression of At.ferrooxidans and the mineral formation. The results showed the biogenic tooeleite exerts significant control on the geochemistry of arsenic contaminated systems.

Keywords: Arsenic(III), Biosynthetic tooeleite, Acidithiobacillus ferrooxidans, Ferrous oxidation

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Lignocellulosic material has drawn significant attention among the scientific community due to its year-round availability as a renewable resource for industrial consumption. Being an economic substrate alternative, various industries are reevaluating processes to incorporate derived compounds from these materials. Varieties of fungi and bacteria have the ability to depolymerize lignocellulosic biomass by synthesizing degrading enzymes. Owing to catalytic activity stability and high yields of conversion, lignocellulolytic enzymes derived from fungi currently have a high spectrum of industrial applications. Moreover, these materials are cost effective, eco-friendly and nontoxic while having a low energy input. Techno-economic analysis for current enzyme production technologies indicates that synthetic production is not commercially viable. Instead, the economic projection of the use of naturally-produced ligninolytic enzymes is promising. This approach may improve the economic feasibility of the process by lowering substrate expenses and increasing lignocellulosic by-product's added value. The present review will discuss the classification and enzymatic degradation pathways of lignocellulolytic biomass as well as the potential and current industrial applications of the involved fungal enzymes.

Keywords: Lignocellulosic biomass, Lignocellulosic by-products, Fungi, Lignocellulolytic enzymes, Catalytic activity

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Khon Kaen 40002, Thailand, d. Department of Chemical Engineering, Faculty of Engineering, Khon Kaen University, Khon Kaen 40002, Thailand, e. Center of Excellence on Hazardous Substance Management (HSM), Bangkok 10330, Thailand, f Department of Civil and Environmental Engineering and Construction, University of Nevada, Las Vegas, NV 89154, USA) Simultaneous manganese adsorption and biotransformation by *Streptomyces violarius* strain SBP1 cell-immobilized biochar, *Science of The Total Environment*, Volume 713 (2020), 136708

Consumption of water containing high proportions of manganese could cause Parkinson's like symptoms and damage the central nervous systems. This study aims to investigate the potential of manganese removal through the development of microbial cell-immobilized biochar. The wood vinegar industry generates a large volume of carbonized wood waste (natural biochar) from the pyrolytic process. This is the first investigation utilizing this low value waste combined with biological treatment for water purification. Raw and hydrogen peroxide-modified biochars were used to immobilize an effective manganese-oxidizing bacterium, *Streptomyces violarius* strain SBP1 (SBP1). The results demonstrated that the modified biochar had a higher proportion of oxygen-containing functional groups leading to better manganese removal. Manganese adsorption by the modified biochar fitted pseudo-second-order and Langmuir models with the maximum adsorption capacity of 1.15 mg g⁻¹. The modified biochar with SBP1 provided the highest removal efficiency at 78%. The advanced synchrotron analyses demonstrated that manganese removal by the biochar with SBP1 is due to the synergistic combination of manganese adsorption by biochars and biological oxidation by SBP1.

Keywords: Biochar, Cell immobilization, Micro X-ray fluorescence spectroscopy, X-ray absorption near edge structure, Wood pyrolysis

José Pinela^a, Alejandra B.Omarini^{bc}, Dejan Stojković^d, Lillian Barros^a, Pablo D.Postemsky^e, Ricardo C.Calhelha^a, Javier Brecci^{ab}, Marcelo Fernández-Lahore^c, Marina Soković^d, Isabel C.F.R.Ferreira^a (a. Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal, b. INCITAP Institute of Earth and Environmental Sciences of La Pampa (CONICET-UNLPam) National Scientific and Technical Research Council-National University of La Pampa. Mendoza 109 (CP6300), Santa Rosa, La Pampa, Argentina, c. Downstream Bioprocessing Laboratory, Jacobs University Bremen gGmbH. Campus Ring 1, CP28759 Bremen, Germany, d. University of Belgrade, Department of Plant Physiology, Institute for Biological Research “Siniša Stanković”, Bulevar despota Stefana 142, Belgrade, Serbia, e. Laboratorio de Biotecnología de Hongos Comestibles y Medicinales, CERZOS-UNS/CONICET, Camino de La Carrindaga Km7, Bahía Blanca 8000, Buenos Aires, Argentina) Biotransformation of rice and sunflower side-streams by dikaryotic and monokaryotic strains of *Pleurotus sapidus*: Impact on phenolic profiles and bioactive properties, *Food Research International*, Volume 132 (2020), 109094

Fungi are known to modify the properties of lignocellulosic materials during solid-state fermentation (SSF). In this study, agricultural side-streams (sunflower seed hulls, rice husks and rice straw) were used as substrates for SSF with dikaryotic and monokaryotic strains of *Pleurotus sapidus*. The phenolic profiles of the mentioned substrates were characterized by LC-DAD/ESI-MSn pre- and post- fermentation. Moreover, antioxidant, cytotoxic and antimicrobial activities were screened against oxidizable cellular substrates, tumour and primary cell lines, and

different bacteria and fungi, respectively. The concentration of phenolic compounds in the crop side-streams was reduced after fermentation with both strains of the fungus. The fermented extracts also displayed lower antioxidant and cytotoxic activities and had no hepatotoxicity. The antimicrobial activity depended upon the crop side-stream and/or SSF conditions. These results indicate that *P. sapidus* represent a good candidate to modify the phenolic fraction presents in crop side-streams with a consequent decrease in its bioactivities. However, the SSF with *P. sapidus* strains play an interesting role in the detoxification of plant materials which can be used for different applications according to the “reduce - reuse - recycle” concept contributing with the sustainable land use and circular economy.

Keywords: Solid-state fermentation, Lignocellulosic substrates, *Pleurotus sapidus*, Phenolic compounds, Antioxidant activity, Antimicrobial activity

Biomarker

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Predictive biomarkers aid selection of personalized therapy targeted to molecular alterations within an individual's tumor. Patients' responses to targeted therapies are commonly followed by treatment resistance. Here, we survey liquid biopsies as alternatives to tumor biopsies to assess predictive and therapy response biomarkers. We examine the potential of liquid biopsies to meet the challenges of minimal residual disease monitoring after curative intent treatment for earlier detection of disease recurrence. We focus on blood, the most commonly collected minimally invasive clinical sample, and on the two most widely studied assays, circulating tumor DNA and circulating tumor cells.

KeyWords: personalized cancer medicine, liquid biopsy, circulating tumor DNA, circulating tumor cells, predictive biomarkers, treatment response biomarkers, minimal residual disease monitoring, targeted and immunotherapy, sensitivity and specificity, treatment resistance

Christian Bime, Sara M.Camp, Nancy Casanova, Radu C.Oita, Juliet Ndukum, Heather Lynn, Joe G.N.Garcia (College of Medicine, University of Arizona Health Sciences, Tucson, Arizona) **The acute respiratory distress syndrome biomarker pipeline: crippling gaps between discovery and clinical utility, Translational Research, Available online 26 (2020), 006010**

Recent innovations in translational research have ushered an exponential increase in the discovery of novel biomarkers, thereby elevating the hope for deeper insights into “personalized” medicine approaches to disease phenotyping and care. However, a critical gap exists between the fast pace of biomarker discovery and the successful translation to clinical use. This gap underscores the fundamental biomarker conundrum across various acute and chronic

disorders: how does a biomarker address a specific unmet need? Additionally, the gap highlights the need to shift the paradigm from a focus on biomarker discovery to greater translational impact and the need for a more streamlined drug approval process. The unmet need for biomarkers in acute respiratory distress syndrome (ARDS) is for reliable and validated biomarkers that minimize heterogeneity and allow for stratification of subject selection for enrollment in clinical trials of tailored therapies. This unmet need is particularly highlighted by the ongoing SARS-CoV-2/COVID-19 pandemic. The unprecedented numbers of COVID-19-induced ARDS cases has strained health care systems across the world and exposed the need for biomarkers that would accelerate drug development and the successful phenotyping of COVID-19-infected patients at risk for development of ARDS and ARDS mortality. Accordingly, this review discusses the current state of ARDS biomarkers in the context of the drug development pipeline and highlight gaps between biomarker discovery and clinical implementation while proposing potential paths forward. We discuss potential ARDS biomarkers by category and by context of use, highlighting progress in the development continuum. We conclude by discussing challenges to successful translation of biomarker candidates to clinical impact and proposing possible novel strategies.

Keywords: Diagnostic biomarkers in ARDS, Angiopoeitin-2 (Ang-2), Vascular endothelial growth factor (VEGF), Surfactant proteins, Selectins, Proinflammatory cytokines, Anti-inflammatory cytokines, Cytozymes

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Dietary characteristics and oxidative stress are closely linked to the wellbeing of individuals. In recent years, various urinary biomarkers of food and oxidative stress have been proposed for use in wastewater-based epidemiology (WBE), in efforts to objectively monitor the food consumed and the oxidative stress experienced by individuals in a wastewater catchment. However, it is not clear whether such biomarkers are suitable for wastewater-based epidemiology. This study presents a suite of 30 urinary food and oxidative stress biomarkers and evaluates their applicability for WBE studies. This includes 22 biomarkers which were not previously considered for WBE studies. Daily per capita loads of biomarkers were measured from 57 wastewater influent samples from nine Australian catchments. Stability of biomarkers were assessed using laboratory scale sewer reactors. Biomarkers of consumption of vitamin B2, vitamin B3 and fibre, as well as a component of citrus had per capita loads in line with reported literature values despite susceptibility of degradation in sewer reactors. Consumption biomarkers of red meat, fish, fruit, other vitamins and biomarkers of stress had per capita values inconsistent with literature findings, and/or degraded rapidly in sewer reactors, indicating that they are unsuitable for use as WBE biomarkers in the traditional quantitative sense. This study serves to communicate the suitability of food and oxidative stress biomarkers for future WBE research.

Keywords: Food, Diet, Stress, Biomarkers, Wastewater-based epidemiology, Wastewater

Asla Pitkänen, Tomi Paananen, Jenni Kyyriäinen, Shalini Das Gupta, Mette Heiskanen, Niina Vuokila, Ivette Bañuelos-Cabrera, Niina Lapinlampi, Natallie Kajevu, Pedro Andrade, Robert Ciszek, Leonardo Lara-Valderrábano, Xavier Ekolle Nnode-Ekane, Noora Puhakka(A.I. Virtanen Institute for Molecular Sciences, University of Eastern Finland, PO Box 1627, FIN-70211 Kuopio, Finland) Biomarkers for posttraumatic epilepsy, *Epilepsy & Behavior*, Available online (2020), 107080

A biomarker is a characteristic that can be objectively measured as an indicator of normal biologic processes, pathogenic processes, or responses to an exposure or intervention, including therapeutic interventions. Biomarker modalities include molecular, histologic, radiographic, or physiologic characteristics. To improve the understanding and use of biomarker terminology in biomedical research, clinical practice, and medical product development, the Food and Drug Administration (FDA)–National Institutes of Health (NIH) Joint Leadership Council developed the BEST Resource (Biomarkers, EndpointS, and other Tools). The seven BEST biomarker categories include the following: (a) susceptibility/risk biomarkers, (b) diagnostic biomarkers, (c) monitoring biomarkers, (d) prognostic biomarkers, (e) predictive biomarkers, (f) pharmacodynamic/response biomarkers, and (g) safety biomarkers. We hypothesize some potential overlap between the reported biomarkers of traumatic brain injury (TBI), epilepsy, and posttraumatic epilepsy (PTE). Here, we tested this hypothesis by reviewing studies focusing on biomarker discovery for posttraumatic epileptogenesis and epilepsy. The biomarker modalities reviewed here include plasma/serum and cerebrospinal fluid molecular biomarkers, imaging biomarkers, and electrophysiologic biomarkers. Most of the reported biomarkers have an area under the receiver operating characteristic curve greater than 0.800, suggesting both high sensitivity and high specificity. Our results revealed little overlap in the biomarker candidates between TBI, epilepsy, and PTE. In addition to using single parameters as biomarkers, machine learning approaches have highlighted the potential for utilizing patterns of markers as biomarkers. Although published data suggest the possibility of identifying biomarkers for PTE, we are still in the early phase of the development curve. Many of the seven biomarker categories lack PTE-related biomarkers. Thus, further exploration using proper, statistically powered, and standardized study designs with validation cohorts, and by developing and applying novel analytical methods, is needed for PTE biomarker discovery.

Keywords: Epileptogenesis, Exosome, Machine learning, Magnetic resonance imaging, microRNA, traumatic brain injury

Naseer Ullah Khan^a, Jing Lin^a, Xukun Liu^a, Haiying Li^b, Wei Lu^b, Zhuning Zhong^b, Huajie Zhang^a, Muhammad Waqas^a, Liming Shen^a (a. College of Life Science and Oceanography, Shenzhen University, Shenzhen 518060, PR China, b. Department of Endocrinology, Guiyang First People's Hospital, Guiyang 550002, Guizhou, PR China) Insights into predicting diabetic nephropathy using urinary biomarkers, *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics*, Volume 1868, Issue 10 (2020), 140475

Diabetic nephropathy (DN) is a serious complication of diabetes caused by changes in the structure and function of the kidneys. It is important to detect diagnostic biomarkers of DN at an

early stage, in which the drug can slow the loss of kidney function and prevent disease progression. In recent years, a variety of biological markers related to DN have been discovered, which is of great significance for predicting the occurrence and development of diseases. Due to the simplicity of non-invasive collection, urine is an ideal biological sample for the discovery of new biomarkers of kidney disease. We reviewed some new urinary biomarkers related to early DN patients, including urinary proteins, peptides, and exosomes biomarkers. We also highlight the proteins associated with tubular damage, glomerular damage, inflammation and oxidative stress marker. Despite the promise of these new urinary biomarkers, we next proposed a review of the most recent publications reporting on larger cohorts, focusing on those that aim at qualification or validation. This review provides important data to better understand biomarkers related to the pathophysiology of DN, and these markers have been increasingly studied for disease progression to provide effective human treatment.

Keywords: Biomarker, Diabetic nephropathy, Exosomes, Peptide, Proteomics

Jun Shoji (Division of Ophthalmology, Department of Visual Sciences, Nihon University School of Medicine, 30-1 Ohayaguchi-kamicho, Itabashi-ku, Tokyo 173-8610, Japan) Ocular allergy test and biomarkers on the ocular surface: Clinical test for evaluating the ocular surface condition in allergic conjunctival diseases, *Allergology International*, Volume 69, Issue 4 (2020) Pages 496-504

Allergic conjunctival diseases (ACDs) are inflammatory diseases of the conjunctiva and cornea caused predominantly by the IgE-mediated immediate hypersensitivity response. Allergic conjunctival diseases include allergic conjunctivitis, vernal keratoconjunctivitis (VKC), atopic keratoconjunctivitis (AKC), and giant papillary conjunctivitis. In clinical practice of ACDs, an ocular allergy test using biomarker measurement is a crucial examination technique for diagnosing, evaluating severity, and determining the efficacy of medical treatment. The ocular allergy test includes the tear test for evaluating the concentration of biomarkers in tears and an ocular surface test for assessing the expression levels of messenger ribonucleic acid (mRNA) biomarkers on the ocular surface. The clinical usefulness of several biomarkers has been demonstrated in patients with ACDs; specifically, eosinophil cationic protein and eotaxin-2 as eosinophilic inflammation biomarkers; interleukin-4 and thymus and activation regulated chemokine (CCL17/TARC) as Th2 inflammation biomarkers; eotaxin, tumor necrosis factor- α and soluble IL-6 receptor as giant papillae biomarkers; and osteopontin and periostin as allergic inflammation and remodeling biomarkers. Furthermore, the ocular allergy test, quantitative evaluation methods using biomarkers have allowed for better understanding of the immunological and pathophysiological mechanisms of ACDs. Therefore, the search for a biomarker is important to make an ocular allergy test useful. In previous ocular allergy tests, the biomarkers for allergic inflammation in patients with chronic ACDs including VKC and AKC were substantial. However, the selection of biomarkers associated with the early phase reaction of immediate hypersensitivity and innate immunity responses needs to be addressed in future investigations.

Keywords: Eosinophil cationic protein, Eotaxin-2, Histamine H4 receptor, Ocular allergy test, Th2 chemokine

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Radiation Biology, Norwegian Radium Hospital, Oslo University Hospital, Ullernchausseen 70, 0379 Oslo, Norway, b. Department of Core Facilities, Norwegian Radium Hospital, Oslo University Hospital, Ullernchausseen 70, 0379 Oslo, Norway, c. Norwegian Computing Center, Gaustadalléen 23A, 0373 Oslo, Norway, d. Department of Gynaecologic Oncology, Norwegian Radium Hospital, Oslo University Hospital, Ullernchausseen 70, 0379 Oslo, Norway, e. Institute for Cancer Genetics and Informatics, Norwegian Radium Hospital, Oslo University Hospital, Ullernchausseen 70, 0379 Oslo, Norway, f. Department of Medical Physics, Norwegian Radium Hospital, Oslo University Hospital, Ullernchausseen 70, 0379 Oslo, Norway, g. Department of Physics, University of Oslo, Sem Sælands vei 24, 0371 Oslo, Norway) Combining imaging- and gene-based hypoxia biomarkers in cervical cancer improves prediction of chemoradiotherapy failure independent of intratumour heterogeneity, *EBioMedicine*, Volume 57 (2020), 102841

Background: Emerging biomarkers from medical imaging or molecular characterization of tumour biopsies open up for combining the two and exploiting their synergy in treatment planning of cancer patients. We generated a paired data set of imaging- and gene-based hypoxia biomarkers in cervical cancer, appraised the influence of intratumour heterogeneity in patient classification, and investigated the benefit of combining the methodologies in prediction of chemoradiotherapy failure.

Methods: Hypoxic fraction from dynamic contrast enhanced (DCE)-MR images and an expression signature of six hypoxia-responsive genes were assessed as imaging- and gene-based biomarker, respectively in 118 patients.

Findings: Dichotomous biomarker cutoff to yield similar hypoxia status by imaging and genes was defined in 41 patients, and the association was validated in the remaining 77 patients. The two biomarkers classified 75% of 118 patients with the same hypoxia status, and inconsistent classification was not related to imaging-defined intratumour heterogeneity in hypoxia. Gene-based hypoxia was independent on tumour cell fraction in the biopsies and showed minor heterogeneity across multiple samples in 9 tumours. Combining imaging- and gene-based classification gave a significantly better prediction of PFS than one biomarker alone. A combined dichotomous biomarker optimized in 77 patients showed a large separation in PFS between more and less hypoxic tumours, and separated the remaining 41 patients with different PFS. The combined biomarker showed prognostic value together with tumour stage in multivariate analysis.

Interpretation: Combining imaging- and gene-based biomarkers may enable more precise and informative assessment of hypoxia-related chemoradiotherapy resistance in cervical cancer.

Funding: Norwegian Cancer Society, South-Eastern Norway Regional Health Authority, and Norwegian Research Council.

Keywords: Prognostic biomarker, Medical imaging, Gene expression signature, Hypoxia, Intratumour heterogeneity, Cervical cancer

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Minas Gerais, Av. Prof. Alfredo Balena, 190, Bairro Santa Efigênia, Belo Horizonte, Minas Gerais 30130-100, Brazil, c. Hospital das Clínicas da Universidade Federal de Minas Gerais, Av. Prof. Alfredo Balena, 110, Bairro Santa Efigênia, Belo Horizonte, Minas Gerais 30130-100, Brazil, d. Centro de Ciências da Saúde, Universidade Federal do Recôncavo da Bahia, Av. do Cajueiro 1015, Cajueiro, Santo Antonio de Jesus 44574-490, Bahia, Brazil)
Acute kidney injury biomarkers in the critically ill, Clinica Chimica Acta, Volume 508, (2020) Pages 170-178

Acute kidney injury (AKI) is a highly common complication in intensive care units (ICUs). Novel biomarkers might accelerate the detection and management of AKI. We performed a systematic review aiming to evaluate the performance of biomarkers for early AKI diagnosis in ICUs. MEDLINE, BVS, CINAHL, COCHRANE and EMBASE were searched for studies (2006–2019) on the use of biomarkers for AKI diagnosis. Preselected biomarkers were cystatin C, chitinase-3-like protein-1 (UCHI3L1), neutrophil gelatinase-associated lipocalin (NGAL), interleukin-18 (IL-18), kidney injury molecule-1 (KIM-1) and interferon-gamma-inducible protein 10 (IP-10/CXCL-10), measured in plasma or urine. Eleven articles with total of 2,289 patients were included. The most cited biomarker was NGAL (n = 7 studies; 63.6%). Biomarkers with the highest sensitivity (se) and specificity (sp) were urinary heat shock protein (HSP-72) (se = 100%; sp = 90%) and urinary IL-18 (se = 92%; sp = 100%). All biomarkers' performance was influenced by the presence of comorbidities or AKI etiology. Although some biomarkers showed good performance, there was no externally validated biomarker for early AKI diagnosis. Thus, from this review, we did not indicate a novel biomarker to be promptly used in clinical practice. Prospective studies with a large number of patients are needed to expand knowledge in this field. PROSPERO registration number CRD42016037325.

Keywords: Acute kidney injury, Early diagnosis, biomarkers, Intensive care units, Systematic review

Biofertilizer

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Complete reutilisation of mixed mackerel and brown seaweed wastewater as a high-quality biofertiliser in open-flow lettuce hydroponics, Journal of Cleaner Production, Volume 247, (2020), 119081

Biodegradation using *Bacillus* species can convert mixed fishery wastewater into biofertiliser in a clean manner. Herein, fishery wastewater from mackerel and brown seaweed was tested, and the ratio most suitable for biodegradation was 10:1. During the 72-h biodegradation at the optimum mixing ratio, 36.4% hydrolysis occurred due to stable protease, alginate lyase and laminarinase activities, which chemical oxygen demand decreased by 69.1% and total nitrogen by 62.0%. The highest antioxidant activities toward 2, 2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2'-azino-bis-(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) radicals were 84.9% and 93.1% respectively at 24 h, and the total amino acid content at 72 h was 7715.7 µg mL⁻¹. As a biofertiliser, the 72-h culture broth also met the requirements for standard content of nitrogen (N), phosphorus (P), potassium (K) and heavy metals, and the number of viable cells. In open-flow hydroponics using the produced biofertiliser, 1-month-old lettuce plants exhibited significantly enhanced growth rate compared with controls, with high chlorophyll and carotenoid

content and high antioxidant activity. Moreover, there was no permeation of pathogens in the circular biofertiliser solution. These results indicate the potential of the biofertiliser for the production of high-quality lettuce, and demonstrate the complete reutilisation of mixed fishery wastewater.

Keywords: Mixed fishery wastewater, Complete reutilisation, Biofertiliser, Open-flow hydroponics, Lettuce, Antioxidant

Janerson Jose Coelho, Aoife Hennessy, Imelda Casey, Caio Roberto Soares Bragança TonyWoodcock Nabla Kennedy (Eco-Innovation Research Centre, Department of Science, Waterford Institute of Technology, Waterford, Ireland) Biofertilisation with anaerobic digestates: A field study of effects on soil microbial abundance and diversity, Applied Soil Ecology, Volume 147 (2020), 103403

There is much interest in understanding the effects of repeated applications of anaerobic digestates on soil microbial communities, as well as the biofertiliser value of the microbial community in the digestates. The objective of this study was to evaluate the effects of repeated applications of different types of digestates on soil microbial abundance and diversity in a grassland. Microbial communities in the biofertiliser and soil were quantified by gene copy numbers (GCN) (16S/18S quantitative polymerase chain reaction (qPCR)), deoxyribonucleic acid (DNA) sequencing (Illumina) and colony forming units (CFU). The fertilisation trial was conducted over two years in a ryegrass-dominated grassland. Fertiliser treatments included four different types of digestate, undigested cattle slurry, a nitrogen control with calcium ammonium nitrate (CAN) 27 % N, and a no-fertilisation control. Treatments were randomised in blocks with three replicates. Bacteria had the highest GCN in the anaerobic digestates, followed by archaea; fungi had the lowest. Genes from microorganisms with agronomic/environmental importance were detected in the digestates, including N-fixing bacteria, plant-growth promoting bacteria (PGPB), nitrifying and denitrifying bacteria, arbuscular mycorrhizal fungi (AMF), cellulolytic microbes, methanogens and saprotrophic organisms; however, most of them were found in very low abundances. AMF (*Acaulospora*) and methanogens were found in considerably higher abundances than other microbes with recognised soil-plant effects or functions. Soil bacterial, fungal and archaeal GCN were not significantly influenced by the type of fertiliser ($p > 0.05$), and only temporary effects of the application of digestates were noted on the soil bacterial and fungal CFU populations ($p < 0.05$). The application of digestates had no detectable impact on the soil microbial diversity. Microbial DNA sequences found in abundance in the digestates were not found or only found in low abundance in the soil, an indication that dominant microorganisms present in the biofertiliser failed to establish in soil and/or replace the native microbial populations there, possibly due to niche incompatibilities and competitiveness of indigenous soil microbes.

Keywords: Archaea, Bacteria, Biofertilisers, Fungi, Soil microbiology

Biocomposting

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731235, India) Vermiremediation of cotton textile sludge by *Eudrilus eugeniae*: Insight into metal budgeting, chromium speciation, and humic substance interactions, Bioresource Technology, Volume 314 (2020), 123753

Information on prospective metal remediation by *Eudrilus eugeniae* during vermicomposting of cotton textile sludge (CTS) is rather scarce. This investigation, therefore, evaluates the sanitization efficiency of this species in CTS and CTS + cow-dung (CD) based feedstocks against aerobic composting. Accordingly, reduction in Pb, Cd, Cr, and Zn concentrations was between 50 and 70% under vermicomposting. Budget equations substantiated that humic compound mediated chelation was the dominant route of metal removal, against nominal bioaccumulation by earthworms. Correlation statistics revealed that formation of humic compounds (humic acid, fulvic acid, and humin) greatly influenced the transition of toxic Cr⁶⁺ to benign Cr³⁺ during vermicomposting. Moreover, increase in total N content and P availability was significantly greater under vermicomposting than composting. Thus, *E. eugeniae* efficiently stabilized the feedstocks by reducing pH, Ca, S, and organic C and CTS + CD(2:1) was the most favorable feedstock for *E. eugeniae* vermicomposting in respect of metal detoxification and nutrient stabilization.

Keywords: Textile waste, Vermi-stabilization, Chromium detoxification, Metal removal

Biopesticide

Bertrand Fournier^{ab}, Sofia Pereira Dos Santos^a, Julia A.Gustavsen^c, Gwenaél Imfeld^d, Frédéric Lamy^a, Edward A.D.Mitchell^{ef}, Matteo Mota^a, Dorothea Noll^a, Chantal Planchamp^g, Thierry J.Heger^a (a. Soil Science and Environment Group, CHANGINS, University of Applied Sciences and Arts Western Switzerland, Route de Duillier 50, 1260 Nyon, Switzerland, b. Institute of Environmental Science and Geography, University of Potsdam, Karl-Liebknecht-Str. 24-25, 14476 Potsdam, Germany, c. Avenue Ignace Paderewski 12, 1110 Morges, Switzerland, d. Université de Strasbourg, Laboratory of Hydrology and Geochemistry of Strasbourg (LHyGeS), UMR 7517 CNRS/EOST, 1 Rue Blessig, 67084 Strasbourg Cedex, France, e. Laboratory of Soil Biodiversity, University of Neuchâtel, Rue Emile Argand 11, 2000 Neuchâtel, Switzerland, f. Jardin Botanique de Neuchâtel, Chemin du Pertuis-du-Sault 58, 2000 Neuchâtel, Switzerland, g. Soil and Biotechnology Division, Federal Office for the Environment (FOEN), 3003 Bern, Switzerland) Impact of a synthetic fungicide (fosetyl-Al and propamocarb-hydrochloride) and a biopesticide (*Clonostachys rosea*) on soil bacterial, fungal, and protist communities, Science of The Total Environment, Volume 738, (2020), 139635

The use of synthetic pesticides in agriculture is increasingly debated. However, few studies have compared the impact of synthetic pesticides and alternative biopesticides on non-target soil microorganisms playing a central role in soil functioning.

We conducted a mesocosm experiment and used high-throughput amplicon sequencing to test the impact of a fungal biopesticide and a synthetic fungicide on the diversity, the taxonomic and functional compositions, and co-occurrence patterns of soil bacterial, fungal and protist communities.

Neither the synthetic pesticide nor the biopesticide had a significant effect on microbial α -diversity. However, both types of pesticides decreased the complexity of the soil microbial network. The two pesticides had contrasting impacts on the composition of microbial

communities and the identity of key taxa as revealed by microbial network analyses. The biopesticide impacted keystone taxa that structured the soil microbial network. The synthetic pesticide modified biotic interactions favouring taxa that are less efficient at degrading organic compounds. This suggests that the biopesticides and the synthetic pesticide have different impact on soil functioning.

Altogether, our study shows that pest management products may have functionally significant impacts on the soil microbiome even if microbial α -diversity is unaffected. It also illustrates the potential of high-throughput sequencing analyses to improve the ecotoxicological risk assessment of pesticides on non-target soil microorganisms.

Keywords: Biological control agents, Microbial community, Microbiome, Non-target microorganism, Pest management, Soil biodiversity, Synthetic pesticide

Laura Mejias^{ab}, Mònica Estrada^a, Raquel Barrena^a, Teresa Gea^a (a. GICOM Research Group, Department of Chemical, Biological and Environmental Engineering School of Engineering, Edifici Q, Universitat Autònoma de Barcelona, 08193, Bellaterra, Barcelona, Spain, b. Aeris Tecnologías Ambientales S.L, Carrer Santa Rosa, 38, local, 08290 Cerdanyola del Vallès, Barcelona, Spain) A novel two-stage aeration strategy for *Bacillus thuringiensis* biopesticide production from biowaste digestate through solid-state fermentation, *Biochemical Engineering Journal*, Volume 161 (2020), 107644

A novel aeration strategy has been developed at lab and bench-scale for *Bacillus thuringiensis* (Bt) derived biopesticides production through solid-state fermentation, using a mixture of digestate and biowaste as substrates. A Box-Behnken design was performed to select key parameters of the spore production process, being temperature and biodegradability the factors with a significant effect. Further tests confirmed the importance of oxygen content for spore production. Thus, a two-stage aeration strategy consisting of a microaeration phase followed by a high-rate aeration period was developed and tested. The production strategy was validated in a 22-L reactor using two different strains (Bt kusrtaki, Btk, and israelensis, Bti), demonstrating the robustness of the protocol. Maximum production of 1.3×10^8 spores g⁻¹ dry matter for Btk and 4×10^8 spores g⁻¹ dry matter for Bti were obtained, representing a final yield of 5 and 29 spores produced per initial CFU, respectively.

Keywords: circular economy, digestate, biopesticide, *Bacillus thuringiensis*, aeration strategy

CindyBallardo^{ab}, María del Carmen Vargas-García^c, Antoni Sánchez^a, Raquel Barrena^a, Adriana Artola^a (a. Composting Research Group, Department of Chemical, Biological and Environmental Engineering, Escola d'Enginyeria, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, 08193 Barcelona, Spain, b. Universidad Nacional del Centro del Perú, Centro de Investigación en Residuos Sólidos, Av. Mariscal Castilla N 3989-4089, Huancayo, Peru, c. Departamento de Microbiología, Universidad de Almería, Almería, Spain) Adding value to home compost: Biopesticide properties through *Bacillus thuringiensis* inoculation, *Waste Management*, Volume 106, (2020), Pages 32-43

Home and community composting are considered potential tools for the self-management of organic waste. The production of added value products from biowaste is an encouraging step

further to valorise this waste stream. To increase the profits of homemade compost, this paper presents a strategy to produce enriched home compost with biopesticide properties through a simple and low-cost process. *Bacillus thuringiensis* (Bt) was inoculated in a home composter bin through a solid inoculum previously prepared using the same waste as substrate. The process was monitored and compared with a home composting control process without inoculation. Final composts were analysed and compared in terms of physicochemical and microbiological properties, respiration and germination indices, indicating the suitability of both to be used as organic amendments. Also, a standardized toxicity test proved that Bt-enriched compost can be safely applied to the soil. Microbiological analysis revealed highly diverse communities in both cases, with limited differences at phylum taxonomic level, but dissimilar relative abundances of species within phylum. Bacteroidetes and Proteobacteria were dominant, with the presence of species able to transform organic matter from vegetal origin, but not usually related to compost. Bt-crystal toxin was clearly present in Bt-enriched compost, indicating the coexistence of Bt with the different microbial populations till the end of the composting process. Although Bt has been widely investigated due to its biopesticide properties, the incorporation of this microorganism to home composting level has not been previously reported.

Keywords: *Bacillus thuringiensis*, Biopesticide, Enriched compost, Microbiocenosis, Home composting

Luca Finetti^a, Federica Ferrari^b, Girolamo Caló^b, Stefano Cassanelli^c, Morena De Bastiani^a, Stefano Civolani^{ad}, Giovanni Bernacchia^a (a. Department of Life Sciences and Biotechnology, University of Ferrara, Ferrara, Italy, b. Department of Medical Sciences, Section of Pharmacology, University of Ferrara, Ferrara, Italy, c. Department of Life Sciences, University of Modena and Reggio Emilia, Reggio Emilia, Italy, d. InnovaRicerca s.r.l. Monestirolo, Ferrara, Italy) **Modulation of *Drosophila suzukii* type 1 tyramine receptor (DsTAR1) by monoterpenes: a potential new target for next generation biopesticides, Pesticide Biochemistry and Physiology, Volume 165 (2020), 104549**

This study proposes a biochemical and molecular model for the interaction between the *Drosophila suzukii* type 1 tyramine receptor (DsTAR1) and monoterpenes.

A preliminary molecular and functional characterization of DsTAR1 cDNA revealed that a 1.8 kb long ORF codes for a 600 amino acid polypeptide featuring seven transmembrane domains, as expected for a GPCR. A stable HEK 293 cell line expressing DsTAR1 was tested for responsiveness to tyramine (TA) and octopamine (OA). In intracellular calcium mobilization studies, TA led to a concentration-dependent increase in $[Ca^{2+}]_i$ ($pEC_{50} \sim 6.40$), completely abolished by pre-incubation with the antagonist yohimbine 1 μM . Besides, in dynamic mass redistribution (DMR) studies, TA evoked a positive DMR signal in a concentration-dependent manner ($pEC_{50} \sim 6.80$).

The recombinant cell line was then used to test three monoterpenes (thymol, carvacrol and α -terpineol) as putative ligands for DsTAR1. The terpenoids showed no agonist effects in both DMR and calcium mobilization assays, but they increased the potency of the endogenous ligand, TA, acting as positive allosteric modulators.

Moreover, expression analysis on adults *D. suzukii*, exposed for 24, 72 or 120 h to a sublethal concentration of the three monoterpenes, showed a downregulation of DsTAR1.

This evidence has led to hypothesize that the downregulation of DsTAR1 might be a compensatory mechanism in response to the positive allosteric modulation of the receptor induced by monoterpenes.

Therefore, these findings might be useful for the development of a new generation of biopesticides against *Drosophila suzukii*, targeting TAR1.

Keywords: *Drosophila suzukii*, Tyramine receptor, Essential oils, Monoterpenes, Biopesticides, Dynamic mass redistribution

Rani Rai, Surindra Suthar (School of Environment & Natural Resources, Doon University, Dehradun 248001, Uttarakhand, India) Composting of toxic weed *Parthenium hysterophorus*: Nutrient changes, the fate of faecal coliforms, and biopesticide property assessment, Bioresource Technology, Volume 311 (2020), 123523

This study aimed to investigate; composting of toxic weed *Parthenium* with cow dung in (2:1, and 1:1 ratio); and the changes in *Escherichia coli* and *Salmonella* population; as well as the antimicrobial property of ready compost. Organic carbon decreased by 45–52% while total nitrogen, total potassium, available phosphorus increased by 1.87- to 3.21-, 1.65- to 1.83-, and 4.03- to 3.33-folds, respectively in *Parthenium* setups. Germination index value (110–132%) indicates no phytotoxicity of composted *Parthenium*. *E. coli* reduced by 6.87 to 6.90 log population (<1000 CFU g⁻¹, safe limit) while *Salmonella* was in non-detectable limit in compost samples. Results of the antimicrobial test indicate a strong biocidal activity by non-sterilized compost extract against plant pathogens *Xanthomonas citris*, *Xanthomonas campestris*, and *Erwinia carotovora*. *Xanthomonas* spp. It is concluded that thermophilic composting could convert *Parthenium* into a product with biomanure and biopesticide property for sustainable agriculture production.

Keywords: Invasive weed, Congress grass, C/N ratio, Faecal coliforms, Black rot disease, Germination index

Jianguo Feng^a, Rong Wang^a, Zhiyang Chen^a, Shengwei Zhang^a, Shuzhong Yuan^a, Hongen Cao^a, Seid Mahdi Jafari^b, Wenchao Yang^a (a. College of Horticulture and Plant Protection, Yangzhou University, Yangzhou 225009, China, b. Department of Food Materials and Process Design Engineering, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran) Formulation optimization of D-limonene-loaded nanoemulsions as a natural and efficient biopesticide, Colloids and Surfaces A: Physicochemical and Engineering Aspects, Volume 596 (2020), 124746

D-limonene is an important constituent of citrus fruits, such as oranges and lemons, and can be extracted as a natural essential oil for controlling the agricultural pests because of its antifungal and insecticidal activities. However, the hydrophobicity of D-limonene hinders its full potential and excellent performance. In this research, the effect of emulsifier type, dosage, and emulsification method on the formation and stability of D-limonene-loaded nanoemulsions was investigated by sample appearance, microstructural observations, droplet size measurement, and multiple light scattering analysis. Nanoemulsions prepared with emulsifier (EL-40) exhibited the highest stability, with an appropriate HLB (Hydrophilic Lipophilic Balance) value of 13.5. The stability of nanoemulsions increased at higher emulsifier dosage from 2% to 6%. Also, nanoemulsions fabricated by dropwise addition of aqueous phase (deionized water) into D-limonene as the oil phase premixed with emulsifier were the most stable samples. The optimized

formulation of D-limonene-loaded nanoemulsions was determined as: 10 % D-limonene, 6% EL-40, and 84 % deionized water. The quality indicators of this formulation were acceptable in terms of FAO standards. Finally, D-limonene-loaded nanoemulsions could inhibit the growth of various fungal pathogens, including *Pyricularia oryzae* (rice blast), *Rhizoctonia solani* (rice sheath blight), *Colletotrichum gloeosporioides* (pepper anthracnose), and *Phomopsis amygdali* (peach shoot blight). This research provides a practical solution for the formulation of stable and effective nanoemulsions containing D-limonene for the control of agricultural crop diseases.

Keywords: D-limonene, Nanoemulsions, Stability, Antifungal activity, Emulsification method

P.Vivekanandhan^a, S.Bedini^b, M.S.Shivakumar^a (a. Molecular Entomology Laboratory, Department of Biotechnology, School of Biosciences, Periyar University, Salem 636 011, Tamil Nadu, India, b. Department of Agriculture, Food, and Environment, University of Pisa, via del Borghetto 80, 56126 Pisa, Italy) **Isolation and identification of entomopathogenic fungus from Eastern Ghats of South Indian forest soil and their efficacy as biopesticide for mosquito control, Parasitology International, Volume 76 (2020), 102099**

The repeated usage of chemical insecticides, responsible for insecticide resistance in mosquitoes and environmental toxicity. Currently effective and environmental-safe control strategies are needed for the control disease-vector mosquitoes. Entomopathogens can be an effective alternative to chemical insecticide. Herein we isolated and tested 46 soil-borne entomopathogenic fungi belonging to six genera, namely *Beauveria* sp., *Metarhizium* sp., *Fusarium* sp., *Aspergillus* sp., *Trichoderma* sp., and *Verticillium* sp., fungi conidia were tested on *Aedes aegypti*, *Anopheles stephensi* and *Culex quinquefasciatus* larvae. Bioassays results show that *M. anisopliae* fungal isolate causes a 100%, 98.6% and 92% mortality within six days, on *Aedes aegypti*, *Anopheles stephensi* and *Culex quinquefasciatus*, respectively. *M. anisopliae* treated three mosquito larvae have lower lifetime with LT50 values in *A. stephensi*, 2.931 days; *A. aegypti*, 2.676 days and *C. quinquefasciatus*, 3.254 days. 18 s rDNA sequence analysis confirmed that the isolated fungus are belonging to the genus of *M. anisopliae*-VKKH3, *B. bassiana*-VKBb03, and *V. lecanii*-VKPH1. Our results clearly show that *M. anisopliae* has good potential, as a low-cost, environmentally safe tool for the control of *A. aegypti*, *A. stephensi*, and *C. quinquefasciatus* mosquitoes.

Keywords: Entomopathogenic fungus, *Aedes aegypti*, *Anopheles stephensi*, *Culex quinquefasciatus*, Larval bioassay, Microbial pesticide, Eco-friendly

M.S.Abd El-Atti^a, A.M.Khalil^a, A.A.Elsheakh^b, Wesam S.Elghohary^b (a. Zoology Department, Faculty of Science, Zagazig University, Zagazig, 44519, Egypt, b. Plant Protection Research Institute, Agriculture Research Center, Doki, Giza, Egypt) **Biological control of *Monacha cartusiana* “glassy clover land snails” by microbial biopesticides Biozed and Biogard, using bait technique, Biocatalysis and Agricultural Biotechnology, (2020), 101572**

The effectiveness of microbial derived insecticides (Biozed and Biogard) were tested for controlling the subversive clover snails causing wastage of economic plants at Sharkia Governorate, Egypt, using poisonous baits technique. The toxicity index, LC50 and relative potency values reveals the potential activity of Biozed (fungal) than Biogard (bacterial) against *M. cartusiana* snails. Biogard caused no mortalities among treated clover snails at all at the first

day of exposure. Mortality percentages appeared after one week and increased gradually with increasing concentrations and time of treatments. The highest concentrations of Biozed (0.75%) and Biogard (3.9%) caused 66.6% and 40% mortalities respectively after 28 days of exposure. From the biochemical parameters, an increment of total proteins, AST, ALT, α -esterase levels while a strong reduction on the total lipids, β -esterase and Phenoloxidase levels were observed after treatments with LC25 of biocides for three weeks. Histopathological investigations on the digestive and hermaphrodite glands revealed that sublethal concentration of Biozed produced tubular disruptions, vacuolation, excessive luminal secretions in digestive gland tissues. Malformed sperms and oocytes were spotted in ovotestis acini treated with Biozed. Biogard caused extensive luminal secretions, hemocytes infiltration and lysis of peripheral cells of digestive tubules while hermaphroditic acini showed disrupted sperms and oocytes.

Keywords: *Monacha cartusiana*, Biozed, Biogard, Toxicity, Biochemistry, Histopathology

Biodegradation

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Combining electro-oxidation (EO) with biodegradation for real oil sands process water (OSPW) treatment was evaluated in terms of naphthenic acid (NA) biodegradation enhancement. Ion mobility spectrometry (IMS) qualitative analysis showed that EO by graphite was able to degrade the different NA clusters in OSPW including: classical, oxidized and heteroatomic NAs. Applying EO even at current density as low as 0.2 mA/cm² was still able to reduce classical NAs and acid extractable fraction (AEF) by 19% and 7%, respectively. EO pretreatment preferentially broke long carbon chains and highly cyclic carboxylic fractions of NAs in OSPW to improve the biodegradation of NAs. Aerobic biodegradation for 40 days reduced NAs by up to 30.9% when the samples were pre-treated with EO. Applying EO at current densities below 2 mA/cm² maintained current efficiency as high as 48% and resulted in improvement in the biodegradation rate of remaining NAs by up to 2.7 folds. It was further revealed that applying EO before biodegradation could reduce the biodegradation half-life of classical NAs by up to 4.4 folds. 16S amplicon sequencing analysis showed that the samples subjected to biodegradation had increased abundances of Sphingomonadales and Rhodocyclales with increasing applied current density for EO pre-treatments.

Keywords: Electro-oxidation, OSPW, Naphthenic acids, Biodegradation

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PR China) Biodegradation of n-alkanes in crude oil by three identified bacterial strains, Fuel, Volume 275 (2020) 117897

In this study, aerobic biodegradation of crude oil was simulated using *Pseudomonas aeruginosa* XJ16, *Bacillus cereus* XJ20, and *Acinetobacter lwoffii* XJ19 bacteria for 90 days, for semi-quantitative calculation of concentration, demonstrating that n-alkanes (C14–C35) were biodegraded by the three strains at different ratios and rates. *P. aeruginosa* XJ16 showed the highest biodegradative potential for n-alkanes, with total biodegradation ratio of 98.2% in 10 days. In comparison, the total biodegradation ratio by *B. cereus* XJ20 increased gradually and achieved 98.8% after 90 days; whereas that by *A. lwoffii* XJ19 was much lower even after 90 days (29.3%). In addition, *P. aeruginosa* XJ16 and *B. cereus* XJ20 exhibited stronger biodegradation efficiencies for C18–C32 n-alkanes (95.4%–99.7%) than *A. lwoffii* XJ19 (9.05%–73.0%). However, all three bacterial strains exhibited comparably good biodegradation efficiencies for C33–C35 n-alkanes (60.2%–86.4%). Moreover, the biodegradation rate constants and biodegradation rates were of the decreasing order: *P. aeruginosa* XJ16 > *B. cereus* XJ20 > *A. lwoffii* XJ19. *P. aeruginosa* XJ16 and *B. cereus* XJ20 biodegrade n-alkanes with relatively low carbon numbers more easily than those with high carbon numbers. However, *A. lwoffii* XJ19 is more likely to biodegrade n-alkanes with relatively high carbon numbers. On day 10, surface tension ($\text{mN}\cdot\text{m}^{-1}$) declined from 70.6 to 35.9 by treatment with *P. aeruginosa* XJ16, to 31.3 with *B. cereus* XJ20, and to 34.1 with *A. lwoffii* XJ19. As biosurfactant-producing and hydrocarbon-degrading bacteria, these three strains have the potential to be used for bioremediation of hydrocarbon pollutants.

Keywords: Bacterial species, n-Alkanes (C14–C35), Biodegradation ratio, Biodegradation rate, Bioremediation

Yusuke Kambe^a, Yuji Mizoguchi^{ab}, Ken Kuwahara^{ac}, Takahiko Nakaoki^c, Yoshiaki Hirano^b, Tetsuji Yamaoka^a (a. Department of Biomedical Engineering, National Cerebral and Cardiovascular Center (NCVC) Research Institute, 6-1 Kishibe-Shimmachi, Suita, Osaka, 564-8565, Japan, b. Faculty of Chemistry, Materials and Bioengineering, Kansai University, 3-3-35 Yamatecho, Suita, Osaka, 564-8680, Japan, c. Department of Materials Chemistry, Ryukoku University, Seta, Otsu, 520-2194, Japan) **Beta-sheet content significantly correlates with the biodegradation time of silk fibroin hydrogels showing a wide range of compressive modulus, Polymer Degradation and Stability, Volume 179 (2020) 109240**

Elasticity and biodegradability are required for hydrogel scaffolds in soft tissue engineering and vary among target tissues. To identify the unique effects of these properties on tissue regeneration, a factor that alters only one of these properties independent of the other is needed. Here, we evaluated various properties of 15 types of silk fibroin (SF) physical hydrogels with different SF concentrations and molecular weights, and found that the compressive modulus and biodegradability did not correlate with each other significantly. This suggested the possibility of a factor that affected only one of the properties. SF concentration and water content of the hydrogels changed both the compressive modulus and biodegradability simultaneously. In contrast, the β -sheet content in SF hydrogels correlated only with the biodegradation time significantly, suggesting that the β -sheet content may be used to study the effect of biodegradation time on tissue regeneration. In addition, an SF hydrogel was modified with a peptide derived from the β -sheet forming GAGAGS/Y repeated region in SF heavy-chain,

resulting in no significant difference in the compressive modulus but a significantly delayed biodegradation time. These results suggest the potential for SF hydrogels as a group of materials with made-to-order elasticity and biodegradability for soft tissue engineering applications.

Keywords: Silk fibroin, Physical hydrogel, Compressive test, Enzymatic degradation, Soft tissue engineering

Haiping Huang^{ab}, Mengsha Yin^b, Denglin Han^a (a. School of Geosciences, Yangtze University, Wuhan 430100, Hubei, PR China, b. Department of Geoscience, University of Calgary, 2500 University Drive NW, Calgary, AB T2N 1N4, Canada) **Novel parameters derived from alkylchrysenes to differentiate severe biodegradation influence on molecular compositions in crude oils, Fuel, Volume 268 (2020) 117366**

Solvent extracted bitumens from oil sands in the Athabasca region, West Canada and Liaohe Basin, NE China and oils from the Bongor Basin, SW Chad have been geochemically characterized to investigate biodegradation influence on molecular compositions. All samples in each case history were derived from the same source rock systems and have a similar maturity level. The variations in molecular compositions are merely caused by variable levels of biodegradation. GC–MS analysis results based on overall saturated and aromatic hydrocarbon distributions illustrated that biodegradation influences on Athabasca oil sands were less severe than these in Liaohe oil sands and Bongor oils but biodegradation level assignment is inconclusive and confusion. Novel biodegradation parameters based on methylchrysene (MCh) isomer distributions and relative abundance between alkylchrysenes and alkylphenanthrenes were proposed to differentiate biodegradation influence at heavy to severe biodegradation levels. The 3-MCh is proved to be the most stable methylchrysene isomer and the ratio of 3-MCh/ Σ MCh can serve as a novel biodegradation parameter. Meanwhile, alkylchrysenes show much higher ability to resist biodegradation than alkylphenanthrenes and the ratio of C0-1Ch/C2P was proposed as another novel biodegradation parameter. While the nature of organic source input may exert some impacts on the initial values of these novel parameters, continuous increases in these two parameters with intensified biodegradation levels may provide a supplemental tool for biodegradation influence assessment especially when biodegradation approaches to severe levels.

Keywords: Biodegradation level, Biomarkers, Aromatic hydrocarbon, Alkylchrysenes

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Three biodegradation were carried out in soils with activator, non-activator and no activator. For oil-addicted biodegradation, macro-alkanes were devoured (soil S1:3313 mg C18-C30/kg, soil S2: 2741 mg C18-C30/kg) in soils with activator, which was 3.8 times of that for non-oil-addicted biodegradation. For oil-addicted biodegradation, high respiratory activity (S1: 0.8

CO₂/kg soil, S2: 0.6 mg CO₂/kg soil) and rapid growth rate (S1: 48 %, S2: 36 %) of oil-addicted microbe with activator were observed. Moreover, for oil-addicted biodegradation, low consumption of NH₄⁺-N (22 mg/kg) and acetic acid (410 mg/kg) were observed, which were 1/8 and 4/5 for non-oil-addicted biodegradation. Meanwhile, rapid growth and high respiratory activity of the genera *Pseudomonas*, *Diaminobutyricimonas*, *Dyadobacter* and *Galbitalea* were observed. It indicated that macro-alkanes instead of organic matter such as aromatic protein I and II, fulvic acid-like, soluble microbial metabolites, humic acid-like was utilized rapidly for oil-addicted biodegradation due to less consumption of NH₄⁺-N and acetic acid.

Keywords: Oil-addicted biodegradation, Activator, Macro-alkanes, Low consumption of NH₄⁺-N, Oil-contaminated soil

Matthew Rodrigue^a, Vijaikrishnah Elango^b, David Curtis^a, Autumn W.Collins^a, John H.Pardue^{ab} (a. Department of Civil & Environmental Engineering, Louisiana State University, Baton Rouge, LA 70803, United States of America, b. Hazardous Substance Research Center, Louisiana State University, Baton Rouge, LA 70803, United States of America) **Biodegradation of MC252 polycyclic aromatic hydrocarbons and alkanes in two coastal wetlands, Marine Pollution Bulletin, Volume 157 (2020) 111319**

Complementary microbial and geochemical assessment techniques investigated the biodegradation of PAHs and alkanes in salt marshes impacted by crude oil following the Macondo spill. Contamination was observed in the top 10 cm of the marsh profile based on PAH analysis and measurement of the $\delta^{13}\text{C}$ signature of impacted marsh soils. Measurement of evolution of ¹³C depleted CO₂ indicated mineralization of crude oil ranging from 2.7–12.1 mg CO₂-C/m²-hr. Changes in weathering ratios of alkylated phenanthrenes and dibenzothiophenes indicated loss of these 3-ring PAHs consistent with biodegradation. A diverse microbial population was observed at both locations dominated by Gammaproteobacteria and including known hydrocarbon degraders such as *Marinobacter* and *Alcanivorax*. There was shared richness between sites and across seasons but results suggested substantial turnover of phylotypes in space and time. Biodegradation of alkanes and alkylated PAHs occurred when oxygen was provided in laboratory reactors but not in the absence of oxygen.

Keywords: PAHs, Gulf Coast, MC252 oil, Biodegradation, Stable isotopes

Allyn H.Maeda^a, Shinro Nishi^b, Yuji Hatada^b, Yukari Ohta^b, Kanna Misaka^a, Marie Kunihiro^a, Jiro F.Mori^a, Robert A.Kanaly^a (a. Department of Life and Environmental System Science, Graduate School of Nanobiosciences, Yokohama City University, Yokohama, Kanagawa, Japan, b. Institute of Biogeosciences, Japan Agency for Marine-Earth Science and Technology (JAMSTEC), Yokosuka, Kanagawa, Japan) **Chemical and genomic analyses of polycyclic aromatic hydrocarbon biodegradation in *Sphingobium barthaii* KK22 reveals divergent pathways in soil sphingomonads, International Biodeterioration & Biodegradation, Volume 151 (2020) 104993**

Polycyclic aromatic hydrocarbons (PAHs) are hazardous pollutants that are biodegraded by soil bacteria and the soil sphingomonads are thought to be major contributors to PAH biodegradation. To predict PAH environmental fates it is necessary to understand the chemistry and genetics of PAH biodegradation by sphingomonads. When the soil sphingomonad *Sphingobium barthaii* KK22 was exposed to low molecular weight (LMW) PAHs and

biotransformation products were investigated by comprehensive chemical analyses, at least twenty products were identified by different techniques and both intradiol- and extradiol-aromatic ring cleavage pathways were found to be active in this organism. Sphingomonads, a large and diverse group, have been studied in regard to PAH biodegradation, however intradiol-ring cleavage of LMW PAHs has never been reported. Whole genome sequencing and prediction of *S. barthaii* KK22 functional genes revealed sets of aromatic ring-hydroxylating oxygenases and PAH biotransformation genes. Combined with chemical analyses results, novel, near complete PAH biotransformation pathways for soil sphingomonads were constructed. In conjunction with quantitative assays, a comprehensive view of PAH biodegradation was obtained that revealed divergent downstream pathways that advanced our understanding of the PAH biotransformation capabilities of these versatile soil bacteria and shall aid in predictions of PAH environmental fate during soil bioremediation.

Keywords: biodegradation

Tor Nordam^{ab}, Synnøve Lofthus^c, Odd Gunnar Brakstad^a (a. SINTEF Ocean, Trondheim, Norway, b. Department of Physics, Norwegian University of Science and Technology, Trondheim, Norway, c. Department of Biotechnology and Food Science, Norwegian University of Science and Technology, Trondheim, Norway) Modelling biodegradation of crude oil components at low temperatures, Chemosphere, Volume 254 (2020) 126836

For oil spilled at sea, the main weathering processes are evaporation, emulsification, photo-oxidation, dispersion and biodegradation. Of these, only biodegradation may completely remove hydrocarbons from the environment in the long term, as the other processes only serve to transform and dilute the oil components. As petroleum development is moving north, the probability of Arctic oil spills increases. Hence, it is imperative to develop methods for comprehensive risk assessment of oil spills in cold and ice-covered waters. Accurate biodegradation rates are an essential part of this, as they are required to predict the long-term effects of marine oil spills. In this paper, we present experimentally determined biodegradation rates for the component groups which are used to represent oil in the OSCAR oil spill model. The experiments have been carried out at seawater temperatures of , , , and . We show that for the lighter and more soluble oil components, the changes in degradation rates between and are well captured by a constant scaling law. At lower temperatures, and for heavier and less soluble components, the rates are not well described by a constant, probably indicating that oil properties become important for the biodegradation rate.

Keywords: biodegradation, Oil spill modeling

Biosensor

Jiong-Ju Hao, Ke-Da Gu, Lei Xia, Yu-Jie Liu, Zhi-Feng Yang, Hong-Wei Yang (Department of Physics, College of Science, Nanjing Agricultural University, Nanjing 210095, PR China) Research on low-temperature blood tissues detection biosensor based on one-dimensional superconducting photonic crystal, Communications in Nonlinear Science and Numerical Simulation, Volume 89 (2020) 105299

This paper presents a one-dimensional superconducting photonic crystal (sc-PhC) refractive index biosensor with high sensitivity which consists of a periodic arrangement of superconductors and semiconductors. The biosensor has high sensitivity and accuracy in the refractive index range of 1.0 to 2.2 RIU below the critical temperature. The resonance wavelength and defect refractive index of the biosensor have a high linear correlation coefficient, and the linear correlation coefficient of all experimental groups in this paper is higher than 0.999. The sensitivity of the biosensor decreases with increasing temperature, and when the external temperature increases from 80K to 134K, the sensitivity decreases from 6.04396 $\mu\text{m}/\text{RIU}$ to 5.71703 $\mu\text{m}/\text{RIU}$ gradually. And then, the performance of biosensor in blood component detection is researched by FDTD (finite-difference time-domain) method. The result shows that the sensor has higher sensitivity and shows the same change law in the detection of refractive index changes (1.35RIU-1.47RIU) within a small range such as blood components. When the external temperature is increased from 80K to 134K, the sensitivity of the biosensor gradually decreases from 6.85789 $\mu\text{m}/\text{RIU}$ to 6.48073 $\mu\text{m}/\text{RIU}$.

Keywords: Photonic crystal, Superconductor, Biosensor, Low-temperature, FDTD

Xin Lu, Jiadi Sun, Xiulan Sun (State Key Laboratory of Food Science and Technology, School of Food Science and Technology, National Engineering Research Center for Functional Food, Synergetic Innovation Center of Food Safety and Nutrition, Jiangnan University, Wuxi, Jiangsu, 214122, PR China) Recent advances in biosensors for the detection of estrogens in the environment and food, TrAC Trends in Analytical Chemistry, Volume 127 (2020) 115882

Endocrine-disrupting chemicals (EDCs) have become increasingly prevalent in environment samples across the world, posing a serious threat to human health. In particular, estrogenic EDCs have received considerable public attention due to the ways in which they interfere with the normal endocrine functions of humans and animals. In recent years, biosensors for detecting estrogenic EDCs have made considerable progress. This review summarizes recent developments in biosensors for the detection of estrogens in the environment and food, including molecule-based biosensors, cell-based biosensors, and model organism-based biosensors. In particular, this review considered works published in 2017–2019 that focused on methods for the detection of estrogens and the use of nanomaterials for biosensors development. In this work, the advantages and limitations of various types of biosensors were compared, and projections for the future development of biosensors for monitoring estrogens in the environment and food were discussed.

Keywords: EDCs, 17 β -estradiol, Bisphenol A, Biosensor, Nanomaterial

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In the review, the principles and main purposes of using multienzyme systems in electrochemical biosensors are analyzed. Coupling several enzymes allows an extension of the spectrum of detectable substances, an increase in the biosensor sensitivity (in some cases, by several orders of magnitude), and an improvement of the biosensor selectivity, as showed on the examples of amperometric, potentiometric, and conductometric biosensors. The biosensors based on cascade, cyclic and competitive enzyme systems are described alongside principles of function, advantages, disadvantages and practical use for real sample analyses in various application areas (food production and quality control, clinical diagnostics, environmental monitoring). The complications and restrictions regarding the development of multienzyme biosensors are evaluated. The recommendations on the reasonability of elaboration of novel multienzyme biosensors are given.

Keywords: Biosensor, Enzyme cascade, Enzyme recycling, Multienzyme system, Electrochemistry, Amperometry

Ru Wang^a, Jun Jia^b (a. Physical Education Department, Tianjin University of Commerce, Tianjin 300134, Tianjin, China, b. Institute of Social Science and Sport, Tianjin Maritime College, Tianjin 300350, Tianjin, China) Design of intelligent martial arts sports system based on biosensor network technology, Measurement, Volume 165 (2020) 108045

Biosensor is a new type of analytical detection tool, which can be applied to various industries with its sensitivity, accuracy, easy operation, and online monitoring in vivo. Biosensors have a broad market in sports science, and can be applied to timely monitoring of sports training. It will also become an important method and technology of sports education and sports scientific research. The purpose of this article is to study the design of intelligent martial arts sports system based on biosensor network technology. This article studies the physical condition of martial arts athletes by installing biosensors on them, and uses a single variable method and mathematical statistics to record various martial arts athletes. The state of sports is designed by using big data intelligent monitoring system to design network nodes and real-time data transmission through network technology, so as to ensure the health of martial arts athletes and monitor the status of martial arts athletes in real time. Then compared with the traditional situation of remote mobilization, the feasibility of the application of intelligent martial arts sports system under the biosensor biosensor network technology is verified, and the intelligent martial arts sports system under the biosensor network technology is designed. Experimental data shows that the design of the intelligent martial arts sports system under the biosensor network technology effectively protects martial arts athletes and improves performance, and avoids injuries caused by intense sports. The experimental data show that the design of intelligent martial arts sports system under the biosensor network technology has guiding significance for the development of future martial arts sports system.

Keywords: Bio-sensor, Network technology, Martial arts sports system, Real-time monitoring

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applications in agri-food safety, TrAC Trends in Analytical Chemistry, Volume 127 (2020) 115898

This review focuses on the ways in which screen-printed carbon electrodes have been tailored with different biorecognition elements, including enzymes, antibodies, and aptamers, often with other modifiers, such as mediators and nanoparticles, to produce electrochemical biosensors for a variety of analytes of importance in agri-food safety. Emphasis is placed on the strategies of biosensor fabrication and the performance characteristics of the devices. As well as biosensors for a range of analytes in different agri-food matrices, we have also included reports on novel devices that have potential in agri-food safety but as yet have not been applied in this area.

Keywords: Screen-printed carbon, Biosensor, Enzyme, Antibody, Aptamer, Amperometry, Voltammetry, Agri-food safety

Dorothy Koveal, Carlos Manlio, Díaz-García, Gary Yellen (Department of Neurobiology, Harvard Medical School, Boston, MA, USA) Fluorescent Biosensors for Neuronal Metabolism and the Challenges of Quantitation, Current Opinion in Neurobiology, Volume 63 (2020) Pages 111-121

Over the past decade, genetically encoded fluorescent biosensors that report metabolic changes have become valuable tools for understanding brain metabolism. These sensors have been targeted to specific brain regions and cell types in different organisms to track multiple metabolic processes at single cell (and subcellular) resolution. Here, we review genetically encoded biosensors used to study metabolism in the brain. We particularly focus on the principles needed to use these sensors quantitatively while avoiding false inferences from variations in sensor fluorescence that arise from differences in expression level or environmental influences such as pH or temperature.

Keywords: Biosensor

Hiroki Hayashi^a, Naoki Sakamoto^a, Sho Hideshima^b, Yoshitaka Harada^c, Mika Tsuna^c, Shigeki Kuroiwa^b, Keishi Ohashi^b, Toshiyuki Momma^{ab}, Tetsuya Osaka^{ab} (a. Graduate School of Advanced Science and Engineering, Waseda University, 3-4-1 Okubo, Shinjuku, Tokyo 169-8555, Japan, b. Research Organization for Nano & Life Innovation, Waseda University, 513 Waseda-tsurumaki-cho, Shinjuku, Tokyo 162-0041, Japan, c. Food Research Center, Nippon Flour Mills Co., Ltd., 5-1-3 Midorigaoka, Atsugi, Kanagawa 243-0041, Japan) Tetrameric jacalin as a receptor for field effect transistor biosensor to detect secretory IgA in human sweat, Journal of Electroanalytical Chemistry, Volume 873 (2020) 114371

Secretory immunoglobulin A (s-IgA), found in biological fluids, is useful for monitoring condition on mental health to prevent depression. In this study, the non-invasive detection of s-IgA in human sweat was demonstrated using field effect transistor (FET) biosensors modified with a plant lectin, jacalin, as a receptor. The s-IgA molecules were detected with greater sensitivity using the jacalin-immobilized FET biosensors as compared to the sensitivity shown by Fab-immobilized FET biosensors. Jacalin, which is a small lectin tetramer, has four glycan-binding sites and can capture a large number of s-IgA molecules within the charge-detectable region in terms of Debye length. Moreover, the jacalin-immobilized FET biosensor could detect

s-IgA at concentrations ranging from 0.1 µg/mL to 100 µg/mL. Additionally, by using a filtration process to eliminate the interference of other components found in human sweat, our FET sensing system could specifically and quantitatively detect s-IgA. Therefore, our results show the utility of this device in monitoring mental stress.

Keywords: Field effect transistor biosensor, Secretory immunoglobulin A, Jacalin, Human sweat, Mental stress

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Low yield and low titer of natural products are common issues in natural product biosynthesis through microbial cell factories. One effective way to resolve such bottlenecks is to design genetic biosensors to monitor and regulate the biosynthesis of target natural products. In this review, we evaluate the most recent advances in the design of genetic biosensors for natural product biosynthesis in microorganisms. In particular, we examine strategies for selection of genetic parts and construction principles for the design and evaluation of genetic biosensors. We also review the latest applications of transcription factor- and riboswitch-based genetic biosensors in natural product biosynthesis. Lastly, we discuss challenges and solutions in designing genetic biosensors for the biosynthesis of natural products in microorganisms.

Keywords: genetic biosensor, biosynthetic pathway, transcription factor, riboswitch, natural product

Bioengineering

Hongling Zhang^a, Zhifang Zhao^a, Guofeng Ma^b, Lina Sun^a (a. Key Laboratory of Eco-restoration of Regional Contaminated Environment, Ministry of Education, Shenyang University, Shenyang 110044, China, b. Institute of Technical Innovation, Shenyang University, Shenyang 110044, China) **Quantitative evaluation of soil anti-erodibility in riverbank slope remediated with nature-based soil bioengineering in Liaohe River, Northeast China, Ecological Engineering, Volume 151 (2020) 105840**

Soil bioengineering techniques are considered as the cost-effective, nature-friendly, self-repairing and sustainable technique to deal with erosion problems on slopes and enhance riverbank stability, especially for shallow-seated landslides. Research on soil anti-erodibility and stability is one of the keys to understand mechanism of riverbank soil erosion. Three different types of nature-based bioengineering measures were conducted in Liaohe River Protected area and soil erodibility was evaluated in comparison with natural riverbank after four years. On the

basis of soil intrinsic properties, 14 index parameters were selected to evaluate soil anti-erodibility, at the same time, soil shear strength and root dry weight were also used to assess soil stability. Results showed that nature-based bioengineering measures apparently increased riverbank stability by improving soil anti-erodibility and shear strength. Additionally, soil shear strength analysis was in agreement with soil anti-erodibility results, indicating riverbank slope soil stability in descending order were FT (Fiber roll + live stakes slope protection technique) > NT (Nonwoven fabric + live stakes slope protection technique) > CT (Condensed live stakes slope protection technique) > CK (natural riverbank). Furthermore, soil silt and silty clay, aggregate status, organic matter, root system and soil cohesion are the main factors controlling soil erodibility.

Keywords: Nature-based bioengineering measures, Liaohe River Protected area, Soil erodibility, Stability evaluation

Masahiro Yanagiya MD, Kentaro Kitano MD, PhD, Takuma Yotsumoto MD, Hiromichi Asahina PhD, Kazuhiro Nagayama MD, PhD, Jun Nakajima MD, PhD (Department of Thoracic Surgery, The University of Tokyo Graduate School of Medicine, Tokyo, Japan) Transplantation of Bioengineered Lungs Created From Recipient-Derived Cells Into a Large Animal Model, Seminars in Thoracic and Cardiovascular Surgery, Available online 27 April 2020

The use of bioartificial lungs may represent a breakthrough for the treatment of end-stage lung disease. The present study aimed to evaluate the feasibility of transplanting bioengineered lungs created from autologous cells. Porcine decellularized lung scaffolds were seeded with porcine recipient-derived airway and vascular cells. The porcine recipient-derived cells were collected from lung tissue obtained by pulmonary wedge resection. Following culture of autologous cells in the scaffolds, the resulting grafts were unilaterally transplanted into porcine recipients (n = 3). Allograft left unilateral lung transplantation was performed in the control group (n = 3). Left unilateral transplantation of decellularized grafts was also performed in a separate control group (n = 2). In vivo functions were assessed for 2 hours after transplantation. Histologic evaluation and immunostaining showed the presence of airway and vascular cells in the bioengineered lungs. No animals survived in the decellularized transplant group, whereas all animals survived in the bioengineered transplant and allotransplant groups. However, bioengineered lung grafts showed marked bullous changes. The oxygen exchange was comparable between the bioengineered lung graft transplant and allograft transplant groups. However, the carbon dioxide gas exchange of the bioengineered lung graft transplant group was significantly lower than that of the allograft transplant group at 2 hours after transplantation (4.10 ± 0.87 mm Hg vs 24.7 ± 10.1 mm Hg, $P = 0.02$). Transplantation of bioartificial lung grafts created from autologous cells was feasible in the super-acute phase. However, bullous changes and poor carbon dioxide gas exchange remain limitations of this method.

Keywords: Lung regeneration, Thoracic surgery, Lung transplantation

Verónica Guadalupe Lira-Caballero^a, Mario Roberto Martínez-Menez^a, Angélica Romero-Manzanares^b, Edmundo García-Moya^b, José Donald Ríos-Berber^a, Erasmo Rubio-Granados^a (a. Department of Hydrosciences, Postgraduate College, 56264 Montecillo, Texcoco, Mexico, b. Department of Botany, Postgraduate College, 56264 Montecillo, Texcoco, Mexico) Morphometry of gullies and bioengineering for sediment retention in the

**Mixteca Region of Oaxaca, Mexico, Ecohydrology & Hydrobiology, Volume 20 (2020)
Pages 289-300**

Bioengineering is a technical option which uses selected biological elements to retain soil and rehabilitate areas with gullies. With this aim, bioengineering practices were implemented to recover areas affected by gully erosion in a micro-watershed located in the Mixteca, an important region in the Mexican state of Oaxaca. The restoration plan was to rehabilitate an old stone check dam located in the lower part of the watershed and the establishment of live barriers with *Erytrina americana* Miller, upstream in the main gullies contributing to the drainage system. To assess the morphometry of the micro-watershed, a digital elevation model was generated by a drone. To assess the efficiency of rehabilitation practices, the volume of sediments retained by the structures was quantified by topographic surveys. Results show that the live barriers combined with the check dam retained as sediments weight 1,304.99 Mg. As the micro-watershed area is 37.06 hectares, without bioengineering structures, the specific degradation would have reached 35.27 Mg ha⁻¹y⁻¹. Thus, sediments retention obtained with the bioengineering system has proven to be efficient in decreasing waterflow speed and initiating the rehabilitation of gullied lands.

Keywords: Live barriers, Bioengineering, Gullies, Specific degradation, Sediments

Shanglin Chen^{ab}, Meng-Hsuan Hsieh^c, Shu-Hong Li^b, Jun Wu^b, Richard D. Weisel^{bd}, Yen Chang^e, Hsing-Wen Sung^c, Ren-Ke Li^{bd} (a. Department of Cardiac Surgery, Fuwai Hospital, National Center for Cardiovascular Diseases, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China, b. Toronto General Hospital Research Institute, Division of Cardiovascular Surgery, University Health Network, Toronto, Canada, c. Department of Chemical Engineering and Frontier Research Center on Fundamental and Applied Sciences of Matters, National Tsing Hua University, Hsinchu, Taiwan, ROC, d. Division of Cardiac Surgery, Department of Surgery, University of Toronto, Toronto, Canada, e. Taipei Tzu Chi Hospital, Buddhist Tzu Chi Medical Foundation and School of Medicine, Tzu Chi University, Hualien, Taiwan, ROC) **A conductive cell-delivery construct as a bioengineered patch that can improve electrical propagation and synchronize cardiomyocyte contraction for heart repair, Journal of Controlled Release, Volume 320 (2020) Pages 73-82**

Cardiac tissue engineering is of particular importance in the combination of contracting cells with a biomaterial scaffold, which serves as a cell-delivery construct, to replace cardiomyocytes (CMs) that are lost as a result of an infarction, to restore heart function. However, most biomaterial scaffolds are nonconductive and may delay regional conduction, potentially causing arrhythmias. In this study, a conductive CM-delivery construct that consists of a gelatin-based gelfoam that is conjugated with a self-doped conductive polymer (poly-3-amino-4-methoxybenzoic acid, PAMB) is proposed as a cardiac patch (PAMB-Gel patch) to repair an infarcted heart. A nonconductive plain gelfoam (Gel patch) is used as a control. The electrical conductivity of the PAMB-Gel patch is approximately 30 times higher than that of the Gel patch; as a result, the conductive PAMB-Gel patch can substantially increase electrical conduction between distinct clusters of beating CMs, facilitating their synchronous contraction. In vivo epicardial implantation of the PAMB-Gel patch that is seeded with CMs (the bioengineered

patch) in infarcted rat hearts can significantly enhance electrical activity in the fibrotic tissue, improving electrical impulse propagation and synchronizing CM contraction across the scar region, markedly reducing its susceptibility to cardiac arrhythmias. Echocardiography shows that the bioengineered conductive patch has an important role in the restoration of cardiac function, perhaps owing to the synergistic effects of its conductive construct and the synchronously beating CMs. These experimental results reveal that the as-proposed bioengineered conductive patch has great potential for repairing injured cardiac tissues.

Keywords: Myocardial infarction, Cardiac arrhythmia, Conductive polymer, Electrical impulse propagation, Cardiomyocyte synchronization

Xufeng Xue¹, Ryan P.Wang², Jianping Fu¹³⁴ (1. Department of Mechanical Engineering, University of Michigan, Ann Arbor, MI, USA, 2. Greenhills School, Ann Arbor, MI, USA, 3. Department of Biomedical Engineering, University of Michigan, Ann Arbor, MI, USA, 4. Department of Cell and Developmental Biology, University of Michigan Medical School, Ann Arbor, MI, USA) **Modeling of human neurulation using bioengineered pluripotent stem cell culture, Current Opinion in Biomedical Engineering, Volume 13 (2020) Pages 127-133**

Leveraging the developmental potential and self-organizing property of human pluripotent stem cells, researchers have developed tractable models of human embryonic development. Owing to their compatibility to live imaging, genome editing, mechanical perturbation and measurement, these models offer promising quantitative experimental platforms to advance human embryology and regenerative medicine. Herein, we provide a review of recent progress in using human pluripotent stem cells to generate models of early human neural development or neurulation, including neural induction and regional patterning of the neural tube. These models, even in their nascent developmental stages, have already revealed intricate cell-cell signaling and mechanoregulation mechanisms likely involved in tissue patterning during early neural development. We also discuss future opportunities in modeling early neural development by incorporating bioengineering tools to control precisely neural tissue morphology and architecture, morphogen dynamics, intracellular signaling events, and cell–cell interactions to further development of this emerging field and expand its applications.

Keywords: Neurulation, Embryonic development, Human pluripotent stem cells, Embryo models

Xiaohua Yu^{abc}, Paulos Y. Mengsteab^{abcd}, Ganesh Narayanan^{abc}, Lakshmi S.Nair^{abcde}, Cato T. Laurencin^{abcdefg} (a. Connecticut Convergence Institute for Translation in Regenerative Engineering, University of Connecticut Health, Farmington, CT 06030, USA, b. Raymond and Beverly Sackler Center for Biological, Physical and Engineering Sciences, University of Connecticut Health, Farmington, CT 06030, USA, c. Department of Orthopedic Surgery, University of Connecticut Health, Farmington, CT 06030, USA, d. Department of Biomedical Engineering, University of Connecticut, Storrs, CT 06269, USA, e. Department of Materials Science and Engineering, University of Connecticut, Storrs, CT 06269, USA, f. Department of Chemical and Biomolecular Engineering, University of Connecticut, Storrs, CT 06269, USA, g. Department of Reconstructive Sciences, University of Connecticut Health, Farmington, CT 06030, USA) **Enhancing the Surface Properties of a Bioengineered**

Anterior Cruciate Ligament Matrix for Use with Point-of-Care Stem Cell Therapy, Engineering, Available online 7 May 2020

We have previously developed a poly(L-lactic) acid (PLLA) bioengineered anterior cruciate ligament (ACL) matrix that has demonstrated enhanced healing when seeded with primary ACL cells prior to implantation in a rabbit model, as compared with the matrix alone. This suggests that improving cell adhesion on the matrix may beneficially affect the healing response and long-term performance of the bioengineered ACL matrix. One regenerative engineering approach involves enhancing the surface properties of the matrix to support cell adhesion and growth in combination with point-of-care stem cell therapy. Herein, we studied the cell adhesion properties of PLLA braided microfiber matrices enhanced through the physical adsorption of fibronectin and air plasma treatment. We evaluated the kinetics and binding efficiency of fibronectin onto matrices at three time points and three fibronectin concentrations. Incubating the matrix for 120 min in a solution of 25 $\mu\text{g}\cdot\text{mL}^{-1}$ fibronectin achieved the greatest binding efficiency to the matrix and cellular adhesion. Exposing the matrices to air plasma treatment for 5 min before fibronectin adsorption significantly enhanced the cell adhesion of rabbit bone marrow-derived mesenchymal stem cells (R-BMMSCs) 24 h post cell seeding. Finally, cellular proliferation was monitored for up to 21 d, the matrices were exposed to air plasma treatment, and fibronectin adsorption was found to result in enhanced cell number. These findings suggest that exposure to air plasma treatment and fibronectin adsorption enhances the cellular adhesion of PLLA braided microfiber matrices and may improve the clinical efficacy of the matrix in combination with point-of-care stem cell therapies.

Keywords: Anterior cruciate ligament, Ligament, Poly (L-lactic) acid plasma treatment, Fibronectin, Stem cells, Adhesion

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Protein nanocompartments (PNCs) are self-assembling biological nanocages that can be harnessed as platforms for a wide range of nanobiotechnology applications. The most widely studied examples of PNCs include virus-like particles, bacterial microcompartments, encapsulin nanocompartments, enzyme-derived nanocages (such as lumazine synthase and the E2 component of the pyruvate dehydrogenase complex), ferritins and ferritin homologues, small heat shock proteins, and vault ribonucleoproteins. Structural PNC shell proteins are stable, biocompatible, and tolerant of both interior and exterior chemical or genetic functionalization for use as vaccines, therapeutic delivery vehicles, medical imaging aids, bioreactors, biological control agents, emulsion stabilizers, or scaffolds for biomimetic materials synthesis. This review

provides an overview of the recent biomedical and bioengineering advances achieved with PNCs with a particular focus on recombinant PNC derivatives.

Keywords: Nanoparticle, Nanocage, Virus-like particle, Bacterial microcompartment, Encapsulin, Lumazine synthase, Ferritin, Small heat shock protein, Vault

Maxime Tisserant^{ab}, Philippe Janssen^c, André Evette^c, Eduardo González^d, Paul Cavaillé^c, Monique Poulin^{ab} (a. Département de Phytologie, Faculté des Sciences de l'Agriculture et de l'Alimentation, Université Laval, 2425 rue de l'Agriculture, Québec G1V 0A6, Canada, b. Québec Centre for Biodiversity Science, Department of Biology, McGill University, Stewart Biology Building, 1205 Dr. Penfield Avenue, Montréal, Québec H3A 1B1, Canada, c. Univ. Grenoble Alpes, INRAE, LESSEM, F-38402 St-Martin-d'Hères, France, d. Department of Biology, Colorado State University, Biology Bldg, 251 W Pitkin St., Fort Collins, CO 80521, USA) **Diversity and succession of riparian plant communities along riverbanks bioengineered for erosion control: a case study in the foothills of the Alps and the Jura Mountains, Ecological Engineering, Volume 152 (2020) 105880**

Soil bioengineering for riverbank stabilization involves the use of living plant materials to treat unstable or eroding riverbanks. These near-natural structures may harbor a higher plant richness and vegetation cover compared to classical civil engineering structures such as ripraps, but little information exists on vegetation dynamics during secondary succession on stabilized riverbanks. We hypothesized that soil bioengineering, by means of active introduction of early successional *Salix* shrubs, can foster successional trajectories of riparian plant communities, unlike civil engineering. We sampled three types of riverbank stabilization structures: pure bioengineering structures, mixed structures (combining riprap and bioengineering techniques) and ripraps, across a 14-year sequence on 42 sites located along 23 different streams running through the foothills of the Alps and the Jura Mountains (France and Switzerland). We quantified species richness and density and compared the temporal patterns of four groups of species that normally appear sequentially in natural succession on riverbanks (ruderal, hygrophilous, shade-tolerant, competitive species), as well as non-native species. Plant community composition differed greatly between ripraps and the two types of bioengineered sites, and ligneous species typical of advanced successional stages (*Cornus sanguinea*, *Corylus avellana*) spontaneously established in the oldest bioengineered sites. In general, richness of total species was higher in stabilization structures using soil bioengineering (including mixed structures) than in riprapped sites. In particular, the number of shade-tolerant and competitive species in bioengineered sites was double that found at ripraps after 14 years. Yet, richness of shade-tolerant species increased over time only on purely bioengineered sites, and their density there was almost twice that in mixed structures. Neither the type of stabilization structure nor time explained the variability in richness and density of non-native species across sites. Our study showed that along streams running through foothills, where erosion processes are usually intense, vegetation of bioengineered riverbanks exhibits successional dynamics similar to those theoretically found in natural conditions. Bioengineering can therefore foster ecological processes while stabilizing eroding riverbanks along foothill streams, thus satisfying human needs for infrastructure protection with less impact on the riparian ecosystem than riprap structures.

Keywords: Bioengineering, Mixed techniques, Ripraps, Riverbank stabilization, Vegetation succession, Willow fascines

Pollen Biotechnology

Saqer S. Alotaibi^a, Samy M. Sayed^b, ManalAlosaimi^a, Raghad Alharthi^a, Aseel Banjar^a, Nosaiba Abdulqader^a, Reem Alhamed^a (a. Biotechnology Department, College of Science, Taif University, Taif, Saudi Arabia, b. Faculty of Agriculture, Cairo University, Giza 12613, Egypt)**Pollen molecular biology: Applications in the forensic palynology and future prospects: A review, Saudi Journal of Biological Sciences, Volume 27 (2020) Pages 1185-1190**

Palynology, which is the study of pollen and spores in an archaeological or geological context, has become a well-established research tool leading to many significant scientific developments. The term palynomorph includes pollen of spermatophytes, spores of fungi, ferns, and bryophytes, as well as other organic-walled microfossils, such as dinoflagellates and acritarches. Advances in plant genomics have had a high impact on the field of forensic botany. Forensic palynology has also been used and applied more recently to criminal investigation in a meaningful way. However, the use of pollen DNA profiling in forensic investigations has yet to be applied. There were earlier uses of dust traces in some forensic analyses that considered pollen as a type of botanical dust debris. Pollen grains can be studied for comparative morphological data, clues to unexpected aspects relating to breeding systems, pollination biology and hybridization. This can provide a better understanding of the entire biology of the group under investigation. Forensic palynology refers to the use of pollen and other spores when it is used as evidence in legal cases to resolve criminal issues by proving or disproving relationships between people and crime scenes. This overview describes the various contributions and the significance of palynology, its applications, different recent approaches and how it could be further employed in solving criminal investigations.

Keywords: Palynology, Forensic, Forensic palynology, Pollen, Spores

Phanthiwa Khongkarat^a, Rico Ramadhan^b, Preecha Phuwapraisirisan^c, Chanpen Chanchao^d (a. Program in Biotechnology, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Bangkok 10330, Thailand, b. Department of Chemistry, Faculty of Science and Technology, Airlangga University, Surabaya 60115, Indonesia, c. Department of Chemistry, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Bangkok 10330, Thailand, d. Department of Biology, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Bangkok 10330, Thailand) **Safflospermidines from the bee pollen of *Helianthus annuus* L. exhibit a higher in vitro antityrosinase activity than kojic acid, Heliyon, Volume 6 (2020) e03638**

Background: Ozone deterioration in the atmosphere has become a severe problem causing overexposure of ultraviolet light, which results in humans in melanin overproduction and can lead to many diseases, such as skin cancer and melasma, as well as undesirable esthetic appearances, such as freckles and hyperpigmentation. Although many compounds inhibit melanin overproduction, some of them are cytotoxic, unstable, and can cause skin irritation. Thus, searching for new natural compounds with antityrosinase activity and less/no side effects is still required. Here, bee pollen derived from sunflower (*Helianthus annuus* L.) was evaluated. Materials and methods

Sunflower bee pollen (SBP) was collected from *Apis mellifera* bees in Lopburi province, Thailand in 2017, extracted by methanol and sequentially partitioned with hexane and dichloromethane (DCM). The *in vitro* antityrosinase activity was evaluated using mushroom tyrosinase and the half maximal inhibitory concentration (IC₅₀) is reported. The antioxidation activity was determined using the 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay and reported as the half maximal effective concentration. Two pure compounds with antityrosinase activity were isolated by silica gel 60 column chromatography (SG60CC) and high performance liquid chromatography (HPLC), and their chemical structure deduced by Nuclear Magnetic Resonance (NMR) analysis.

Results: The DCM partitioned extract of SBP (DCMSBP) had an antityrosinase activity (IC₅₀, 159.4 µg/mL) and was fractionated by SG60CC, providing five fractions (DCMSBP1–5). The DCMSBP5 fraction was the most active (IC₅₀ = 18.8 µg/mL) and further fractionation by HPLC gave two active fractions, revealed by NMR analysis to be safflospermidine A and B. Interestingly, both safflospermidine A and B had a higher antityrosinase activity (IC₅₀ of 13.8 and 31.8 µM, respectively) than kojic acid (IC₅₀ of 44.0 µM). However, fraction DCMSBP5 had no significant antioxidation activity, while fractions DCMSBP1–4 showed a lower antioxidation activity than ascorbic acid.

Conclusion: Safflospermidine A and B are potential natural tyrosinase inhibitors.

Keywords: Biotechnology, Natural product chemistry, Pharmaceutical chemistry, Antityrosinase, *Apis mellifera*, Bee pollen, Purification, Safflospermidine

Fan Yang^{ab}, Tai Wang^{abc}, Lingtong Liu^a (a. Key Laboratory of Plant Molecular Physiology, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China, b. College of Life Science, University of Chinese Academy of Sciences, Beijing 100093, China, c. Innovative Academy of Seed Design, Chinese Academy of Sciences, Beijing 100093, China) Pollen germination is impaired by disruption of a Shaker K⁺ channel OsAKT1.2 in rice, *Journal of Plant Physiology*, Volume 248 (2020) 153140

Potassium homeostasis is essential for pollen development and pollen-pistil interactions during the sexual reproduction of flowering plants. Here, we described the role of a Shaker K⁺ channel, OsAKT1.2, in rice pollen germination and growth. OsAKT1.2 is specifically expressed in the tricellular pollen, mature pollen grains and growing pollen tubes. Using CRISPR gene editing, we found that knockout lines did not differ from wildtype in vegetative growth, but showed decreased pollen germination rate both in the germination medium and *in vivo*. OsAKT1.2-GFP fusion protein was localized in the plasma membrane and enriched at the pollen tube tip. OsAKT1.2 could complement the yeast strain which is deficient in K⁺ intake. These findings suggest that OsAKT1.2 is associated with pollen germination and tube elongation in rice.

Keywords: K⁺ channel, OsAKT1.2, Potassium, Rice, Pollen germination

Mohammad Saleem Wani^a, Maroof Hamid^b, Younas Rasheed Tantray^a, Raghubir Chand Gupta^a, A.H.Munshi^c, Vijay Singh^a (a. Department of Botany, Punjabi University, Patiala, Punjab 147002, India, b. Centre for Biodiversity & Taxonomy, Department of Botany, University of Kashmir, Srinagar 190006, J & K, India, c. Department of Botany, University of Kashmir, Jammu & Kashmir 190006, India) *In vitro* pollen germination of *Betula utilis*, a typical tree line species in Himalayas, *South African Journal of Botany*, Volume 131 (2020) Pages 214-221

The study was conducted to determine the optimum medium for in vitro pollen germination for *B. utilis* based on germination percentages and length of the pollen tube. Studies about pollen germination and tube growth of *B. utilis* are limited. Therefore, this study aimed to investigate the effects of sucrose (1, 3, 5, 10 and 15%), boric acid (25, 50, 100 and 200 ppm), calcium nitrate (50, 100, 200, 300 and 400 ppm), magnesium sulfate (50, 100, 200 and 300 ppm) and potassium nitrate (50, 100 and 200 ppm) and time of incubation on pollen germination and tube growth. Pollen germination rates and tube growth were recorded periodically at 2, 4, 6, and 10 h. The length varied significantly with different concentrations and incubation time. The germination rate and pollen tube length varied significantly with different concentrations and incubation time. Pollen germination was maximal ($98 \pm 6.1\%$) when the germination medium contained 10% sucrose solution supplemented with 100 ppm H_3BO_3 , 300 ppm $\text{Ca}(\text{NO}_3)_2$, 200 ppm MgSO_4 and 100 ppm KNO_3 , after 6 h of incubation. In addition, results revealed that pollen grains collected immediately after anther dehiscence showed the best germination ability but gradually decreased with time.

Keywords: *Betula utilis*, Pollen grains, Pollen germination, Pollen tube growth

Yi Ren^a, Jiayan Pan^a, Zhike Zhang^a, Jietang Zhao^a, Xinhua He^b, Yonghua Qin^a, Guibing Hu^a (a. State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources/Guangdong Provincial Key Laboratory of Postharvest Science of Fruits and Vegetables/Key Laboratory of South China Horticultural Crop Biology and Germplasm Enhancement, Ministry of Agriculture, College of Horticulture, South China Agricultural University, Guangzhou, China, b. State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, College of Agriculture, Guangxi University, Nanning, China) **Identification of an up-accumulated polyamine oxidase 2 in pollen of self-incompatible ‘Wuzishatangju’ mandarin using comparative proteomic analysis, *Scientia Horticulturae*, Volume 266 (2020) 109279**

Self-incompatibility (SI) is one of the main factors causing seedless fruits in *Citrus*. ‘Wuzishatangju’ (*Citrus reticulata* Blanco) is a natural bud sport from a self-compatible and seedy cultivar ‘Shatangju’. Our previous study showed that gametophytic SI caused seedlessness of ‘Wuzishatangju’. However, it is not clear what factors are responsible for its SI response. In this study, pollen tube growth kinetics was observed in the pistils of ‘Wuzishatangju’ using pollination combination of ‘Wuzishatangju’ (♀) × ‘Wuzishatangju’ (♂) and ‘Wuzishatangju’ (♀) × ‘Shatangju’ (♂). The protein profiles of pollen between ‘Wuzishatangju’ and ‘Shatangju’ were compared by quantitative proteomics analysis based on tandem mass tag technology. Pollen tube from self-pollination of ‘Wuzishatangju’ vigorously germinated in stigma while stopped elongating at the upper site of the style. Pollen from ‘Shatangju’ germinated and pollen tube reached the base of style, suggesting that the mutation plays a role in pollen of ‘Wuzishatangju’. Proteomic analysis indicated that a polyamine oxidase 2 (CrPAO2) was up-accumulated in pollen of ‘Wuzishatangju’ and catalyzed the spermine and spermidine oxidation leading to produce H_2O_2 . The potential roles of CrPAO2 causing SI reaction in ‘Wuzishatangju’ were discussed.

Keywords: Citrus reticulata, Proteomics, Self-incompatibility, Polyamine oxidase, Hydrogen peroxide

Magdalena Węglińska^a, Roman Szostak^a, Agnieszka Kita^b, Agnieszka Nems^b, Sylwester Mazurek^a (a. Department of Chemistry, University of Wrocław, 14 F. Joliot-Curie, 50-383, Wrocław, Poland, b. Department of Food Storage and Technology, Faculty of Biotechnology and Food Science, Wrocław University of Environmental and Life Sciences, 37 Chelmońskiego, 51-630, Wrocław, Poland) **Determination of nutritional parameters of bee pollen by Raman and infrared spectroscopy, Talanta, Volume 212 (2020) 120790**

Vibrational spectroscopy was applied to determine macronutrient levels, total polyphenols (TPs) content, antioxidant activity, pH and color parameters in bee pollens. Raman, attenuated total reflection and diffuse reflectance spectra in the mid- and near-infrared regions were recorded for the homogenized pollen granules. Combining spectral data and the results of reference analyses, partial least squares (PLS) models were constructed and validated. The relative standard errors of prediction (RSEP) were calculated for the calibration and validation sets. Regarding macronutrient analysis, the latter were found to be in the 1.7–2.3%, 2.5–3.6% and 2.6–3.3% ranges for protein, reducing sugars and fat determination, respectively. These errors amounted to 3.1–3.5% for TPs and 2.2–3.4% for antioxidant activity quantification, respectively, whereas they were found to be in the 1.5–2.3% and 1.6–3.2% ranges for pH and the color parameters' determination.

Keywords: Bee pollen, Nutrients, Quantitative analysis, Raman spectroscopy, NIR spectroscopy, IR spectroscopy, Chemometrics

Ya Zhao^a, Yamei Yan^b, Wangting Zhou^a, Dan Chen^a, Kaiyin Huang^a, Shijie Yu^a, Jia Mi^b, Lu Lu^b, Xiaoxiong Zeng^a, Youlong Cao^b (a. College of Food Science and Technology, Nanjing Agricultural University, Nanjing 210095, People's Republic of China, b. National Wolfberry Engineering Research Center, Yinchuan 750002, People's Republic of China) **Effects of polysaccharides from bee collected pollen of Chinese wolfberry on immune response and gut microbiota composition in cyclophosphamide-treated mice, Journal of Functional Foods, Volume 72 (2020) 104057**

The gut microbiota has emerged as an important contributor to the immune system and it is believed to be regulated by dietary fiber. In this study, therefore, the immunomodulatory and gut microbiota modulatory effects of polysaccharides from bee collected pollen of Chinese wolfberry (WBPPS) in cyclophosphamide (CTX)-treated mice were investigated. The results showed that WBPPS could enhance thymus and spleen indices and promote production of immune-related cytokines (IgA, TNF- α , TGF- β 1 and IL-10) in serum of CTX-treated mice. In addition, WBPPS could significantly improve hepatic function and oxidative stress in CTX-treated mice via increasing the levels of GSH, SOD and CAT and decreasing the levels of ALT and MDA. More importantly, WBPPS remarkably increased the relative abundances of Family_XIII, Ruminococcaceae and Saccharimonadaceae while decreased the relative abundances of Tannerellaceae, Marinifilaceae and Rikenellaceae, which were closely associated with immune traits. Overall, WBPPS might be developed as a promising immunomodulator in functional foods.

Keywords: Bee collected pollen, Chinese wolfberry, Polysaccharide, Gut microbiota, Immunoregulation

Hushuai Nie, Cheng Cheng, Jinping Hua (Laboratory of Cotton Genetics, Genomics and Breeding, Key Laboratory of Crop Heterosis and Utilization of Ministry of Education, Beijing Key Laboratory of Crop Genetic Improvement, College of Agronomy and Biotechnology; China Agricultural University, No. 2, Yuanmingyuan West Rd, Haidian District, Beijing 100193, PR China) Mitochondrial proteomic analysis reveals that proteins relate to oxidoreductase activity play a central role in pollen fertility in cotton, Journal of Proteomics, Volume 225 (2020) 103861

otton (*Gossypium hirsutum* L.) is an important economic crop. Cytoplasm male sterility (CMS) has been used to develop hybrid system and to produce hybrid seeds in cotton, but the molecular mechanism of CMS remains unclear. Mitochondria are semi-autonomous organelles, which play an important role in the reproduction of flowering plants. Male sterility has been proved associated with mitochondrial dysfunction in plants. In present study, a new strategy of proteomic sequencing data-independent acquisition (DIA) was used to analysis protein abundance across CMS lines 2074A (cytoplasm of *Gossypium harknessii*, D2-2) and 2074S (cytoplasm of *G. hirsutum*, AD1), and their maintainer 2074B. Comparing with transcriptome results showed that there is little consistence between proteome and transcriptome. A total of 2095 protein species were identified in three materials, and 186 and 161 differentially proteins were detected in the comparisons of 2074A vs 2074B, and 2074S vs 2074B, respectively. Among them, 49 and 50 proteins were specific existed in anther, and mainly participated in oxidoreductase activity, carbohydrate metabolism, fatty acid metabolism, cell aging, wax or cutin deposition and signal transduction. Gh_A07G0770 and Gh_D05G1908 were specific up-regulated in sterility lines, and the other genes Gh_D08G1196, Gh_D12G1971, Gh_A11G1250, Gh_D08G0388 were down-regulated, which presented similar expression tendency verified by qRT-PCR, transcriptome and proteome results. These six genes related to lipid synthesis, response to oxidative stress and cell aging, suggested them being involved in CMS occurrence. Using virus-induced gene silencing (VIGS) system, sterility obtained demonstrated the silencing Gh_A11G1250 in maintainer 2074B led to partial anthers abortion. Gh_A11G1250 encoded a mitochondrial localization of peroxisomal-like protein, participated in response to reactive oxygen species (ROS). Twenty-two proteins interacting with Gh_A11G1250 mainly related to chlorophyll biosynthetic process, photoperiodism and flowering, which showed different expression pattern between the male sterile line 2074A and maintainer 2074B. This novel research based on mitochondrial proteomics comparison confirmed that DAPs related to oxidative stress are critical to pollen abortion.

Biological significance: Cytoplasm male sterility (CMS) system is utilized widely for hybrid production in cotton. However, the genetic and molecular mechanisms of CMS still need to be further elucidated. Up till now, fewer comprehensive comparisons of the mitochondrial proteomes from cotton CMS line and maintainer line have been reported. In this study, we performed a novel comparison of mitochondrial protein profiles in two CMS lines and their common maintainer line. Based on our results, we found a potential protein related to oxidative stress led to the anthers abortion. These results accumulate data to interpret the molecular mechanisms of CMS in cotton.

Keywords: Cytoplasm male sterility (CMS), Mitochondrion proteomics, Oxidative stress, Reactive oxygen species (ROS), Virus-induced gene silencing (VIGS), Upland cotton

Biotechnology Policy Issue

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Assessment of factors affecting innovation policy in biotechnology, Journal of Innovation & Knowledge, Volume 5, Issue 3, (July–September 2020) Pages 180-190

Nearly three decades have passed since the new knowledge and technologies like genetics and biotechnology have emerged. By passing through various periods in which labor force, resources and capital, each one at a certain time, have been comparative and competitive advantages for a more powerful economy, biotechnology is one of the advanced technologies that countries are investing in, in order to achieve sustainable development in the current century. The capabilities of this knowledge are the creation of fundamental and gradual innovations, in addition to the several applications that generate wealth for countries. For this purpose, innovation policies in biotechnology have been addressed here. This study draws on the resource based theory and examines the research development policies, international-corporate collaboration policies and government supportive innovation policies. The statistical population of this study consisted of 165 responses from the directors and experts active in the field of biotechnology industry in Iran (pharmaceutical, food and agriculture). Research hypotheses were tested using SMART PLS software. The results of the research revealed that research development policies, international corporate collaboration policies and government supportive innovation policies have a significant impact on the development of biotechnology innovation activities. In addition, we have discussed the implications of the study as well as given some future directions.

Keywords: Biotechnology, Innovation, Innovation policy, Government support

Agricultural Biotechnology

Ricardo Pelai, Shannon M. Hagerman, Robert Kozak (Faculty of Forestry, University of British Columbia, Canada)
Biotechnologies in agriculture and forestry: Governance insights from a comparative systematic review of barriers and recommendations, Forest Policy and Economics, Volume 117 (August 2020) 102191

The application of biotechnological innovations has increased in agriculture and forestry over the past two decades. Numerous benefits of biotechnologies are documented; however, implementation is controversial and continues to face technical, biophysical and societal barriers. The longer history of agricultural biotechnology holds potential lessons for emerging proposals in forestry, and vice versa. Using a systematic review and content analysis of the scholarly literature in agriculture and forestry (235 articles) between 1989 and 2017, we compare these two sectors in terms of justifications for the use of biotechnologies, barriers to and recommendations for implementation, and types of evidence considered. The primary benefit of biotechnologies identified in the agricultural literature is food security, whereas forest

productivity and adaptation to climate change are the most common motivating justifications in a forest context. We find a relatively greater emphasis in the forestry literature on regulatory and legal barriers. Both fields emphasize recommendations to address barriers related to lack of knowledge and governance processes despite relatively less emphasis on these items as identified barriers. Relatively few (32%) forestry articles were informed by insights from the social sciences and humanities as compared with 51% of those in agriculture. We discuss the implications of anticipated public opposition to tree biotechnology and associated perceptions of risk unique to trees. We also discuss biotechnology governance dilemmas within an “upstream” approach, highlighting the need for meaningful ways of involving stakeholders, rights holders and different publics at the earliest possible stage of the implementation of biotechnologies.

Keywords: Biotechnology governance, Risk governance, Systematic review, Innovation governance

Heiko Rischer, Géza R Szilvay, Kirsi-Marja, Oksman-Caldentey (VTT Technical Research Centre of Finland Ltd., FI-02044 VTT, Espoo, Finland) Cellular agriculture — industrial biotechnology for food and materials, Cellular agriculture — industrial biotechnology for food and materials, Current Opinion in Biotechnology, Volume 61 (February 2020) Pages 128-134

Fundamental changes of agriculture and food production are inevitable. Providing food for an increasing population will be a great challenge that coincides with the pressure to reduce negative environmental impacts of conventional agriculture. Biotechnological manufacturing of acellular products for food and materials has already been piloted but the full profit of cellular agriculture is just beginning to emerge. Cultured meat is a promising technology for animal-based proteins but still needs further development. The concept of plant cells as food offers a very attractive alternative to obtain healthy, protein-rich and nutritionally balanced food raw material. Moreover, cultured microbes can be processed into a wide range of biosynthetic materials. A better control over structural properties will be increasingly important in all cultured cell applications.

Keywords: Animal cells, Plant cells, Microbial cells

Liliana Aguilar-Marcelino¹, Pedro Mendoza-de-Gives¹, Laith Khalil Tawfeeq Al-Ani²³, María Eugenia López-Arellano¹, Olga Gómez-Rodríguez⁴, Edgar Villar-Luna⁵, David Emmanuel Reyes-Guerrero¹ (1. Centro Nacional de Investigación Disciplinaria en Salud Animal e Inocuidad, INIFAP, Jiutepec, Mexico, 2. Department of Plant Protection, College of Agriculture, University of Baghdad, Baghdad, Iraq, 3. School of Biology Science, Universiti Sains Malaysia, 11800 Minden, Pulau Pinang, Malaysia, 4. Fitopatología, Colegio de Postgraduados, Texcoco, Mexico. 5. CONACYT-Instituto Politécnico Nacional, CIIDIR-IPN, Unidad Michoacán, Jiquilpan, Mexico.) Chapter 26 - Using molecular techniques applied to beneficial microorganisms as biotechnological tools for controlling agricultural plant pathogens and pest, Molecular Aspects of Plant Beneficial Microbes in Agriculture (2020) Pages 333-349

In this chapter we present an overview of the use of molecular techniques applied to beneficial microorganisms as biotechnological tools for the control of pathogens and pests of agricultural plants. The content of the chapter addresses issues such as: agricultural pests, diversity of pests that affect economically important media: viruses, bacteria, fungi, nematodes, protozoa, mites, and insects. The biological methods are based in use the natural enemies. On the other hand, we the use of the biological control method to reduce pests in agriculture, the study of different natural enemies and attacks against pests such as bacteria, fungi and nematodes. Respect to the molecular techniques chapter also highlights techniques such as: RACE-PCR, RT-PCR, cloning of genes, nested PCR and qPCR or Real-time PCR. The omics products show great efficacy in the detection of the metabolome and the expressome of several biological control agents, such as *Trichoderma* spp. and other microorganisms.

Keywords: Biological control, Omics, Natural enemies, Plant pathogens, Pest, *Trichoderma*

Chiara Forti^a, Carla Gualtieri^a, Andrea Pagano^a, Susana de Sousa Araújo^b, Alma Balestrazzi^a, Anca Macovei^a (a. Department of Biology and Biotechnology “L. Spallanzani”, University of Pavia, Pavia, Italy, b. Institute of Chemical and Biological Technology António Xavier, New University of Lisbon (ITQB-NOVA), Oeiras, Portugal) Chapter 5 - Genome editing in the context of seed research: How these novel biotechnology tools can change the future face of agricultural crop development, *Advancement in Crop Improvement Techniques* (2020) Pages 77-88

Considering the major challenges in agricultural research such as the need to increase productivity and the quality of cultivated species under environmental constraints to feed the ever-growing population of the planet, genome editing has the powerful potential to accelerate crop improvement. Within this context, genome editing is perceived as an effective and precise tool to modify plant genomes and improve their quality. Crop performance is strongly dependent on seed quality traits. Moreover, seeds can be considered as common denominators to address both plant productivity and improved human nutrition. In this chapter, we intend to take into account the application of genome editing techniques focusing on seed quality traits, including aspects related to seed vigor, dormancy, germination, and features covering seed nutritional/biochemical composition to address current and future crop improvements.

Keywords: Agriculture, Biotechnology, Genome editing, Nutrition, Seeds

Kusam Lata Rana^a, Divjot Kour^a, Ajar Nath Yadav^a, Neelam Yadav^b, Anil Kumar Saxena^c (a. Department of Biotechnology, Akal College of Agriculture, Eternal University, Baru Sahib, India, b. Gopi Nath P.G. College, Veer Bahadur Singh Purvanchal University, Jaunpur, India, c. ICAR-National Bureau of Agriculturally Important Microorganisms, Kusmaur, India) Chapter 16 - Agriculturally important microbial biofilms: Biodiversity, ecological significances, and biotechnological applications, *New and Future Developments in Microbial Biotechnology and Bioengineering: Microbial Biofilms, Current Research and Future Trends in Microbial Biofilms* (2020) Pages 221-265

A biofilm is an assemblage, aggregation, or community of microbial cells bounded by a polymeric matrix comprising polysaccharides that are associated with an inert or biotic surface. Biofilm formation is a universal trait, exhibited by microbes, when growing attached to natural and artificial surfaces. Microbial biofilms are an attractive subject, due to their important roles in

the different sectors including agriculture, environment, industry, and health. Biofilms in agriculture have acquired interest due to their immense possibilities in crop production, protection, and improvement through their role in colonization of surface soils, roots/shoots of plants, and enabling proliferation in the desired niche, as well as enhancing soil fertility. Biofilm-forming microbes have been reported worldwide and they belong to Gram-positive, Gram-negative species, cyanobacteria, archaea, fungi, and microalgae. The microbial biofilm formation has been reported by all three domain systems of archaea, bacteria, and eukarya of different phylum including Actinobacteria, Ascomycota, Bacteroidetes, Basidiomycota, Chloroflexi, Crenarchaeota, Cyanobacteria, Euryarchaeota, Firmicutes, Oomycetes, and Proteobacteria. The most dominant genera involve in biofilms formation belong to *Agrobacterium*, *Anabaena*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Bradyrhizobium*, *Burkholderia*, *Gluconacetobacter*, *Paenibacillus*, *Pseudomonas*, *Rhizobium*, *Trichoderma*, *Xanthomonas*, and *Xylella*. The agriculturally-important microbial communities and their interactions can have several implications on climate change, plant nutrition, plant protection, biofertilization, and bioremediation for sustainable agriculture and environments. This chapter deals with the fundamental aspects of biofilms, mechanisms of formation, the genes that are involved, biodiversity, and biotechnological applications in agriculture, industry, environmental studies, and allied sectors.

Keywords: Agriculturally important microbial biofilms, Biodiversity, EPS, Plant growth promotion, Soil fertility, Sustainable agriculture

Neal Gutterson PhD (Corteva Agrisciences, Johnston, Iowa, United States) Chapter 27 - Commercialization and Applications of Agricultural Biotechnology, Biotechnology Entrepreneurship (Second Edition), Leading, Managing and Commercializing Innovative Technologies (2020) Pages 385-398

The agricultural biotechnology sector (Ag Biotech) shares a common scientific foundation with the therapeutic biotechnology sector, including similar characteristics of a lengthy time to market for emerging products. But the challenges, goals, and opportunities for agricultural applications of biotechnology provide a very different context for innovation and entrepreneurs. Now just 35 years old, we are witnessing a blossoming of biotechnology applications to both crops and microbes. The “conventional” agricultural trait segment continues to focus on two product categories, herbicide tolerance and insect resistance. The advent of CRISPR–Cas technology for genome editing is in its infancy still, but it holds significant promise. However, Ag Biotech applications to chemistries, biopesticides, microbials, and natural products offer increasingly valuable opportunities, based on a combination of market demand for “greener” solutions, and the reduced time to market. These sectors offer new business opportunities that, such as the first wave of Ag Biotech, enable entrepreneurs to think about creating disruptive businesses, not just disruptive technologies for today’s business models, including the application of biotechnology tools to data generation that offer farmer insights.

Keywords: Biotech traits, seeds, herbicide tolerance, insect resistance, crop protection, intellectual property, biologicals, AgBio, Ag Biotech, regulatory approval, innovation, business model

Bioenergy

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To meet the demands for resources, food and energy, especially in fast developing countries in the Global South, new infrastructure investments, technologies and supply chains are required. It is essential to manage a transition that minimises the impacts on global environmental degradation while benefits local socio-economic development. Food-bioenergy integration optimising natural capital resources and considering wider environmental and socio-economic sustainability offers a way forward. This study presents an integrative approach enabling whole systems modelling to address the interlinkage and interaction of resource-food-bioenergy systems and optimise supply chains considering poly-centric decision spaces. Life cycle sustainability assessment, optimisation, agent-based modelling and simulation were coupled to build an integrated systems modelling framework applicable to the resource-food-bioenergy nexus. The model building blocks are described before their applications in three case studies addressing agricultural residues and macro-fungi in the Philippines, sugar cane biorefineries in South Africa, and Nipa palm biofuel in Thailand. Our case studies revealed the great potential of untapped biomass including agricultural waste and non-food biomass grown on marginal lands. Two value chain integration case studies – i.e. straw-fungi-energy in Philippines and sugar-energy in Africa – have been suggested as sustainable solutions to recover waste as value-added products to meet food and energy security. Case studies highlight how an integrative modelling framework can be applied to address multi-level questions, taking into account decision-making at different levels, which contribute to an overall sustainability goal.

Keywords: Agent-based modelling, Optimisation, Bioenergy supply chain, LCA, Nipa palm, Fungi

Fabício Rodrigues Costa^a, Carlos Antonio Alvares Soares Ribeiro^a, Gustavo Eduardo Marcatti^a, Alexandre Simões Lorenzon^a, Thaisa Ribeiro Teixeira^a, Getulio Fonseca Domingues^a, Nero Lemos Martins de Castro^a, Alexandre Rosa dos Santos^b, Vicente Paulo Soares^a, Sady Júnior Martins da Costa de Menezes^c, Pedro Henrique Santos Mota^a, Lucas Arthur de Almeida Telles^a, José Romário de Carvalho^b (a. Federal University of Viçosa/UFV, 36570-000, Viçosa, MG, Brazil, b. Federal University of Espírito Santo/UFES, Department of Rural Engineering, 29500-000, Alegre, ES, Brazil, c. Federal University Rural of Rio de Janeiro – Instituto Três Rios, Department of Environmental Sciences, 25802-100, Três Rios, RJ, Brazil) **GIS applied to location of bioenergy plants in tropical agricultural areas, Renewable Energy, Volume 153, (June 2020) Pages 911-918**

This study aimed to develop an optimal set and size model of bioenergy facilities using a GIS framework. Data from sugarcane plantations were used to create case scenarios. Spatial analysis was accomplished by applying a two-phase approach: identification of suitable zones to locate

bioenergy facilities and identification of ideal areas. These analyses led to a location-allocation model, using Maximize Capacitated Coverage option, in order to assign sugarcane supply areas to potential bioenergy facilities. Nine themes, as well their respective weights, generated by AHP, were used to create a visual depiction of potential sites. This layer was reclassified into five categories, using Natural Breaks (Jenks) method. Various scenarios of bioenergy plants installation were simulated. Around 50% of the area is unsuitable for bioenergy plants. A total of 1,737 potential sites were detected for implanting bioenergy plants. The best regions to locate bioenergy plants were peripheral areas. Cumulative biomass transportation distances dramatically reduce as the number of facilities increases. There is a reduction of 31% in total and average distances when comparing a 4-plant scenario with a single plant scenario. Proposed scenarios can support decision making with different numbers of bioenergy plants. Proposed methodology can be adapted to areas of other countries.

Keywords: Geotechnology, Spatial analysis, Multi-criteria analysis

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The Canadian province of British Columbia (BC) provides an informative case study of bioenergy development, because it relies heavily on fossil fuels but has enormous bioenergy potential. We have examined the potential contribution of bioenergy to reducing BC's GHG emissions. The approach of combining life cycle assessment and economic evaluation to prioritize options should be applicable generally. Biomass availability, including forestry resources, agricultural waste and municipal solid waste, is estimated. Through simplified Life Cycle Assessment, GHG reduction potential of biogas, bioethanol, biofuels from hydrothermal liquefaction, and district heating are quantified, along with the associated GHG reduction costs. The analysis shows that existing biomass resources could yield 110–176 PJ per year, reducing GHG emissions by 13.0–15.7%. Bioenergy from waste streams is already cost-effective and should be prioritized in the short term. However, bioenergy from forestry resources, especially conversion to liquid biofuels, is prohibitively expensive, with GHG reduction cost exceeding CAD \$300/t CO₂-eq. The total extra cost required to achieve full utilization of BC's biomass resources is estimated as 0.8–2.4 billion dollars. To close the cost gaps between bioenergy and fossil fuels, both technological improvement and external cost adjustment through measures like carbon taxation will be needed.

Keywords: Bioenergy, Greenhouse gas reduction, Life cycle assessment, Economic assessment, GHG abatement costs

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Resource and Environmental Sustainability and the College of Sustainability, Dalhousie University, 6299 South St., Halifax, Nova Scotia, Canada, c. Department of Resource Economics and Environmental Sociology, University of Alberta, 116 St. & 85 Ave., Edmonton, Alberta, Canada, d. Canadian Council for Aboriginal Business, 2 Berkeley Street, Suite 202, Toronto, Ontario, Canada.) Open for bioenergy business? Perspectives from Indigenous business leaders on biomass development potential in Canada, *Energy Research & Social Science*, Volume 64, (June 2020) 101446

Canada is one of the world's top five energy producers and, within Canada's energy sector, the bioenergy economy is rapidly expanding. This research was conducted to identify perceived risks, barriers, benefits, and opportunities relating to the development of biomass energy by Indigenous business leaders and/or their communities. Eighteen Indigenous business leaders from forestry, energy, and allied natural resource sectors were interviewed to understand their perspectives on bioenergy. Results included that views on bioenergy feasibility differed between business leaders in northern versus southern Canada. There was no agreement among business leaders as to risks and benefits (neutral, positive, negative) for Indigenous businesses and communities engaging in bioenergy initiatives. Many of the benefits of bioenergy were related by participants to opportunities for increasing community self-reliance and increasing connectedness to Canadian mainstream economic and governance systems. Indigenous-led policy interventions are especially important in new industries like bioenergy in the boreal where Indigenous traditional territories, communities and businesses intersect and thus are likely to be impacted by new developments and partnerships.

Keywords: Bioeconomy, Bioenergy, Indigenous development, Partnership, Renewable energy, Canada

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Transition towards renewable low carbon energy is a fundamental element of climate change mitigation, energy from biomass technologies are targeted within many country's decarbonisation strategies. Decision makers globally face many challenges developing strategies to drive this transition; models are increasingly used to road-test policy interventions before their implemented. A Bioenergy Literature Database was developed of 124,285 papers published 2000–2018. These document an exponential rise in research focusing on biomass and bioenergy. On average 35.4% of papers apply modelling analyses, 99.5% of these use bespoke models rather than high profile Integrated Assessment Models (IAMs) or Energy System Models – although it is these high profile models that are widely used in policy development. A review of the role of bioenergy within energy models is undertaken with a key objective of critiquing their performances in analysing bioenergy research questions. IAMs are found to be widely applied to investigate the impact of bioenergy within wider energy and environmental systems, e.g. for reducing emissions. Energy System Models focus on bioenergy processes, technologies and

feedstocks, although don't capture wider environmental, economic and social themes. Specialist Bioenergy Models offer methods for bespoke analyses of all bioenergy issues, their narrow system boundaries generate targeted outputs but wider effects such as land-use change may not be captured. Caution is required when interpreting modelling outputs, particularly when used to inform policy. It's not feasible to develop all-encompassing bioenergy models covering all nuances between systems, but there is strong argument for using multiple models in parallel to build robust overall conclusions.

Keywords: Bioenergy, Models, Energy system models, Integrated assessment models, Policy development, Review

Michael Hoel (Department of Economics, University of Oslo, P.O. Box 1095, Blindern, N-0317, Oslo, Norway) The rise and fall of bioenergy, Journal of Environmental Economics and Management, Volume 101 (May 2020) 102314

If bioenergy has a less negative impact on the climate than fossil energy, it may be optimal to have a significant increase in the use of bioenergy over time. Due to the difference in the way the climate is affected by the two types of energy, the future time path of the use of bioenergy may be non-monotonic: It may be optimal to first have an increase in its use, and later a reduction. Optimal taxes/subsidies are derived both for the first-best case and for the case of a constraint on the size of the fossil tax.

Keywords: Bioenergy, Renewable energy, Climate policy, Carbon tax, Second best, Subsidies

Muhammad Mansur Abdulwakil, Abdul Samad Abdul-Rahim, Mohd Alsaleh (Department of Economics, Faculty of Economics and Management, Universiti Putra Malaysia, 43400, Serdang, Selangor, Malaysia) Bioenergy efficiency change and its determinants in EU-28 region: Evidence using Least Square Dummy Variable corrected estimation, Biomass and Bioenergy, Volume 137 (June 2020) 105569

Applying the data envelopment approach, this paper computes efficiency change (EFFCH) in terms of its components: pure technical and scale efficiency changes. The least squares dummy variable corrected (LSDVC) method was employed to examine the determinants of efficiency change of bioenergy industry of the EU28 countries covering the period 1990–2013. Results show that the bioenergy industry recorded an average annual rate of progress in efficiency change of 3.8% during the period studied. Interestingly, the region recorded a technical progress with both pure technical efficiency change and scale efficiency change increasing over the study period, however, scale efficiency was the major contributor to efficiency with annual increase of 4.5%. We also found variations in regional performance with EU developing region experiencing a slightly higher increase in efficiency at 3.86% while this figure is at 3.76% for the EU developed countries. Empirical finding show that economic growth, gross fixed capital formation, inflation and size of biomass input affected EFFCH of bioenergy industry of the EU28 region significantly during the period studied. Policy implications of these results are that the bioenergy industry should relentlessly pursue technical progress and aim to improve both technical and scale efficiencies simultaneously through optimal allocation of resources.

Keywords: Efficiency change, Pure technical efficiency change, Scale efficiency change, Bioenergy industry, Non parametric approach, Biased corrected least squares dummy variables

Leila Ahmadi, Miyuru Kannangara, Farid Bensebaa (National Research Council, Canada, 1200 Montréal Road, Ottawa, ON, Canada) Cost-effectiveness of small scale biomass supply chain and bioenergy production systems in carbon credit markets: A life cycle perspective, Sustainable Energy Technologies and Assessments, Volume 37 (February 2020) 100627

Numerous tools and policies are being developed to promote and incentivize the development and deployment of clean fuel technologies. Carbon emission trading is known as one of the most effective market-based tools to control the generation of carbon emissions. Evaluating the best scenarios to deploy, clean energy solutions must include technology, supply chain, carbon emission and investments analyses. There is still a debate about the feasibility and sustainability of bioenergy scenarios for the different markets. Adapting life cycle assessment (LCA) and techno-economic analysis (TEA) tools, this study compared the cost-effectiveness of four bio-based energy generation pathways with a diesel-based power generation as the baseline scenario within the context of Canadian remote and rural communities. This analysis provides a ranking of these bioenergy pathways and highlights the potential carbon offsets and credits of the bio-based pathways in comparison with the baseline scenario. Additional tools including multi-criteria decision making (MCDM) are required to provide a complete decision-making platform.

Keywords: Carbon credits, Emissions trading, Life cycle assessment (LCA), Techno-economic analysis (TEA), Bioenergy production, Wood feedstock, Combined heat and power (CHP)

Nano Biotechnology

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Fe³⁺ reduction coupled to nitrification and Fe²⁺ oxidation coupled to denitrification, occurring in anoxic sediments of aquatic ecosystems, play an important role in global nitrogen cycle. Till date, limited research was done in applying this phenomenon to wastewater treatment. In this study, we fabricated and evaluated an anoxic up-flow packed bed continuous reactor that mimics the Fe redox cycle coupled to microbial mediated simultaneous removal of NH₄⁺-N and COD. The process was initially developed using synthetic wastewater and was later applied to treat low C/N secondary treated wastewater generated from a conventional sewage treatment plant in Chennai, India. Studies were carried out for 500 days to evaluate the performance of the novel process using laboratory synthesized Granulated Nanoscale Oxyhydroxides of Fe (GNOF) as electron acceptor in a 3.92 L capacity anoxic up-flow packed bed reactor. The reactor was operated at different loading rates by varying the Hydraulic Retention Time (HRT) between 24 h and 4 h. Enhanced removals of NH₄⁺-N (93.20 ± 2.37 %), TN (86.45 ± 6.04 %), and COD (66.47 ± 13.90 %) were attained at 12 h HRT as a result of co-existence of ammonia oxidizing bacteria, denitrifiers, and anammox species. Enhanced performance was obtained by evolving

anammox in a gradient of $\text{NH}_4^{+}\text{-N}$ and $\text{NO}_2^{-}\text{-N}$ in the reactor. This work demonstrates the use of GNOF for the first time in continuous packed bed reactor for the anoxic removal of $\text{NH}_4^{+}\text{-N}$ and COD from secondary treated wastewater. This process holds economic advantages compared to other biological nitrogen removal techniques: (i) as the requirement of oxygen is substituted by GNOF, (ii) occurrence of simultaneous nitrification and denitrification in the single reactor maintains the pH and hence alkalinity addition is not required, and (iii) sludge disposal costs are less. The recycling of GNOF inside the reactor makes this process more sustainable and suitable for practical applications.

Keywords: Anoxic, Up-flow packed bed reactor, Low C/N secondary treated wastewater, Simultaneous nitrification-denitrification, Granulated nanoscale oxyhydroxides of Fe

Biomimicry

Shimin Liu^a, Jinsong Bao^a, Yuqian Lu^b, Jie Li^a, Shanyu Lu^a, Xuemin Sun^a (a. College of Mechanical Engineering, Donghua University, Shanghai, China, b. Department of Mechanical Engineering, The University of Auckland, New Zealand) **Digital twin modeling method based on biomimicry for machining aerospace components, Journal of Manufacturing Systems, Available online 14 May 2020**

High-performance aerospace component manufacturing requires stringent in-process geometrical and performance-based quality control. Real-time observation, understanding and control of machining processes are integral to optimizing the machining strategies of aerospace component manufacturing. Digital Twin can be used to model, monitor and control the machining process by fusing multi-dimensional in-context machining process data, such as changes in geometry, material properties and machining parameters. However, there is a lack of systematic and efficient Digital Twin modeling method that can adaptively develop high-fidelity multi-scale and multi-dimensional Digital Twins of machining processes. Aiming at addressing this challenge, we proposed a Digital Twin modeling method based on biomimicry principles that can adaptively construct a multi-physics digital twin of the machining process. With this approach, we developed multiple Digital Twin sub-models, e.g., geometry model, behavior model and process model. These Digital Twin sub-models can interact with each other and compose an integrated true representation of the physical machining process. To demonstrate the effectiveness of the proposed biomimicry-based Digital Twin modeling method, we tested the method in monitoring and controlling the machining process of an air rudder.

Keywords: Digital twin, Mimicry, Information modeling, Machining, Digital twin mimic model (DTMM), Model based definition (MBD)

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School for Integrative Sciences and Engineering, 21 Lower Kent Ridge Road, 119077, Singapore) Biomimicry of microbial polysaccharide hydrogels for tissue engineering and regenerative medicine – A review, Carbohydrate Polymers, Volume 241 (2020) 116345

Hydrogels as artificial biomaterial scaffolds offer a much favoured 3D microenvironment for tissue engineering and regenerative medicine (TERM). Towards biomimicry of the native ECM, polysaccharides from Nature have been proposed as ideal surrogates given their biocompatibility. In particular, derivatives from microbial sources have emerged as economical and sustainable biomaterials due to their fast and high yielding production procedures. Despite these merits, microbial polysaccharides do not interact biologically with human tissues, a critical limitation hampering their translation into paradigmatic scaffolds for in vitro 3D cell culture. To overcome this, chemical and biological functionalization of polysaccharide scaffolds have been explored extensively. This review outlines the most recent strategies in the preparation of biofunctionalized gellan gum, xanthan gum and dextran hydrogels fabricated exclusively via material blending. Using inorganic or organic materials, we discuss the impact of these approaches on cell adhesion, proliferation and viability of anchorage-dependent cells for various TERM applications.

Keywords: Microbial polysaccharide hydrogel, Tissue engineering and regenerative medicine (TERM), Biofunctionalization, Material blending, Cell proliferation

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3. Annual Review-Plant Pathology
4. Annual Review- Ecology and Systematics
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