EIACP PROGRAM CENTER RESOURCE PARTNER

On

ENVIRONMENTAL BIOTECHNOLOGY

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EIACP-PC RESOURCE PARTNER

on

ENVIRONMENTAL BIOTECHBNOLOGY

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5. Abstracts

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 Forest & Climate Change, Govt. of India. 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. To buildup more awareness to safe the environment as well as for the betterment of livelihood for each and every classess of people in India, now the centre is revump as Environmental Information Awareness, Capacity building and livelihood programme (EIACP) Programme center – Resource Partner

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

This is the 42nd publication of Abstract Volume of this EIACP 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 2023. In this issue, various topics like Bioenergy, Bioengineering, Bio-degradation, Bio-remediation, Bio-transformation etc. have been covered. We are grateful to the various libraries and their staff for their cooperation extended to us during the collection of the articles.

Abstract Format

The format of the abstract is as follows:

Abstract:	The abstracts are arranged in different subheads.
Author:	Name of the authors are given in the order in which they appear in the original document. These names are given in succession.
Address of Authors:	Address of the author is given in parenthesis at the end of the author's name. When the address of any other author is found, it is written after wards delimited by stop(.).
Locus:	The name of the journal is followed by the volume number, issue number, year of publication and the page no.

GENERAL INFORMATION

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

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

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

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

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

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

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

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

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

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

1. Bacterial Biofertilizer
2. Algal Biofertilizer

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

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

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

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

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

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

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

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

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

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

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

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

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

Biomimicry: Biomimicry is an applied science that derives inspiration for solutions to human problems through the study of natural designs, systems and processes. Biomimicry on the other hand, which is not a science, is a more subtle way which we can benefit from nature. It is the modern, often high tech, equivalent of the historical practices of emulating nature. . The science of biomimicry is a newly developing field but the application of biomimicry has been around since the beginning of man. The biomimetic technologies (flight controls, bio-robotics, ventilation systems, etc.) and potential technologies (fin geometry, nacre materials, etc.) improve performance. The use of biomimicry as an approach to sustainable engineering, specifically the environmental components.

ABBREVIATIONS USED IN ADDRESSES AND CITED JOURNALS

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

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

Asa J. Lewis, Xiaoyan Yun, Max G. Lewis, Erica R. McKenzie, Daniel E. Spooner, Marie J. Kurz, Rominder Suri, Christopher M. Sales. ([a]Department of Civil, Architectural, and Environmental Engineering, Drexel University, 3100 Market St., Philadelphia, PA, 19104, USA, [b]Civil and Environmental Engineering Department, Temple University, Philadelphia, PA, 19122, USA, [c]Department of Biology, Temple University, Philadelphia, PA, 19122, USA, [d]Department of Biology, Commonwealth University of Pennsylvania, Lock Haven University, Lock Haven, PA, 17745, USA, [e]Academy of Natural Sciences of Drexel University, Philadelphia, PA, 19103, USA, [f]Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, 37831, USA) Impacts of divalent cations (Mg2+ and Ca2+) on PFAS bioaccumulation in freshwater macroinvertebrates representing different foraging modes. Environmental Pollution, Volume 331, Part 2 (2023): 121938

Per- and polyfluoroalkyl substances (PFAS) have extensively contaminated freshwater aquatic ecosystems where they can be transported in water and partition to sediment and biota. In this paper, three freshwater benthic macroinvertebrates with different foraging modes were exposed to environmentally relevant concentrations of eight perfluoroalkyl carboxylates (PFCA), three perfluoroalkyl sulfonates (PFSA), and three fluorotelomer sulfonates (FTS) at varying divalent cation concentrations of magnesium (Mg2+) and calcium (Ca2+). Divalent cations can impact PFAS partitioning to solids, especially to sediments, at higher concentrations. Sediment dwelling worms (Lumbriculus variegatus), epibenthic grazing snails (Physella acuta), and sediment-dwelling filter-feeding bivalves (Elliptio complanata) were selected due to their unique foraging modes. Microcosms were composed of synthetic sediment, culture water, macroinvertebrates, and PFAS and consisted of a 28-day exposure period. L. variegatus had significantly higher PFAS bioaccumulation than P. acuta and E. complanata, likely due to higher levels of interactions with and ingestion of the contaminated sediment. “High Mg2+” (7.5 mM Mg2+) and “High Ca2+” (7.5 mM Ca2+) conditions generally had statistically higher bioaccumulation factors (BAF) than the “Reference Condition” (0.2 mM Ca2+ and 0.2 mM Mg2+) for PFAS with perfluorinated chain lengths greater than eight carbons. Long-chain PFAS dominated the PFAS profiles of the macroinvertebrates for all groups of compounds studied (PFCA, PFSA, and FTS). These results indicate that the study organism has the greatest impact on bioaccumulation, although divalent cation concentration had observable impacts between organisms depending on the environmental conditions. Elevated cation concentrations in the microcosms led to significantly greater bioaccumulation in the test organisms compared to the experimental reference conditions for long-chain PFAS.

Keywords: Bioavailability; Uptake mechanism; Fate and transport; PFAS profiles; Environmental relevance

A.J. Piro, S.J. Taipale, H.M. Laiho, E.S. Eerola, K.K. Kahilainen. ([a]Lammi Biological Station, University of Helsinki, Pääjärventie 320, FI-16900, Lammi, Finland, [b]Department of Biological and Environmental Science, University of Jyväskylä, P.O. Box 35 (YA), FI-40014, Jyväskylä, Finland). Fish muscle mercury concentration and bioaccumulation fluctuate year-round - Insights from cyprinid and percid fishes in a humic boreal lake. Environmental Research, Volume 231, Part 2(2023): 116187

Boreal lakes demonstrate pronounced seasonality, where the warm open-water season and subsequent cold and ice-covered season dominate natural cycles. While fish muscle total mercury concentration (mg/kg) [THg] is well documented in open-water summer months, there is limited knowledge on the ice-covered winter and spring mercury dynamics in fish from various foraging and thermal guilds. This year-round study tested how seasonality influences [THg] and its bioaccumulation in three percids, perch (Perca fluviatilis), pikeperch (Sander lucioperca), ruffe (Gymnocephalus cernua), and three cyprinids, roach (Rutilus rutilus), bleak (Alburnus alburnus), and bream (Abramis brama) in deep boreal mesotrophic Lake Pääjärvi, southern Finland. Fish were sampled and [THg] was quantified in the dorsal muscle during four seasons in this humic lake. Bioaccumulation regression slopes (mean ± STD, 0.039 ± 0.030, range 0.013–0.114) between [THg] and fish length were steepest during and after spawning and shallowest during autumn and winter for all species. Fish [THg] was significantly higher in the winter-spring than summer-autumn in all percids, however, not in cyprinids. The lowest [THg] was observed in summer and autumn, likely due to recovery from spring spawning, somatic growth and lipid accumulation. Fish [THg] was best described by multiple regression models (R2adj: 52–76%) which included total length and varying combinations of seasonally changing environmental (water temperature, total carbon, total nitrogen, and oxygen saturation) and biotic factors (gonadosomatic index, and sex) in all species. The seasonal variation in [THg] and bioaccumulation slopes across multiple species suggests a need for standardized sampling seasons in long-term monitoring to avoid any seasonality bias. From the fisheries and fish consumption perspective in seasonally ice-covered lakes, monitoring of both winter-spring and summer-autumn would improve knowledge of [THg] variation in fish muscle.

Keywords: Growth dilution; Spawning; Starvation; Season; Mercury; Winter

Abbi S. Brown, Xiaoyan Yun, Erica R. McKenzie, Christopher G. Heron, Jennifer A. Field, Christopher J. Salice. ([a]Environmental Science and Studies Program, Towson University, Towson, MD, USA, [b]Civil and Environmental Engineering Department, Temple University, Philadelphia, PA, USA, [c]Department of Environmental and Molecular Toxicology, College of Agricultural Sciences, Oregon State University, Corvallis, OR, USA). Spatial and temporal variability of per- and polyfluoroalkyl substances (PFAS) in environmental media of a small pond: Toward an improved understanding of PFAS bioaccumulation in fish .Science of The Total Environment,Volume 880(2023): 163149

Per- and polyfluoroalkyl substances (PFAS) are highly fluorinated compounds with many industrial applications, for instance as ingredients in fire-suppressing aqueous film-forming foams (AFFF). Several PFAS have been demonstrated to be persistent, bioaccumulative and toxic. This study better characterizes the bioaccumulation of PFAS in freshwater fish through a spatial and temporal analysis of surface water and sediment from a stormwater pond in a former Naval air station (NAS) with historic AFFF use. We sampled environmental media from four locations twice per week for five weeks and sampled fish at the end of the sampling effort. The primary PFAS identified in surface water, sediment, and biota were perfluorooctane sulfonate (PFOS) and perfluorohexane sulfonate (PFHxS) followed by perfluorooctanoic acid (PFOA) in environmental media and perfluoroheptane sulfonate (PFHpS) in biota. We observed significant temporal variability in surface water concentrations at the pond headwaters following stochastic events such as heavy rainfall for many compounds, particularly PFHxS. Sediment concentrations varied most across sampling locations. In fish, liver tissue presented the highest concentrations for all compounds except PFHxS, which was highest in muscle tissue, suggesting the influence of fine-scale aqueous PFAS fluctuations on tissue distribution. Calculated log bioaccumulation factors (BAFs) ranged from 0.13 to 2.30 for perfluoroalkyl carboxylates (PFCA) and 0.29–4.05

for perfluoroalkane sulfonates (PFSA) and fluctuated greatly with aqueous concentrations. The variability of PFAS concentrations in environmental media necessitates more frequent sampling efforts in field-based studies to better characterize PFAS contamination in aquatic ecosystems as well as exercising caution when considering single time-point BAFs due to uncertainty of system dynamics.

Keywords: Aquatic toxicology; AFFF; Perfluorooctane sulfonate (PFOS); Perfluorohexane sulfonate (PFHxS); Water; Sediment

Tao Hu, Jiachao Zhang, Xueyan Xu, Xiaoli Wang, Changzhi Yang, Chao Song, Shuguang Wang, Shan Zhao. ([a]Shandong Key Laboratory of Water Pollution Control and Resource Reuse, School of Environmental Science and Engineering, Shandong University, Qingdao, 266237, China, [b]Analysis and Test Center, Qilu University of Technology (Shandong Academy of Sciences), Jinan, 250014, China, [c]Shandong Yellow River Delta National Nature Reserve Administration Committee, Dongying, 257091, China). Bioaccumulation and trophic transfer of antibiotics in the aquatic and terrestrial food webs of the Yellow River Delta. Chemosphere,Volume 323(2023): 138211

Antibiotic pollution caused by aquaculture industries is a common problem in the wetland of the Yellow River Delta (YRD). Aquatic and terrestrial food webs coexist and interact in wetlands. However, there are few comparative studies on antibiotics in these two food webs. This study investigated the occurrence, bioaccumulation, and trophic transfer of 19 antibiotics in the aquatic and terrestrial food webs of the YRD, and discussed the effects of physicochemical parameters in different food webs. The total concentrations of antibiotics in aquatic organisms and terrestrial organisms ranged from 11.61 to 63.08 ng/g dry weight (dw) and 4.21–9.11 ng/g dw, respectively. BAF (bioaccumulation factor), BSAFa (biota sediment accumulation factor), and BSAFt (biota soil accumulation factor) were used to explore the bioaccumulation capacity of antibiotics. The calculation results of these three factors showed that fluoroquinolones (FQs) had the highest bioaccumulation capacity. As for the trophic transfer, the total concentrations of antibiotics were biodiluted in the aquatic food web while biomagnified in the terrestrial food web. Physicochemical parameters of the antibiotics showed that log Kow (octanol-water partition coefficient)/log Dow (pH-dependent distribution coefficient) and log Koa (octanol-air partition coefficient) were good predictors for antibiotic bioaccumulation in the aquatic and terrestrial organisms of the YRD, respectively. In addition, the increasing log Dow and log Koa led to a rise of TMF (trophic magnification factor) in the aquatic food web while a decrease of TMF in the terrestrial food web. Overall, these results provide insights into the mechanisms on bioaccumulation and trophic transfer of antibiotics in different food webs.

Keywords: Antibiotics; Bioaccumulation; Trophic transfer; Terrestrial food web; Aquatic food web

Robert P. Mason, Kate L. Buckman, Emily A. Seelen, Vivien F. Taylor, Celia Y. Chen. ([a]Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA, [b]Department of Biological Sciences, Dartmouth College, Hanover, NH 03755, USA, [c]University of Southern California, LA, CA 90089, USA, [d]Department of Earth Sciences, Dartmouth College, Hanover, NH 03755, USA). An examination of the factors influencing the bioaccumulation of methylmercury at the base of the estuarine food web. Science of The Total Environment,Volume 886(2023): 163996

Estuarine systems have received ongoing mercury (Hg) inputs from both point sources and regional contamination and have high legacy Hg in sediments. This is an environmental concern given that coastal seafood is an important vector for human exposure to methylmercury (MeHg). The base of the food chain represents the most important trophic steps for MeHg bioaccumulation. The magnitude of the uptake by phytoplankton, and their consumers, is influenced by many factors, in addition to sediment and water MeHg concentrations, that impact MeHg assimilation into phytoplankton and the trophic transfer to higher trophic levels, both benthic and pelagic. For forage fish, such as mummichogs (Fundulus heteroclitus), abiotic and biotic (bioenergetic) factors can influence their MeHg content, and diet is also important as they feed both on benthic and pelagic prey. Given that the importance of sediment MeHg versus pelagic MeHg sources has been debated, we updated a phytoplankton bioaccumulation model, and coupled this with a bioaccumulation model for MeHg concentration in mummichog tissue to examine the controlling factors for sites, from Maine to Maryland, USA, ranging widely in their Hg concentrations and other variables. The study highlighted the importance of DOC in modulating uptake into the pelagic food web, but also demonstrated the importance of diet in controlling mummichog MeHg. Finally, the relative importance of MeHg source - sediment or water column – was correlated with the level of Hg contamination. Sediment-derived MeHg was a more important source for highly Hg contaminated systems. As water column and sediment MeHg are not strongly correlated for the studied ecosystems, their importance as a source of MeHg to mummichogs varies with location. The study highlights the differences across ecosystems in MeHg bioaccumulation pathways, and that uptake into phytoplankton is an important variable controlling forage fish concentration.

Keywords: Mercury; Methylmercury; Phytoplankton; Forage fish; Mummichogs; Bioaccumulation; Model; Multi-estuary analysis

Marco Parolini, Matteo Stucchi, Roberto Ambrosini, Andrea Romano. (Department of Environmental Science and Policy, University of Milan, via Celoria 26, I-20133 Milan, Italy). A global perspective on microplastic bioaccumulation in marine organisms. Ecological Indicators,Volume 149(2023): 110179

Microplastic (MP) contamination of marine ecosystems has been confirmed as an environmental issue of global concern. A growing number of monitoring surveys has extensively documented the occurrence and distribution of a wide array of MPs of different sizes, shapes, colours, and polymeric compositions in seawater, sediments, and marine organisms worldwide. The presence of MPs in marine organisms has been explored in many species belonging to different taxonomic groups collected in diverse geographical locations. These studies have revealed the ingestion and the bioaccumulation of MPs in organisms at each trophic level, confirming the ubiquity of MP contamination in marine ecosystems. This systematic review aimed at summarizing the results of the vast literature concerning the bioaccumulation of MPs in marine organisms to 1) shed light on potential differences in MP body burden among different taxonomic groups and 2) investigate the spatial and temporal variation of MP bioaccumulation at the global level. Our analyses showed that, independently of the geographic origin of the sample, the MP body burden significantly differed among trophic levels and/or taxonomic groups. Zooplankton showed the lowest MP levels, while the highest levels were observed in vertebrates other than fish (i.e. mammals, birds and reptiles). In contrast, no temporal or geographical differences in MP bioaccumulation were noted, independently of the taxonomic groups. These results confirmed that all marine organisms can ingest and accumulate MPs, but the large variability in body burden within and among the taxonomic groups precludes the opportunity to identify global patterns of contamination.

Keywords: Body burden; Ecological indicators; Microplastics; Marine organisms; Oceans

Mengru Fu, Jiaqi Tan, Shanqi Zhou, Peng Liu, Zhihua Qiao, Yanna Han, Wei Zhang, Cheng Peng.([a]State Environmental Protection Key Laboratory of Environmental Risk Assessment and Control on Chemical Process, School of Resource and Environmental Engineering, East China University of Science and Technology, Shanghai 200237, China, [b]Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA, [c]Xi'an Thermal Power Research Institute Co. Ltd., Suzhou branch, Suzhou 215000, China). Acrylonitrile butadiene styrene microplastics aggravate the threat of decabromodiphenyl ethane to Eisenia fetida: Bioaccumulation, tissue damage, and transcriptional responses. Science of The Total Environment, Volume 889(2023): 164303

Little is known about how brominated flame retardants (NBFRs) and microplastics (MPs) co-pollution influences soil organisms. Here, we investigated the impacts of acrylonitrile butadiene styrene (ABS)-MPs in soil on the 28-d dynamic bioaccumulation, tissue damage, and transcriptional responses of decabromodiphenyl ethane (DBDPE) in Eisenia fetida by simulating different pollution scenarios (10 mg kg−1 DBDPE, 10 mg kg−1 DBDPE accompanied by 0.1 % ABS-MPs, and 10 mg kg−1 DBDPE accompanied by 0.1 % ABS-resin). The results show ABS resin did not influence DBDPE bioaccumulation or distribution, but ABS-MPs, particularly 74–187 μm size of MPs, prolonged DBDPE equilibrium time and significantly promoted DBDPE bioaccumulation in tissue (1.76–2.38 folds) and epidermis (2.72–3.34 folds). However, ABS-MPs and ABS-resin reduced DBDPE concentrations of intestines by 22.2–30.6 % and 37.3 %, respectively. DBDPE-MPs caused more serious epidermis and intestines damages than DBDPE. Additionally, compared to the control, DBDPE significantly up-regulated 1957 genes and down-regulated 2203 genes; meanwhile, DBDPE-MPs up-regulated 1475 genes and down-regulated 2231 genes. DBDPE and DBDPE-MPs both regulated lysosome, phagosome, and apoptosis as the top 3 enriched pathways, while DBDPE-MPs specifically regulated signaling pathways and compound metabolism. This study demonstrated that the presence of ABS-MPs aggravated the biotoxicity of DBDPE, providing scientific information for assessing the ecological risks of MPs and additives from e-waste in soil.

Keywords: Acrylonitrile butadiene styrene microplastics; Decabromodiphenyl ethane; Bioaccumulation; Transcriptomics; Earthworm

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Arsenic, Cd, and Pb environmental fate is influenced when the traditional permanent flooding rice production systems are replaced by water-saving and soil conservation practices, urging for additional strategies that avoid their bioaccumulation in rice grain. The aim of this two-years

field study was to evaluate the effects of fresh and field-aged biochar on As, Cd, and Pb bioaccumulation, and on As speciation, in rice grain produced in different growing environments (flooding versus sprinkler and conventional tillage versus direct seeding). Biochar produced from holm-oak pruning residues (pyrolysis at 550 °C, 48 h), in a single application (28 Mg ha−1), reduced As bioaccumulation in rice grain in the permanent flooding system to non-quantifiable concentrations (e.g., from 0.178 mg kg−1 to <0.04 mg kg−1, for inorganic-As, respectively), an effect which remained under field-aging conditions, increasing rice commercial value. When adopting sprinkler irrigation, the undesirable increase in Cd bioaccumulation in rice, relatively to the anaerobic system, was counteracted by biochar application, reducing its bioaccumulation in kernels between 32 and 80 %, allowing a simultaneous control of metals and metalloids bioaccumulation in rice. The bioaccumulation of Pb was also prevented with biochar application, with a reduction in its concentration four- to 13-times, in all the management systems, relatively to the non-amended plots, under fresh biochar effects. However, Pb immobilization decreased with biochar field-aging, indicating that the biochar application may have to be repeated to maintain the same beneficial effect. Therefore, the present study shows that the implementation of sprinkler irrigation with holm-oak biochar could reduce the risk of heavy metals(loids) bioaccumulation in rice grains and, thereby, ensuring food safety aspects, particularly under fresh biochar effects.

Keywords: Oryza sativa L.; Toxic trace elements; Sprinkler irrigation; Flooding irrigation; Mediterranean environment; Soil amendments

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Although gut microbes can affect the accumulation and metabolism of arsenic (As), the microbes contributing to these processes remain largely unknown. Therefore, this study aimed to investigate the bioaccumulation and biotransformation of arsenate [As(V)] and arsenobetaine (AsB) in mice with a disordered gut microbiome. We used cefoperazone (Cef) to construct a mouse model of gut microbiome disruption along with 16S rRNA sequencing to elucidate the effect of gut microbiome destruction on the biotransformation and bioaccumulation of As(V) and AsB. This revealed the role of specific bacteria in As metabolism. Gut microbiome destruction increased the bioaccumulation of As(V) and AsB in various organs and reduced the excretion of As(V) and AsB in the feces. Further, gut microbiome destruction was found to be important for the biotransformation of As(V). Interference with Cef can significantly decrease Blautia and Lactobacillus while increasing Enterococcus, leading to increase As accumulation in mice and enhanced methylation. We also identified Lachnoclostridium, Erysipelatoclostridium, Blautia, Lactobacillus, and Enterococcus as biomarkers involved in As bioaccumulation and biotransformation. In conclusion, specific microbes can increase As accumulation in the host, exacerbating its potential health risks.

Keywords: Arsenic; Gut microbiome; Cefoperazone; Blautia; Lactobacillus; Enterococcus

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Mesocosms allow the simulation of environmentally relevant conditions and can be used to establish more realistic scenarios of organism exposure to nanoparticles. An indoor mesocosm experiment simulating an aquatic stream ecosystem was conducted to assess the toxicokinetics and bioaccumulation of silver sulfide nanoparticles (Ag2S NPs) and AgNO3 in the freshwater invertebrates Girardia tigrina, Physa acuta and Chironomus riparius, and determine if previous single-species tests can predict bioaccumulation in the mesocosm. Water was daily spiked at 10 μg Ag L−1. Ag concentrations in water and sediment reached values of 13.4 μg Ag L−1 and 0.30 μg Ag g−1 in the Ag2S NP exposure, and 12.8 μg Ag L−1 and 0.20 μg Ag g−1 in the AgNO3. Silver was bioaccumulated by the species from both treatments, but with approximately 1.5, 3 and 11 times higher body Ag concentrations in AgNO3 compared to Ag2S NP exposures in snails, chironomids and planarians, respectively. In the Ag2S NP exposures, the observed uptake was probably of the particulate form. This demonstrates that this more environmentally relevant Ag nanoform may be bioavailable for uptake by benthic organisms. Interspecies interactions likely occurred, namely predation (planarians fed on chironomids and snails), which somehow influenced Ag uptake/bioaccumulation, possibly by altering organisms´ foraging behaviour. Higher Ag uptake rate constants were determined for AgNO3 (0.64, 80.4 and 1.12 Lwater g−1organism day−1) than for Ag2S NPs (0.05, 2.65 and 0.32 Lwater g−1organism day−1) for planarians, snails and chironomids, respectively. Biomagnification under environmentally realistic exposure seemed to be low, although it was likely to occur in the food chain P. acuta to G. tigrina exposed to AgNO3. Single-species tests generally could not reliably predict Ag bioaccumulation in the more complex mesocosm scenario. This study provides methodologies/data to better understand exposure, toxicokinetics and bioaccumulation of Ag in complex systems, reinforcing the need to use mesocosm studies to improve the risk assessment of environmental contaminants, specifically NPs, in aquatic environments.

Keywords: Nanomaterials; Uptake and elimination; Exposure routes; Sediments; Single-species tests; Risk assessment

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The extensive utilization of both legacy and novel brominated flame retardants (BFRs) leads to high environmental concentrations, which would be bioaccumulated by organisms and further transferred through the food webs, causing potential risks to humans. In this study, five BFRs, that showed high detection frequencies and concentrations in sediments from an e-waste dismantling site in Southern China, namely 2,3,4,5,6-pentabromotoluene (PBT), hexabromobenzene (HBB), 1,2-bis(2,4,6-tribromophenoxy) ethane (BTBPE), decabromodiphenyl ethane (DBDPE), and decabromodiphenyl ether (BDE209), were selected as target pollutants in the lab-constructed aquatic food web as part of a micro-ecosystem, to investigate their distribution, bioaccumulation, and trophic transfer patterns. The significant correlations between different samples in the food web indicated that the dietary uptake appeared to influence the levels of BFRs in organisms. Significant negative correlations were observed between the trophic level of organisms and the lipid-normalized concentrations of BTBPE and DBDPE, indicating the occurrence of trophic dilution after 5-month exposure. However, the average values of bioaccumulation factors (BAFs) were from 2.49 to 5.17 L/kg, underscoring the importance of continued concern for environmental risks of BFRs. The organisms occupying higher trophic levels with greater bioaccumulation capacities may play a pivotal role in determining the trophic magnification potentials of BFRs. This research provides a helpful reference for studying the impacts of feeding habits on bioaccumulation and biomagnification, as well as for identifying the fate of BFRs in aquatic environment.

Keywords: BFRs; Dietary uptake; Distribution, Bioaccumulation; Trophic transfer

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In this work, a wide-scope liquid chromatography-tandem mass spectrometry (LC-MS/MS) method for the quantitative determination of environmental levels of multiclass drugs and their metabolites in water and fish samples was developed. The method allowed the reliable determination of 44 drugs, covering a rather wide range of chemistries and physicochemical characteristics. In order to obtain a reliable and robust analytical protocol, different combinations of extraction and cleanup techniques were systematically examined. Aqueous samples were extracted using a simple Oasis HLB SPE enrichment protocol with pH-optimized sample percolation (pH 3). The extraction of cryo-homogenized biota samples was performed using double extraction with MeOH basified with 0.5% NH3, which allowed high extraction recoveries for all target analytes. The problem of the coextracted lipid matrix, which is known to be the key obstacle for reliable biota analysis, was systematically examined in a series of model cleanup experiments. A combination of cryo-precipitation, filtration, and HLB SPE cleanup was proposed as a protocol, which allowed reliable and robust analysis of all target compounds at low ng/g levels. At the final conditions, the method which was validated at three concentration levels showed high extraction recoveries (68–97%), acceptable matrix effects (12 to −32%), accuracies (81–129%), and reproducibilities (3–32%) for all analytes. The developed method was used to determine drug concentrations in river water and in feral freshwater fish, including whole fish and muscle tissue, from the Sava River (Croatia), in order to estimate their corresponding bioaccumulation potential. With respect to bioaccumulation potential in whole fish and fish muscle, the most relevant drugs were lisinopril, sertraline, terbinafine, torsemide, diazepam, desloratadine, and loratadine with estimated bioaccumulation factors ranging from 20 to 838 and from 1 to 431, respectively.

Keywords: Pharmaceuticals; Biota; Surface water; Organic contaminants; Bioaccumulation

Yiye Jiang, Yanhong Zeng, Ruifeng Lu, Yanting Zhang, Ling Long, Xiaobo Zheng, Xiaojun Luo, Bixian Mai. ([a]State Key Laboratory of Organic Geochemistry and Guangdong Key Laboratory of Environmental Protection and Resources Utilization, Guangzhou Institute of Geochemistry, Chinese Academy of Sciences, Guangzhou 510640, China, [b]University of Chinese Academy of Sciences, Beijing 100049, China, [c]Guangdong-Hong Kong-Macao Joint Laboratory for Environmental Pollution and Control, Guangzhou Institute of Geochemistry, Chinese Academy of Sciences, Guangzhou 510640, China, [d]CAS Center for Excellence in Deep Earth Science, Guangzhou 510640, China, [e]Guangdong Laboratory for Lingnan Modern Agriculture, Guangdong Provincial Key Laboratory of Agricultural & Rural Pollution Abatement and Environmental Safety, College of Natural Resources and Environment, South China Agricultural University, Guangzhou 510642, China). Application of amino acids nitrogen stable isotopic analysis in bioaccumulation studies of pollutants: A review. Science of The Total Environment, Volume 879(2023): 163012

Accurately quantifying trophic positions (TP) to describe food web structure is an important element in studying pollutant bioaccumulation. In recent years, compound-specific nitrogen isotopic analysis of amino acids (AAs-N-CSIA) has been progressively applied as a potentially reliable tool for quantifying TP, facilitating a better understanding of pollutant food web transfer. Therefore, this review provides an overview of the analytical procedures, applications, and limitations of AAs-N-CSIA in pollutant (halogenated organic pollutants (HOPs) and heavy metals) bioaccumulation studies. We first summarize studies on the analytical techniques of AAs-N-CSIA, including derivatization, instrumental analysis, and data processing methods. The N-pivaloyl-i-propyl-amino acid ester method is a more suitable AAs derivatization method for quantifying TP. The AAs-N-CSIA application in pollutant bioaccumulation studies (e.g., Hg, MeHg, and HOPs) is discussed, and its application in conjunction with various techniques (e.g., spatial analysis, food source analysis, and compound tracking techniques, etc.) to research the influence of pollutant levels on organisms is summarized. Finally, the limitations of AAs-N-CSIA in pollutant bioaccumulation studies are discussed, including the use of single empirical values of βglu/phe and TDFglu/phe that result in large errors in TP quantification. The weighted βglu/phe and the multi-TDFglu/phe models are still challenging to solve for accurate TP quantification of omnivores; however, factors affecting the variation of βglu/phe and

TDFglu/phe are unclear, especially the effect of pollutant bioaccumulation in organisms on internal AA metabolic processes.

Keywords: Amino acid; Nitrogen isotopic composition; Trophic position; Bioaccumulation; Trophic magnification factors

Wenhui Song, Yankun Du, Dengtan Li, Zongyuan Xiao, Bing Li, Jinling Wei, Xinjie Huang, Chuanwei Zheng, Jinhua Wang, Jun Wang, Lusheng Zhu. (College of Resources and Environment, Shandong Agricultural University, Key Laboratory of Agricultural Environment in Universities of Shandong, 61 Daizong Road, Taian 271018, China). Polyethylene mulch film-derived microplastics enhance the bioaccumulation of atrazine in two earthworm species (Eisenia fetida and Metaphire guillelmi) via carrier effects. Journal of Hazardous Materials, Volume 455(2023): 131603

Microplastics (MPs) may significantly affect the bioavailability of coexisting pollutants in soil by adsorption-desorption behavior. However, the mechanisms underlying these interaction remain unclear. Herein, the influence of unused polythylene mulch film-derived MPs (MFMPs) and farmland residual polyethylene mulch film-derived MPs (MFMPs-aged) on the adsorption-desorption behavior and bioavailability of atrazine (ATZ) in soil were investigated. The adsorption kinetics and the adsorption isotherms of ATZ on soil, MFMPs, and MFMPs-aged fitted well by the pseudo-second-order model and the Langmuir model, respectively. ATZ were easier to desorb from soil, MFMPs, and MFMPs-aged in the simulated earthworm digestive fluid than that in the CaCl2 solution. The adsorption and desorption capacities of MFMPs and MFMPs-aged for ATZ were higher than those of soil, especially for MFMPs-aged. The existence of MPs in soil strengthened the adsorption and desorption capacities of ATZ, and the strengthened effects were promoted by the addition amount and aging process of MPs. Moreover, the occurrence of MPs significantly increased the bioaccumulation of ATZ in earthworms, especially for MFMPs-aged. This study deepens the knowledge of the interaction mechanisms of mulch film-derived MPs and pesticide pollution.

Keywords: Microplastics; Mulch film; Atrazine; Adsorption-desorption; Bioaccumulation

Lu Qiao, Lu Chen, Zhen Yang, Jinhua Xu, Jinlong Song, Xingyang Li, Huiwu Sun, Yingchun Mu. ([a]Key Laboratory of Control of Quality and Safety for Aquatic Products, Ministry of Agriculture and Rural Affairs, Chinese Academy of Fishery Sciences, Beijing, 100141, China, [b]College of Food Science and Engineering, Bohai University, Jinzhou, 121000, China). Bioaccumulation and elimination, acute toxicity analysis and risk assessment of diflubenzuron in common carp (Cyprinus carpio). Chemosphere (2023): 139154

Diflubenzuron has been applied in agriculture and aquaculture, and its residues in ecological environment and food chain could result in chronic exposure and long-term toxicity effects for human health. However, limited information is available regarding diflubenzuron levels in fish and associated risk assessment. This study performed the analysis for dynamic bioaccumulation and elimination distribution of diflubenzuron in carp tissues. The results indicated that diflubenzuron was absorbed and enriched by fish body along with higher enrichment in lipid-rich tissues of fish. The peak concentration in carp muscle reached 6-fold of diflubenzuron concentration in aquaculture water. The median lethal concentration (LC50) of diflubenzuron at 96 h was 12.29 mg/L, presented low toxicity to carp. Risk assessment results showed that the chronic risk from dietary exposure to diflubenzuron through carp consumption for Chinese residents of children and adolescents, adults and elderly people were acceptable, while posed a certain risk for young children. This study provided the reference for pollution control, risk assessment and scientific management of diflubenzuron.

Keywords: Diflubenzuron; Bioaccumulation and elimination; Pharmacokinetic analysis; Acute toxicity; Risk assessment

Bioremediation

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Efficient decontamination of oil contaminated soils is not always easy, especially when the contamination is aged. In this work, we have opted for bioremediation techniques, with a low environmental impact, whose treatments were selected according to the area and soil to be treated. Thus, an industrial area, which had had fuel oil spills for decades, was our decontamination target, using bioremediation techniques that included bioaugmentation with bacteria (autochthonous bacterial consortium), phytoremediation with a plant (Medicago sativa L.) and bioaugmentation with a fungus (Pleurotus ostreatus). These treatments were tested alone and in combination to observe any possible synergies. The evaluation of these treatments for the degradation of the total aliphatic and aromatic fractions of total petroleum hydrocarbons (TPH), showed a higher efficiency (18–48 %) in the degradation of the aliphatic fractions for all the treatments compared with natural attenuation (11 %). By contrast, lower efficiencies were obtained for the aromatic fractions (0–35 %) compared with natural attenuation, which did not decrease. The removal of these fractions was only effective in the combined treatment using all three organisms: the plant, the bacteria, and the fungus, where the bioaugmentation enhanced the plant-microorganism interaction in the root system. The selection of the biological treatments to a specific contaminated site and the evaluation of decontamination by the aromatic and aliphatic chain profiles, leads to a better understanding of the degradation of the different fractions of fuel.

Keywords: Old-polluted soil; Environmentally friendly bioremediation; Autochthonous bacterial consortium; Bioaugmentation; Phytoremediation; Mycoremediation

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A class of organic priority pollutants known as PAHs is of critical public health and environmental concern due to its carcinogenic properties as well as its genotoxic, mutagenic, and cytotoxic properties. Research to eliminate PAHs from the environment has increased significantly due to awareness about their negative effects on the environment and human health. Various environmental factors, including nutrients, microorganisms present and their abundance, and the nature and chemical properties of the PAH affect the biodegradation of PAHs. A large spectrum of bacteria, fungi, and algae have ability to degrade PAHs with the biodegradation capacity of bacteria and fungi receiving the most attention. A considerable amount of research has been conducted in the last few decades on analyzing microbial communities for their genomic organization, enzymatic and biochemical properties capable of degrading PAH. While it is true that PAH degrading microorganisms offer potential for recovering damaged ecosystems in a cost-efficient way, new advances are needed to make these microbes more robust and successful at eliminating toxic chemicals. By optimizing some factors like adsorption, bioavailability and mass transfer of PAHs, microorganisms in their natural habitat could be greatly improved to biodegrade PAHs. This review aims to comprehensively discuss the latest findings and address the current wealth of knowledge in the microbial bioremediation of PAHs. Additionally, recent breakthroughs in PAH degradation are discussed in order to facilitate a broader understanding of the bioremediation of PAHs in the environment.

Keywords: Polycyclic aromatic hydrocarbons; Bioremediation; Bacteria; Algae; Fungi; Biodegradation

Eric A. Seagren. (Department of Civil, Environmental, and Geospatial Engineering, Michigan Technological University, Houghton, MI, United States). Bioremediation, Reference Module in Biomedical Sciences. Elsevier (2023): https://doi.org/10.1016/B978-0-12-824315-2.00413-9

Bioremediation uses biodegradation processes to either eliminate environmental contaminants or reduce their risks. Biodegradation processes transform organic contaminants, sometimes resulting in complete conversion to inorganic products (mineralization), or alter the transport of inorganic contaminants. In some cases, naturally-occurring intrinsic bioremediation is sufficient for risk reduction; however, numerous factors can limit biodegradation in the environment. Engineered bioremediation strategies focus on promoting biodegradation and overcoming limitations. In situ bioremediation approaches treat the contamination in place, and are classified by the technique for adding stimulating amendments. Ex situ bioremediation technologies involve excavation of the contaminated materials and treatment in different types of bioreactors.

Keywords: Bioaugmentation; Biodegradation; Bioremediation; Biostimulation; Biotransformation; Cometabolism; Engineered bioremediation; Ex situ bioremediation; In situ bioremediation; Intrinsic bioremediation; Mineralization; Monitored Natural Attenuation; Phytoremediation

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This review aims to give a detailed overview of various bioremediation technologies used for the decontamination of polychlorinated biphenyl (PCB)-polluted environments; discuss the bioaugmentation approaches employed to treat PCB-polluted soil, sediment, and wastewater; explore the limitations of bioaugmentation and the strategies to improve its efficiency; give an update on the current state of biodegradation studies on PCB and their mechanisms; explore the future research prospects on bioremediation based on the articles discussed in the current review. Extensive analysis of original works has revealed that the various bioremediation strategies displayed varying efficiencies with most found to be efficient. Coupling of treatment methods has been found effective in the decontamination of polluted sites. The biodegradation of PCB revealed that the concentrations of highly-chlorinated PCB can be substantially reduced under sequential anaerobic and aerobic processes. The study revealed that the concentrations of PCB in contaminated media declined largely due to the degradation of congeners with one or more chlorine atoms. Various enzymes participated in the degradation of PCB and include multicomponent dioxygenase (bphA, E, F, and G), dehydrogenases (bphB), second dioxygenase (bphC), and hydrolase (bphD). The review provides novel biological treatment strategies for the management of PCB-contaminated sites.

Keywords: Bioaugmentation; Biodegradation; Polychlorinated biphenyls; PCB-degrading genes; Bioremediation technologies

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This work aimed to validate the removal of total petroleum hydrocarbons (TPH) in a pilot system (on-site). Six piles of oil-contaminated soil were treated with 1) bioremediation (BIO) by three simultaneous technologies (bioaugmentation (bacterial consortium), phyto- (Panicum maximum) and vermiremediation (Pontoscolex corethrurus)), and compared with 2) natural attenuation (NA). Removal of alkanes, polycyclic aromatics (PAH), total petroleum hydrocarbons (TPH), and bacterial diversity were evaluated at 0, 35, 70, and 112 days. Biomass and number of shoots of P. maximum, the secondary vegetation, and the abundance of meso and macrofauna were measured initially and at the end. After 112 days, BIO significantly removed more alkanes (76%), PAH (68%), and TPH (76%) than NA treatment (23%, 19%, 24%). P. maximum biomass increased significantly (300%), with 97.3 ± 11.8 shoots m^{-2}. After 112 days, the secondary plants Lippia dulcis, Taraxacum officinale, Bidens pilosa and bacterial phylum Actinobacteria (18%) were the most abundant. The abundance of the earthworm Protozapotecia australis was reduced, while the most abundant group of mesofauna was Acari (56%–71%). This combination of technologies improved the development of grass and secondary plants, which generated a more favorable microhabitat for soil organisms to remove TPH more efficiently.

Keywords: Bacterial consortium; Field bioremediation; Panicum maximum; Pontoscolex corethrurus; Oil contamination

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The increasing anthropogenic and technogenic activities to compensate the raising population and unending demands of humans ended in severe pollution and detrimental damage to the environment. This environmental pollution due to lethal pollutants, toxic heavy metals and organic wastes has been drastically affecting the ecosystem of the living organisms. These are forced to enter into the food chain as they tend to accumulate in the agricultural soils. In order to eliminate these pollutants from the soils the bioremediation will be an efficient tool and this can be achieved by plant growth promoting rhizobacteria and by green wastes. In this study the plant growth promoting rhizobacteria (PGPR) and green wastes are evaluated for their effectiveness in bioremediating the toxic contaminants. Green wastes are rich sources of naturally occurring polyphenols which are potential eliminating agents of these pollutants, they can perform metal chelation, reduction, antibiotic properties, adsorption, complexation and by supplying the nutrients. However, PGPRs are well known plant life saviors from various biotic and abiotic stresses; they are also the bioremediating agents as they perform heavy metal elimination by various methods. In this study, it is also depicted that the combined application of PGPR and green wastes result in the significant method to bioremediate the contaminated sites. The bioremediation by PGPRs and green wastes is the prominent effective way to terminate the pollutants compared to phytoremediation.

Keywords: Bioremediation; Bioresources; Green waste; Heavy metals; PGPR

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Fundo, RS, Brazil, [b]Graduate Program in Mining, Metallurgical and Materials Engineering (PPGE3M), Federal University of Rio Grande do Sul (UFRGS), Porto Alegre, RS, Brazil, [c]Graduate Program in Food Science and Technology (PPGCTA), University of Passo Fundo (UPF), Passo Fundo, RS, Brazil). Biochar-immobilized Bacillus spp. for heavy metals bioremediation: A review on immobilization techniques, bioremediation mechanisms and effects on soil. Science of The Total Environment, Volume 881(2023): 163385

Heavy metals contamination present risks to ecosystems and human health. Bioremediation is a technology that has been applied to minimize the levels of heavy metals contamination. However, the efficiency of this process varies according to several biotic and abiotic aspects, especially in environments with high concentrations of heavy metals. Therefore, microorganisms immobilization in different materials, such as biochar, emerges as an alternative to alleviate the stress that heavy metals have on microorganisms and thus improve the bioremediation efficiency. In this context, this review aimed to compile recent advances in the use of biochar as a carrier of bacteria, specifically Bacillus spp., with subsequent application for the bioremediation of soil contaminated with heavy metals. We present three different techniques to immobilize Bacillus spp. on biochar. Bacillus strains are capable of reducing the toxicity and bioavailability of metals, while biochar is a material that serves as a shelter for microorganisms and also contributes to bioremediation through the adsorption of contaminants. Thus, there is a synergistic effect between Bacillus spp. and biochar for the heavy metals bioremediation. Biomineralization, biosorption, bioreduction, bioaccumulation and adsorption are the mechanisms involved in this process. The application of biochar-immobilized Bacillus strains results in beneficial effects on the contaminated soil, such as the reduction of toxicity and accumulation of metals in plants, favoring their growth, in addition to increasing microbial and enzymatic activity in soil. However, competition and reduction of microbial diversity and the toxic characteristics of biochar are reported as negative impacts of this strategy. More studies using this emerging technology are essential to improve its efficiency, to elucidate the mechanisms and to balance positive and negative impacts, especially at the field scale.

Keywords: Immobilization; Bacillus; Heavy metals; Biochar; Microorganism carriers

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Phthalic acid esters (PAEs) are known as the most widely used plasticizer as well as one of the ubiquitously distributed emerging pollutants. Biodegradation and bioremediation via application of PAEs-degrading microbes is promising. In this study, a novel marine microbe, Gordonia hongkongensis RL-LY01, was isolated from mangrove sediment showing high di-(2-ethylhexyl) phthalate (DEHP) degradation capacity. Strain RL-LY01 could degrade a wide range of PAEs and the degradation kinetics of DEHP followed the first-order decay model. Meanwhile, good environmental adaptability, preference to alkaline conditions and good tolerance to salinity and metal ions was shown. Further, metabolic pathway of DEHP in strain RL-LY01 was proposed, with di-ethyl phthalate, phthalic acid, benzoic acid and catechol as intermediates. Additionally, one known mono-alkyl phthalate hydrolase gene (mehpH) was identified. Finally, the excellent performance during bioremediation of artificial DEHP-contaminated saline soil and sediment indicated strain RL-LY01 employs great application potential for the bioremediation of PAE-contaminated environments.

Keywords: Phthalic acid esters; Gordonia hongkongensis; Biodegradation; Bioremediation; Saline soil

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The purpose of this study was to investigate the development of biotechnologies related to the bioremediation of soil contaminated by agrochemicals using fungi through technological prospecting with patent mapping and analysis of scientific products. Due to the high complexity of biotechnologies involving microorganisms, it is observed that the state of the art is still in development, with several technological advantages already elucidated and important challenges to be overcome. Patent mapping revealed that the number of granted or pending patents showed a positive trend. In this context, a high number of patent documents were observed that describe processes and methods aimed at the preparation and application of fungi in soil bioremediation, as well as biotechnologies that use consortia of different strains of fungi or fungi and bacteria and advanced approaches involving genetic engineering. In short, it was found that inventions related to the investigated biotechnology have been protected mainly in China, the USA, Japan, and the European Union, with emphasis on the technological impact of patents in India. Finally, the findings indicated that soil bioremediation with the use of fungi presents a potential for development due to a series of technological and environmental aspects.

Keywords: Bioremediation; Fungi; NVivo; Patents; Patent mapping; Technological prospecting

Guofang Xu, Siyan Zhao, Jinting Liu, Jianzhong He. (Department of Civil and Environmental Engineering, National University of Singapore, 117576, Singapore). Bioremediation of organohalide pollutants: progress, microbial ecology, and emerging computational tools. Current Opinion in Environmental Science & Health, Volume 32(2023): 100452

Organohalide chemicals such as polychlorinated biphenyls (PCBs), polybrominated diphenyl ethers (PBDEs), and polyfluoroalkyl substances (PFASs) are prevalent contaminants in the environment. Recent findings that certain microbes could attenuate these pollutants suggest the potential to develop bioremediation technologies using functional microorganisms to combat this pollution crisis. A timely review on bioremediation progress and emerging tools that can be used to facilitate bioremediation design is needed. Thus far, bioremediation of PCBs and PBDEs is at the developing stage from laboratory investigation to field application, whereas exploring potent microbes remains the central task for PFASs. Successful bioremediation is underpinned by a collection of interactive microbes; however, relevant microbial ecology questions affecting bioremediation performance are underexplored. Machine learning, quantum chemistry, and biomolecular modeling are prospective tools to optimize system operation, predict environmental fate of chemicals, and explore functional enzymes, but their application in bioremediation only emerged recently. This review summarizes recently discovered microbes and genes involved in biodegradation of organohalide pollutants, highlights practical and ecological questions, and discusses potential application of computational tools in bioremediation of organohalide pollutants.

Keywords: Bioremediation; Organohalide pollutants; Microbial ecology; Machine learning; Quantum chemistry; Biomolecular modelling

Jarosław Chwastowski, Paweł Staroń. (Department of Engineering and Chemical Technology, Cracow University of Technology, 24 Warszawska St., 31-155 Cracow, Poland). Immobilization of Phaffia rhodozyma cells in biopolymer for enhanced Cr(VI) bioremediation. Colloids and Surfaces A: Physicochemical and Engineering Aspects, Volume 672 (2023): 131698

The presented study investigated the use of Phaffia rhodozyma cells immobilized in natural biopolymer for improved bioremediation of toxic chromium compounds from aqueous solutions. Cells were immobilised in the shape of spheres (PRS) and flat coatings (PRC) with the use of sodium alginate. The bioremediation process was conducted through sorption and the reduction of Cr(VI). The biosorption was best described by the Langmuir isotherm model (R2 = 0.982, 0.985, 0.992 for Free cells, PRS and PRC, respectively) and for the kinetics, the Weber-Morris for unmodified cells and pseudo-second order model for PRS/PRC was the best fit according to the correlation coefficient (R2 >0.9). Fourier-transform infrared spectroscopy (FTIR) analysis showed that the sorption process is probably of chemical nature. The reduction of Cr(VI) to Cr(III) was carried out by the result of the difference between values obtained from colorimetry with the 1,5-diphenylcarbazide (DPC)–Cr(VI) complex and overall Cr concentration obtained from atomic absorbance spectrometry. The P. rhodozyma was able to detoxicate chromate up to 99%. The comparison of immobilization shapes showed that PRC has higher bioremediation properties than PRS by about 15% in terms of chromium removal from aqueous solutions. The 3 cycles of adsorption/desorption without decrease in efficiency showed that the PRS and PRC can be used multiple times for the removal of chromium ions from environment.

Keywords: Chromium; Toxicity; Bioremediation; Yeast cells; Immobilization

Shivananda Behera, Surajit Das. (Laboratory of Environmental Microbiology and Ecology (LEnME), Department of Life Science, National Institute of Technology, Rourkela 769 008, Odisha, India). Potential and prospects of Actinobacteria in the bioremediation of environmental pollutants: Cellular mechanisms and genetic regulations. Microbiological Research, Volume 273(2023): 127399

Increasing industrialization and anthropogenic activities have resulted in the release of a wide variety of pollutants into the environment including pesticides, polycyclic aromatic hydrocarbons (PAHs), and heavy metals. These pollutants pose a serious threat to human health as well as to the ecosystem. Thus, the removal of these compounds from the environment is highly important. Mitigation of the environmental pollution caused by these pollutants via bioremediation has become a promising approach nowadays. Actinobacteria are a group of eubacteria mostly known for their ability to produce secondary metabolites. The morphological

features such as spore formation, filamentous growth, higher surface area to volume ratio, and cellular mechanisms like EPS secretion, and siderophore production in Actinobacteria render higher resistance and biodegradation ability. In addition, these bacteria possess several oxidoreductase systems (oxyR, catR, furA, etc.) which help in bioremediation. Actinobacteria genera including Arthrobacter, Rhodococcus, Streptomyces, Nocardia, Microbacterium, etc. have shown great potential for the bioremediation of various pollutants. In this review, the bioremediation ability of these bacteria has been discussed in detail. The utilization of various genera of Actinobacteria for the biodegradation of organic pollutants, including pesticides and PAHs, and inorganic pollutants like heavy metals has been described. In addition, the cellular mechanisms in these microbes which help to withstand oxidative stress have been discussed. Finally, this review explores the Actinobacteria mediated strategies and recent technologies such as the utilization of mixed cultures, cell immobilization, plant-microbe interaction, utilization of biosurfactants and nanoparticles, etc., to enhance the bioremediation of various environmental pollutants.

Keywords: Actinobacteria; Pollutants; Bioremediation; Cellular mechanism; Genetic regulation

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Microbial bioremediation is a highly effective method to degrade phthalates in the environment. However, the response of native microbial communities to the exogenously introduced microorganism remains unknown. In this study, the native fungal community was monitored by amplicon sequencing of the fungal ITS region during the restoration process of the di-n-butyl phthalate (DBP)-contaminated soils with Gordonia phthalatica QH-11T. Our results showed that the diversity, composition, and structure of the fungal community in the bioremediation treatment did not differ from the control, and no significant correlations were found between number of Gordonia and variation of fungal community. It was also observed that DBP pollution initially increased the relative abundance of plant pathogens and soil saprotrophs first, but their proportions returned to the initial level. Molecular ecological network analysis showed that DBP pollution increased the network complexity, while the network was not significantly altered by bioremediation. Overall, the introduction of Gordonia was shown to not have a long-term impact on the native soil fungal community. Therefore, this restoration method can be considered safe in terms of soil ecosystem stability. The present study provides a deeper insight into the effect of bioremediation on fungal communities and provides an extended basis to further explore the ecological risks of introducing exogenous microorganisms.

Keywords: Phthalate esters; Bioremediation; Gordonia sp.; Fungal community; Microbiome

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Faculty of Chemical Engineering and Environmental Protection, Technical University Gheorghe Asachi of Iasi, Romania, [c]Department of Pharmaceutical Sciences, North Carolina Central University, USA, [d]Department of Livestock Products Technology, (Meat Science) Veterinary College and Research Institute, Namakkal, Tamil Nadu, India, [e]Department of Botany and Microbiology, College of Science, King Saud University, PO Box-2455, Riyadh, 11451, Saudi Arabia, [f]University Centre for Research & Development, Chandigarh University, Mohali, 140103, India). Bioremediation efficiency of free and immobilized form of Aspergillus niger and Aspergillus tubigenesis biomass on tannery effluent. Environmental Research, Volume 231, Part 3 (2023): 116275

Untreated tannery effluent discharge, which causes severe environmental pollution. This research was performed to assess the bioremediation (multi-pollutant adsorption) potential of pre-identified and multi metal tolerant Aspergillus niger and Aspergillus tubigenesis through a stirred tank bioreactor in free and immobilized form. Physicochemical property analysis results showed that most of the tannery effluent properties were beyond the permissible limits. These A. niger and A. tubigenesis effectively immobilized on corncob and coir solid support material. The stirred tank bioreactor based bioremediation study revealed that the fungal biomass (Aspergillus niger and Aspergillus tubigenesis) immobilized coir and corncob material demonstrated remarkable multi-pollutant (TSS: 22.5% & 13.5%, TS: 29% & 22%, BOD: 21% & 10%, TDS: 28% & 19%, COD: 30% & 22%, Cr: 27% & 19%, Cu: 28% & 12%, and Pb: 48% & 29% respectively) adsorption potential in a week of treatment. Moreover, it reduced the toxicity of tannery effluent and promotes the sprouting of Oriza sativa seeds, as demonstrated by petri plate bioassay. These finding suggest that the metal-tolerant fungal isolates A. niger and A. tubigenesis demonstrated impressive bioremediation proficiencies in an immobilized state. A field investigation is required to assess the feasibility of this strategy on tannery effluent.

Keywords: Tannery effluent; Aspergillus niger; Aspergillus tubigenesis; Immobilization; Bioremediation

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This study presents a smart technological framework to efficiently remove azithromycin from natural soil resources using bioremediation techniques. The framework consists of several modules, each with different models such as Penicillium Simplicissimum (PS) bioactivity, soft computing models, statistical optimisation, Machine Learning (ML) algorithms, and Decision Tree (DT) control system based on Removal Percentage (RP). The first module involves designing experiments using a literature review and the Taguchi Orthogonal design method for cultural conditions. The RP is predicted as a function of cultural parameters using Response Surface Methodology (RSM) and three ML algorithms: Instance-Based K (IBK), KStar, and

Locally Weighted Learning (LWL). The sensitivity analysis shows that pH is the most important factor among all parameters, including pH, Aeration Intensity (AI), Temperature, Microbial/Food (M/F) ratio, and Retention Time (RT), with a p-value of <0.0001. AI is the next most significant parameter, also with a p-value of <0.0001. The optimal biological conditions for removing azithromycin from soil resources are a temperature of 32 °C, pH of 5.5, M/F ratio of 1.59 mg/g, and AI of 8.59 m3/h. During the 100-day bioremediation process, RP was found to be an insignificant factor for more than 25 days, which simplifies the conditions. Among the ML algorithms, the IBK model provided the most accurate prediction of RT, with a correlation coefficient of over 95%.

Keywords: Azithromycin; Bioremediation; Machine learning; Penicillium simplicissimum; Taguchi design

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Global concern about petroleum hydrocarbon pollution has intensified and gained scientific interest due to its noxious nature, high persistence in environmental matrices, and low degradability. One way to address this is by combining remediation techniques that could overcome the constraints of traditional physio-chemical and biological remediation strategies. The upgraded concept of bioremediation to nano-bioremediation in this direction offers an efficient, economical, and eco-friendly approach to mitigate petroleum contaminants. Here, we review the unique attributes of different types of nanoparticles and their synthesis procedures in remediating various petroleum pollutants. This review also highlights the microbial interaction with different metallic nanoparticles and their consequential alteration in microbial as well as enzymatic activity which expedites the remediating process. Besides, the latter part of the review explores the application of petroleum hydrocarbon degradation and the application of nano supports as immobilizing agents for microbes and enzymes. Further, the challenges and the future prospects of nano-bioremediation have also been discussed.

Keywords: Enzymes; Immobilization; Microbes; Nanomaterial; Nanoparticles; Nanotoxicity

Biotransformation

Natalia Guevara, Marta Vázquez, Pietro Fagiolino. (Facultad de Química, Universidad de la República. Montevideo, Uruguay). Biotransformation/metabolism. Reference Module in Biomedical Sciences, Elsevier (2023): https://doi.org/10.1016/B978-0-12-824315-2.00336-5

Lipophilic xenobiotics and endobiotics are converted in the body by enzymatic reactions to hydrophilic products that are readily excreted in urine and/or bile. For this purpose, sequential enzymatic reactions take place, and several enzymes are involved. In addition, efflux transporters also have an important role in metabolism. Owing to the importance of biotransformation in reducing xenobiotics concentration and blocking functional groups, the process is subject to transcriptional regulation. Nevertheless, there are multiple factors that account for intra and interindividual variability in biotransformation.

Keywords: Age; Biotransformation; Efflux transporters; Enzymatic reactions; Epigenetics; Genetics; Phases I–II enzymes; Sex; Transcriptional regulation; Xenobiotic and drug metabolism

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The current study was aimed to enhance the solubility, dispersibility and biotransformation efficacy of ellagic acid (EA) by preparing food-derived ellagic acid-Undaria pinnatifida polysaccharides solid dispersion (EA/UPP SD). The results demonstrated that the solubility of EA/UPP SD was improved from 0.014 mg/mL to 0.383 mg/mL, and the enhancement was related to converting to a more amorphous state and restraining its self-aggregation during the mechanochemical process. The structure of EA/UPP SDs was mostly maintained by hydrogen bonds and hydrophobic interactions between EA and UPP. Moreover, the result of in vitro anaerobic incubations showed the biotransformation process was improved with EA/UPP SD addition to substrate due to the advance of microbial accessibility in EA dispersion. Altogether, these results indicated that the EA/UPP SDs expanded the application of EA by increasing the solubility and dispersity, and provided a theoretical basis for bioconversion efficiency enhancement.

Keywords: Ellagic acid; Undaria pinnatifida polysaccharides; Solid dispersion; Solubility; Dispersity; Biotransformation

Zhuo Gao, Shujun Yi, Mengzhu Xue, Kecheng Zhu, Rongyan Yang, Tiecheng Wang, Hongwen Sun, Lingyan Zhu. ([a]College of Natural Resources and Environment, Northwest A&F University, Yangling, Shaanxi Province 712100, PR China, [b]Key Laboratory of Plant Nutrition and The Agri-environment in Northwest China, Ministry of Agriculture, Yangling, Shaanxi 712100, PR China, [c]College of Environmental Science and Engineering, Nankai University, Tianjin 300071, PR China). Microbial biotransformation mechanisms of PFPiAs in soil unveiled by metagenomic analysis. Journal of Hazardous Materials, Volume 448 (2023) : 130896

As alternatives of long-chain PFASs (Poly- and perfluoroalkyl substances), perfluoroalkyl phosphinic acids (PFPiAs) are increasingly observed in the environment, but their environmental behaviors have not been well understood. Here, the microbial biotransformation of C6/C6 and C8/C8 PFPiA in two soils (Soil N and Y) was investigated. After 252 d and 330 d of incubation with PFPiAs in Soil N and Y respectively, the levels of PFPiAs decreased distinctly, accompanied by the increasing perfluorohexaphosphonic acid (PFHxPA) or perfluorooctanophosphonic acid (PFOPA) formation, magnifying PFPiAs were susceptible to C-P cleavage, which was also confirmed by the density functional theory calculations. The half-lives of the PFPiAs were longer than one year, while generally shorter in Soil N than in Soil Y and that of C6/C6 was shorter than C8/C8 PFPiA (392 d and 746 d in Soil N, and 603 and 1155 d in Soil Y, respectively). Metagenomic sequencing analysis revealed that Proteobacteria as the primary host of the potential functional genes related to CP bond cleavage might be the crucial phyla contributing to the biotransformation of PFPiAs. Meanwhile, the more intensive interactions between the microbes in Soil N consistently contribute to its greater capacity for transforming PFPiAs.

Keywords: PFPiAs; Biotransformation; DFT; Potential functional gene; CP bond cleavage

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The aim of this study was to explore the effects of herbal drug pharmacokinetic interactions on the biotransformation of molnupiravir and its metabolite β-D-N4-hydroxycytidine (NHC) in the blood and brain. To investigate the biotransformation mechanism, a carboxylesterase inhibitor, bis(4-nitrophenyl)phosphate (BNPP), was administered. Not only molnupiravir but also the herbal medicine Scutellaria formula-NRICM101 is potentially affected by coadministration with molnupiravir. However, the herb-drug interaction between molnupiravir and the Scutellaria formula-NRICM101 has not yet been investigated. We hypothesized that the complex bioactive herbal ingredients in the extract of the Scutellaria formula-NRICM101, the biotransformation and penetration of the bloodbrain barrier of molnupiravir are altered by inhibition of carboxylesterase. To monitor the analytes, ultrahigh-performance liquid chromatography tandem mass spectrometry (UHPLCMS/MS) coupled with the microdialysis method was developed. Based on the dose transfer from humans to rats, a dose of molnupiravir (100mg/kg, i.v.), molnupiravir (100mg/kg, i.v.) + BNPP (50mg/kg, i.v.), and molnupiravir (100mg/kg, i.v.) + the Scutellaria formula-NRICM101 extract (1.27g/kg, per day, for 5 consecutive days) were administered. The results showed that molnupiravir was rapidly metabolized to NHC and penetrated into the brain striatum. However, when concomitant with BNPP, NHC was suppressed, and molnupiravir was enhanced. The blood-to-brain penetration ratios were 2% and 6%, respectively. In summary, the extract of the Scutellaria formula-NRICM101 provides a pharmacological effect similar to that of the carboxylesterase inhibitor to suppress NHC in the blood, and the brain penetration ratio was increased, but the concentration is also higher than the effective concentration in the blood and brain.

Keywords: molnupiravir; β-D-N4-hydroxycytidine; herb-drug interaction; NRICM101; pharmacokinetics

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Universidad Autónoma de Nuevo León, UANL, San Nicolás de los Garza, Mexico, [d]Centro de Investigación en Biotecnología y Nanotecnología, Facultad de Ciencias Químicas, Parque de Investigación e Innovación Tecnológica, Universidad Autónoma de Nuevo León, Apodaca, Mexico, [e]Institute for Bioengineering, School of Engineering, University of Edinburgh, Edinburgh EH9 3JL, United Kingdom, [f]School of Natural and Environmental Sciences, Group of Biotechnology and Molecular Biology, The University of Newcastle, Devonshire Building, NE1 7RU, United Kingdom, [g]Department of Bioengineering, Mc Gill University, McConnell Engineering Building, 3480 University, Room 350, Montreal, Quebec H3A 0E9, Canada). New perspectives into Gluconobacter-catalysed biotransformations. Biotechnology Advances, Volume 65 (2023): 108127

Different from other aerobic microorganisms that oxidise carbon sources to water and carbon dioxide, Gluconobacter catalyses the incomplete oxidation of various substrates with regio- and stereoselectivity. This ability, as well as its capacity to release the resulting products into the reaction media, place Gluconobacter as a privileged member of a non-model microorganism class that may boost industrial biotechnology. Knowledge of new technologies applied to Gluconobacter has been piling up in recent years. Advancements in its genetic modification, application of immobilisation tools and careful designs of the transformations, have improved productivities and stabilities of Gluconobacter strains or enabled new bioconversions for the production of valuable marketable chemicals. In this work, the latest advancements applied to Gluconobacter-catalysed biotransformations are summarised with a special focus on recent available tools to improve them. From genetic and metabolic engineering to bioreactor design, the most recent works on the topic are analysed in depth to provide a comprehensive resource not only for scientists and technologists working on/with Gluconobacter, but for the general biotechnologist.

Keywords: Gluconobacter; Biotransformations; Whole-cell immobilisation; Genetic engineering; Industrial biotechnology; Process intensification; Green chemistry

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Volume 892 (2023): 164230

Biological aqua crust (BAC), as a novel biological crust with high arsenic (As) immobilization capacity, might be an ideal nature-based solution for As removal in mine drainage. This study examined the As speciation, binding fraction and biotransformation genes in the BACs to find out the underlying mechanism of As immobilization and biotransformation. Results showed that the BACs could immobilize As from mine drainage up to 55.8 g/kg, and their As immobilization concentrations were 1.3–6.9 times higher than that of sediments. Extremely high As

immobilization capacity was attributed to the processes of bioadsorption/absorption and biomineralization driven by Cyanobacteria. The high abundance of As(III) oxidation genes (27.0 %) enhanced microbial As(III) oxidation, resulting in >90.0 % of As(V) with low toxicity and mobility in the BACs. The increase in abundances of aioB, arsP, acr3, arsB, arsC and arsI with As was the key process for microbiota in the BACs for resistance to the As toxicity. In conclusion, our findings innovatively confirmed the potential mechanism of As immobilization and biotransformation mediated by the microbiota in the BACs and highlighted the important role of BACs for As remediation in mine drainage.

Keywords: Biological aqua crust; Arsenic remediation; Arsenic biotransformation genes; Mine drainage

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Benzotriazole ultraviolet stabilizers (BUVSs) are emerging pollutants that are widely detected in aquatic ecosystems. While structure-dependent effects of BUVSs are reported, the relationship between biotransformation and toxicity outcomes remains unclear. In this study, zebrafish embryos were exposed to two common BUVSs (UV-234 and UV-326) at 1, 10, and 100 µg/L for up to 7 days. Comparison of their uptake and biotransformation revealed that the bioaccumulation capacity of UV-234 was higher than that of UV-326, while UV-326 was more extensively biotransformed with additional conjugation reactions. However, UV-326 showed low metabolism due to inhibited phase II enzymes, which may result in the comparable internal concentrations of both BUVSs in larval zebrafish. Both BUVSs induced oxidative stress while decreased MDA, suggesting the disturbance of lipid metabolism. The subsequent metabolomic profiling revealed that UV-234 and UV-326 exerted different effects on arachidonic acid, lipid, and energy metabolism. However, both BUVSs negatively impacted the cyclic guanosine monophosphate / protein kinase G pathway. This converged metabolic change resulted in comparable toxicity of UV-234 and UV-326, which was confirmed by the induction of downstream apoptosis, neuroinflammation, and abnormal locomotion behavior. These data have important implications for understanding the metabolism, disposition, and toxicology of BUVSs in aquatic organisms.

Keywords: Benzotriazole ultraviolet stabilizers; Biotransformation; Metabolomics; Neuroinflammation; Locomotion behavior

Hefei Wang, Zeming Wang, Jibao Deng, Jian Wang, Yanzheng Gao. (Institute of Organic Contaminant Control and Soil Remediation, College of Resources and Environmental Sciences, Nanjing Agricultural University, Nanjing 210095, PR China).Conductive black carbon promoted biotransformation of undissolved 2, 2′-dinitrobiphenyl by mediating electron transfer. Science of The Total Environment, Volume 882(2023): 163619

With low bioaccessbility, persistence of the undissolved organic pollutants in soil and sediments poses threat to health of the resident. Although ubiquitous black carbon catalyzes a wide range of biogeochemical reactions in nature, its role in biotransformation of the compounds in non-aqueous phase like 2, 2′-nitrobiphenyl remains unclear. Reduction rate constants of 2, 2′-dinitrobiphenyl by Shewanella oneidensis MR-1 increased from 0.0044 h−1 by 7-fold to 0.035 h−1 in the presence of black carbons produced at pyrolysis temperature of 250–900 °C. Accordingly, electrical conductivity of black carbon was enhanced from 0 to 5.56 S·cm−1. The reactivity of black carbon for catalyzing the biotransformation positively correlated with its electrical conductivity (R2 > 0.89), which was strongly associated with conductive graphitic clusters in it. The surface oxygenated groups in black carbon were likely not involved in the bioreduction. This work attaches importance to role of the ubiquitous black carbon in natural biotransformation of the undissolved pollutants, and elucidates new mechanism for the biotransformation.

Keywords: Black carbon; Shewanella oneidensis MR-1; Biotransformation; 2, 2′-nitrobiphenyl; electron transfer

Camila L.V. Bastolla, Daína Lima, Jacó J. Mattos, Vera H.V. Dias, Bárbara P.H. Righetti, Carlos H.A.M. Gomes, Herculano Cella, Isis M.M. Reis, Miguel Saldaña-Serrano, Clarissa P. Ferreira, Márcia C. Bícego, Satie Taniguchi, Flávia L. Zacchi, Afonso C.D. Bainy. ([a] Laboratory of Biomarkers of Aquatic Contamination and Immunochemistry, LABCAI, Department of Biochemistry, Federal University of Santa Catarina, UFSC, Florianópolis, Santa Catarina, Brazil, [b]Aquaculture Pathology Research Center, NEPAQ, Department of Aquaculture, Federal University of Santa Catarina, UFSC, Florianópolis, Santa Catarina, Brazil, [c]Laboratory of Marine Mollusks, LMM, Department of Aquaculture, Federal University of Santa Catarina, UFSC, Florianópolis, Santa Catarina, Brazil, [d]Laboratory of Marine Organic Chemistry, Oceanographic Institute, University of São Paulo, São Paulo, Brazil, [e]Laboratory of Algae Cultivation, LCA, Department of Aquaculture, Federal University of Santa Catarina, UFSC, Florianópolis, Brazil, [f]Fishery Engineering and Biological Sciences Department, Santa Catarina State University, Laguna 88790-000, Brazil). Comparative biochemical and molecular responses of biotransformation and antioxidant systems in three species of Crassostrea (Sacco, 1897) oysters exposed to chrysene. Comparative Biochemistry and Physiology Part C: Toxicology & Pharmacology, Volume 270 (2023): 109642

Chrysene (CHR) is among the most persistent polycyclic aromatic hydrocarbons (PAH) in water and a priority compound for pollutants monitoring, due to its carcinogenic, mutagenic and genotoxic potential. Aquatic animals exposed to CHR may present alterations of biomarkers involved in the biotransformation and oxidative stress-related parameters. The aim of this study was to investigate differences in antioxidant and biotransformation (phase I and II) systems of Crassostrea gigas, C. gasar and C. rhizophorae and its effects resulting from CHR exposure. Adult oysters of these species were exposed to 10 μg L−1 of CHR for 24 h and 96 h. In gills, the transcripts CYP1-like, CYP2-like, CYP2AU1-like, GSTO-like, MGST-like, SULT-like were evaluated after 24 h of exposure. The activity of SOD, CAT, GPx, GR and G6PDH were analyzed in gills and digestive glands after 96 h of exposure. CHR bioaccumulated in tissues. Differences in the remaining levels of CHR in water after 96 h were observed in aquaria containing C. gigas or C. gasar oysters and may be associated to the different filtration rates between these species. Downregulate of biotransformation genes were observed in gills of C.

gasar (CYP2AU1-like and GSTO-like) and C. rhizophorae (CYP1-like1, CYP2-like, MGST-like and SULT-like), suggesting that biotransformation responses may be species-specific. Differential activity of antioxidant enzymes were observed in gills and digestive gland of oysters exposed to CHR. Biochemical responses suggested that C. gigas and C. gasar are more responsive to CHR. Differential responses observed among the three Crassostrea species can be related to evolutionary differences, ecological niches and adaptation to environment.

Keywords: PAH; Oyster; Biomarker; Oxidative stress; Cytochrome P450

Carolin Seller, Laura Varga, Elizabeth Börgardts, Bernadette Vogler, Elisabeth Janssen, Heinz Singer, Kathrin Fenner, Mark Honti. ([a]Eawag, Swiss Federal Institute of Aquatic Science and Technology, 8600 Dübendorf, Switzerland, [b]Department of Chemistry, University of Zürich, 8057 Zürich, Switzerland, [c]Department of Sanitary and Environmental Engineering, Budapest University of Technology and Economics, 1111 Budapest, Hungary, [d]ELKH-BME Water Research Group, 1111 Budapest, Hungary). Do biotransformation data from laboratory experiments reflect micropollutant degradation in a large river basin? Water Research, Volume 235(2023): 119908

Identifying a chemical's potential for biotransformation in the aquatic environment is crucial to predict its fate and manage its potential hazards. Due to the complexity of natural water bodies, especially river networks, biotransformation is often studied in laboratory experiments, assuming that study outcomes can be extrapolated to compound behavior in the field. Here, we investigated to what extent outcomes of laboratory simulation studies indeed reflect biotransformation kinetics observed in riverine systems. To determine in-field biotransformation, we measured loads of 27 wastewater treatment plant effluent-borne compounds along the Rhine and its major tributaries during two seasons. Up to 21 compounds were detected at each sampling location. Measured compound loads were used in an inverse model framework of the Rhine river basin to derive k’bio,field values – a compound-specific parameter describing the compounds’ average biotransformation potential during the field studies. To support model calibration, we performed phototransformation and sorption experiments with all the study compounds, identifying 5 compounds that are susceptible towards direct phototransformation and determining Koc values covering four orders of magnitude. On the laboratory side, we used a similar inverse model framework to derive k’bio,lab values from water-sediment experiments run according to a modified OECD 308-type protocol. The comparison of k’bio,lab and k’bio,field revealed that their absolute values differed, pointing towards faster transformation in the Rhine river basin. Yet, we could demonstrate that relative rankings of biotransformation potential and groups of compounds with low, moderate and high persistence agree reasonably well between laboratory and field outcomes. Overall, our results provide evidence that laboratory-based biotransformation studies using the modified OECD 308 protocol and k’bio values derived thereof bear considerable potential to reflect biotransformation of micropollutants in one of the largest European river basins.

Keywords: Biotransformation kinetics; Laboratory-field comparison; Micropollutants; Bayesian model frameworks

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Microbiology of the Czech Academy of Sciences, Třeboň, Czech Republic). Green alga Chlamydomonas reinhardtii can effectively remove diclofenac from the water environment – A new perspective on biotransformation. Journal of Hazardous Materials, Volume 455, (2023): 131570

The use of unicellular algae to remove xenobiotics (including drugs) from wastewaters is one of the rapidly developing areas of environmental protection. Numerous data indicate that for efficient phycoremediation three processes are important, i.e. biosorption, bioaccumulation, and biotransformation. Although biosorption and bioaccumulation do not raise any serious doubts, biotransformation is more problematic since its products can be potentially more toxic than the parent compounds posing a threat to organisms living in a given environment, including organisms that made this transformation. Thus, two questions need to be answered before the proper algae strain is chosen for phycoremediation, namely what metabolites are produced during biotransformation, and how resistant is the analyzed strain to a mixture of parent compound and metabolites that appear over the course of culture? In this work, we evaluated the remediation potential of the model green alga Chlamydomonas reinhardtii in relation to non-steroidal anti-inflammatory drugs (NSAIDs), as exemplified by diclofenac. To achieve this, we analysed the susceptibility of C. reinhardtii to diclofenac as well as its capability to biosorption, bioaccumulation, and biotransformation of the drug. We have found that even at a relatively high concentration of diclofenac the algae maintained their vitality and were able to remove (37.7%) DCF from the environment. A wide range of phase I and II metabolites of diclofenac (38 transformation products) was discovered, with many of them characteristic rather for animal and bacterial biochemical pathways than for plant metabolism. Due to such a large number of detected products, 18 of which were not previously reported, the proposed scheme of diclofenac transformation by C. reinhardtii not only significantly contributes to broadening the knowledge in this field, but also allows to suggest possible pathways of degradation of xenobiotics with a similar structure. It is worth pointing out that a decrease in the level of diclofenac in the media observed in this study cannot be fully explained by biotransformation (8.4%). The mass balance analysis indicates that other processes (total 22%), such as biosorption, a non-extractable residue formation, or complete decomposition in metabolic cycles can be involved in the diclofenac disappearance, and those findings open the prospects of further research.

Keywords: Non-steroidal anti-inflammatory drug; Diclofenac; Biotransformation; Chlamydomonas reinhardtii

Xin Wang, Qian Wu, Zhou-Zheng Wang, Wen-Jie Ma, Jun Qiu, Nian-Si Fan, Ren-Cun Jin. ([a]School of Engineering, Hangzhou Normal University, Hangzhou 310018, China, [b]School of Life and Environmental Sciences, Hangzhou Normal University, Hangzhou 311121, China). Biotransformation-mediated detoxification of roxarsone in the anammox process: Gene regulation mechanism. Chemical Engineering Journal, Volume 467 (2023): 143449

Roxarsone is a common organoarsenic feed additive used in livestock and poultry breeding, while the ecotoxicity of organic arsenic remains a concern. Therefore, the effects of roxarsone on the anaerobic ammonium oxidation (anammox) process and responding mechanism were investigated in this study. The minimum nitrogen removal efficiency (NRE) of anammox process was 64.0% under roxarsone stress. Meanwhile, the reactive oxygen species (ROS) content increased by 1.5–2.3 times, and electron transport system activity (ETSA) decreased by

22.9±5.0%. The total antioxidant capacity (T-AOC) level first increased and then decreased, resulting in an imbalance between ROS production and antioxidant defense. The copy numbers of arsenic resistance genes significantly increased, indicating that roxarsone was transformed in the anammox system. Co-occurrence networks manifested that arsenic resistance genes were significantly positively correlated with dominant genera. The detoxification mediated by biotransformation mitigated the toxicity of roxarsone and the side effects of oxidative stress. This work provides insights into the response and mechanism of anammox consortia to roxarsone and promotes the efficient treatment of wastewater containing organic arsenic by the anammox process.

Keywords: Anammox; Roxarsone; Arsenic biotransformation; ROS; Oxidative stress; Microbial community

Hiep T. Nguyen, Tien H. Du, Jin Gi Hong, Seungdae Oh. ([a]Department of Civil Engineering, KyungHee University, Yongin-si, Gyeonggi-do, Republic of Korea, [b]Department of Civil Engineering and Construction Engineering Management, California State University, Long Beach, CA, United States). Cometabolic biotransformation mediates the detoxification of oxytetracycline in Flavobacterium-enriched microbiome. Journal of Environmental Chemical Engineering, Volume 11, Issue 3 (2023): 109932

Oxytetracycline (OTC), a widely used antibiotic that is readily detectable in the environment, potentially has a number of negative ecological consequences. The present study revealed the key role of the cometabolic breakdown of OTC in activated sludge microbiomes, which led to a high removal efficiency and detoxification of both OTC and its derivatives. An AS bioreactor was established to treat environmentally relevant levels of OTC. The bioreactor achieved an overall OTC removal efficiency of 94–97% at the steady state, with cometabolic biotransformation as the primary contributor to this ahead of other removal routes such as direct metabolic biodegradation, biosorption, and phosphorolysis. A novel biotransformation pathway for OTC proposed in this study involved dehydration, hydroxylation, ring cleavage, and alcohol dehydrogenation, distinguishing it from previously reported pathways. Although transformation products with potentially higher toxicity than OTC formed during the biotransformation process, the AS microbiome eliminated the overall toxicity of both OTC and its derivatives, as illustrated by both molecular structure-based toxicity simulations and antimicrobial susceptibility testing. Analysis of microbiome sequence data revealed the bacterial populations potentially facilitating cometabolic (e.g., Tolumonas) and direct metabolic (e.g., Flavobacterium) biotransformation. Overall, our study provides new insights into the removal routes and kinetics for OTC in AS microbiomes and the key species that potentially promote OTC transformation and detoxification.

Keywords: Oxytetracycline; Cometabolism; Direct metabolism; Biotransformation; Detoxification; Flavobacterium

Donglin Wang, Quan Ma, Hui Lin, Jie Zhou, Suxia Yuan, Baiwen Ma, Yaohui Bai, Jiuhui Qu. ([a]Key Laboratory of Drinking Water Science and Technology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China, [b]University of Chinese Academy of Sciences, Beijing, 100049, China, [c]Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, Beijing, 100081, China). Enhancement of micropollutant biotransformation by adding manganese sand in constructed wetlands. Heliyon, Volume 9, Issue 4 (2023): e15092

Recent investigations have shown that the addition of manganese (Mn) sand to constructed wetlands (i.e., Mn-amended CWs) can improve the performance of organic micropollutants

(MPs) removal. In addition to the direct oxidation and adsorption of Mn oxides, the indirect role of Mn oxides in MP biotransformation is crucial to the removal of MPs but has seldom been referred to. Herein, we constructed lab-scale CWs with or without the addition of natural Mn sand (~35% Mn oxides) to decipher the influence of Mn oxides on the biotransformation of the six selected MPs which commonly existed in the wastewater. The experimental results showed that the addition of Mn sand to CWs can improve the removal of MPs (8.48% atrazine, 13.16% atenolol, and 6.27% sulfamethoxazole [pairwise Wilcoxon test $p < 0.05$]). Combining the detection of transformation products and metagenomic sequencing, we found that the enhanced removal of atrazine in the Mn-amended CWs was mainly due to the bioaugmented hydroxylation process. The enrichment of biotransformation-related genes and associated microbes of atenolol and sulfamethoxazole in Mn-amended CWs indicated that the addition of Mn sand to CWs can strengthen the biotransformation of MPs. Furthermore, we found that these MP-biodegrading microbes were widely present in the full-scale CWs. Overall, our research provides fundamental information and insights for further application of Mn-amended CWs in MP removal.

Keywords: Wetland treatment; Manganese oxides; Organic micropollutants; Metagenomic assembled genomes; Biodegradation

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The measurement of nanoparticles (NPs) in a biological matrix is essential in various toxicity studies. However, the current knowledge has limitations in differentiating particulate and ionic forms and further identification of their biotransformation. Herein, we evaluate the biotransformation and differential lung clearance kinetics of particulate and ionic forms using PEGylated silver NPs (AgNP-PEGs; 47.51 nm) and PEGylated gold NPs (AuNP-PEGs; 11.76 nm). At 0, 3, and 6 h and 1, 3, 7, and 14 days after a single pharyngeal aspiration in mice at 25 μg/mouse, half of the lung is digested by proteinase K (PK) to separate particulates and ions, and the other half is subjected to the acid digestion method for comparison. The quantitative and qualitative evaluation of lung clearance kinetics suggests that AgNP-PEGs are quickly dissolved and transformed into insoluble silver sulfide (Ag2S), which shows a fast-clearing early phase (0 −6 h; particle T1/2: 4.8 h) and slow-clearing late phase (1 −14 days; particle T1/2: 13.20 days). In contrast, AuNP-PEGs were scarcely cleared or biotransformed in the lungs for 14 days. The lung clearance kinetics of AgNPs and biotransformation shown in this study can be informed by the PK digestion method and cannot be obtained using the acid digestion method.

Keywords: Particokinetics; Lung burden; Dissolution; Toxicokinetics; Inhalation

Dandan Cao, Xiaomei Zhu, Jian Zhang, Xuedong Wang. (State Key Laboratory of Bioreactor Engineering, East China University of Science and Technology, 130 Meilong Road, Shanghai 200237, China). A combined strategy to enhance phytosterols biotransformation to 22-hydroxy-23,24-bisnorchol-4-ene-3-one by Mycobacterium neoaurum. Process Biochemistry, Volume 128 (2023): 94-97

A combined strategy for the overexpression of cholesterol oxidase M2 (ChoM2) and in situ removal of inhibitory intermediates was applied to promote the production efficiency of 22-hydroxy-23,24-bisnorchol-4-ene-3-one (HBC) from phytosterols (PS) biotransformation by Mycobacterium neoaurum (M. neoaurum). Firstly, the rate-limiting step of PS to phytostenones was overcome by increasing the activity of ChoM2. Under this condition, PS transformation period was reduced from 84 h to 72 h, and the productivity of HBC was increased by 17%, in g/L/d from 9.36 (84 h) to 10.92 (72 h). Meanwhile, the overexpressed ChoM2 caused an excessive accumulation of the inhibitory intermediates, phytostenones, which hindered PS biotransformation. Accordingly, in situ removal of the inhibitory intermediates through adding 5 g/L of resin D101 (a macroporous styrene-divinylbenzene copolymer resin) at the beginning of the biotransformation further reduced the PS transformation time to 60 h, and the productivity was increased by 41% from 9.36 to 13.21 g/L/d.

Keywords: Phytosterols biotransformation; Cholesterol oxidase (ChoM2); 22-Hydroxy-23,24-bisnorchol-4-ene-3-one; Phytostenones; In situ removal

Biomarker

Rafael Paez, Michael N. Kammer, Nicole T. Tanner, Samira Shojaee, Brent E. Heideman, Tobias Peikert, Meridith L. Balbach, Wade T. Iams, Boting Ning, Marc E. Lenburg, Christopher Mallow, Lonny Yarmus, Kwun M. Fong, Stephen Deppen, Eric L. Grogan, Fabien Maldonado. ([a]Department of Medicine, Division of Allergy, Pulmonary and Critical Care Medicine, Vanderbilt University Medical Center, Nashville, TN, [b]Department of Medicine, Division of Hematology-Oncology, Vanderbilt University Medical Center, Nashville, TN, [c]Department of Thoracic Surgery, Vanderbilt University Medical Center, Nashville, TN, [d]Department of Medicine, Division of Pulmonary, Critical Care, Allergy and Sleep Medicine, Medical University of South Carolina, Charleston, SC, [e]Department of Medicine, Division of Pulmonary and Critical Care Medicine, Mayo Clinic, Rochester, MN, [f]Vanderbilt University School of Medicine, Nashville, TN, [g]Vanderbilt-Ingram Cancer Center, Nashville, TN, [h]Department of Medicine, Section of Computational Biomedicine, Boston University School of Medicine, Boston, MA, [i]Division of Pulmonary, Critical Care and Sleep Medicine, University of Miami, Miami, FL, [j]Division of Pulmonary and Critical Care Medicine, Johns Hopkins University, Baltimore, MD, [k]University of Queensland Thoracic Research Centre, The Prince Charles Hospital, Brisbane, QLD, Australia, [l]Tennessee Valley Healthcare System, Nashville, TN). Update on biomarkers for the stratification of indeterminate. pulmonary nodules, Chest, (2023): https://doi.org/10.1016/j.chest.2023.05.025

Topic Importance: Lung cancer is the leading cause of cancer related deaths. Early detection and diagnosis are critical as survival decreases with advanced stages. Approximately 1.6 million nodules are incidentally detected every year on chest computed tomography in the United States.

This number of nodules identified is likely much larger after accounting for screening detected nodules. Most of these nodules, whether incidentally or screening-detected, are benign. Despite this, many patients undergo unnecessary invasive procedures to rule out cancer as our current stratification approaches are suboptimal, particularly for intermediate probability nodules. Thus, non-invasive strategies are urgently needed.

Review Findings: Biomarkers have been developed to assist through the continuum of lung cancer care and include blood protein-based biomarkers, liquid biopsies, quantitative imaging analysis (radiomics), exhaled volatile organic compounds, bronchial or nasal epithelium genomic classifiers, among others. While many biomarkers have been developed, few have been integrated into clinical practice as they lack clinical utility studies demonstrating improved patient centered outcomes.

Summary: Rapid technological advances and large network collaborative efforts will continue to drive the discovery and validation of many novel biomarkers, but ultimately, randomized clinical utility studies demonstrating improved patient outcomes will be required to bring biomarkers into clinical practice.

Keywords: biomarkers; early detection; indeterminate pulmonary nodules; lung cancer

Marco Garcia-Vaquero, Armin Mirzapour-Kouhdasht. (School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland). A review on proteomic and genomic biomarkers for gelatin source authentication: Challenges and future outlook. Heliyon, Volume 9, Issue 6 (2023): e16621

Biomarkers are compounds that could be detected and used as indicators of normal and/or abnormal functioning of different biological systems, including animal tissues and food matrices. Gelatin products of animal origin, mainly bovine and porcine, are currently under scrutiny mainly due to the specific needs of some sectors of the population related to religious beliefs and their dietary prohibitions, as well as some potential health threats associated with these products. Thus, manufacturers are currently in need of a reliable, convenient, and easy procedure to discern and authenticate the origin of animal-based gelatins (bovine, porcine, chicken, or fish). This work aims to review current advances in the creation of reliable gelatin biomarkers for food authentication purposes based on proteomic and DNA biomarkers that could be applied in the food sector. Overall, the presence of specific proteins and peptides in gelatin can be chemically analysed (i.e., by chromatography, mass spectroscopy, electrophoresis, lateral flow devices, and enzyme-linked immunosorbent assay), and different polymerase chain reaction (PCR) methods have been applied for the detection of nucleic acid substances in gelatin. Altogether, despite the fact that numerous methods are currently being developed for the purpose of detecting gelatin biomarkers, their widespread application is highly dependent on the cost of the equipment and reagents as well as the ease of use of the various methods. Combining different methods and approaches targeting multiple biomarkers may be key for manufacturers to achieve reliable authentication of gelatin's origin.

Keywords: Proteomic; Genomic; Biomarker; Gelatin; Halal; Kosher

Jan Pańczak, Paweł Kosakowski, Adam Zakrzewski. (AGH University of Science and Technology, Faculty of Geology, Geophysics and Environmental Protection, 30 Mickiewicza Av., 30-059 Krakow, Poland). Biomarkers in fossil resins and their

palaeoecological significance. Earth-Science Reviews, Volume 242 (2023): https://doi.org/10.1016/j.earscirev.2023.104455

Fossil resins are the one of several fossil tree products, together with leaves, wood, seeds, or pollen. As an emanation of organic matter, resins are made of organic compounds, predominantly terpenes. Terpenes are broadly identified from various living organisms such as higher plants, fungi, or bacteria. In fossil resins, these compounds occur in several forms – usually mono-, sesqui-, di-, and tri-terpenes. Some terpenes present in fossil resins provide information about their ancestors and the paleoenvironmental conditions during the resin expulsion. These compounds, known as biomarkers, preserve the original shapes of molecules or occur as altered structures. Due to the chromatographic methods, insight into the chemical structure of fossil resins is enabled and biomarkers might be detected. In this study, information about the state-of-the-art chromatographic research concerning fossil resins was gathered. The biomarkers found in fossil resins were divided into compounds providing chemotaxonomic (botanical biomarkers) and environmental information (other biomarkers). Botanical biomarkers provide high utility in paleobotanical studies. The initial identification of a source tree, gymnosperm, or angiosperm is possible, due to certain chemical patterns of these types. Moreover, in chemotaxonomic studies, the restriction to more specific taxonomic levels, especially to the level of family, is usually possible, thanks to the occurrence of specific biomarkers. Many terpenes that are known to have an ecological function in extant plants are also found in fossil resins; however, their presence does not clearly indicate the ecological properties of trees due to the advanced alterations of the chemical structure. However, some specific environmental biomarkers found in fossil resins (e.g. succinic acid or rosane) might provide information about the paleoenvironment during the resin deposition.

Keywords: Gas chromatography–mass spectrometry; Amber; Terpenes; Chemical structure; Chemotaxonomy

Sheetal Rajpal, Ankit Rajpal, Manoj Agarwal, Virendra Kumar, Ajith Abraham, Divya Khanna, Naveen Kumar..([a]Department of Computer Science, University of Delhi, Delhi, India, [b]Department of Computer Science, Hans Raj College, University of Delhi, Delhi, India, [c]Department of Nuclear Magnetic Resonance Imaging, All India Institute of Medical Sciences, New Delhi, India, [d]Faculty of Computing and Data Science, FLAME University, Lavale, Pune, Maharashtra, India, [e]Functional Genomics Lab, Institute of Genomics and Integrative Biology, Delhi (IGIB), India), XAI-CNVMarker: Explainable AI-based copy number variant biomarker discovery for breast cancer subtypes, Biomedical Signal Processing and Control, Volume 84 (2023): 104979

Breast cancer is a leading cause of cancer-related deaths among women. The multi-omic data has revolutionized the methodology to unravel molecular heterogeneity in breast cancer. As genetic variations captured from Copy Number Variation (CNV) data are considered the most stable amongst the multi-omic data, it leads to robust biomarkers. Thus, this paper targets the discovery of a set of CNV biomarkers for dissecting this heterogeneity. The existing algorithms yield biomarkers, too huge to be interpreted clinically. So, in this paper, we have proposed XAI-CNVMarker—an explainable AI-based post-hoc biomarker discovery framework to discover a small set of interpretable biomarkers. We exploit the power of deep learning to build DLmodel—a deep learning model for breast cancer classification. Subsequently, the trained model is analyzed using different explainable AI methods to arrive at a set of 44 CNV biomarkers. Using 5-fold cross-validation, we obtained a classification accuracy of 0.712 (± 0.048) at a 95% confidence interval. Gene set analysis revealed 37 subtype-specific enriched

Reactome and Kegg pathways, 21 druggable genes, and 13 biomarkers linked with the prognostic outcome. Finally, we validated the efficacy of the identified biomarkers on METABRIC. Thus, the proposed framework demonstrates the role of explainable AI in discovering clinically reliable biomarkers.

Keywords: Explainable AI; CNV; Biomarker; Deep learning; Breast cancer subtypes; Gradient

Rui Ji, Yue Li, Ruihao Huang, Jingkang Xiong, Xiaoqi Wang, Xi Zhang. ([a]Medical Center of Hematology, Xinqiao Hospital, State Key Laboratory of Trauma, Burn and Combined Injury, Army Medical University, Chongqing 400037, China, [b]Jinfeng Laboratory, Chongqing 400037, China) Recent advances and research progress in biomarkers for chronic graft versus host disease, Critical Reviews in Oncology/Hematology, Volume 186 (2023): 103993

Chronic graft-versus host disease (cGVHD) is a major risk for patients undergoing allogeneic hematopoietic stem cell transplantation. With the emergence of novel therapies and the increased understanding of the mechanisms underlying cGVHD, there are more options for cGVHD treatment. Regardless of improvements in treatment, diagnosis mainly depends on identification of symptoms, which makes precise treatment a challenge. Numerous biomarkers for cGVHD have been validated and have demonstrated strong associations with prognosis and response to treatment. The most common biomarkers mainly include critical types of immune cells, chemokines, cytokines, microRNAs, and autoantibodies, all of which play important roles in the development of cGVHD. Compared to traditional tools, biomarkers have several advantages, for example, they can be applied for early diagnosis, to identify cGVHD risk before onset, and predict which therapy is most likely to benefit patients. In this review, we summarize biomarkers with potential clinical value and discuss future applications.

Keywords: Hematopoietic stem cell transplantation; Chronic graft-versus-host disease; Cellular biomarker

Audrey Catteau, Antoine Le Guernic, Mélissa Palos Ladeiro, Odile Dedourge-Geffard, Marc Bonnard, Isabelle Bonnard, Laurence Delahaut, Anne Bado-Nilles, Jean-Marc Porcher, Christelle Lopes, Olivier Geffard, Alain Geffard. ([a]Université de Reims Champagne-Ardenne (URCA), UMR-I 02 SEBIO, UFR Sciences Exactes et Naturelles, Campus Moulin de La Housse, BP 1039, 51687, Reims, France, [b]Institut National de L'Environnement et des Risques (INERIS), UMR-I 02 SEBIO (Stress Environnementaux et Biosurveillance des Milieux Aquatiques), BP 2, 60550, Verneuil-en-Halatte, France, [c]Univ Lyon, Université Lyon 1, CNRS, Laboratoire de Biométrie et Biologie Evolutive UMR 5558, 69622, Villeurbanne, France, [d]INRAE, UR RiverLy, Laboratoire D'écotoxicologie, F-69625, Villeurbanne, France) Integrative biomarker response - Threshold (IBR-T): Refinement of IBRv2 to consider the reference and threshold values of biomarkers, Journal of Environmental Management, Volume 341 (2023): 118049

The Integrated Biomarker Response (IBR) is one of the most used index in biomonitoring, especially the IBRv2 integrating a reference condition. However, some limitations remain for its routine and large-scale use. The IBRv2 is proportional to the total number of biomarkers, is dependent on the nature of biomarkers and considers all biomarkers modulations, even small and biologically non-significant. In addition, IBRv2 relies on reference values but the references are often different between each study, making it difficult to compare results between studies and/or

campaigns. To overcome these limitations, the present work proposed a new index called IBR-T ("Integrated Biomarker Response – Threshold") which considers the threshold values of biomarkers by limiting the calculation of the IBR value to biomarkers with significant modulations. The IBRv2 and the IBR-T were calculated and compared on four datasets from active biomonitoring campaigns using Dreissena polymorpha, a bivalve widely used in freshwater biomonitoring studies. The comparison between indices has demonstrated that the IBR-T presents a better correlation ($0.907 < r2 < 0.998$) with the percentage of biomarkers significantly modulated than the IBRv2 ($0.002 < r2 < 0.759$). The IBRv2 could not be equal to 0 ($0.915 <$ intercept <1.694) because the value was dependent on the total number of biomarkers, whereas the IBR-T reached 0 when no biomarker was significantly modulated, which appears more biologically relevant. The final ranking of sites was different between the two index and the IBR-T ranking tends to be more ecologically relevant that the IBRv2 ranking. This IBR-T have shown an undeniable interest for biomonitoring and could be used by environmental managers to simplify the interpretation of large datasets, directly interpret the contamination status of the site, use it to decision-making, and finally to easily communicate the results of biomonitoring studies to the general public.

Keywords: Dreissena polymorpha; Biomonitoring; Integration; Diagnostic; Water quality; Caging

Erica E. Fortune, Alexandra K. Zaleta, M. Claire Saxton. ([a]Cancer Support Community, Research and Training Institute, Philadelphia, PA, USA, [b]Cancer Support Community, Washington, DC, USA) Biomarker testing communication, familiarity, and informational needs among people living with breast, colorectal, and lung cancer, Patient Education and Counseling, Volume 112 (2023): 107720

Objectives-This study aims to characterize patient experiences with biomarker testing, including history of biomarker testing, related communication and education, self-perceived familiarity and informational needs.

Methods-436 U.S. adults diagnosed with lung (38%), colorectal (35%) or breast cancer (27%) from 2018 to 2022 completed a survey. Two logistic regressions were conducted to predict patients' familiarity with biomarker testing and informational needs.

Results-Despite high biomarker testing rates (85%), half of respondents reported low familiarity with biomarker testing and three-quarters reported outstanding informational needs. Regression models indicate those patients who have greater health literacy and report having conversations with their oncologists about biomarker testing have more familiarity with biomarker testing and less informational needs, even after controlling for important sociodemographic factors.

Conclusions-There is an opportunity to improve patients' familiarity with biomarker testing and decrease outstanding informational needs by focusing on factors such as health literacy and patient-provider communication, which could further cultivate patients' understanding of the importance of biomarker testing in cancer care.

Practice implications-These findings underscore the importance of patient-provider relationships and the need for additional tools that assist providers in assessing patients' health literacy and facilitating conversations with patients, especially those focused on complex topics such as biomarker testing.

Keywords: Biomarkers; Cancer; Communication; Health literacy; Patient education

Ross L Prentice, Sowmya Vasan, Lesley F Tinker, Marian L Neuhouser, Sandi L Navarro, Daniel Raftery, GA Nagana Gowda, Mary Pettinger, Aaron K Aragaki, Johanna W Lampe, Ying Huang, Linda Van Horn, JoAnn E Manson, Robert B Wallace, Yasmin Mossavar-Rahmani, Jean Wactawski-Wende, Simin Liu, Linda Snetselaar, Barbara V Howard, Rowan T Chlebowski, Cheng Zheng. ([1]Division of Public Health Sciences, Fred Hutchinson Cancer Center, Seattle, WA, United States, [2]School of Public Health, University of Washington, Seattle, WA, United States, [3]Department of Anesthesiology and Pain Medicine, University of Washington, Seattle, WA, United States, [4]Department of Preventive Medicine, Northwestern University, Chicago, IL, United States, [5]Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, United States, [6]College of Public Health, University of Iowa, Iowa City, IA, United States, [7]Department of Epidemiology and Population Health, Albert Einstein College of Medicine, Bronx, NY, United States, [8]Department of Epidemiology and Environmental Health, University of Buffalo, Buffalo, NY, United States, [9]Department of Epidemiology, School of Public Health, Brown University, Providence, RI, United States, [10]Department of Medicine, Georgetown University Medical Center, and MedStar Health Research Institute, Hyattsville, MD, United States, [11]The Lundquist Institute, Torrance, CA, United States, [12]Department of Biostatistics, University of Nebraska Medical Center, Omaha, NE, United States) Metabolomics Biomarkers for Fatty Acid Intake and Biomarker-Calibrated Fatty Acid Associations with Chronic Disease Risk in Postmenopausal Women, The Journal of Nutrition (2023): 2663-2677

Background-A substantial observational literature relating specific fatty acid classes to chronic disease risk may be limited by its reliance on self-reported dietary data.

Objectives-We aimed to develop biomarkers for saturated (SFA), monounsaturated (MUFA), and polyunsaturated (PUFA) fatty acid densities, and to study their associations with cardiovascular disease (CVD), cancer, and type 2 diabetes (T2D) in Women's Health Initiative (WHI) cohorts.

Methods-Biomarker equations were based primarily on serum and urine metabolomics profiles from an embedded WHI human feeding study (n = 153). Calibration equations were based on biomarker values in a WHI nutritional biomarker study (n = 436). Calibrated intakes were assessed in relation to disease incidence in larger WHI cohorts (n = 81,894). Participants were postmenopausal women, aged 50–79 when enrolled at 40 United States Clinical Centers (1993–1998), with a follow-up period of ~20 y.

Results-Biomarker equations meeting criteria were developed for SFA, MUFA, and PUFA densities. That for SFA density depended somewhat weakly on metabolite profiles. On the basis of our metabolomics platforms, biomarkers were insensitive to trans fatty acid intake. Calibration equations meeting criteria were developed for SFA and PUFA density, but not for MUFA density. With or without biomarker calibration, SFA density was associated positively with risk of CVD, cancer, and T2D, but with small hazard ratios, and CVD associations were not statistically significant after controlling for other dietary variables, including trans fatty acid and fiber intake. Following this same control, PUFA density was not significantly associated with CVD risk, but there were positive associations for some cancers and T2D, with or without biomarker calibration.

Conclusions-Higher SFA and PUFA diets were associated with null or somewhat higher risk for clinical outcomes considered in this population of postmenopausal United States women. Further research is needed to develop even stronger biomarkers for these fatty acid densities and their major components. This study is registered with clinicaltrials.gov identifier: NCT00000611.

Keywords: biomarker; cancer; cardiovascular disease; type 2 diabetes; metabolomics; saturated fatty acids; monounsaturated fatty acids; polyunsaturated fatty acids

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Biomarker detection has attracted increasing interest in recent years due to the minimally or non-invasive sampling process. Single entity analysis of biomarkers is expected to provide real-time and accurate biological information for early disease diagnosis and prognosis, which is critical to the effective disease treatment and is also important in personalized medicine. As an innovative single entity analysis method, nanopore sensing is a pioneering single-molecule detection technique that is widely used in analytical bioanalytical fields. In this review, we overview the recent progress of nanopore biomarker detection as new approaches to disease diagnosis. In highlighted studies, nanopore was focusing on detecting biomarkers of different categories of communicable and noncommunicable diseases, such as pandemic COVID-19, AIDS, cancers, neurologic diseases, etc. Various sensitive and selective nanopore detecting strategies for different types of biomarkers are summarized. In addition, the challenges, opportunities, and direction for future development of nanopore-based biomarker sensors are also discussed.

Keywords: Nanopore; Biomarkers; Analytical bioanalytical methods; Single-molecule analysis; Human diseases; Lab assays and diagnosis

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In this review, we evaluate the role of fluid biomarkers related to neurodegenerative diseases. Such conditions present diagnostic challenges due to phenotypic heterogeneity, longitudinal evolution, overlap between diagnostic entities, and variability in progression. Biomarkers can potentially provide insight into diagnosis, progression, prognostication, and treatment efficacy. This review covers recent advances in fluid biomarkers including beta-amyloid, tau protein, neurofilament light chain, alpha-synuclein and glial fibrillary protein, and briefly touches upon imaging biomarkers. For each biomarker, we discuss the pathophysiological correlates, clinical uses, accuracy, and limitations.

Keywords: Biomarkers; Neurodegenerative Disease; Alzheimer's Disease; Cerebrospinal Fluid; Plasma; Diagnosis

Anna D. Barker, Mario M. Alba, Parag Mallick, David B. Agus, Jerry S.H. Lee. ([1]Lawrence J. Ellison Institute for Transformative Medicine, Los Angeles, California, USA. [2]Complex Adaptive Systems Initiative and School of Life Sciences, Arizona State University, Tempe, Arizona, USA. [3]Department of Pharmacology and Pharmaceutical Sciences, USC Alfred E. Mann School of Pharmacy, University of Southern California, Los Angeles, California, USA. [4]Canary Center at Stanford for Cancer Early Detection, Stanford University, Stanford, California, USA, [5]Department of Radiology, Stanford University, Stanford, California, USA, [6]Keck School of Medicine, University of Southern California, Los Angeles, California, USA, [7]Viterbi School of Engineering, University of Southern California, Los Angeles, California, USA) An Inflection Point in Cancer Protein Biomarkers: What Was and What's Next, Molecular & Cellular Proteomics (2023): 100569

Biomarkers remain the highest value proposition in cancer medicine today – especially protein biomarkers. Yet despite decades of evolving regulatory frameworks to facilitate the review of emerging technologies, biomarkers have been mostly about promise with very little to show for improvements in human health. Cancer is an emergent property of a complex system and deconvoluting the integrative and dynamic nature of the overall system through biomarkers is a daunting proposition. The last two decades have seen an explosion of multi-omics profiling and a range of advanced technologies for precision medicine, including the emergence of liquid biopsy, exciting advances in single cell analysis, artificial intelligence (machine and deep learning) for data analysis and many other advanced technologies that promise to transform biomarker discovery. Combining multiple omics modalities to acquire a more comprehensive landscape of the disease state, we are increasingly developing biomarkers to support therapy selection and patient monitoring. Furthering precision medicine, especially in oncology, necessitates moving away from the lens of reductionist thinking towards viewing and understanding that complex diseases are, in fact, complex adaptive systems. As such, we believe it is necessary to re-define biomarkers as representations of biological system states at different hierarchical levels of biological order. This definition could include traditional molecular, histologic, radiographic, or physiological characteristics, as well as emerging classes of digital markers and complex algorithms. To succeed in the future, we must move past purely observational individual studies and instead start building a mechanistic framework to enable integrative analysis of new studies within the context of prior studies. Identifying information in complex systems and applying theoretical constructs, such as information theory, to study cancer as a disease of dysregulated communication could prove to be "game changing" for the clinical outcome of cancer patients.

Stine Andersen, Alexander Lynge Reese-Petersen, Natalia Braams, Mads Jønsson Andersen, Søren Mellemkjær, Asger Andersen, Harm Jan Bogaard, Federica Genovese, Jens Erik Nielsen-Kudsk. ([a,] Department of Cardiology, Aarhus University Hospital, Denmark, [b]Nordic Bioscience, Denmark, [c]Department of Pulmonology, Amsterdam University Medical Center, the Netherlands) Biomarkers of collagen turnover and wound healing in chronic thromboembolic pulmonary hypertension patients before and after pulmonary endarterectomy. International Journal of Cardiology, Volume 384 (2023): 82-88

Background-In chronic thromboembolic pulmonary hypertension (CTEPH), fibrotic remodeling of tissue and thrombi contributes to disease progression. Removal of the thromboembolic mass by pulmonary endarterectomy (PEA) improves hemodynamics and right ventricular function, but the roles of different collagens before as well as after PEA are not well understood.

Methods-In this study, hemodynamics and 15 different biomarkers of collagen turnover and wound healing were evaluated in 40 CTEPH patients at diagnosis (baseline) and 6 and 18 months after PEA. Baseline biomarker levels were compared with a historical cohort of 40 healthy subjects.

Results-Biomarkers of collagen turnover and wound healing were increased in CTEPH patients compared with healthy controls, including a 35-fold increase in the PRO-C4 marker of type IV collagen formation and a 55-fold increase in the C3M marker of type III collagen degradation. PEA reduced pulmonary pressures to almost normal levels 6 months after the procedure, with no further improvement at 18 months. There were no changes in any of the measured biomarkers after PEA.

Conclusions-Biomarkers of collagen formation and degradation are increased in CTEPH suggesting a high collagen turnover. While PEA effectively reduces pulmonary pressures, collagen turnover is not significantly modified by surgical PEA.

Keywords: Chronic thromboembolic pulmonary hypertension; Biomarkers; Collagen; Right heart failure

Paul D. Wagner, Sudhir Srivastava. (Cancer Biomarkers Research Group, Division of Cancer Prevention, National Cancer Institute, Bethesda, USA). National Cancer Institute's early detection research network: A model organization for biomarker research, Journal of the National Cancer Center (2023): 93-99

For many cancers a primary cause of poor survival is that they are detected at a late stage when therapies are less effective. Although screening methods exist to detect some types of cancer at an early stage, there are currently no effective methods to screen for most types of cancer. Biomarkers have the potential to improve detection of early-stage cancers, risk stratification, and prediction of which pre-cancerous lesions are likely to progress and to make screening tests less invasive. Although thousands of research articles on biomarkers for early detection are published every year, few of these biomarkers have been validated and shown to be clinically useful. This reflects both the inherent difficulty in detecting early-stage cancers and a disconnect between the process of discovering biomarkers and their use in the clinic. To overcome this limitation the US National Cancer Institute created the Early Detection Research Network. It is a highly collaborative program that brings together biomarker discoverers, assay developers, and clinicians. It provides an infrastructure that is essential for developing and validating biomarkers and imaging methods for early cancer detection and has successfully completed several multicenter validation studies.

Keywords: Biomarkers; Early detection; Validation; Collaboration; Data sharing

Maciej L. Goniewicz. (Department of Health Behavior, Roswell Park Comprehensive Cancer Center, Elam and Carlton Streets, Buffalo NY 14226, United States). Biomarkers of Electronic Nicotine Delivery Systems (ENDS) use, Addiction Neuroscience, Volume 6 (2023):100077

This perspective summarizes available evidence on biomarkers of exposure in electronic nicotine delivery system (ENDS) users to aid the overall assessment of the health consequences of using

ENDS. Identification of novel biomarkers of exposure specific to ENDS use remains challenging because chemicals emitted from ENDS devices have many familiar sources. The biomarker levels of many tobacco-related toxicants measured in biological samples collected from ENDS users did not differ significantly from non-users, except for nicotine metabolites and a small number of biomarkers of exposure to volatile organic compounds and tobacco-specific tobacco nitrosamines. Several studies have shown that while exposed to nicotine, long-term exclusive ENDS users showed significantly lower levels of toxicant biomarkers than cigarette smokers. Studies have also shown that concurrent users of ENDS and combustible cigarettes ('dual users') are not reducing overall exposure to harmful toxicants compared to exclusive cigarette smokers. Because of an absence of validated ENDS-specific biomarkers, we recommend combining several biomarkers to differentiate tobacco product user groups in population-based studies and monitor ENDS compliance in randomized controlled trials. Using a panel of biomarkers would provide a better understanding of health effects related to ENDS use.

Keywords: Electronic Nicotine Delivery Systems; ENDS; E-cigarettes; Vaping; Biomarkers; Exposure

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By its many virtues, non-biomarker-reliant molecular detection has recently shown bright prospects for cancer screening but its clinical application is hindered by the shortage of measurable criteria that are analogous to biomarkers. Here, we report a digital biomarker, as a new-concept serum biomarker, of hepatocellular carcinoma (HCC) found with SERS-based biosensors and a deep neural network "digital retina" for visualizing and explicitly defining spectral fingerprints. We validate the discovered digital biomarker (a collection of 10 characteristic peaks in the serum SERS spectra) with unsupervised clustering of spectra from an independent sample batch comprised normal individuals and HCC cases; the validation results show clustering accuracies of 95.71% and 100.00%, respectively. Furthermore, we find that the digital biomarker of HCC shares a few common peaks with three clinically applied serum biomarkers, which means it could convey essential biomolecular information similar to these biomarkers. Accordingly, we present an intelligent method for early HCC detection that leverages the digital biomarker with similar traits as biomarkers. Employing the digital biomarker, we could accurately stratify HCC, hepatitis B, and normal populations with linear classifiers, exhibiting accuracies over 92% and area under the receiver operating curve values above 0.93. It is anticipated that this non-biomarker-reliant molecular detection method will facilitate mass cancer screening.

Keywords: Digital biomarker; Surface-enhanced Raman scattering; Biosensor for cancer detection; Intelligent Detection for cancer; Hepatocellular carcinoma

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Bioscience and Biotechnology, University of Tabriz, Tabriz, Iran, [c]Pharmaceutical Analysis Research Center, Tabriz University of Medical Sciences, Tabriz, Iran). Recent progress and challenges in the application of molecularly imprinted polymers for early-stage screening of neurodegenerative diseases-related protein biomarkers, Microchemical Journal (2023): 108931

Proteomics is an essential technology in medicine and biotechnology. Protein profiling and its application in disease diagnosis have attracted a lot of attention from scientists. Highly selective detection of target proteins will be beneficial in clinical diagnosis, treatment of diseases, therapeutic monitoring, control of bioreactors, and the detection of microorganisms/toxins. In recent years, researchers have paid much attention to developing biosensors for the monitoring of proteins as biomarkers of neurodegenerative diseases. In this review, essential protein biomarkers of neurodegenerative diseases are mentioned. This review reports the use of molecularly imprinted polymer (MIPs)-based biosensors for the recognition of protein biomarkers of neurodegenerative diseases. The major emphasis is based on immune-, geno-, and enzyme-based sensors. Also, the critical role of various types of MIPs and innovative/efficient methods integrated with optical and electrical biosensing systems, micro/nano-electromechanical systems, lateral flow, and microfluidic platforms were surveyed. Importantly, the advantages and the limitations of MIPs-based biosensors are investigated, critically. The advantages of using smartphones in data analysis and integration of lateral flow tests with MIPs-based biosensors in increasing the sensitivity of target proteins monitoring are discussed. Hope, the critical discussions of this review provide new perspectives for the scientists to overcome limitations of traditional methods in the early-stage diagnosis of neurodegenerative diseases. Also, discussion about the critical role of MIPs in the biosensing of protein biomarkers opens a new horizon for the point of care analysis of neurodegenerative disease in near future.

Keywords: Protein biomarkers; Neurodegenerative disease; Molecularly imprinted polymer; Bioanalysis

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This article describes the use of prognostic, predictive, and response biomarkers that have been developed for autosomal dominant polycystic kidney disease and their use in clinical care or drug development. We focus on biochemical markers that can be assayed in patients' blood and urine and their association with the outcome of decreased glomerular filtration rate. There have been several studies on prognostic biomarkers. The most promising ones have been markers of tubular injury, inflammation, metabolism, or the vasopressin-urinary concentration axis. So far, none have been shown to be superior to kidney volume-based biomarkers. Several biomarkers are additive to kidney volume and genotype in prognostic models, but there have been few direct comparisons between the biochemical markers to identify the best ones. Moreover, there is a lack of uniformity in the statistical tools used to assess and compare biomarkers. There have been few reports of predictive and response biomarkers, and none are suitable surrogate endpoints. The U.S. Food and Drug Administration's Biomarker Qualification Program provides a regulatory pathway to approve biomarkers for use across multiple drug-development programs.

Keywords: Biomarker; Prognosis; Surrogate endpoint; Polycystic kidney disease; Clinical trial

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The management of neuroendocrine tumors (NETs) represents a clinical challenge due to heterogeneity of their clinical behaviour, molecular biology and response to treatment. Over the years, several circulating biomarkers have been developed for the early diagnosis and follow-up of NETs. The specific secretory products of tumors associated with a secretory syndrome (functioning tumors) may be used as diagnostic and/or prognostic biomarkers while the most common non-specific circulating biomarkers, that may be increased in both functioning and non-functioning tumors, are chromogranin A and the neuron specific enolase. However, the diagnostic accuracy as well as the prognostic and predictive value of these biomarkers are limited and novel techniques of multianalyte analysis of regulators of tumor biology have been developed. The NETest has been most extensively studied and proved to be useful in NET diagnosis, early detection of post-operative recurrence and prediction of response to treatment but further investigation establishing higher level of evidence is required for implementation in clinical practice.

Keywords: Neuroendocrine; biomarker; predictive; prognostic; chromogranin A; 5-HIAA; NETest

Micha Kaiser, Jan M. Bauer, Steffen Otterbach, Lucia A. Reisch, Alfonso Sousa-Poza. ([a]El-Erian Institute of Behavioural Economics and Public Policy, University of Cambridge, Trumpington Street, Cambridge CB2 1QA, United Kingdom, [b]Department of Management, Society and Communication, Copenhagen Business School, Dalgas Have 15, Frederiksberg 2000, Denmark, [c]Institute for Health Care & Public Management, University of Hohenheim, Fruwirthstrasse 48, Stuttgart 70599, Germany). The association between commuting and cardiovascular disease: A biomarker-based analysis of cross-sectional cohort data from the UK Biobank, Preventive Medicine, Volume 172 (2023): 107521

This study used cross-sectional UK Biobank data to estimate the influence of active and passive commuting modes and commuting distance on cardiovascular disease (CVD) -related biomarkers as measures of health outcomes. The analysis applied logistic regression to assess the risk of exhibiting individual biomarker values outside a predefined reference interval and standard linear regression to estimate the relation between commuting practices and a composite CVD index. The study sample comprised 208,893 UK Biobank baseline survey participants aged 40 to 69 who use various modes of transport to commute to work at least once a week. Participants were recruited and interviewed between 2006 and 2010 at 22 centers geographically dispersed across England, Scotland, and Wales. The data set included these participants' sociodemographic and health-related information, including lifestyle indicators and biological measures. The primary outcome was a shift from low to high-risk blood serum levels in eight cardiovascular biomarkers: total cholesterol, low density lipoprotein, high density lipoprotein, triglycerides, apolipoprotein A and B, C-reactive protein, and lipoprotein (a). Our results indicated a small negative association between the composite risk index for CVD biomarkers and weekly commuting distance. Although estimates for active commuting modes (cycling, walking) may admittedly be sensitive to different covariate adjustments, our specifications show them to be positively associated with select CVD biomarkers. Commuting long distances by car is negatively associated with CVD-related biomarkers, while cycling and walking might be positively associated. This biomarker-based evidence, although limited, is less susceptible to residual confounding than that from distant outcomes like CVD mortality.

Keywords: Active commuting; Biomarker; cardiovascular disease risk; Cycling; Physical activity

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Objective-Evaluate serum and urine biomarker panels for their capabilities in discriminating between individuals (13–34-years-old) with healthy hips versus those with developmental dysplasia of the hip (DDH) prior to diagnosis of secondary hip osteoarthritis (OA).

Design-Urine and serum were collected from individuals (15–33 years old) with developmental dysplasia of the hip, prior to and following diagnosis of hip osteoarthritis (OA), and from age-matched healthy-hip controls. Samples were analyzed for panels of protein biomarkers with potential for differentiation of hip status using receiver operator characteristic curve (area under curve (AUC)) assessments.

Results-Multiple urine and serum biomarker panels effectively differentiated individuals with DDH from healthy-hip controls in a population at risk for developing secondary hip OA with the best performing panel demonstrating an AUC of 0.959. The panel comprised of two serum and two urinary biomarkers provided the highest combined values for sensitivity, 0.85, and specificity, 1.00, while a panel of four serum biomarkers provided the highest sensitivity, 0.93, while maintaining adequate specificity, 0.71.

Conclusion-Results of this indicate that panels of protein biomarkers measured in urine and serum may be able to differentiate young adults with DDH from young adults with healthy hips. These data suggest the potential for clinical application of a routine diagnostic method for cost-effective and timely screening for DDH in at-risk population. Further development and validation of these biomarker panels may result in highly sensitive and specific tools for early diagnosis, staging, and prognostication of DDH, as well as treatment decision making and monitoring capabilities.

Keywords: Dysplasia; Osteoarthritis; Biomarker; Mechanism

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Wisconsin, Milwaukee, WI, USA). Correlation Between Biomarkers and Treatment Outcomes in Diverse Cancers: A Systematic Review and Meta-Analysis of Phase I and II Immunotherapy Clinical Trials, European Journal of Cancer (2023): 112927

Background-Many immuno-oncology (IO) trials are conducted without biomarker selection. We performed a meta-analysis of phase I/II clinical trials evaluating immune checkpoint inhibitors (ICIs) to determine the association between biomarkers and clinical outcomes, if any.

Methods-A PubMed search for phase I/II clinical trials with drugs approved by the Food and Drug Administration (labeled, off-label, combined with investigational ICIs or other treatment modalities) from 2018 to 2020 was performed. The objective response rate (ORR), progression-free survival (PFS), and overall survival (OS) were compared between biomarker-positive and biomarker-negative groups, using studies that explored the correlation of biomarkers with outcomes.

Results-Overall, 174 clinical studies that included 19,178 patients were identified and 132 studies investigated >30 correlative biomarkers, that included PD-L1 expression (≥1%, 111 studies), tumor mutational burden (20 studies), and microsatellite instability/mismatch repair deficiency (10 studies). Overall, 123, 46, and 30 cohorts (drugs, tumor types, or biomarkers) with 11,692, 3,065, and 2,256 patient outcomes for ORR, PFS, and OS, respectively, were analyzed in correlation with biomarkers. Meta-analyses demonstrated that ICIs in patients with biomarker-positive tumors were associated with higher ORR (odds ratio 2.15 [95% CI, 1.79-2.58], $p<0.0001$); and longer PFS (hazard ratio [HR] 0.55 [95% CI, 0.45-0.67], $p<0.0001$), and OS (HR 0.65 [95% CI, 0.53-0.80], $p<0.0001$) compared with those with biomarker-negative tumors. Significance for ORR and PFS was retained in multivariate analysis ($p<0.001$) (OS, not included owing to the small number of trials reporting OS).

Conclusion-Our data suggest that IO biomarkers should be used in patient selection for ICIs. Prospective studies are warranted.

Keywords: Immune checkpoint inhibitor; Immunotherapy; Meta-analysis; Tumor biomarker

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Biomarkers are new tools framed in precision and personalized medicine. Hereditary hemorrhagic telangiectasia (HHT) is a rare genetic vascular disease with disturbances in the angiogenic pathways. Descriptive evidence supports that some angiogenesis-related molecules are differently detected in HHT patients compared to healthy subjects. These molecules are also related to diagnosis, prognosis, complications and therapy monitoring in other common vascular diseases. Despite the need for improving knowledge before applying them in daily clinical practice, there are good candidates to be considered as potential biomarkers in HHT and other vascular diseases. In the present review, the authors aim to summarize and discuss current evidence regarding the main putative angiogenic biomarkers by describing the biological role of each biomarker, the evidence related to HHT and their potential use in this and other common vascular diseases from a clinical point-of-view.

Keywords: Hereditary hemorrhagic telangiectasia; Biomarkers; Translational medicine; Angiogenesis; Rare diseases

Biofertilizer

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The demand for food to feed the growing world population has been promoting the indiscriminate use of chemical fertilizers, which can be detrimental to the environment. In order to maintain high crop productivity without damaging the ecosystem, biofertilizers have emerged as alternative to reduce the use of chemical fertilizers. So, environmentally safer biofertilizer can replace the exploitation of more toxic chemical fertilizer. Here, the fly Drosophila melanogaster was used to study the potential toxicity of the biofertilizer Beifort®. Flies were exposed to high concentrations of Beifort® in the diet (1.8 mL/L, 9.0 mL/L and 18 mL/L), and morphological and behavioral endpoints of toxicity were analyzed (development from egg to adult age, flies longevity, climbing performance, memory and learning of an associative learning, larvae digestive tract damage and plasmid DNA break). Beifort® did not modify flies development, survival, digestive track cell damage, locomotor activity or memory. Beifort® did not induce DNA breakage in vitro and had no toxicity to the non-target D. melanogaster after in vivo exposure. Thus, in addition of promoting the sustainable use of agricultural wastes, the exploitation of Beifort® can contribute to decrease the use of chemical fertilizers.

Keywords: Biofertilizer; Toxicity; Drosophila melanogaster; Beifort; Behavior; Development

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Combustion and depletion of fossil fuels, open burning of agricultural wastes, and use of hazardous chemicals in biofuels production route are some major challenges among scientific community. In the present study these obstacles were mitigated simultaneously. Initially, rice straw biomass was delignified using a combined eco-friendly laccase-assisted sodium chlorite (LASC) pretreatment. The combined pretreatment strategy of rice straw biomass reduced 55.6% lignin and increased the total available carbohydrate by 1.43 fold. Further, enzymatic digestion of LASC pretreated rice straw using a formulated cellulase cocktail from Aspergillus flavus MDU-5 and Trichoderma citrinoviride MDU-1 liberated 526.68 mg/g sugars with high saccharification yield (84.0%). The enzymatic hydrolysates thus obtained were found to contain

7.43–16.78 g/L sugars. The cellulolytic hydrolysates when fermented with Saccharomyces cerevisiae NCIM-3640 produced 3.02–7.28 g/L bioethanol, with high yield (72.96–85.31% of the theoretical value). Parallelly, lignin extracted from waste pretreatment stream showed biopesticidal activity against the larvae of H. armigera; whereas, the evaluation of residual material (after hydrolysis and fermentation) exhibited biofertilizer properties. These findings suggests that the environmentally benign LASC pretreatment, cellulase cocktail, and utilization of waste stream for the production of biopesticide and biofertilizer may provide a promising strategy in the development of holistic lignocellulosic biorefinery process.

Keywords: Rice straw; Biorefinery; Pretreatment; Bioethanol; Biopesticide; Biofertilizer

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For years, agrochemical fertilizers have been used in agriculture for crop production. However, intensive utilization of chemical fertilizers is not an ecological and environmental choice since they are destroying soil health and causing an emerging threat to agricultural production on a global scale. Under the circumstances of the increasing utilization of chemical fertilizers, cultivating microalgae to produce biofertilizers would be a wise solution since desired environmental targets will be obtained including (1) replacing chemical fertilizer while improving crop yields and soil health; (2) reducing the harvest of non-renewable elements from limited natural resources for chemical fertilizers production, and (3) mitigating negative influences of climate change through CO_2 capture through microalgae cultivation. Recent improvements in microalgae-derived-biofertilizer-applied agriculture will be summarized in this review article. At last, the recent challenges of applying biofertilizers will be discussed as well as the perspective regarding the concept of circular bio-economy and sustainable development goals (SDGs).

Keywords: Biofertilizer; Carbon capture; Circular bioeconomy; Microalgae cultivation; Sustainable development goals

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Technology, Kollam 691 505, Kerala, India, [c]Microbial Processes and Technology Division, CSIR- National Institute for Interdisciplinary Science and Technology (CSIR-NIIST), Trivandrum 695 019, Kerala, India). Biomass valorization of agriculture wastewater grown freshwater diatom Nitzschia sp. for metabolites, antibacterial activity, and biofertilizer, Bioresource Technology, Volume 377 (2023): 128976

The sustainable utilization of agricultural wastewater is a major global challenge. This study evaluated the impact of agricultural fertilizer on the biomass potential of Nitzschia sp. for metabolite production, antibacterial activity, and slow release biofertilizer. Cultivation of Nitzschia sp. in agriculture wastewater (0.5 mg ml−1) exhibited maximum cell density (12×105 cells ml−1), protein content (10.0 mg g−1), and lipid content (14.96%). Carbohydrate and phenol content increases in a dose-dependent manner with 8.27 mg g−1 and 2.05 mg g−1 at a concentration of 2 mg ml−1 respectively. There was a 2.1-fold increment in chrysolaminarin content. Both gram-negative and gram-positive bacteria were susceptible to the antibacterial activity of the biomass. The effects of using diatom biomass as a biofertilizer were evaluated on the growth of periwinkle plants, which showed significant improvements in leaf development, branching at an early stage, flowering, and a marked increase in shoot length. Diatom biorefinery holds immense potential in addressing agriculture wastewater recycling and sustainable generation of high-value compounds.

Keywords: Nitzschia sp.; Non-point pollution; Diatom; Catharanthus roseus; Agriculture fertilizer

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Although substantial quantities of Nile perch waste/wastewater are generated in Northeastern and Central Africa, only a small fraction of Nile perch waste is reutilized, with the resultant environmental pollution threatening aquatic life. Therefore, it was investigated whether Nile perch wastewater (NPWW) can be processed to produce a quality biofertilizer and thus completely reused. To achieve this purpose, NPWW degradation was conducted in a 1 L flask for 72 h using a microbial consortium of three Bacillus species. After 72 h biodegradation, the number of viable cells was 5.6 × 107 CFU/mL, the degree of protein hydrolysis was 48.7%, and the removal efficiency of chemical oxygen demand concentration and total nitrogen in NPWW was 52.5% and 44.0%, respectively, with C/N ratios of 5.5−6.4. Small molecules resulting from biodegradation comprised 52.9% hydrophilic amino acids and exhibited 73.9%, 98.9%, and 93.3% of free radical-scavenging activity for DPPH, ABTS, and OH-, respectively. The resultant biofertilizer was non-phytotoxic beyond a 50-fold dilution, and a 1000-fold dilution of the biofertilizer in barley hydroponics resulted in significantly higher stem and leaf growth than the control and commercial fertilizer. The biofertilizer-fed barley leaves exhibited a higher production of photosynthetic pigments and significantly higher antioxidant activity (92.5% for DPPH and 91.8% for ABTS) than the leaves in the control and commercial fertilizer groups. These findings indicate that the biodegraded NPWW rich in small molecules can be used as a biostimulant for sustainable agriculture.

Keywords: Nile perch wastewater; Biodegradation; Antioxidant peptides; Sustainable biofertilizer; Barley hydroponics

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Microalgae are source of macro- and micronutrients, phytohormones, lipids and carbohydrates, in addition to having an excellent adaptive capacity to the most diverse environments. Due to this, they have gained prominence in the biofertilizer industry. In this work, we evaluated the potential Desmodesmus abundans L2B Bold biofertilizer in bean cultivar "Pérola". Microalgal biomass (107 cells mL−1) was applied to bean plants by manual irrigation starting at 15 days after sowing (DAS) and then every 10 days thereafter. The total number of pods and seeds, leaf fresh and dry mass, root dry mass, and total fresh and dry mass were positively influenced by microalgae biofertilizer. The leaf pigments were significantly ($p < 0.05$) increased with the use of D. abundans L2B Bold. This increase was of approximately 30% in chlorophyll a and b content with the application of biofertilizer 17 DAS and 7% in the middle of the crop cycle (37 DAS). The biofertilizer also significantly ($p < 0.05$) impacted foliar enzymatic activity with superoxide dismutase (SOD) being increased during all the crop cycle. Phenylalanine ammonia-lyase (PAL) presented higher activity under microalgae use, being increased approximately 120%–1500% in biofertilized plants in the middle and at the end of the crop cycle, respectively. There were significant($p < 0.05$) increases in K and Ca of seed beans contents with the application of biofertilizer. Based on our results, we conclude that D. abundans L2B Bold has great potential for use as a biofertilizer in bean crop.

Keywords: Microalgae; Plant growth; Biofertilization; Bean mineral composition

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At present, the exploitation of biofertilizers is revealing the vast potential for the advancement of sustainable and organic agriculture and the improvement of arable soil quality. Therefore, we investigated the capacity of an innovative phosphorus biofertilizer to enhance the activity and diversity of the soil microbiome inhabiting chemically degraded soil (type Abruptic Luvisol). The two-year field experiment comprised a control treatment (FC) devoid of microbial enrichment, an optimal dose of fertilizer containing beneficial microorganisms (FA100) and a dose of fertilizer that was 40 % below this optimal level and contained microorganisms (FA60). Phosphorus biofertilizer increased soil enzymatic activity immediately after application and between the corresponding treatments in subsequent sampling times, it alleviated the effects of metabolic stress, improved phytoavailable phosphorus content and increased maize yield.

Identification based on the terminal restriction fragments size revealed the presence of microorganisms important for soil health such as phosphorus solubilizers, nitrogen fixers, biological control agents, entomopathogens, mycorrhizal fungi, bioremediators and plant growth promoters. Next Generation Sequencing (NGS) showed that the application of phosphorus biofertilizer changed the relative abundance of different microbial phyla, classes and orders, increased the diversity of soil microorganisms and indicated that the composition of the soil microbiome was also dependent on the sampling time. The prediction of bacterial community function using PICRUSt demonstrated that the application of biofertilizer raised the number of functional sequences associated with metabolism and cell processes, including phosphorus compound pathways. FUNGuild showed that saprotrophic and symbiotrophic fungi were more abundant in microbiologically enriched treatments. Our results proved that the phosphorus biofertilizer used offers a sustainable and promising solution to the problem of reducing traditional mineral fertilizer inputs while ensuring soil microorganism welfare and enhancing land productivity, and, what is more, it can be effectively exploited in regenerative agriculture and as a factor used to enhance resilience to climate change.

Keywords: Biofertilizer; Microbial diversity; Climate change; Sustainable agriculture; Degraded soil; Soil phosphorus

Zhiping Zhang, Fuke Ai, Yameng Li, Shengnan Zhu, Qiyou Wu, Zhisai Duan, Hanchuan Liu, Liyang Qian, Quanguo Zhang, Yang Zhang. (Key Laboratory of New Materials and Facilities for Rural Renewable Energy, MOA of China, Henan Agricultural University, Zhengzhou 450002, China) Co-production process optimization and carbon footprint analysis of biohydrogen and biofertilizer from corncob by photo-fermentation, Bioresource Technology, Volume 375(2023): 28814

In this study, corncob was taken as substrate, the co-production process of biohydrogen and biofertilizer by photo-fermentation was investigated and its carbon footprint analysis was conducted to evaluate the carbon transfer pathway. Biohydrogen was produced by photo-fermentation, and the hydrogen producing residues were immobilized by sodium alginate. Cumulative hydrogen yield (CHY) and nitrogen release ability (NRA) was taken as references, and the effect of substrate particle size on the co-production process was evaluated. Results showed that due to the porous adsorption properties, corncob size of 120 mesh was the optimal one. Under that condition, the highest CHY and NRA were 71.16 mL/g TS and 68.76%, respectively. The carbon footprint analysis indicted that 7.9% carbon element was released as carbon dioxide, 78.3% carbon element was immobilized in the biofertilizer, and 13.8% carbon element was lost. This work is significant of the biomass utilization and clean energy production.

Keywords: Corncob size; Carbon footprint; Cumulative hydrogen yield; Nitrogen release

Tianyu Du, Qufei Hu, Haiyun He, Wenjing Mao, Zhou Yang, Hong Chen, Linna Sun, Meizhi Zhai. ([a]College of Forestry, Northwest A&F University, Yangling, Shaanxi, China, [b]Taiyuan State-Owned Forest Farm, Taiyuan, Shanxi, China, [c]Shannxi Walnut Engineering Technology Research Center, Yangling, China). Long-term organic fertilizer and biofertilizer application strengthens the associations between soil quality index, network complexity, and walnut yield, European Journal of Soil Biology, Volume 116 (2023): 103492

Although various combinations of organic-inorganic fertilizers can enhance plant yields, the effects of different fertilization regimes on the associations between rhizosphere soil microorganisms and plant productivity are poorly understood. In this study, we investigated the rhizosphere soil microbial composition and structure and the relationships among rhizospheric microorganisms, soil properties, and yield in a walnut (Juglans regia L.) orchard after 7 years of applying different fertilization regimes. The combinations of organic and inorganic fertilizers were found to enhance walnut yield, soil quality index (SQI), and soil biodiversity (bacterial and fungal) ($P < 0.05$). The soil microbial community composition and co-occurrence networks of rhizosphere soil (RS) and bulk soil (BS) showed different responses to fertilization. Bacillus and Pseudomonas were mainly enriched in RS, whereas Fusarium was significantly more abundant in BS ($P < 0.05$) under a combined chemical fertilizer, organic fertilizer, and biofertilizer treatment (F + O + BO). Network analysis revealed that organic fertilizer and biofertilizer reduced the competition and network complexity among rhizosphere microbial communities (edges: RS = 388, BS = 967; modularity: RS = 0.790, BS = 0.834). Furthermore, SQI, microbial diversity, and network complexity were significantly correlated with walnut yield ($P < 0.01$), among which SQI explained the highest proportion of the variation in yield (SOI: RS = 78.02%; BS = 81.18%). In addition, both yields and soil microbial community composition were significantly affected by pH, SOM, TN, and SMBN. Collectively, these findings have important implications for our understanding of the relationship between woody plants and rhizospheric microorganisms.

Keywords: Long-term fertilization; Soil properties; Rhizosphere soil microorganism; Yield

Biocomposting

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This study aimed to demonstrate the importance of goat manure, sawdust, and green waste (lettuce, potatoes, carrots, and cabbage) as nutrient sources for soil and crops in family farming. Macro and micronutrient concentrations were determined. Two bio-composts were formed, one with a mixture of goat manure, sawdust and agricultural waste and the other without manure only sawdust and agricultural waste. The physicochemical properties of the soil, residues, and bio-compost were measured. Sawdust had high total organic carbon (TOC) and low total nitrogen (TN), P, K, Ca, and Mg levels, whereas goat manure had high TOC, TN, K, Ca, Mg, and P levels. The soil treated with the solid bio-composts (with and without goat manure) had significant effects, with the pH value reaching 7.0, suggesting that the bio-composts were safe for agricultural use. The manure bio-compost was rich in TOC, TN, P, Ca, and K macronutrients but poor in Mg. The manure-free bio-compost had high TOC and TN levels. However, both bio-composts had low C:N ratios. Finally, the experiments revealed high Fe and Mn and low Cu and Zn concentrations. These results clearly revealed that growth of maximum plant height (71 cm) were significantly influenced by bio-compost and suggest that the levels of TOC, TN, P, K, Ca, Mg, Fe, Mn, Cu, and Zn were reliable and thus do not present restrictions for agricultural use.

Keywords: Hylocereus costaricensis; Microorganisms; Granulometry; Organic; Compounds; Composting

Biopesticides

Golafarin Ghoreishi, Raquel Barrena, Xavier Font. (GICOM research group, Department of Chemical, Biological and Environmental Engineering, Universitat Autònoma de Barcelona, Edifici Q, Carrer de les Sitges, 08193 Bellaterra (Cerdanyola del Vallès), Barcelona, Spain). Using green waste as substrate to produce biostimulant and biopesticide products through solid-state fermentation, Waste Management, Volume 159 (2023): 84-92

Although the use of green waste as a substrate in different types of microbial bioprocessing has a major impact on improving green waste valorization, very little information has been provided on this issue. The purpose of this paper is to study the feasibility of using green waste to produce a biostimulant (Indole-3-acetic acid (IAA)) and biopesticide (conidial spore) through solid-state fermentation. Trichoderma harzianum was selected as the inoculum of the process and the green waste was a mixture of grass clippings and pruning waste. An experiment was designed to study the effect of tryptophan concentration, proportion of grass and pruning waste, and substrate moisture on IAA and spore production. The results show that washing and using phosphate buffer has a beneficial effect on green waste quality in terms of bioproduction. The maximum IAA and spore productions reported in the current study were 101.46 µg g−1 dry matter and 3.03 × 109 spore g−1 dry matter, respectively. According to the results, IAA production increases with a higher amount of tryptophan and grass. However, the number of spores increased with lower amounts of tryptophan and grass. The model suggested the following optimized parameters for the production of spores and IAA: tryptophan 0.45 %, grass 61 %, and moisture 74 %. The effect of fermentation time was also studied, and the results show that the maximum IAA and spore production was obtained on days 3 and 7, respectively.

Keywords: Green waste; Solid-state fermentation; Trichoderma harzianum; Indole-3-acetic acid

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Worldwide, P. marginatus causes 75% of estimated economic loss in papaya farming, with an increase in production costs. The extract of plant essential oils (PEO) has the potential to control P. marginatus by degrading its wax coatings to death; however, it is less studied in the East African agroecosystem. Therefore, this study was conducted to evaluate the efficacy of four PEO from (neem, citrus, garlic, and castor) against P. marginatus at different concentrations (0.5%, 1%, and 1.5%) with and without 0.2% adjuvants separately as a biopesticide. The experiment was conducted in a completely randomized design with four replications per treatment concentration. The papaya seeds (Carina variety) were used in the experiment. After 3 weeks from transplanting, 50 P. marginatus specimens were inoculated in each plant. Before treatment application, insect abundance, leaf curling, yellowing, and soot mold were assessed. Then, 24 h, 48 h, and 72 h after biopesticide application, insect mortality was assessed. The results showed a significant difference ($p = 0.001$) for all assessment intervals in PEOs. However, for the PEOs in combination with the adjuvants, the results were significantly different (p = 0.001) only at 24 h. It was found that among the biopesticides, neem oil (1.5%) + isopropyl alcohol was highly effective (95.5%) after 72 h followed by (Imidacloprid (91%), citrus oil 1.5% (90.7%) and neem oil (1.5%) + paraffin oil (81.0%). But also, there were significant differences among treatments on leaf curling, yellowing, and soot mold reduction in papaya plants 21 days after spray. We conclude that neem oil (1.5%) + 0.2% isopropyl alcohol, neem oil (1.5%) + paraffin oil, and citrus oil (1.5%) significantly controlled P. marginatus. Thus, we recommend adopting these formulations for papaya farmers to control P. marginatus in their farms; however, simple formulations which can be easily accessed by smallholder farmers are essential.

Keywords: Adjuvants; Botanical pesticides; Carica papaya; Invasive pests; Pest management

Biodegradation

Haitai Dong, Xingzu Wang, Shun Lu, Ye Ma, Cheng Song, Sha Wang, Hong Liu. ([a]Chongqing Institute of Green and Intelligent Technology, Chinese Academy of Sciences, Chongqing 400714, China, [b]Chongqing School, University of Chinese Academy of Sciences, Chongqing 400714, China, [c]niversity of Chinese Academy of Sciences, Beijing 100049, China). Microbial fuel cell-based biosensor for monitoring anaerobic biodegradation of poly (3-hydroxybutyrate-co-4-hydroxybutyrate), Polymer Degradation and Stability, Volume 214 (2023): 110409

Poly-3-hydroxybutyrate-co-4-hydroxybutyrate (P34HB) polymer, which is a common type of polyhydroxyalkanoates (PHAs), may provide alternative solutions to the white pollution issues. In this study, its anaerobic biodegradation was investigated through the microbial fuel cell (MFC) system, by monitoring several parameters, including the time-dependent changes in the electrical signals, the concentration of the P34HB degradation products, biogas production, the weight loss of P34HB films, and the morphological and chemical structure of the test materials during the degradation. Notably, the electrical signal was selected as an indicator to online monitor the anaerobic biodegradation of P34HB films. After 40 days of degradation, the coulombic yield biodegradability (Q-biodegradability) of P34HB films reached 37.59%. A linear relationship among the weight loss biodegradability of P34HB films and Q-biodegradability with high correlation coefficient of $R2 = 0.998$ was established. The results suggested that the anaerobic biodegradability of P34HB films can be efficient measured by using the Q-biodegradability compared to conventional methods. Microbial community analysis also indicated that the genus Desulfovibrio and Enterobacter contributed to the biodegradation of P34HB films and the electrical signals production via the cooperation among other microorganisms. This study presented the online monitoring of the anaerobic biodegradation of P34HB films through MFC-based sensors, which provided an alternative approach to evaluate the anaerobic biodegradability of biodegradable plastics.

Keywords: Microbial fuel cell (MFC); P34HB films; Anaerobic biodegradation; Electrical signals; Microbial community

Aubrey Dickson Chigwada, Memory Tekere. (Department Environmental Sciences, College of Agriculture and Environmental Sciences, University of South Africa (UNISA), Florida Campus, Roodepoort, 1709, South Africa). The plastic and microplastic waste

menace and bacterial biodegradation for sustainable environmental clean-up a review, Environmental Research, Volume 231, Part 1 (2023): 116110

Environment plastic litter accumulation is a significant concern, needing urgent advancements in plastic waste management. Recent investigations into plastic biodegradation by bacteria and their enzymes are creating exciting unique opportunities for the development of biotechnological plastic waste treatment methods. This review summarizes information on bacterial and enzymatic biodegradation of plastic in a wide range of synthetic plastics such as polyethylene terephthalate (PET), polyethylene (PE), polypropylene (PP), polystyrene (PS), polyurethane (PUR), polytetrafluoroethylene (PTFE) and polyvinyl chloride (PVC). Plastic biodegradation is facilitated by Acinetobacter, Bacillus, Brevibacillus, Escherichia, Pseudomonas, Micrococcus, Streptomyces, and Rhodococcus bacteria, and enzymes such as proteases, esterases, lipases, and glycosidases. Molecular and analytical procedures used to analyze biodegradation processes are outlined, as are the obstacles in verifying plastic breakdown using these methods. Taken together, the findings of this study will contribute significantly to the construction of a library of high-efficiency bacterial isolates and consortiums and their enzymes for use in plastic biosynthesis. This information is useful to researchers investigating plastic bioremediation and a supplement to the scientific and grey literature already accessible. Finally, the review focuses on expanding the understanding of bacterial capacity to break-down plastic utilizing modern biotechnological methods, bio-nanotechnological-based materials, and their future role in resolving pollution problems.

Keywords: Biodegradation; Microbial consortium; Plastic waste; Plastic remediation

Subramani Abilaji, Kuppusamy Sathishkumar, Jayaraman Narenkumar, Mohamad S. Alsalhi, Sandhanasamy Devanesan, Punniyakotti Parthipan, Balakrishnan Muthuraj, Aruliah Rajasekar. ([a]Environmental Molecular Microbiology Research Laboratory, Department of Biotechnology, Thiruvalluvar University, Vellore, 632 115, Tamil Nadu, India, [b]Rhizosphere Biology Laboratory, Department of Microbiology, Bharathidasan University, Tiruchirappalli, 620 024, Tamil Nadu, India, [c]Department of Environmental & Water Resources Engineering, School of Civil Engineering, Vellore Institute of Technology, Vellore, 632 014, Tamil Nadu, India, [d]Department of Physics and Astronomy, College of Science, King Saud University, P.O. Box 2455; Riyadh, 11451, Saudi Arabia, [e]Department of Biotechnology, Faculty of Science and Humanities, SRM Institute of Science and Technology, Kattankulathur, Chengalpattu, Tamil Nadu 603 203, India, [f]Center for Membrane and Cell Physiology, Department of Molecular Physiology and Biological Physics, University of Virginia, School of Medicine, Charlottesville, Virginia 22903, United States). Sequential photo electro oxidation and biodegradation of textile effluent: Elucidation of degradation mechanism and bacterial diversity, Chemosphere, Volume 331 (2023): 138816

Textile effluent contains a highly toxic and refractory azo dyes. Eco-friendly method for efficient decolorization and degradation of textile effluent is essential. In the present study, treatment of textile effluent was carried through sequential electro oxidation (EO) and photo electro oxidation (PEO) using RuO2–IrO2 coated titanium electrode as an anode and cathode followed by biodegradation. The pre-treatment of textile effluent by photo electro oxidation for 14 h exhibited 92% of decolorization. Subsequent biodegradation of the pre-treated textile effluent enhanced the reduction of chemical oxygen demand to 90%. Metagenomics results exhibited that Flavobacterium, Dietzia, Curtobacterium, Mesorhizobium, Sphingobium, Streptococcus, Enterococcus, Prevotellaand Stenotrophomonas bacterial communities majorly involved in the

biodegradation of textile effluent. Hence, integrating sequential photo electro oxidation and biodegradation proposed an efficient and eco-friendly approach for treating textile effluent.

Keywords: Textile effluent; Electrooxidation; Metagenomics; Biodegradation

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A new strain, Stenotrophomonas maltophilia GYH, used trichloromethane (TCM) as the only carbon source for its growth was isolated. This strain was the first reported bacterium with TCM aerobic degradation ability. The initial TCM concentration of 8.93 mg·L-1 resulted in a degradation efficiency of 100% and a mineralization efficiency of 52% under the role of the strain. Based on the carbon balance and chlorine balance, the strain GYH could convert about 40 μg organic C contained by TCM to 20.4 μg inorganic C and 19.4 μg C by biomass, along with the complete dechlorination of TCM in 84 h. The maximum specific growth and biodegradation rates were 0.078 and 0.018 h-1, respectively. Two TCM-degrading genes were cloned and successfully expressed in the constructed strains, with 66.45% and 23.61% dechlorination efficiency. In combination with gas and ion chromatography detection and genetic analysis, an aerobic biodegradation pathway of TCM was proposed. TCM was finally converted to CO2, Cl-, and biomass under the aerobic degradation of the GYH. Such results supply fundamental knowledge for future research to effectively explain the molecular mechanism of TCM aerobic biodegradation and expand the potential industrial application of TCM biodegradation in polluted environments.

Keywords: TCM; Aerobic biodegradation; Dechlorination; Genetic analysis; Biodegradation pathway

Louisa F. James-Pearson, Kevin J. Dudley, Valentino Setoa Junior Te'o, Bharat K.C. Patel. ([1]School of Biology and Environmental Science, Queensland University of Technology, Brisbane, Queensland, Australia). A hot topic: thermophilic plastic biodegradation, Trends in Biotechnology (2023): https://doi.org/10.1016/j.tibtech.2023.03.016

Biological degradation of plastic waste is an environmentally and economically friendlier alternative to current recycling practices and enables the cycling of plastic monomers back into virgin-quality plastics. However, due to slow reaction rates, there is a lack of an industrially viable biodegradation strategy for most plastics. Here, we highlight the applicability of a thermophilic biodegradation strategy over a mesophilic approach, to enhance enzyme accessibility and catalyze plastic biodegradation. Thus, at reactions closer to the melting temperature or glass transition temperature of plastics, thermophilic reactions can offer an alternative direction to conventional plastic biodegradation strategies.

Keywords: mesophilic; plastic biodegradation; pretreatment; protein engineering; thermophilic

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Versatility and desirable attributes of synthetic plastics have greatly contributed towards their wide applications. However, vast accumulation of plastic wastes in environment as a result of their highly recalcitrant nature has given rise to plastic pollution. Existing strategies in alleviating plastic wastes accumulation are inadequate, and there is a pressing need for alternative sustainable approaches in tackling plastic pollution. In this context, plastic biodegradation has emerged as a sustainable and environmental-friendly approach in handling plastic wastes accumulation, due to its milder and less energy-intensive conditions. In recent years, extensive research effort has focused on the identification of microorganisms and enzymes with plastic-degrading abilities. This review aims to provide a timely and holistic view on the current status of plastic biodegradation, focusing on recent breakthroughs and discoveries in this field. Furthermore, current challenges associated to plastic biodegradation are discussed, and the future perspectives for continuous advancement of plastic biodegradation are highlighted.

Keywords: Plastics; Biodegradation; Enzymes; Biocatalyst; Upcycling

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Phenols and formaldehyde are often simultaneously discharged into the environment with sewage, and due to their highly toxic to organisms, few have been reported to be degraded simultaneously. This study investigated the simultaneous biodegradation of phenol and formaldehyde using the highly efficient formaldehyde-degrading fungus Aspergillus nomius SGFA1, which was previously isolated and identified in our laboratory. The response surface methodology was used to optimize the biodegradation conditions of phenol and formaldehyde; the optimum temperature, initial pH, and glucose content were determined to be 28.1 °C, 5.0, and 0.89%, respectively, under which the maximum degradation rates of phenol and formaldehyde reached 89.7% and 85.3%, respectively. Mass balance and stoichiometric analysis revealed 0.26 g·g−1 and 0.05 g·g−1 conversions of phenol and formaldehyde carbon to biomass, respectively. The degradation pathway demonstrated that phenol hydroxylase (PHE) and formaldehyde dehydrogenase (FALDH) were the key enzymes for phenol and formaldehyde degradation, with enzyme activities reaching maxima of 0.008 and 1.09 U·mg−1 at 8 and 6 h, respectively. This study demonstrated the ability of A. nomius SGFA1 to effectively remove phenol and formaldehyde simultaneously, providing new information on the use of microorganisms to reduce environmental pollution.

Keywords: Biodegradation; Formaldehyde; Phenol; Response surface methodology; Aspergillus nomius

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With the benefits of coming at low-cost, being light-weight and having a high formability and durability, conventional plastics are widely used in both industry and daily life. However, because of their durability and extensive half-life with poor degradability and the low recycling rate, large amounts of plastic waste are accumulated in various environments, posing a significant threat to organisms and ecosystems. Compared to conventional physical and chemical degradation, biodegradation of plastic might become a promising and environmentally friendly solution for this problem. One of the aims of this review is to briefly describe the impact of plastics (especially microplastics). To facilitate rapid advancements in the area of plastic biodegradation, this paper provides a comprehensive review of the candidate organisms capable of biodegrading plastics and originating from four categories including natural microorganisms, artificially derived microorganisms, algae and animal organisms. In addition, the potential mechanism during plastic biodegradation and associated driving factors are summarized and discussed. Furthermore, the recent biotechnological progress (e.g. synthetic biology, systems biology, etc.) is highlighted as being key for future research. Finally, innovative research avenues for future studies are proposed. Concluding, our review is addressing the practical application of plastic biodegradation and the plastic pollution, thus necessitating more sustainable developments.

Keywords: Conventional plastics; Biodegradation; Candidate organisms; Biodegradation mechanisms; Correlative factors

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Microplastic (MP) and Nanoplastic (NP) contamination have become a critical ecological concern due to their persistent presence in every aspect of the ecosystem and their potentially harmful effects. The current approaches to eradicate these wastes by burning up and dumping adversely impact the environment, while recycling has its own challenges. As a result, applying degradation techniques to eliminate these recalcitrant polymers has been a focus of scientific investigation in the recent past. Biological, photocatalytic, electrocatalytic, and, recently, nanotechnologies have been studied to degrade these polymers. Nevertheless, it is hard to degrade MPs and NPs in the environment, and these degradation techniques are comparatively inefficient and require further development. The recent research focuses on the potential use of

microbes to degrade MPs and NPs as a sustainable solution. Therefore, considering the recent advancements in this important research field, this review highlights the utilization of organisms and enzymes for the biodegradation of the MPs and NPs with their probable degradation mechanisms. This review provides insight into various microbial entities and their enzymes for the biodegradation of MPs. In addition, owing to the lack of research on the biodegradation of NPs, the perspective of applying these processes to NPs degradation has also been looked at. Finally, a critical evaluation of the recent development and perspective for future research to improve the effective removal of MPs and NPs in the environment through biodegradation is also discussed.

Keywords: Microplastics; Nanoplastics; Biodegradation; Microorganisms; Enzymes; Mechanism

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Heavy oil is one of the most significant unconventional petroleum resources and one of its formation mechanisms is biodegradation. The characterization of the molecular compositions of petroleum is crucial for determining the various degrees of biodegradation. In this work, detailed investigations of acids and polar NSO compounds in different levels of biodegraded oils from the Bongor Basin (Chad) were carried out by negative ion electrospray ionization (-ESI) Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS). The present findings show that the heteroatomic compounds of biodegraded crude oils are predominantly composed of N1, N1O1, O1, O2, O3 and O4 species. The relative content of N1, N1O1 and O1 species tend to decrease and those of O2, O3 and O4 species appear to increase with the increasing of biodegradation. The ratio of acyclic and cyclic acids (A/C ratio) of the O2 species increase with an increase of biodegradation, indicating the increasing of O2 class during microbial alteration. A new parameter, i.e. the ratio of (O2 + O3 + O4)/(N1 + O1) species, is presented to quantificationally define biodegradation levels. This parameter is inversely proportional to API gravity and has a favorable positive correlation with total acid number (TAN), suggesting acidic compounds are formed by the microbial alteration of N1 and O1 class and are more presented in advanced biodegradation. A modified ternary diagram including N1, O1 and O2 + O3 + O4 species describe the detailed changes of nitrogen- and oxygen- containing compounds. Data points with a high level of biodegradation tend to shift to O2 + O3 + O4 species end-member and retreat from N1 species end-member, showing the relative content of O2 + O3 + O4 species increase and those of N1 species decrease with increasing biodegradation which may due to the formation of organic acids in degradation oil. The ratio of (O2 + O3 + O4)/(N1 + O1) species and the modified ternary diagram provide new parameters to estimate the biodegradation degree and TAN in crude oil.

Keywords: ESI FT-ICR MS; Biodegradation; Petroleum acids; Polar NSO compounds; Bongor Basin

Yimin Xie, Naiwen Chen, Zhiwei Liang, Yihuai Huang, Hojae Shim. (Department of Civil and Environmental Engineering, Faculty of Science and Technology, University of Macau, Macau SAR 999078, China) Biodegradation of dibutyl phthalate and diethyl phthalate by indigenous isolate Bacillus sp. MY156: Characterization, stoichiometry, enzyme activity, and physiological response to cell surface, Journal of Water Process Engineering, Volume 53 (2023): 103862

An indigenous bacterial strain, Bacillus sp. MY156, was isolated from a local wastewater treatment plant and utilized for degradation of dibutyl phthalate (DBP) and diethyl phthalate (DEP). The isolate showed a substrate preference of DBP to DEP. The optimal biodegradation conditions were pH 7, 30 °C, 0.2 (in terms of OD600) inoculum size, and 2 % (v v−1) bacterial load. The biodegradation of DBP and DEP as sole carbon source was comprehensively investigated via degradation kinetics and mass balance analysis. The isolate achieved complete degradation and over 80 % removal of 300 mg L−1 DBP within 60 h and 200 mg L−1 DEP in 5 days. The biodegradation of DBP and DEP fitted the inhibitory kinetic model, and the maximum degradation rates for DBP and DEP were 183.34 and 66.90 mg L−1 day−1, respectively. The cell surface responses to biodegradation were investigated by analyses of morphology, Fourier transform-infrared, and extracellular polymeric substance. The potential intermediates were mono-n-butyl phthalate, mono-ethyl phthalate, phthalic acid, and protocatechuic acid by β-oxidation, hydrolysis, and decarboxylation. The esterase and dehydrogenase activities reached the highest at the initial and middle phases during biodegradation. The docking studies also elucidated the relevant enzyme preferred DBP to DEP via binding energy and bond distance.

Keywords: Dibutyl phthalate; Diethyl phthalate; Biodegradation; Stoichiometry; Esterase

Yifeng Xu, Ying Gu, Lai Peng, Ning Wang, Shi Chen, Chuanzhou Liang, Yiwen Liu, Bing-Jie Ni. ([a]Hubei Key Laboratory of Mineral Resources Processing and Environment, Wuhan University of Technology, Luoshi Road 122, Wuhan, Hubei, 430070, China, [b]Shenzhen Research Institute of Wuhan University of Technology, Shenzhen, 518000, Guangdong, China, [c]Centre for Technology in Water and Wastewater, School of Civil and Environmental Engineering, University of Technology Sydney, Sydney, NSW, 2007, Australia). Unravelling ciprofloxacin removal in a nitrifying moving bed biofilm reactor: Biodegradation mechanisms and pathways, Chemosphere, Volume 320 (2023): 138099

Although moving bed biofilm reactors (MBBRs) have shown excellent antibiotic removal potentials, the information on underlying mechanisms is yet limited. This work assessed the removal of ciprofloxacin in an enriched nitrifying MBBR by clarifying the contribution of adsorption and microbial-induced biodegradation. Results demonstrated the considerable biomass adsorption (55%) in first 30 min. Limiting nitrite oxidizing bacteria growth or inhibiting nitrification would lead to lower adsorption capacities. The highest ciprofloxacin biodegradation rate constant was 0.082 L g SS−1 h−1 in the presence of ammonium, owing to ammonia oxidizing bacteria (AOB)-induced cometabolism, while heterotrophs played an insignificant role (~9%) in ciprofloxacin biodegradation. The developed model also suggested the importance of AOB-induced cometabolism and metabolism over heterotrophs-induced biodegradation by analyzing the respective biodegradation coefficients. Cometabolic biodegradation pathways of ciprofloxacin mainly involved the piperazine ring cleavage, probably alleviating antimicrobial activities. It implies the feasibility of nitrifying biofilm systems towards efficient antibiotic removal from wastewater.

Keywords: Biofilm; Antibiotic; Cometabolism; Biodegradation pathways; Ammonia oxidizing bacteria

Lebohang Gerald Motsoeneng, Vizelle Naidoo, Lukhanyo Mekuto. (Department of Chemical Engineering, University of Johannesburg, Johannesburg 2028, South Africa) Biogas production and metabolite profiling from anaerobic biodegradation of free cyanide using municipal waste activated sludge, Bioresource Technology Reports, Volume 22 (2023): 101442

This study investigated the biodegradation of free cyanide (FCN) under anaerobic conditions using municipal waste activated sludge (MWAS) for subsequent biogas production and metabolite profiling in an airtight stirred tank bioreactor. The pH, temperature, and agitation speed were set at 9.5, 35 °C and 85 rpm respectively and the experiment was ran for 14 days at 100 mg FCN/L. After the biodegradation process, the metabolites were extracted using ethyl acetate and thereafter, metabolite profiling was performed using LC-QTOF-MS/MS. The microorganisms achieved an FCN biodegradation efficiency of 99.6 %, while the maximum biogas produced were 229 mL and 179 mg COD/L for captured and dissolved biogas respectively. 248 metabolites were detected and these included tert-butyl[amino(H1,2,4,-triazol-1-yl)methylidene] carbamate, 8-hydroxyquinone, 2.5-difluro-1H-imadazole-4-carboxylic acid, oleoyl ethyl amide (OEtA) and pterin; metabolites of medical significance. The findings of this study demonstrated that it is possible to produce value-added products from anaerobic cyanide treatment processes, which can be applied in various fields.

Keywords: Anaerobic biodegradation; Free cyanide; Biogas; Municipal waste activated sludge; Metabolites

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The activated sludge process at wastewater treatment plants is important to prevent discharge of organic pollutants to the environment. Determination of biodegradation kinetics in activated sludge is challenging for mixtures that cover a diverse range of structures. The aims of this study were to (1) design a closed aerobic biodegradation batch test with activated sludge and (2) develop a sample preparation procedure that is compatible with LC-MS and Solid Phase Microextraction (SPME) coupled to GC-MS. A headspace:sludge ratio of 4:1 was sufficient to ensure aerobic conditions in activated sludge for 7 days at co-solvent concentrations <0.01%. Ethanol was added to sub-samples (50%) to stop biodegradation, extract sorbed chemicals and allow storage at −18 °C without ice formation. The ethanol extracted the chemicals from the sludge before filtration (0.2 μm). The filtrate was diluted in ultrapure water to <12% ethanol before analysis by SPME GC-MS/MS and was suitable for direct injection on LC-MS/MS. Biodegradation was distinguished from sorption through abiotic controls using autoclaved poisoned sludge. Linalool, naphthalene, α-isomethylionone, phenanthrene, citronellol, drometrizole, 2-ethylhexyl 4-methoxycinnamate, dicyclohexyl phthalate, BP-1, BP-3, methyl-, ethyl-, propylparaben, alkyl sulfates and isethionates degraded within 48 h in activated sludge, while musk ketone, tonalide and 1,3,5-trichlorobenzene did not. A 10 times reduction of sludge density did not markedly affect the microbial diversity but slowed biodegradation kinetics (partly explained by theory). This study demonstrated a ‘cold’ alternative to an OECD 314b test and how biodegradation kinetics can be determined for mixtures of diverse chemicals in closed batch tests with activated sludge.

Keywords: UV filters; Plasticizers; Fragrances; Preservatives

Shodai Hino, Norioki Kawasaki, Naoko Yamano, Tsutomu Nakamura, Atsuyoshi Nakayama. (Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), 1-8-31 Midorigaoka, Ikeda, Osaka, 563-8577, Japan) Effects of particle size on marine biodegradation of poly(l-lactic acid) and poly(ε-caprolactone), Materials Chemistry and Physics, Volume 303 (2023): 127813

The rising quantity of non-degradable microplastics in the world's oceans is becoming a major environmental and health issue. In this context, the advent of biodegradable plastics is a key step. However, information about the degradation of these polymers in the marine environment is scarce. In this study, the effect of particle size on laboratory-scale non-enzymatic hydrolysis, enzymatic hydrolysis, and seawater biodegradation of polymers was investigated. Compostable and biodegradable polymers, such as poly(l-lactic acid) (PLA) and poly(ε-caprolactone) (PCL), were cryo-milled and segregated into different size fractions. While non-enzymatic hydrolysis remained largely unaffected by the particle size, the enzymatic hydrolysis rate tended to increase with decreasing particle size for both polymers. The results indicated that the enzymatic hydrolysis rate could be accelerated by making the polymer particles finer. Furthermore, the seawater biodegradation rate and logarithm of the specific surface area were positively correlated. Therefore, it was expected that seawater biodegradation could also be accelerated. The hydrolysis rate of PLA in seawater, however, was not accelerated even with the smallest particle size, suggesting that the specific surface area, as well as the number of bacteria and concentration of extracellular enzymes on the particle surface, are essential for its seawater biodegradation.

Keywords: Marine biodegradation; Microplastics; Particle size; Poly(l-lactic acid); Poly(ε-caprolactone)

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The plasticized film was made of polylactide and birch tar, which was used in a concentration of 1, 5 and 10 % by weight. Tar was added to the polymer to obtain materials with antimicrobial properties. The main purpose of this work is to characterize and biodegradation of this film after the end of its use. Therefore, the following analyzes were performed: enzymatic activity of microorganisms in the presence of polylactide (PLA) film containing birch tar (BT), biodegradation process in compost, barrier changes and structural properties of the film before

and after biodegradation and bioaugmentation. Biological oxygen demand BOD21, water vapor permeability (Pv), oxygen permeability (Po), scanning electron microscopy (SEM) and enzymatic activity of microorganisms were assessed. Microorganism strains Bacillus toyonensis AK2 and Bacillus albus AK3 were isolated and identified, which constituted an effective consortium increasing the susceptibility of polylactide polymer material with tar to biodegradation in compost. Analyses with the use of the above-mentioned strains had an impact on the change of physicochemical properties, e.g. the presence of biofilm on the surface of the analyzed films and the reduction of the barrier properties of the film, which translates into the recorded susceptibility to biodegradation of these materials. The analyzed films can be used in the packaging industry, and after use, subjected to intentional biodegradation processes, including bioaugmentation.

Keywords: Polylactide; Birch tar; Biodegradation-compost

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Exposure to polycyclic aromatic hydrocarbons (PAHs) from tobacco smoke has been linked to many negative health effects. Studies on the biodegradation of PAHs by human microbiota and detailed pathways for their anaerobic biodegradation are scarce despite their importance in getting rid of these toxic compounds. In a previous study for our group, we determined the ability of oral bacterial isolates in the anaerobic biodegradation of anthracene as a model of PAHs. Three isolates with the highest anthracene degradation ability were selected for the present study which include Limosilactobacillus fermentum, Veillonella parvula, and Streptococcus anginosus. In this study, we aimed at exploring and elucidating the anthracene anaerobic biodegradation pathways in selected Firmicutes oral isolates. Metabolites throughout the pathway were detected by gas chromatography coupled with mass spectroscopy (GC-MS) using anthracene as sole source of carbon. After incubation for 3 days, anthracene was undetected in the supernatant of L. fermentum and V. parvula, while a residual of 3% of anthracene was detected in presence of S. anginosus. Results revealed that anaerobic biodegradation by L. fermentum and V. parvula started with hydroxylation and dehydrogenation producing 9,10- anthraquinone and ended up with simpler structures such as catechol, while S. anginosus hydroxylation for anthracene resulted in the production of 1,2-anthracenediol and ended up with catechol and phthalic acid. The biodegradation of anthracene by oral bacteria could convert it to other toxic metabolites such as anthraquinone and catechol which were reported to have potential carcinogenic effects. Moreover, fatty acids detected as biodegradation metabolites could be one of the causes of smokers' heart-related diseases. Thus, this study explored oral metabolites resulting from smoking under anaerobic conditions towards elucidating the role of oral microbiota in health and disease states.

Keywords: Anthracene; Anaerobic biodegradation; Oral firmicutes; Streptococcus anginosus; Limosilactobacillus fermentum; Veillonella parvula

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Plastics have become an essential part of life. When it enters the environment, it migrates and breaks down to form smaller size fragments, which are called microplastics (MPs). Compared with plastics, MPs are detrimental to the environment and pose a severe threat to human health. Bioremediation is being recognized as the most environmentally friendly and cost-effective degradation technology for MPs, but knowledge about the biodegradation of MPs is limited. This review explores the various sources of MPs and their migration behavior in terrestrial and aquatic environments. Among the existing MPs removal technologies, biodegradation is considered to be the best removal strategy to alleviate MPs pollution. The biodegradation potential of MPs by bacteria, fungi and algae is discussed. Biodegradation mechanisms such as colonization, fragmentation, assimilation, and mineralization are presented. The effects of MPs characteristics, microbial activity, environmental factors and chemical reagents on biodegradation are analyzed. The susceptibility of microorganisms to MPs toxicity might lead to decreased degradation efficiency, which is also elaborated. The prospects and challenges of biodegradation technologies are discussed. Eliminating prospective bottlenecks is necessary to achieve large-scale bioremediation of MPs-polluted environment. This review provides a comprehensive summary of the biodegradability of MPs, which is crucial for the prudent management of plastic waste.

Keywords: Microplastics; Biodegradation; Bacteria; Fungi; Algae; PETase

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In this study, a set of comprehensive experiments were conducted to explore the effects of temperature on the biodegradation, bioavailability, and generation of reactive oxygen species (ROS) by thermally enhanced biodegradation (TEB) under benzene and BaP co-contaminated conditions. The biodegradation rates of benzene increased from 57.4% to 88.7% and 84.9%, and the biodegradation efficiency of BaP was enhanced from 15.8% to 34.6% and 28.6%, when the temperature was raised from the ambient temperature of 15 °C to 45 °C and 30 °C, respectively. In addition, the bioavailability analysis results demonstrated that the water- and butanol-

extractable BaP increased with elevated temperatures. High enzymatic activities and PAH-RHDα gene in gram-positive bacteria favored the long-term elevated temperatures (30 and 45 °C) compared to gram-negative bacteria. Moreover, ROS species (O2•− and •OH) generation was detected which were scavenged by the increased superoxide dismutase and catalase activities at elevated temperatures. Soil properties (pH, TOC, moisture, total iron, Fe3+, and Fe2+) were affected by the temperature treatments, revealing that metal-organic-associated reactions occurred during the TEB of benzene–BaP co-contamination. The results concluded that biodegradation of benzene–BaP co-contamination was greatly improved at 45 °C and that microbial activities enhanced the biodegradation under TEB via the increased bioavailability and generation and degradation of ROS.

Keywords: Bioavailability; ROS; Thermally enhanced biodegradation; PAH-RHDα genes; Soil properties

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Coal biodegradation is promising for sustainable energy development. Studying proteomics in coal biodegradation is effective for identifying different proteins and analyzing corresponding biological strategies. However, previous research on this topic is limited. Here, Fusarium sp. NF01 was proven to degrade lignite based on surface morphology, functional groups, and chemical composition for the first time. The proteomics of Fusarium sp. NF01 were then quantitatively and qualitatively analyzed using isobaric tandem mass tags and bioinformatics profiling during lignite biodegradation. The results showed that 1.8 g of lignite was biodegraded into 4.7 mL of black droplets, with microstructural changes. The abundance of 18 proteins, including eight upregulated and ten downregulated proteins (fold change, $FC \geq 1.2$ or $FC \leq 0.83$ and P-value ≤ 0.05), significantly changed during the lignite biodegradation process. These proteins were mainly involved in spermidine synthase, PM H+-ATPase, GGT, 6-HDNO, IPS, and AST. Fusarium sp. NF01 adopted multilevel protein-based strategies, such as nutrient transport and synthesis, positive plasma membrane regulation, immunity optimization, and prevention of cell damage and death to respond to the influence of the lignite environment on its growth and metabolism. These findings provide valuable bioinformation for identifying degradation-specific protein molecules and elucidating the biodegradation mechanism of coal.

Keywords: Fusarium; Lignite biodegradation; Proteomics; Tandem mass tag; Response strategy

Biosensor

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Umami substances can provide a palatable flavour for food. In this study, an electrochemical impedimetric biosensor was developed for detecting umami substances. This biosensor was fabricated by immobilising T1R1 onto AuNPs/reduced graphene oxide/chitosan which was in advance electro-deposited onto a glassy carbon electrode. The evaluation by the electrochemical impedance spectrum method showed that the T1R1 biosensor performed well with low detection limits and wide linear ranges. Under the optimised incubation time (60 s), the electrochemical response was linearly related to the concentrations of the detected targets monosodium glutamate and inosine-5′-monophosphate within their respective linear range of 10-14 to 10-9 M and 10-16 to 10-13 M. The low detection limit of monosodium glutamate and inosine-5′-monophosphate was 10−15 M and 10−16 M, respectively. Moreover, the T1R1 biosensor exhibited high specificity to umami substances even in the real food sample. The developed biosensor still retained 89.24% signal intensity after 6-day storage, exhibiting a desirable storability.

Keywords: Umami; Electrochemical biosensor; T1R1 receptor; Electrochemical impedance spectroscopy

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A biosensor is an analytical tool applied for biomarkers' specific and sensitive detection. Using biosensors in clinical settings leads to trustworthy, precise, and quantitative measurements of biomarkers at low concentrations. Nanoengineering presents several benefits compared to traditional clinical diagnostics: the time saving and the ability of nanomaterials for onsite diagnosis of biomarkers. Over the last few years, nanotechnology has enormously contributed to the design and fabrication of biosensors in terms of specificity, biocompatibility, sensitivity, and validity. Besides, nanomaterials enable miniaturization and develop a portable sensing system suitable for commercial purposes. Polyvinylpyrrolidone (PVP) is a water-soluble polymer broadly utilized in various industries, including pharmaceuticals, medicine, cosmetics, etc. In pharmaceuticals, it may be used as a coating agent, binder, pore-former, suspending agent, solubilizer, and other excipients for traditional formulations and new controlled or targeted delivery systems and biosensors. The main goal of this article is to provide a brief overview of recent biosensors using PVP as part of their structure.

Keywords: Polyvinylpyrrolidone; Nanotechnology; Biosensors; Biocompatibility; Sensitivity

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A "on–off" self-powered biosensor was developed based on enzymatic biofuel cells (EBFCs) for sequential detection of microRNA-21 (miRNA-21) and miRNA-155 by capture and release of a single-bioanode enzyme, i.e., glucose oxidase. When miRNA-21 is present, it hybridizes with DNA1 and the glucose oxidase (GOD)-modified DNA2, i.e., DNA2-GOD. Then, GOD oxidizes glucose to produce a large number of electrons, and a significantly increased open-circuit voltage (E1OCV) is observed, corresponding to the "on" state. If miRNA-155 is present, it hybridizes with DNA1 and DNA3-functionalized SiO2 nanosphere@gold nanoparticles, i.e., SiO2@AuNPs-DNA3, and replaces miRNA-21 to release GOD at the bioanode, thus leading to decreased E2OCV, corresponding to the "off" state. The "on–off" self-powered biosensor shows ultra-sensitive detection of miRNA-21 and miRNA-155 with detection limits of 0.17 fM and 0.37 fM, respectively. It is believed that this study provides a feasible model for designing self-powered biosensors for multi-targets detection.

Keywords: "On–off"; Self-powered biosensor; Enzymatic biofuel cells; Capture and release

Sanika Jain, Ritu Panwar, Jyoti Mathur. (Department of Bioscience and Biotechnology, Banasthali Vidyapith, Banasthali, Rajasthan, India). Design and development of colorimetric, whole-cell based, electrochemical biosensors for arsenic detection, Inorganic Chemistry Communications, Volume 153 (2023): 110730

Heavy metal contamination seriously threatens human health since these substances are non-biodegradable and retained by the ecosystem. Pollution caused by heavy metals is a natural and human-caused issue that has resulted in increased heavy metal content in natural environments that is too dangerous for human health. The presence of heavy metals is not only toxic to human health but also has an impact on soil and plant productivity. Among the various contaminants concentration of heavy metals such as As, Pb, Hg, and Cd has increased, causing concern among most of the world's population. Nowadays, biosensors are a potent substitute for traditional analytical methods for regulating water quality, including natural water, process water used in

the food industry during production, and wastewater before it is released into natural water courses. It is an analytical tool that is portable, inexpensive, time-saving, highly sensitive, and selective that produces results in a split second. The analytical gadget synergistically combines microelectronics and biotechnology and comprises a transducer and an immobilized biocomponent. Several harmful compounds, like pesticides, heavy metals, etc., can be detected and measured using water, soil, and food biosensors. The goal is to detect the concentration of heavy metal ions in the soil, water, and food because their toxicity can cause damage to all life forms using biosensor. This review summarizes the principle, types, construction, and application of biosensors for arsenic detection.

Keywords: Arsenic toxicity; Atomic absorption spectroscopy; Detection; Biosensors; Heavy metal

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Synthetic microbial community (SynCom) biosensors are a promising technology for detecting and responding to environmental cues and target molecules. SynCom biosensors use engineered microorganisms to create a more complex and diverse sensing system, enabling them to respond to stimuli with enhanced sensitivity and accuracy. Here, we give a definition of SynCom biosensors, outline their construction workflow, and discuss current biosensing technology. We also highlight the challenges and future for developing and optimizing SynCom biosensors and the potential applications in agriculture and food management, biotherapeutic development, home sensing, urban and environmental monitoring, and the One Health foundation. We believe SynCom biosensors could be used in a real-time and remote-controlled manner to sense the chaos of constantly dynamic environments.

Keywords: synthetic microbial communities; cell-free biosensor; whole-cell biosensor; consortia biosensor; SynCom biosensor

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disposable biosensors for medical diagnostics: Principles, opportunities, and challenges, Advances in Colloid and Interface Science, Volume 317 (2023): 102920

Hydrogels are excellent water-swollen polymeric materials for use in wearable, implantable, and disposable biosensors. Hydrogels have unique properties such as low cost, ease of preparation, transparency, rapid response to external conditions, biocompatibility and self-adhesion to the skin, flexibility, and strain sensitivity, making them ideal for use in biosensor platforms. This review provides a detailed overview of advanced applications of stimuli-responsive hydrogels in biosensor platforms, from hydrogel synthesis and functionalization for bioreceptor immobilization to several important diagnostic applications. Emphasis is placed on recent advances in the fabrication of ultrasensitive fluorescent and electrically conductive hydrogels and their applications in wearable, implantable, and disposable biosensors for quantitative measurements. Design, modification, and assembly techniques of fluorescent, ionically conductive, and electrically conductive hydrogels to improve performance will be addressed. The advantages and performance improvements of immobilizing bioreceptors (e.g., antibodies, enzymes, and aptamers), and incorporating fluorescent and electrically conductive nanomaterials are described, as are their limitations. Potential applications of hydrogels in implantable, wearable, disposable portable biosensors for quantitative detection of the various bioanalytes (ions, molecules, drugs, proteins, and biomarkers) are discussed. Finally, the global market for hydrogel-based biosensors and future challenges and prospects are discussed in detail.

Keywords: Biosensor platforms; Stimuli-responsive hydrogels; Hydrogel synthesis; Conductive hydrogels; Florescent hydrogels; Nanomaterials; Bioreceptor immobilization; Biomarkers

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The effect of the covalent binding between anthocyanins extracted from purple potato peels and beta-lactoglobulin (β-Lg) on its ability to fabricate a green/smart halochromic biosensor combined with pullulan (Pul) was studied. The physical, mechanical, colorimetry, optical, morphological, stability, functionality, biodegradability, and applicability of β-Lg/Pul/Anthocyanin biosensors to monitor the Barramundi fish's freshness during storage were entirely evaluated. The docking and multispectral results proved that β-Lg could be successfully phenolated with anthocyanins and subsequently interacted with Pul via H-bonding and other forces which mainly subsequently form the smart biosensors. Phenolation with anthocyanins significantly heightened the mechanical, moisture resistance, and thermal steadiness of β-Lg/Pul biosensors. Anthocyanins also nearly duplicated the bacteriostatic and antioxidant activities of β-Lg/Pul biosensors. The biosensors changed the color associated with the loss in freshness of the Barramundi fish, mostly due to the ammonia production and pH-alteration throughout fish deterioration. Most importantly, β-Lg/Pul/Anthocyanin biosensors are biodegradable and decomposed within ~30 d of simulated environmental circumstances. Overall, β-Lg/Pul/Anthocyanin smart biosensors could minimize the usage of plastic packaging materials and employ to monitor the freshness of stored fish and fish-stuffs.

Keywords: Anthocyanins; Byproducts; Covalent binding; Green/smart packaging; pH-reactive biosensors; Multifunctionality; Barramundi quality

Yunqiu Zhao, Lin Zhu, Yaxue Ding, Weiting Ji, Kun Liu, Ke Liu, Bei Gao, Xinyi Tao, Yu-Guo Dong, Feng-Qing Wang, Dongzhi Wei. ([a]State Key Laboratory of Bioreactor Engineering, Newworld Institute of Biotechnology, East China University of Science and Technology, Shanghai, 200237, China, [b]Key Laboratory of Biocatalysis and Intelligent Manufacturing (ECUST), China National Light Industry, Shanghai, 200237, China). Simple and cheap CRISPR/Cas12a biosensor based on plug-and-play of DNA aptamers for the detection of endocrine-disrupting compounds, Talanta, Volume 263 (2023): 124761

Endocrine-disrupting compounds (EDCs) are widely distributed in the environment. Here, we present a CRISPR/Cas12a (CAS) biosensor based on DNA aptamers for point-of-care detection of EDCs. Two typical EDCs, 17β-estradiol (E2) and bisphenol A (BPA), were selected to be detected by the CAS biosensors via the plug-and-play of their DNA aptamers. The results indicated that the performance of the CAS biosensors can be well regulated by controlling the trans-cleavage activity of Cas12a on a single-stranded DNA reporter and optimizing the sequence and ratio of DNA aptamer and activator DNA. Ultimately, two reliable and specific biosensors were developed, with the linear range and limit of detection of 0.2–25 nM and 0.08 nM for E2 and of 0.1–250 nM and 0.06 nM for BPA, respectively. Compared to the existing detection methods, the CAS biosensors showed higher reliability and sensitivity with simple operation, short detection time, and no costly equipment.

Keywords: Endocrine-disrupting compounds; DNA aptamers; CRISPR/Cas12a biosensor; 17β-estradiol; Bisphenol A

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Microbial toxins with high toxicity have caused significant threats to human health, economics and ecological environment, attracting considerable attentions around the world. Developing specific, highly sensitive, reliable, rapid and cost-effective detection technologies is essential to confront such threats. In recent years, novel optical biosensors due to their simple design, autonomous operation, fast response, high-frequency monitoring without extensive sample preparation and excellent recognition capability have been applied in the ultrasensitive detection of trace microbial toxins. In this paper, the recent advances of various novel optical biosensors for microbial toxins determination are summarized with emphasis on fluorescent, colorimetric, chemiluminescent, electrochemiluminescent, surface plasmon resonance and surface enhanced Raman scattering biosensors. Furthermore, the advantages, current development status, limitations in practical application, and future prospects of these technologies were also discussed comprehensively. It is expected to promote the future development and wide application of optical biosensors.

Keywords: Microbial toxin; Optical biosensor; Challenges; Future prospect

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Laboratory of Marine Microbiome Engineering, Institute for Advanced Study, Shenzhen University, Shenzhen 518060, PR China, [c]State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China, [d]Institute of Agricultural Resources and Environment, Jiangsu Academy of Agricultural Sciences, Key Laboratory of Saline-Alkali Soil Improvement and Utilization (Coastal Saline-Alkali lands), Ministry of Agriculture and Rural Affairs, Nanjing 210014, China). **On-site Screening Method for Bioavailability Assessment of the Organophosphorus Pesticide, Methyl Parathion, and Its Primary Metabolite in Soils by Paper Strip Biosensor, Journal of Hazardous Materials (2023): 131725**

An important public concern worldwide is soil pollution caused by organophosphorus pesticides and their primary metabolites. To protect the public's health, screening these pollutants on-site and determining their soil bioavailability is important, but doing so is still challenging. This work improved the already-existing organophosphorus pesticide hydrolase (mpd) and transcriptional activator (pobR), and it first designed and constructed a novel biosensor (Escherichia coli BL21/pNP-LacZ) that can precisely detect methyl parathion (MP) and its primary metabolite p-nitrophenol with low background value. To create a paper strip biosensor, E. coli BL21/pNP-LacZ was fixed to filter paper using bio-gel alginate and sensitizer polymyxin B. According to the calibrations of the paper strip biosensor for soil extracts and standard curve, the color intensity of the paper strip biosensor collected by the mobile app may be used to compute the concentration of MP and p-nitrophenol. This method's detection limits were 5.41µg/kg for p-nitrophenol and 9.57µg/kg for MP. The detection of p-nitrophenol and MP in laboratory and field soil samples confirmed this procedure. Paper strip biosensor on-site allows for the semi-quantitative measurement of p-nitrophenol and MP levels in soils in a simple, inexpensive, and portable method.

Keywords: paper strip biosensor; p-nitrophenol; organophosphorus pesticide; screening method; soil

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The gut microbiota has emerged as an important aspect of clinical oncology. The role of microbiota in cancer goes beyond the risks and causes of cancer. Microbiotas are currently known to act at the local epithelial level of the intestine and alter the immune response of intestinal and extra-intestinal tumors. As probiotics are increasingly used in functional foods and pharmaceuticals, rapid and sensitive monitoring of probiotics is important for quality, purity, and safety management. Due to the weaknesses and limitations of routine microbiological techniques, developing advanced state-of-the-art methods is one of the main goals of

researchers. One of the most critical and progressive areas is the nanomaterial-based method. Biosensors are one of the most advanced methods based on nanomaterials. While biosensing technology for the human gut flora has the potential to transform the clinical diagnosis, point-of-care (POC) biosensors that directly detect microbial community disruptions are not currently available in clinical practice. This review study aimed to explore the potential of biosensors in identifying the human gut flora to achieve the best techniques for the first time.

Keywords: Nanomaterial; Nanotechnology; Gut microbiota; Biosensors

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In this work, a Si/InAs/Ge junctionless tunneling field effect transistor (JL-TFET) based biosensor has been simulated. The proposed biosensor turns on with a 0.5 V bias supply voltage to make it suitable for low-power applications. Comparing results of Si/InAs/Ge JL-TFET based biosensors in which fixed (f)-gate is connected to control (c)-gate with that of in which f-gate is not connected to c-gate, a 90% decrease in drain current sensitivity was found. To further improve average subthreshold slope (SS) and sensitivity, we have proposed Si/InAs/Ge JL-TFET based biosensor with asymmetric gate oxide thickness. Simulation results show that the designed Si/InAs/Ge JL-TFET based biosensor with oxide thickness underneath c-gate TOX1 = 2 nm and oxide thickness underneath f-gate TOX2 = 3 nm for biomolecules having a dielectric constant value as 12 exhibits SS = 4.6 mV/dec, and sensitivity = 1.6e4. Accordingly, proposed biosensor has superior electrical characteristics in comparison with the recent state-of-the-art JL-TFET based biosensors.

Keywords: Biosensor; Dielectric modulated TFET; Intra-band tunneling; Steep subthreshold slope; Simulation study

S.V. Bazhenov, U.S. Novoyatlova, E.S. Scheglova, E.V. Prazdnova, M.S. Mazanko, A.G. Kessenikh, O.V. Kononchuk, E.Y. Gnuchikh, Y. Liu, R. Al Ebrahim, G.B. Zavilgelsky, V.A. Chistyakov, I.V. Manukhov. ([a]Moscow Institute of Physics and Technology, 141701, Dolgoprudny, Russia, [b]D.I.Ivanovskiy Academy of Biology and Biotechnology, Southern Federal University, 344090, Stachki av. 194/1, Rostov-on-Don, Russia, [c]Laboratory of Microbiology, BIOTECH University, Volokolamskoe Highway 11, 125080, Moscow, Russia, [d]National Research Center Kurchatov Institute, Kurchatov Genomic Center, Moscow, 123182, Russia). Bacterial lux-biosensors: Constructing, applications, and prospects, Biosensors and Bioelectronics: X, Volume 13 (2023): 100323

This review aims to systematize data on the construction and applications of bacterial lux-biosensors in various fields ranging from investigation of gene regulation and regulatory networks to the new probiotics' search and ecotoxicological research. The typical technical solutions and devices required for diverse tasks applying lux-biosensors are reviewed. Aspects of the application of lux-biosensors in fundamental researches, such as the study of oxidative stress,

heat shock, DNA-damaging, pro- and antioxidant activities, are also considered. This technology allows rapid screening of the biological activities of newly synthesized compounds, which could be applied as components for fuels, household chemicals, and drugs. Works related to the ecological state assessment on water resources are also described. The use of lux-biosensor complexes based on different organisms, including both gram-positive and gram-negative bacteria, makes toxicological investigations more comprehensive. Bacterial lux-biosensors based on Escherichia coli can be used as a model for evaluation of the effect of certain substances on the transmembrane potential in mitochondria, albeit with extrapolation to a certain extent. Another aspect that draws our interest is that biosensors are able to help predict some systemic properties of probiotics. In the future, it's quite promising to see more applications of lux-biosensors for environmental control, microbial-microbial interaction assessment, antioxidant action mechanism studies and toxicological studies in the development of new drugs.

Keywords: Lux-biosensor; Whole-cell biosensor; Luminescence; Gene regulation; Probiotics; Ecotoxicology

Hongyuan Shang, Xiaofei Zhang, Meili Ding, Aiping Zhang. (College of Pharmacy, Shanxi Medical University Taiyuan, 030001, PR China). Dual-mode biosensor platform based on synergistic effects of dual-functional hybrid nanomaterials, Talanta, Volume 260 (2023): 124584

Detection of biomarkers is very vital in the prevention, diagnosis and treatment of diseases. However, due to the poor accuracy and sensitivity of the constructed biosensors, we are now facing great challenges. In addressing these problems, nanohybrid-based dual mode biosensors including optical-optical, optical-electrochemical and electrochemical-electrochemical have been developed to detect various biomarkers. Integrating the merits of nanomaterials with abundant active sites, synergy and excellent physicochemical properties, many bi-functional nanohybrids have been reasonable designed and controllable preparation, which applied to the construction dual mode biosensors. Despite the significant progress, further efforts are still needed to develop dual mode biosensors and ensure their practical application by using portable digital devices. Therefore, the present review summarizes an in-depth evaluation of the bi-functional nanohybrids assisted dual mode biosensing platform of biomarkers. We are hoping this review could inspire further concepts in developing novel dual mode biosensors for possible detection application.

Keywords: Dual mode; Biosensing platform; Nanohybrids; Biomarkers detection

Gideon Opoku, Iddrisu Danlard, Albert Dede, Emmanuel Kofi Akowuah. (Department of Computer Engineering, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana). Design and numerical analysis of a circular SPR based PCF biosensor for aqueous environments, Results in Optics, Volume 12(2023):100432

This paper presents the design and numerical analysis of a circular photonic crystal fiber (PCF) biosensor based on surface plasmon resonance (SPR) for aqueous environments. The proposed biosensor has a geometrical design that uses the cladding at the fiber's exterior to simplify the gold and analyte deposition process. The sensing characteristics and performances of the proposed biosensor are fully investigated with the finite element method. The investigation indicates that the plasmonic material's thickness affects the biosensor's performance. The results of the proposed biosensor demonstrate a wide refractive index range of 1.30 to 1.44, with the highest wavelength or spectral sensitivity as 21,000 nm/RIU and the highest resolution as 9.09×10^{-6} RIU. The proposed biosensor has a straightforward geometric profile. The proposed biosensor is stable and suited for aqueous surroundings and wide-range detection applications.

Keywords: Biosensor; Photonic crystal fiber; Surface plasmon resonance; Wide-ranged; Refractive index; Aqueous environments

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A biosensor based on glutamate oxidase (GluOx) was developed to measure glutamate concentration. The main function of this type of biosensor is related to the structure and catalytic activity of GluOx. Since radiofrequency, as the widest spectrum of electromagnetic fields, can affect the catalytic activity and structure of GluOx, in this study, the effect of these fields on the analytical parameters of the fabricated biosensor was investigated. To build the biosensor a sol-gel solution of chitosan and native GluOx were prepared and then immobilized on the surface of the platinum electrode. Similarly, to investigate the effect of radiofrequency fields on the analytical parameters of the biosensor, instead of the native GluOx, irradiated GluOx was used to build the biosensor. To evaluate the biosensor responses, cyclic voltammetry experiments were performed and voltammograms were considered as biosensor responses. To determine the analytical parameters including detection limit, linear range, and saturation region of the responses, calibration curves were drawn for each of the biosensors. Also the long-term stability and selectivity of the fabricated biosensor were evaluated. Thereafter, the optimum pH and temperature for each of these two biosensors were examined. The results showed that radiofrequency waves harmed the detection and response of biosensors in the saturation region, while they had little effect on the linear region. Such results could be due to the effect of radiofrequency waves on the structure and function of glutamate oxidase. In general, the results indicate that when a glutamate oxidase-based biosensor is used to measure glutamate in radiofrequency fields, corrective coefficients for this type of biosensor should be considered to accurately measure glutamate concentration.

Keywords: Glutamate; Glutamate oxidase; Biosensor; Radiofrequency; Analytical parameters

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Technology has always been a progressive thing to serve human beings in terms of advancement to make lives easier and processes simple. One such revolutionary technology which finds its wide field implication includes the 'Biosensors'. Biosensors, as the name suggested, are a kind of sensor that detects the presence of biological molecules including enzymes, proteins, etc in a sample. Biosensors are been classified based on receptor and transducer. The technology has found its implications in a wide range of fields of biology including medicine, diagnosis, defence, food industry, environmental monitoring, etc. the best example of a biosensor that is widely used and handy is the Glucometer. The biosensors are high throughput detectors that are finding their multi-faceted implication in customer-friendly and budgeted devices for accurate results in limited timings. The present review will provide an overview of the kinds of biosensors and their different applications.

Keywords: Biosensor; Detector; Device; Receptor; Transducer

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The emergence of new compounds during the past decade requires a high-throughput screening method for toxicity assay. The stress-responsive whole-cell biosensor is a powerful tool to evaluate direct or indirect damages of biological macromolecules induced by toxic chemicals. In this proof-of-concept study, nine well-characterized stress-responsive promoters were first selected to assemble a set of blue indigoidine-based biosensors. The PuspA-based, PfabA-based, and PgrpE-based biosensors were eliminated due to their high background. A dose-dependent increase of visible blue signal was observed in PrecA-, PkatG-, and PuvrA-based biosensors, responsive to potent mutagens, including mitomycin and nalidixic acid, but not to genotoxic lead and cadmium. The PrecA, PkatG, and Ppgi gene promoters were further fused to a purple deoxyviolacein synthetic enzyme cluster. Although high basal production of deoxyviolacein is unavoidable, an enhanced visible purple signal in response to mitomycin and nalidixic acid was observed as dose-dependent, especially in PkatG-based biosensors. The study shows that a set of stress-responsive biosensors employing visible pigment as a reporter is pre-validating in detecting extensive DNA damage and intense oxidative stress. Unlike widely-used fluorescent and bioluminescent biosensors, the visual pigment-based biosensor can become a novel, low-cost, mini-equipment, and high-throughput colorimetric device for the toxicity assessment of chemicals. However, combining multiple improvements can further improve the biosensing performance in future studies.

Keywords: Whole-cell biosensor; Pigment biosynthesis; DNA damage; Oxidative stress; Stress response

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An increasing number of electrochemical biosensors have been constructed to detect single bioactive substances with high sensitivity, but not multiple bioactive substances with different properties. Therefore, we incorporated Cu and Fe elements into Prussian blue to form Prussian blue analogues (PBA), in order to improve the electrochemical catalytic activity of Prussian blue. At the same time, MoS2 is used as the material substrate to increase the electrochemical active site of the composite. We have constructed a universal electrochemical sensing platform

using composite materials (CuFe PBA/MoS2) as electrode modification materials for detecting two different types of representative cancer biomarkers, hydrogen peroxide (H2O2) and carcinoembryonic antigen (CEA). The universal electrochemical biosensor showed a significant linear response to both H2O2 and CEA with the lowest detection limits of 0.23 µM and 0.01 ng mL-1, respectively, and it had high selectivity, reproducibility, and stability. The universal electrochemical biosensor is successfully applied to detect H2O2 released from human breast cancer (MCF-7) cells and CEA expressed on the surface of human cervical cancer (HeLa) cells. The developed biosensor has potential in the dynamic detection of the flux of H2O2 and the expression level of CEA from living cells. The high sensitivity of this universal sensor provides a novel strategy for simultaneously detecting multiple cancer biomarkers.

Keywords: Hydrogen peroxide; Carcinoembryonic antigen; CuFe PBA/MoS2 nanocomposites; Electrochemical biosensor

Bioengineering

Julia Rädler, Dhanu Gupta, Antje Zickler, Samir EL Andaloussi. ([1]Biomolecular Medicine, Division of Biomolecular and Cellular Medicine, Department of Laboratory Medicine, Karolinska Institutet, 141 57 Huddinge, Sweden, [2]Department of Paediatrics, University of Oxford, Oxford OX3 9DU, UK) Exploiting the biogenesis of extracellular vesicles for bioengineering and therapeutic cargo loading, Molecular Therapy, Volume 31, Issue 5 (2023): 1231-1250

Extracellular vesicles (EVs) are gaining increasing attention for diagnostic and therapeutic applications in various diseases. These natural nanoparticles benefit from favorable safety profiles and unique biodistribution capabilities, rendering them attractive drug-delivery modalities over synthetic analogs. However, the widespread use of EVs is limited by technological shortcomings and biological knowledge gaps that fail to unravel their heterogeneity. An in-depth understanding of their biogenesis is crucial to unlocking their full therapeutic potential. Here, we explore how knowledge about EV biogenesis can be exploited for EV bioengineering to load therapeutic protein or nucleic acid cargos into or onto EVs. We summarize more than 75 articles and discuss their findings on the formation and composition of exosomes and microvesicles, revealing multiple pathways that may be stimulation and/or cargo dependent. Our analysis further identifies key regulators of natural EV cargo loading and we discuss how this knowledge is integrated to develop engineered EV biotherapeutics.

Keywords: exosomes; microvesicles; drug delivery; EV heterogeneity; EV engineering

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Keywords: Lung transplant; Xenotransplantation; Bioengineering; Ex vivo lung perfusion; Tissue engineering

Hamed Barabadi, Hesam Noqani, Fatemeh Ashouri, Abhinav Prasad, Kamyar Jounaki, Kiana Mobaraki, Yugal Kishore Mohanta, Ebrahim Mostafavi. ([a]Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Iran, [b]Biochemistry and Environmental Toxicology Laboratory, Lab. # 103, School of Environmental Sciences, Jawaharlal Nehru University, New Delhi, 110067, India, [c]Department of Applied Biology, School of Biological Sciences, University of Science and Technology Meghalaya (USTM), 9th Mile, Baridua, Ri Bhoi, 793101, Meghalaya, India, [d]Stanford Cardiovascular Institute, Stanford University School of Medicine, Stanford, CA, United States, [e]Department of Medicine, Stanford University School of Medicine, Stanford, CA, United States): Nanobiotechnological approaches in anticoagulant therapy: The role of bioengineered silver and gold nanomaterials, Talanta, Volume 256 (2023) 124279

Nanotechnology is a novel area that has exhibited various remarkable applications, mostly in medicine and industry, due to the unique properties coming with the nanoscale size. One of the notable medical uses of nanomaterials (NMs) that attracted enormous attention recently is their significant anticoagulant activity, preventing or reducing coagulation of blood, decreasing the risk of strokes, heart attacks, and other serious conditions. Despite successful in vitro experiments, in vivo analyses are yet to be confirmed and further research is required to fully prove the safety and efficacy of nanoparticles (NPs) and to introduce them as valid alternatives to conventional ineffective anticoagulants with various shortcomings and side-effects. NMs can be synthesized through two main routes, i.e., the bottom-up route as a more preferable method, and the top-down route. In numerous studies, biological fabrication of NPs, especially metal NPs, is highly suggested given its eco-friendly approach, in which different resources can be employed such as plants, fungi, bacteria, and algae. This review discusses the green synthesis and characterization of silver nanoparticles (AgNPs) and gold nanoparticles (AuNPs) as two of the most useful metal NPs, and also their alloys in different studies focussing on their anticoagulant potential. Challenges and alternative approaches to the use of these NPs as anticoagulants have also been highlighted.

Keywords: Anticoagulant activity; Green synthesis; Silver nanoparticles; Gold nanoparticles

Hamed Barabadi, Kiana Mobaraki, Fatemeh Ashouri, Hesam Noqani, Kamyar Jounaki, Ebrahim Mostafavi. ([a]Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran, [b]Stanford Cardiovascular Institute, Stanford University School of Medicine, Stanford, CA, United States, [c]Department of Medicine, Stanford University School of Medicine, Stanford, CA, United States,):Nanobiotechnological approaches in antinociceptive therapy: Animal-based evidence for analgesic nanotherapeutics of bioengineered silver and gold nanomaterials, Advances in Colloid and Interface Science, Volume 316 (2023): 102917

Pain management is a major challenge in healthcare systems worldwide. Owing to undesirable side effects of current analgesic medications, there is an exceeding need to develop the effective alternative therapeutics. Nowadays, the application of nanomaterials is being highly considered, as their exceptional properties arising from the nanoscale dimensions are undeniable. With the increasing use of metal NPs, more biocompatible and costly methods of synthesis have been developed in which different biological rescores including microorganisms, plants and algae are employed. Nanobiotechnology-based synthesis of nanosized particles is an ecological approach offering safe production of nanoparticles (NPs) by biological resources eliminating the toxicity attributed to the conventional routes. This review provides an assessment of biosynthesized silver nanoparticles (AgNPs) and gold nanoparticles (AuNPs) as antinociceptive agents in recent studies. Living animal models (mice and rats) have been used for analyzing the effect of biogenic NPs on decreasing the nociceptive pain utilizing different methods such as acetic acid-induced writhing test, hot plate test, and formalin test. Potent analgesic activity exhibited by green fabricated AgNPs and AuNPs represents the bright future of nanotechnology in the management of pain and other social and medicinal issues followed by this unpleasant sensation. Moreover, there NPs showed a protective effects on liver, kidney, and body weight in animal models that make them attractive for clinical studies. However, further research is required to fully address the harmless antinociceptive effect of NPs for clinical usage.

Keywords: Antinociceptive activity; Green synthesis; Silver nanoparticles; Gold nanoparticles

Catarina S. Silva, Banani Kundu, Joana M. Gomes, Emanuel M. Fernandes, Rui L. Reis, Subhas C. Kundu, Albino Martins, Nuno M. Neves. (3B's Research Group, I3Bs–Research Institute on Biomaterials, Biodegradables and Biomimetics, University of Minho, Headquarters of the European Institute of Excellence on Tissue Engineering and Regenerative Medicine, AvePark Parque de Ciência e Tecnologia, Zona Industrial da Gandra, Barco, 4805-017 Guimarães, Portugal, ICVS/3B's–PT Government Associate Laboratory, Braga/Guimarães, Portugal):Development of bilayered porous silk scaffolds for thymus bioengineering, Biomaterials Advances, Volume 147 (2023) 213320

The thymus coordinates the development and selection of T cells. It is structured into two main compartments: the cortex and the medulla. The replication of such complex 3D environment has been challenged by bioengineering approaches. Nevertheless, the effect of the scaffold microstructure on thymic epithelial cell (TEC) cultures has not been deeply investigated. Here, we developed bilayered porous silk fibroin scaffolds and tested their effect on TEC co-cultures. The small and large pore scaffolds presented a mean pore size of 84.33 ± 21.51 μm and 194.90 ± 61.38 μm, respectively. The highly porous bilayered scaffolds presented a high water absorption and water content (> 94 %), together with mechanical properties in the range of the native tissue. TEC (i.e., medullary (mTEC) and cortical (cTEC) cell lines) proliferation is increased in scaffolds with larger pores. The co-culture of both TEC lines in the bilayered porous silk scaffolds presents enhanced cell proliferation and metabolic activity when compared with mTEC in single culture. Also, when the co-culture occurred with cTEC in the small pores layer and mTEC in the large pores layer, a 9.2- and 18.9-fold increase in Foxn1 and Icam1 gene expression in cTEC is evident. These results suggest that scaffold microstructure and the co-culture influence TEC's behaviour. Bilayered silk scaffolds with adjusted microstructure are a valid alternative for TEC culture, having possible applications in advanced thymus bioengineering strategies.

Keywords: Silk fibroin; Bilayered scaffolds; Microarchitecture; Thymic epithelial cells; Thymus bioengineering

Elisa A. Casanova, Adrian Rodriguez-Palomo, Lisa Stähli, Kevin Arnke, Olivier Gröninger, Melanie Generali, Yvonne Neldner, Simon Tiziani, Ana Perez Dominguez, Manuel Guizar-Sicairos, Zirui Gao, Christian Appel, Leonard C. Nielsen, Marios Georgiadis, Franz E. Weber, Wendelin Stark, Hans-Christoph Pape, Paolo Cinelli, Marianne Liebi, SAXS imaging reveals optimized osseointegration properties of

bioengineered oriented 3D-PLGA/aCaP scaffolds in a critical size bone defect model. ([a]Department of Trauma Surgery, University of Zurich, University Hospital Zurich, Zurich, Switzerland, [b]Department of Physics, Chalmers University of Technology, Gothenburg, Sweden, [c]Institute for Chemical and Bioengineering, ETH Zurich, Zurich, Switzerland, [d]Institute for Regenerative Medicine (IREM), Center for Therapy Development and Good Manufacturing Practice, University of Zurich, Zurich, Switzerland, [e]Oral Biotechnology and Bioengineering, Department of Cranio-Maxillofacial and Oral Surgery, Center for Dental Medicine, University of Zurich, Zurich, Switzerland, [f]Swiss Light Source, Paul Scherrer Institute, Villigen, Switzerland, [g]Department of Radiology, Stanford School of Medicine, Stanford, CA, USA, [h]Center for Applied Biotechnology and Molecular Medicine (CABMM), University of Zurich, Zurich, Switzerland, [i]Centre for X-ray Analytics, Swiss Federal Laboratories for Materials Science and Technology (EMPA), St. Gallen, Switzerland): Biomaterials, Volume 294 (2023):121989

Healing large bone defects remains challenging in orthopedic surgery and is often associated with poor outcomes and complications. A major issue with bioengineered constructs is achieving a continuous interface between host bone and graft to enhance biological processes and mechanical stability. In this study, we have developed a new bioengineering strategy to produce oriented biocompatible 3D PLGA/aCaP nanocomposites with enhanced osseointegration. Decellularized scaffolds -containing only extracellular matrix- or scaffolds seeded with adipose-derived mesenchymal stromal cells were tested in a mouse model for critical size bone defects. In parallel to micro-CT analysis, SAXS tensor tomography and 2D scanning SAXS were employed to determine the 3D arrangement and nanostructure within the critical-sized bone. Both newly developed scaffold types, seeded with cells or decellularized, showed high osseointegration, higher bone quality, increased alignment of collagen fibers and optimal alignment and size of hydroxyapatite minerals.

Keywords: Mesenchymal stromal cells; Critical size bone defect; Scaffold; PLGA/aCaP; Extracellular matrix; SAXS tomography

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SummaryBioengineering devices and systems will become a practical and versatile technology in society when sustainability issues, primarily pertaining to their efficiency, sustainability, and human-machine interaction, are fully addressed. It has become evident that technological paths should not rely on a single operation mechanism but instead on holistic methodologies that integrate different phenomena and approaches with complementary advantages. As an intriguing invention, the ferroelectret nanogenerator (FENG) has emerged with promising potential in various fields of bioengineering. Utilizing the changes in the engineered macro-scale electric dipoles to create displacement current (and vice versa), FENGs have been demonstrated to be a compelling strategy for bidirectional conversion of energy between the electrical and mechanical domains. Here we provide a comprehensive overview of the latest advancements in integrating FENGs in bioengineering systems, focusing on the applications with the most potential and the underlying current constraints.

Andrea Schlegel, Hynek Mergental, Constantino Fondevila, Robert J. Porte, Peter J. Friend, Philipp Dutkowski. ([1]Fondazione IRCCS Ca' Granda, Ospedale Maggiore Policlinico, Centre of Preclinical Research, Milan, 20122, Italy, [2]Department of Surgery and Transplantation, Swiss HPB Center, University Hospital Zurich, Switzerland, [3]The Liver Unit, Queen Elizabeth University Hospital Birmingham, United Kingdom, [4]Hepatopancreatobiliary Surgery & Transplantation, General & Digestive Surgery Service, Hospital Universitario La Paz, IdiPAZ, CIBERehd, Madrid, Spain, [5]Erasmus MC Transplant Institute, Department of Surgery, Division of HPB & Transplant Surgery, Erasmus University Medical Center, Rotterdam, the Netherlands, [6]Nuffield Department of Surgical Sciences, University of Oxford, Oxford, UK): Machine perfusion of the liver and bioengineering, Journal of Hepatology, Volume 78, Issue 6 (2023) Pages 1181-1198

With the increasing number of accepted candidates on waiting lists worldwide, there is an urgent need to expand the number and the quality of donor livers. Dynamic preservation approaches have demonstrated various benefits, including improving liver function and graft survival, and reducing liver injury and post-transplant complications. Consequently, organ perfusion techniques are being used in clinical practice in many countries. Despite this success, a proportion of livers do not meet current viability tests required for transplantation, even with the use of modern perfusion techniques. Therefore, devices are needed to further optimise machine liver perfusion – one promising option is to prolong machine liver perfusion for several days, with ex situ treatment of perfused livers. For example, stem cells, senolytics, or molecules targeting mitochondria or downstream signalling can be administered during long-term liver perfusion to modulate repair mechanisms and regeneration. Besides, today’s perfusion equipment is also designed to enable the use of various liver bioengineering techniques, to develop scaffolds or for their re-cellularisation. Cells or entire livers can also undergo gene modulation to modify animal livers for xenotransplantation, to directly treat injured organs or to repopulate such scaffolds with “repaired” autologous cells. This review first discusses current strategies to improve the quality of donor livers, and secondly reports on bioengineering techniques to design optimised organs during machine perfusion. Current practice, as well as the benefits and challenges associated with these different perfusion strategies are discussed.

Keywords: Liver transplantation; machine perfusion; ischemia-reperfusion-injury; mitochondria; bioengineering; regeneration medicine; organoids; scaffolding

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University of Calabria, Rende, Italy): Bioengineering and medical informatics education in MD programs: perspectives from three Italian experiences, International Journal of Medical Informatics, Volume 172 (2023):105002

Given the impact of bioengineering and medical informatics technologies in health care, the design and implementation of education programs able to combine medical curricula with a proper teaching on engineering and informatics is now of paramount importance. In Italy, this goal has to fit in with the existing higher education system, which is structured into Bachelor programs and Master programs. Medicine and Surgery programs, instead, are designed as a six-year single-cycle Degree Program in Medicine and Surgery which comprises both class attendance and hospital internship and training. This program allows students to become Medical Doctors (MD). The different organization of this University program makes it not easy to introduce further contents, namely hard science courses, in the educational program. Notwithstanding this, we present here some recent innovative programs aimed at widening MD curriculum by including biomedical engineering and informatics subjects. In particular, we will introduce three of them. Two are joint-degree programs, the first between Humanitas University and Politecnico di Milano (MEDTEC School), and the second between University of Calabria and University Magna Graecia of Catanzaro (Medicina e Chirurgia TD). The Third one is a Professional Master coupled with an MD degree, based on a joint program among Pavia University, Pisa University, the Institute of Advanced studies in Pavia and the Scuola Superiore S. Anna in Pisa (MEET).

The paper provides a description of the fundamental design principles of the three above mentioned programs, and explores some aspects of the teaching modules, highlighting their positive aspects. In particular, we show how the three different programs allow students to enrich their knowledge by studying engineering subjects and innovative methods and technologies, as well as their applications to patient care.

The MEDTEC program is the first degree program at Italian and international scale which integrates medical and engineering subjects. In the following years, other programs were issued in Italy, defining similar education programs to couple a degree in medicine education with bioengineering and medical informatics, among which Medicina e Chirurgia TD and MEET. We believe the experiences described here in this paper represent the possibility of bridging the gap between medical and technological competencies.

Keywords: Medicine and Technologies; Biomedical Engineering; Medical Informatics; Medical Education; MEDTEC; MEET; Medicina e Chirurgia TD

Dao Shi, Feng Wu, Lingling Huang, Ying Li, Sunkui Ke, Jinyao Li, Zhenqing Hou, Zhongxiong Fan. ([a]Institute of Materia Medica & College of Life Science and Technology, Xinjiang University, Urumqi, 830017, China, [b]College of Materials, Xiamen University, Xiamen 361005, China, [c]Xiamen Key Laboratory of Traditional Chinese Bio-engineering, Xiamen Medical College, Xiamen 361021, China [d]Department of Thoracic Surgery, Zhongshan Hospital of Xiamen University, China): Bioengineered nanogenerator with sustainable reactive oxygen species storm for self-reinforcing sono-chemodynamic oncotherapy, Journal of Colloid and Interface Science, Volume 646,(2023): 649-662

Oxidative stress-based antitumor modalities derived from reactive oxygen species (ROS) storms have attracted increasing attention. Nevertheless, low delivery efficiency, poor selectivity, hypoxia and overexpressed glutathione (GSH) have severely restricted the sustainable generation of the ROS storm in tumor cells. Herein, we design a bioengineered nanogenerator by coordination-driven co-assembly of sonosensitizer indocyanine green (ICG), Fenton-like agent copper ion (CuII) and mitochondrial respiratory inhibitor metformin (MET), which is then camouflaged by a cancer cytomembrane to induce a sustainable intracellular ROS storm for on-demand self-reinforcing sono-chemodynamic oncotherapy. Such a nanogenerator with a core–shell structure, suitable diameter and outstanding stability can efficiently accumulate in tumor regions and then internalize into tumor cells through the camouflaging and homologous targeting strategy of the cancer cytomembrane. The nanogenerator shows an exceptional instability under the triple stimulations of acidic lysosomes, overexpressed GSH and ultrasound (US) radiation, thereby resulting in the rapid disassembly and burst drug release. Interestingly, the released MET significantly enhances the sonodynamic therapy (SDT) efficacy of the released ICG by inhibiting mitochondrial respiration and meanwhile the released CuII obviously reduces ROS elimination by downregulating overexpressed GSH for self-amplifying and self-protecting the intracellular ROS storm. Moreover, such a nanogenerator almost completely achieves the tumor ablation in vivo in a single therapy cycle. Taken together, our bioengineered nanogenerator with a sustainable ROS storm can provide a promising strategy for ROS storm-based oncotherapy.

Keywords: Cancer cytomembrane; Bioengineered coordination nanogenerator; Homologous targeting; Sustainable ROS storm; Sono-chemodynamic oncotherapy

Adam S. Mullis, David L. Kaplan. ([a]Department of Biomedical Engineering, Tufts University, Medford, MA, 02155, USA, [b]Allen Discovery Center, Tufts University, Medford, MA, 02155, USA): Functional bioengineered tissue models of neurodegenerative diseases, Biomaterials, Volume 298(2023): 122143

Aging-associated neurodegenerative diseases, such as Alzheimer's and Parkinson's diseases remain poorly understood and no disease-modifying treatments exist despite decades of investigation. Predominant in vitro (e.g., 2D cell culture, organoids) and in vivo (e.g., mouse) models of these diseases are insufficient mimics of human brain tissue structure and function and of human neurodegenerative pathobiology, and have thus contributed to this collective translational failure. This has been a longstanding challenge in the field, and new strategies are required to address both fundamental and translational needs. Bioengineered tissue culture models constitute a class of promising alternatives, as they can overcome the low cell density, poor nutrient exchange, and long term culturability limitations of existing in vitro models. Further, they can reconstruct the structural, mechanical, and biochemical cues of native brain tissue, providing a better mimic of human brain tissues for in vitro pathobiological investigation and drug development. We discuss bioengineering techniques for the generation of these neurodegenerative tissue models, including biomaterials-, organoid-, and microfluidics-based approaches, and design considerations for their construction. To aid the development of the next generation of functional neurodegenerative disease models, we discuss approaches to incorporate greater cellular diversity and simulate aging processes within bioengineered brain tissues.

Keywords: Bioengineering; Tissue engineering; Neurodegenerative diseases; Human pluripotent stem cells; Organoids; Microfluidics

Han Liu, Hao Zhang, Sicheng Wang, Jin Cui, Weizong Weng, Xinru Liu, Hua Tang, Yan Hu, Xiaoqun Li, Kun Zhang, Fengjin Zhou, Yingying Jing, Jiacan Su. ([a]Institute of Translational Medicine, Shanghai University, Shanghai, 200444, China, [b]Organoid Research Center, Shanghai University, Shanghai, 200444, China, [c]Department of Orthopedics, Shanghai Zhongye Hospital, Shanghai, 200444, China, [d]Department of Orthopedics Trauma, Shanghai Changhai Hospital, Naval Medical University, Shanghai,

200433, China, [e]Shaoxing Institute of Technology at Shanghai University, Shaoxing, 312000, China, [f]Department of Orthopaedics, Honghui Hospital, Xi'an Jiao Tong University, Xi'an, 710000, China, [g]Department of Orthopedics, Xinhua Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, 200092, China): Bone-targeted bioengineered bacterial extracellular vesicles delivering siRNA to ameliorate osteoporosis, Composites Part B: Engineering, Volume 255 (2023): 110610

Osteoporosis (OP), characterized by decreased bone mass and destruction of bone microarchitecture, is the most common bone degenerative disease. Conventional treatments for OP have several side effects, new treatment approaches are needed. Bacterial extracellular vesicles (BEVs) carrying curative molecules have emerged as a promising alternative due to their unique nanosized structures, stable loading capacity, good biocompatibility, ease of modification, and industrialization. In this study, we modified probiotics Escherichia coli Nissle 1917 (ECN) to overexpress hCXCR4 fused with the ClyA on the membrane surface of BEVs. The bone targeted BEVs took advantage of the intrinsic anti-OP function and loaded with SOST siRNA to generate BEVs-hCXCR4-SOST siRNA (BEVs-CSs). The customized BEVs-CSs have exhibited great bone targeting ability without long-term cytotoxicity. In addition, the bioengineered BEVs-CSs can be internalized by bone marrow mesenchymal stem cell and promote their osteogenic differentiation with significant cytocompatibility. Finally, the bifunctional BEVs-CSs successfully reversed the OP in an ovariectomized mouse model. Taken together, such a bioengineered BEVs-based strategy provides an innovative, safe, efficient and promising therapeutic solution for intractable OP treatment.

Keywords: Osteoporosis; Bacterial extracellular vesicle; Bone targeting; Small interfering RNA; Osteogenic differentiation

Pollen Biotechnology

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Ragweed is an invasive plant in Europe, causing hay fever and asthma in allergic patients. Climate change is predicted to increase expansion and allergenicity. Elevated NO2 induced upregulation of a new allergen in ragweed pollen, an enolase, Amb a 12.

of this study was producing ragweed enolase as a recombinant protein and characterizing its physicochemical and immunological features.

Amb a 12 was designed for E. coli and insect cell expression. Physicochemical features were determined by mass spectrometry, circular dichroism measurements and enzymatic activity assay. Immunological characteristics were determined in ELISA, in a mediator release assay and by investigation of association with clinical symptoms. Common allergen sources were screened for similar proteins.

Ragweed enolase was produced as a 48 kDa protein forming oligomers in both expression systems, showing differences in secondary structure content and enzymatic activity depending on expression system. IgE frequency and allergenicity were low regardless of expression system. Enolase-specific serum bound to similar sized molecules in mugwort, timothy grass and birch pollen, as well as food allergen sources, while highest IgE inhibition was achieved with peach pulp extract.

Amb a 12 had high sequence similarity and comparable IgE frequency to enolase allergens from different sources. 50 kDa proteins were found in other pollen and food allergen sources, suggesting that enolases might be pan-allergens in pollen and plant foods.

Keywords: Ragweed; Enolase; Sensitization rate; Plant allergens

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Pollen tube polar growth is a key cellular process during plant fertilization and is regulated by tip-focused exocytosis and endocytosis. However, the spatiotemporal dynamics and localizations of apical exocytosis and endocytosis in the tip region are still a matter of debate. Here, we use a refined spinning-disk confocal microscope coupled with fluorescence recovery after photobleaching for sustained live imaging and quantitative analysis of rapid vesicular activities in growing pollen tube tips. We traced and analyzed the occurrence site of exocytic plasma membrane-targeting of Arabidopsis secretory carrier membrane protein 4 and its subsequent endocytosis in tobacco pollen tube tips. We demonstrated that the pollen tube apex is the site for both vesicle polar exocytic fusion and endocytosis to take place. In addition, we disrupted either tip-focused exocytosis or endocytosis and found that their dynamic activities are closely correlated with one another basing on the spatial organization of actin fringe. Collectively, our findings attempt to propose a new exocytosis and endocytosis-coordinated yin-yang working model underlying the apical membrane organization and dynamics during pollen tube tip growth.

Keywords: Exocytosis; Endocytosis; Actin fringe; Polar growth; Pollen tube tip

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Wuhan 430070, China[c]State Key Laboratory of Natural and Biomimetic Drugs, Institute of Ocean Research, Peking University, Beijing 100191, China[d]Zhejiang Provincial Key Laboratory of Biometrology and Inspection & Quarantine, College of Life Sciences, China Jiliang University, Hangzhou 310018, China). Hydrogen peroxide oxidation modifies the structural properties and allergenicity of the bee pollen allergen profilin, Food Chemistry, Volume 425(2023): 136495

Bee pollen is a byproduct of pollination, which is a necessary process to produce foods. However, bee pollen can induce significant food-borne allergies. We previously identified a bee pollen-derived pan-allergen in the profilin family, Bra c p. Herein, we aimed to reduce Bra c p allergenicity via protein oxidation with hydrogen peroxide and explore the changes induced. Ion-mobility mass spectrometry revealed aggregation of the oxidized product; we also found irreversible sulfonation of the free sulfhydryl group of the Bra c p Cys98 residue to a more stable cysteine derivative. A significant proportion of the α-helices in Bra c p were transformed into β-sheets after oxidation, masking the antigenic epitopes. An immunoassay demonstrated that the IgE-binding affinity of Bra c p was decreased in vitro after oxidation. To our knowledge, this is the first report describing the application of protein oxidation to reduce the allergenicity of profilin family member in foods.

Keywords: Bee pollen allergen; Profilin family; Hydrogen peroxide; Protein oxidation; Allergenicity reduction

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In recent decades, Cinnamomum camphora have gradually become the main street trees in Shanghai. This study aims to investigate the allergenicity of camphor pollen.

A total of 194 serum samples from patients with respiratory allergy were collected and analyzed. Through protein profile identification and bioinformatics analysis, we hypothesized that heat shock cognate protein 2-like protein (HSC70L2) is the major potential allergenic protein in camphor pollen. Recombinant HSC70L2 (rHSC70L2) was expressed and purified, and a mouse model of camphor pollen allergy was established by subcutaneous injection of total camphor pollen protein extract (CPPE) and rHSC70L2.

Specific IgE was found in the serum of 5 patients in response to camphor pollen and three positive bands were identified by Western blotting. Enzyme-linked immunosorbent assay (ELISA), Immune dot blot and Western blot experiments confirmed that CPPE and rHSC70L2 can cause allergies in mice. Moreover, rHSC70L2 induces polarization of peripheral blood CD4+ T cells to Th2 cells in patients with respiratory allergies and mice with camphor pollen allergy. Finally, we predicted the T cell epitope of the HSC70L2 protein, and through the mouse spleen T cell stimulation experiment, we found that the 295EGIDFYSTITRARFE309 peptide induced T cells differentiation to Th2 and macrophages differentiation to the alternatively activated (M2) state. Moreover, 295EGIDFYSTITRARFE309 peptide increased the serum IgE levels in mice.

The identification of HSC70L2 protein can provide novel diagnostic and therapeutic targets for allergies caused by camphor pollen.

Keywords: Allergen; Camphor pollen; Heat shock cognate protein 2-like protein; Respiratory allergic diseases; T cell epitope prediction

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The effect of non-thermal processing on food flavor and aroma components is still unclear. Non-thermal electrohydrodynamic (EHD) drying was applied as a novel technology for the drying of lotus bee pollen. The effect of different output voltage (10, 20, 30, 40, and 50 kV) of EHD on volatile organic compounds (VOCs) was studied, samples of hot air drying (HAD) and natural sun drying (NSD) was also evaluated. Results showed that 147 volatile organic compounds were identified from lotus pollen, and most of them were aldehydes and terpenes. Due to lipid oxidation and protein modification, most aldehydes and terpenes increased with increase of voltage, while alcohol and acid concentrations first increased and then decreased with voltage. The concentration of alcohols accumulated was the highest in natural sun drying, which caused by fermentation when exposed to natural environment for a long time drying. Four VOCs, ethnol M, ethnol D, acetic M, and acetic D, were selected by variable importance in projection variable selection method of partial least squares discriminant analysis as potential markers to distinguish different drying lotus bee pollen. These findings in current work revealed the flavor formation and related mechanism of bee pollen during non-thermal drying.

Keywords: Electrohydrodynamic drying; Lotus bee pollen; Volatile organic compounds; Lipid oxidation; Protein modification

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Lily (Lilium spp.) is an important horticultural crop, but its use is limited due to serious pollen contamination problems. There are many studies on pollen development in model plants, but few on flower crops such as lilies. Gibberellin (GA) is a large class of hormones and plays an important role in plant vegetative growth and reproductive development. GAMYB is a group of

the R2R3-MYB family upregulated by gibberellin, and plays an important role in anther development. Here, we isolated a novel GAMYB, named LoMYB65, from lily, which was closely related to the AtMYB65 and AtMYB33 in Arabidopsis. Fluorescence quantitative PCR results showed that LoMYB65 was mainly expressed in lily anthers. LoMYB65 could be activated by 288 μmol L−1 GA3 treatment and the LoMYB65 protein was located in the nucleus and cytoplasm, and had transactivation in yeast and tobacco leaf cells. The conserved motif within 226 amino acids of the C-terminal of LoMYB65 contributed to its transactivation. Overexpression of LoMYB65 caused dwarf phenotype, unnormal tapetum development, less seeds of siliques in transgenic Arabidopsis plants, the transgenic plants showed partly male sterile. Simultaneously, silencing of LoMYB65 with VIGS (Virus Induced Gene Silencing) in lily anthers caused unnormal pollen development and reduced the pollen amount. Overexpression of LoMYB65 in Arabidopsis and silencing of LoMYB65 in lily resulted in decreased pollen counts, so we speculate that LoMYB65 may be dose-dependent. Overall, these findings suggest that LoMYB65 may play an important role in anther development and pollen formation in lily. LoMYB65 may provide a useful candidate gene for pollenless breeding of lily.

Keywords: Lily; Anther development; Pollen pollution; GAMYB; VIGS

Zhihao Sun, Keke Liu, Chi Chen, Daibo Chen, Zequn Peng, Ran Zhou, Ling Liu, Dengmei He, Wenjing Duan, Hongmei Chen, Chenbo Huang, Zheyan Ruan, Yingxin Zhang, Liyong Cao, Xiaodeng Zhan, Shihua Cheng, Lianping Sun. ([a]Key Laboratory for Zhejiang Super Rice Research, Chinese National Center for Rice Improvement and Stat Key Laboratory of Rice Biology, China National Rice Research Institute, HangZhou 311402, China, [b]Baoqing Northern Rice Research Center, Northern Rice Research Center of China National Rice Research Institute, Baoqing, Heilongjiang 155600, China, [c]College of Agronomy, Heilongjiang Bay Agricultural University, Daqing, Heilongjiang 163711, China). OsLDDT1, encoding a transmembrane structural DUF726 family protein, is essential for tapetum degradation and pollen formation in rice, Plant Science, Volume 329 (2023): 111596

Formation of the pollen wall, which is mainly composed of lipid substances secreted by tapetal cells, is important to ensure pollen development in rice. Although several regulatory factors related to lipid biosynthesis during pollen wall formation have been identified in rice, the molecular mechanisms controlling lipid biosynthesis are unclear. In this study, we isolated the male-sterile rice mutant oslddt1 (leaked and delayed degraded tapetum 1). oslddt1 plants show complete pollen abortion resulting from delayed degradation of the tapetum and blocked formation of Ubisch bodies and pollen walls. OsLDDT1 (LOC_Os03g02170) encodes a DUF726 containing protein of unknown function with highly conserved transmembrane and α/β Hydrolase domains. OsLDDT1 localizes to the endoplasmic reticulum and the gene is highly expressed in rice panicles. Genes involved in regulating fatty acid synthesis and formation of sporopollenin and pollen exine during anther development showed significantly different expression patterns in oslddt1 plants. Interestingly, the wax and cutin contents in mature oslddt1–1 anthers were decreased by 74.07 % and 72.22 % compared to WT, indicating that OsLDDT1 is involved in fatty acid synthesis and affects formation of the anther epidermis. Our results provide as deeper understanding of the role of OsLDDT1 in regulating male sterility and also provide materials for hybrid rice breeding.

Keywords: Rice; Male sterility; OsLDDT1; Fatty acid synthesis; Transmembrane structural protein

Biotechnology Policy Issue

Caizhi Liao, Shadow Xiao, Xia Wang. ([a]Renaissance Diacare, Creative Biosciences Co. Ltd., Guangzhou, China, [b]Australian Institute for Bioengineering and Nanotechnology, The University of Queensland, Brisbane, Australia, [c]Total Precise Venture, Central, Hong Kong SAR, China, [d]Zhejiang University Medical College affiliated Sir Run Run Shaw Hospital, Hangzhou, China). Bench-to-bedside: Translational development landscape of biotechnology in healthcare, Health Sciences Review, Volume 7 (2023): 100097

Biotechnology is a rapidly evolving field that has the potential to transform the way we diagnose and treat diseases and is changing the landscape of healthcare. Great endeavors have been devoted to the field of healthcare biotechnology, and our knowledge of the subject has remarkably improved. By leveraging the latest advancements in molecular biology and genetics, new biotech paradigms are emerging, sparking new searches for novel solutions for human health and well-being. However, the clinical translational development of breakthrough biotechnology discoveries remains an intriguing challenge. Only a few biotech innovations have progressed to new transformative healthcare tools and therapies. In this review, we will outline the clinical translational development landscape of biotechnology in healthcare. Notable discoveries and translational developments in healthcare biotechnology, including classical discoveries and new paradigms, are thoroughly discussed. Even though great challenges remain in the bench-to-bedside translational development process, more groundbreaking biotech ideas are about to be translated into commercial products to bring positive health gains, with a tight multitude of collaboration among research institutes, healthcare providers, and industry partners.

Keywords: Bench-to-bedside; Clinical translational development; Healthcare; Biotechnology; Therapy

Agricultural Biotechnology

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The policy report published by the European Academies Science Advisory Council (EASAC) introduces a new concept, 'Regenerative Agriculture', but but does not provide an exact definition for the term. The roots of the ideological concept lie in the French Enlightenment period, when food supplies of local communities were not a real concern. Nowadays, agriculture struggles to keep up with the population explosion. The EASAC position paper sets ecological farming and large-scale agriculture against each other despite the fact that their common aim is to supply the world population with high quality food and industrial raw materials. The comments in the present paper aim to provide a more nuanced approach to some of the ideas discussed in the EASAC report, with special emphasis on the fact that, although the report formulates noble aims, it does not present concrete suggestions on how they could be achieved economically.

Keywords: EASAC report; Intensive production; Organic production; Pesticides; Antimicrobial resistance; Bio economical and biotechnological approaches

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Of late, global food security has been under threat by the coronavirus disease 2019 (COVID-19) pandemic and the recent military conflict in Eastern Europe. This article presents the objectives of the Sustainable Development Goals and the European Green Deal related to achieving food security and sustainable development in European Union (EU) agriculture, taking the aforementioned threats into account. In addition, it discusses the future of plant agricultural biotechnology and artificial intelligence (AI) systems, considering their potential for reaching the goal of food security. Paradoxically, the present challenging situation may allow politicians and stakeholders of the EU to realize opportunities and use the potential of the biotechnology sector.

Keywords: agricultural biotechnology; artificial intelligence in agriculture; biotechnology sector; food security; new plant breeding techniques

Bioenergy

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economy approach towards sustainable zero-waste environment, Chemosphere, Volume 319 (2023): 138005

The inevitable need for waste valorisation and management has revolutionized the way in which the waste is visualised as a potential biorefinery for various product development rather than offensive trash. Biowaste has emerged as a potential feedstock to produce several value-added products. Bioenergy generation is one of the potential applications originating from the valorisation of biowaste. Bioenergy production requires analysis and optimization of various parameters such as biowaste composition and conversion potential to develop innovative and sustainable technologies for most effective utilization of biowaste with enhanced bioenergy production. In this context, feedstocks, such as food, agriculture, beverage, and municipal solid waste act as promising resources to produce renewable energy. Similarly, the concept of microbial fuel cells employing biowaste has clearly gained research focus in the past few decades. Despite of these potential benefits, the area of bioenergy generation still is in infancy and requires more interdisciplinary research to be sustainable alternatives. This review is aimed at analysing the bioconversion potential of biowaste to renewable energy. The possibility of valorising underutilized biowaste substrates is elaborately presented. In addition, the application and efficiency of microbial fuel cells in utilizing biowaste are described in detail taking into consideration of its great scope. Furthermore, the review addresses the significance bioreactor development for energy production along with major challenges and future prospects in bioenergy production. Based on this review it can be concluded that bioenergy production utilizing biowaste can clearly open new avenues in the field of waste valorisation and energy research. Systematic and strategic developments considering the techno economic feasibilities of this excellent energy generation process will make them a true sustainable alternative for conventional energy sources.

Keywords: Biowaste to energy nexus; Microbial fuel cells; Development of bioreactors; Potential microbes

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India possesses a huge potential in biomass power generation to reduce dependency on fossil fuel imports. Of the available biomass sources, crop residues are particularly interesting as they dispersed resources with varying spatiotemporal availability and features. These residues also have competing applications which differ geographically. In India, state-wise crop-level biomass databases are found to be scarce, and local biomass records are critical to implement decentralized bioenergy projects. The main objective of this study is to critically assess the potential of agricultural crop residues, their subsequent bioenergy, and the syngas production potential in all of India's regions (28 states and 8 UTs). 43 major crop residues produced from 28 different crops produced in different regions of India were taken for this study, considering their recent crop production statistics for the year 2017-18 and following standard estimation procedures. The syngas production potential was estimated using a Python gasification model using input parameters from the literature. Overall, 869.11 MT of gross residue is generated annually, with 288.14 MT (33.15%) of surplus residue. In terms of surplus crop residue, Uttar Pradesh produces the most surplus residue (57.72 MT) and sugarcane ranks first with a national potential of 62.68 MT. For the 2017-18 fiscal year, the bioenergy production potential from surplus crop residue was estimated to be 4.88 EJ. This syngas generation potential is determined to be 37.64% of India's gross residual potential. Upgrading this quantity of syngas via, for example, methanol (MeOH) synthesis is expected to provide 81.7905 MT of MeOH with an equivalent energy content of 1.85 EJ.

Keywords: Biomass availability; Bioenergy; Syngas production; Methanol production

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The progress of clean alternative energy sources is of very essential owing to the increase in an energy crisis and the escalating problems of climatic change. In this regard, bioenergy generation from carbohydrate-rich Lignocellulose biomass (LCB) is a promising technique, owing to its benefits such as ease of availability, decrease in harmful emissions, eco-friendly, energy efficiency and sustainability. The key constituents present in LCB are cellulose, hemicellulose, and lignin. This biological conversion of LCB faces difficulties due to the recalcitrance of lignin. Thus, the delignification of LCB is essential for the removal of complex lignin compounds. The primary technologies employed for the conversion of LCB biomass to bioenergy and pretreatment technologies involved in removing the lignin barrier have been extensively discussed in the present review. Different microorganisms and enzymes used for the delignification and detoxification process have also been studied for the scaling up of industrial bioenergy production from LCB.

Keywords: Lignocellulose biomass; Lignin; Recalcitrant; Delignification; Detoxification; Bioenergy

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The energy demands in Zimbabwe have drastically increased due to the improvement of the country`s economy. To supply the electricity, Zimbabwe imports most of its energy but the demands are yet to be fulfilled. Bio-waste provide an alternative energy source, however, it has not been fully explored and their quantities are currently unknown. Therefore, this study assessed the bio-wastes availability for bioenergy generation in Zimbabwe. Yield data on biomasses were obtained from the international databases of Food and Agricultural Organization which was validated by the data obtained from Zimbabwean Ministry of Lands and Agriculture as well as from research institutes. The information compiled included biomass from agriculture, municipal solid waste, livestock's dung and municipal sewage sludge. Forests were not considered due to the government prohibition of forests exploitations. The results showed that a total of 49 Gtons of bio-wastes are sustainably available producing a total of 539 PJ of energy which constitute ~42.3% of the total energy required in Zimbabwe. Among the available bio-wastes, crop residues with ~48 Gtons produce the largest amount of energy ~502 PJ followed by animal dung ~36.2 PJ, then MSW ~9.1 TJ and lastly by MSS ~0.8 TJ. Assessment of the bio-waste availability is vital for bio-energy technology to be used sustainably implemented in Zimbabwe.

Keywords: Bio-wastes quantities; Energy potential; Mathematical modelling; Bioenergy; Zimbabwe

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Second-generation bioenergy, a carbon neutral or negative renewable resource, is crucial to achieving India's net-zero emission targets. Crop residues are being targeted as a bioenergy resource as they are otherwise burned on-field, leading to significant pollutant emissions. But

estimating their bioenergy potential is problematic because of broad assumptions about their surplus fractions. Here, we use comprehensive surveys and multivariate regression models to estimate the bioenergy potential of surplus crop residues in India. These are with high sub-national and crop disaggregation that can facilitate the development of efficient supply chain mechanisms for its widespread usage. The estimated potential for 2019 of 1313 PJ can increase the present bioenergy installed capacity by 82% but is likely insufficient alone to meet India's bioenergy targets. The shortage of crop residue for bioenergy, combined with the sustainability concerns raised by previous studies, imply a need to reassess the strategy for the use of this resource.

Keywords: Crop residue; Bioenergy potential; Prescribed fires; Survey; Multivariate regression

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Soil acidity may negatively affect plant growth. By-products (bottom ash (BA), biochar (BC), and biogas slurry (BS)) from bioenergy technology may change the physio-chemical properties of acidic soils and affect the plant growth parameters. The current research work was carried out to determine the impact of different bioenergy by-products to enhance soybean growth and production by alleviating the effects of acidic soil. A total of eight treatments of different bioenergy amendments (BA, BC, and BS) and their combined applications were used as follows; T1 (control), T2 (only biogas slurry); T3 (only bottom ash); T4 (only biochar); T5 (biogas slurry + bottom ash); T6 (biogas slurry + biochar); T7 (bottom ash + biochar); T8 (biochar + bottom ash + biogas slurry). Our results depicted that, the synergistic use of amendment mainly, T8 treatment (BC + BA + BS) was found most effective, which significantly prompted the dry biomass and photosynthetic rate by 42.58% and 13.25% over the T6 treatment respectively. Furthermore, the chlorophyll pigments, photochemical activities, and root growth of soybean plants enhanced significantly under T5 and T8 treatments as compared to the control. Finally, amendments significantly increased the yield in T8 treatment by increasing the pod's number, grain number, 100-grain weight and grain yield by 119.6%, 75%, 24.9%, and 83.7% as compared to T1. Conclusively, amendments are very effective in the reclamation of acidic soil

and enhance the post-harvest soil pH at T8 treatment by 41.49% in comparison to T1 treatment. The organic amendments might neutralize the soil pH and change the acidic nature of the soil, which would modify the root growth of soybean and increase the photosynthetic and photochemical activities, resulting in increased soybean growth and yield.

Keywords: Bioenergy waste; Biomass; Photosynthesis; Soil reclamation; Soybean yield

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The current study aims to investigate the physicochemical properties and pyrolysis characteristics (kinetic triplet and thermodynamic parameters) of the invasive grass Cenchrus echinatus to assess its bioenergy potential. A thermogravimetric analyzer was employed to obtain the pyrolysis behavior of the grass under slow non-isothermal conditions. First, a multi-component deconvolution analysis of differential thermogravimetry (DTG) curves using the Fraser–Suzuki function was performed, aiming to quantify the individual devolatilization reactions of hemicellulose (P–HC), cellulose (P–CL), and lignin (P–LG). The survey of the activation energy employing four isoconversional methods (Friedman, Flynn–Wall–Ozawa, Kissinger–Akahira–Sunose, and Starink) indicated the following devolatilization order: P–LG (329.9 − 376.7 kJ mol−1) > P–CL (178.4 − 188.2 kJ mol−1) > P–HC (157.8 − 161.2 kJ mol−1). With values of pre-exponential factors from 1.1 × 1015 to 1.4 × 1031 min−1, as estimated from the kinetic compensation effect, it was deduced that the chemical reactions with simpler nature are predominant. With the method of integral master plot, a geometrical contraction mechanism matched the devolatilization of P–CL, and an nth-order-based reaction model matched the devolatilizations of P–HC and P–LG. Besides, the thermodynamic study suggested that the conversion process is endothermic (ΔH≠ = 153.4 to 245.2 kJ mol−1) and nonspontaneous (ΔG≠ = 146.8 to 174.4 kJ mol−1). With the three kinetic triplets, one overall rate expression for the pyrolysis of invasive grass C. echinatus was established. The simulation results were then compared to experimental kinetic curves, and the agreement was deemed satisfactory. The outcomes from this research recommend the C. echinatus as a promising feedstock for bioenergy production and are decisive for scheming large-scale pyrolysis reactors for this invasive grass.

Keywords: Cenchrus echinatus; Bioenergy potential; Physicochemical characterization; Kinetic triplet; Thermodynamic parameters

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Sciences/Department of Chemical Engineering, University of Santo Tomas, Manila, Philippines Author links open overlay panelRaymond R. Tan Department of Chemical Engineering, De La Salle University, Manila, Philippines). Optimal Multi-Disruption Stream Allocation in a Bioenergy Park via P-Graph, Reference Module in Earth Systems and Environmental Sciences, Elsevier,(2023) https://doi.org/10.1016/B978-0-323-90386-8.00053-X

Bioenergy parks are developed due to potential benefits in the environmental, economic, and social dimensions. Separate bioenergy plants or collocated facilities form collaborations and agree to exchange material and energy products to achieve operational sustainability. Such a highly integrated network is vulnerable to cascading failures caused by one or more disrupted component plants. This disruption will result in capacity reductions, supply chain delays, and the inability to meet contractual obligations to customers. During disruptions, a bioenergy park can still operate under abnormal conditions by allocating the product streams within the network and minimizing the impact of the disturbance. In this work, a P-graph model is proposed for the optimal allocation of product streams in the network when disruptions originate from multiple plants. A penalty cost is deducted from the optimal profit of the bioenergy park and is paid to customers as compensation due to losses for not meeting the baseline demand for products. A bioenergy-based eco-industrial park is used to illustrate the proposed framework.

Keywords: Eco-industrial Park; P-graph Method; Multiple Disruptions; Industrial Symbiosis; Penalty Cost

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Energy is the most essential commodity for a rising nation like India. India's population has grown beyond 1.4 billion, driving a rapid rise in energy consumption. To meet this demand, India must explore all available energy sources, including bioenergy. Bioenergy is a renewable energy created from materials that were oncealive, known as “biomass.” This article examines the current energy situation in India and different biomass conversion technologies that can convert it into bioenergy.

Keywords: Renewable Energy; Biomass; Bioenergy; Energy; Conversion technologies

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The worldwide trend in energy production is moving toward circular economy systems and sustainable availability of sources. Some advanced methods support the economic development of energy production by the utilization of waste biomass, while limiting ecological effects. The use of agro waste biomass is viewed as a major alternative energy source that expressively lowers greenhouse gas emissions. Agricultural residues produced as wastes after each step of agricultural production are used as sustainable biomass assets for bioenergy production. Nevertheless, agro waste biomass needs to go through a few cyclic changes, among which biomass pre-treatment contributes to the removal of lignin and has a significant role in the efficiency and yield of bioenergy production. As a result of rapid innovation in the utilization of agro waste for biomass-derived bioenergy, a comprehensive overview of the thrilling highlights and necessary advancements, in addition to a detailed analysis of feedstock, characterization, bioconversion, and contemporary pre-treatment procedures, appear to be vital. To this end, the current status in the generation of bioenergy from agro biomass through various pre-treatment procedures was examined in this study, along with presenting relevant challenges and a perspective for future investigations.

Keywords: Agro residues; Bioenergy; Biological pre-treatment; Characterization; Municipal solid waste

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Bioenergy is currently a major renewable energy source in Europe but faces an unclear future because of conflicting modelling results and the lack of long-term policy. This paper identifies three challenges and potential opportunities by analysing bioenergy's historical national deployment, current policy support, and possible future roles in Europe. The first challenge is on the supply side. Calculating the supply-consumption dynamics and import dependency of EU bioenergy, we find that the security of bioenergy supply is challenging for liquid biofuels and those countries with the highest per-capita bioenergy consumption in Europe. Second, the definition of “sustainable bioenergy” in modelling studies is sometimes inconsistent with how EU policies label it. Third, on the demand side, there are unique but competing uses for bioenergy without a clear long-term strategy in Europe. We conclude with three opportunities to tackle these challenges for future research. First, utilising the untapped bioenergy potential with low environmental impacts could improve supply security. A clear and harmonised definition of “sustainable bioenergy” could better convey modelling results to policymaking. Finally, understanding where best to use limited sustainable bioenergy supply through sector-coupled energy system models can provide direction for a clearer EU bioenergy strategy towards 2050.

Keywords: Bioenergy; Decarbonisation; Energy policy; Scenarios; Europe

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Nigeria, [d]Department of Computer Science, Aberystwyth University, Penglais Campus, West Wales, United Kingdom, [e]Department of Chemical Engineering, Faculty of Industrial Technology, Universitas Pembangunan Nasional "Veteran", Yogyakarta, Indonesia, [f]Department of Chemistry, Faculty of Science and Technology, Airlangga University, Mulyorejo, Surabaya, 60115, Indonesia) Bioenergy revamping and complimenting the global environmental legal framework on the reduction of waste materials: A facile review, Heliyon, Volume 9, Issue 1(2023): e12860

The challenges posed by climate change/global warming are very alarming, and they have become the focal point of attention for researchers within the global environmental domains. The development of bioenergy can help salvage this situation as a renewable energy source that makes use of recycled waste materials to create useful energy products. This review study found that the development of sustainable bioenergy is environmentally friendly, and it has been proven to be a better means of recycling waste materials into final energy products for sustainable development. The study hereby concluded and recommended that environmental policies concerning the sustainable development of bioenergy should be adopted within the various nations' local laws and the global environment at large, as this will result in adhering strictly to international environmental legal frameworks regulating the prevention and reduction of waste materials. The possible correlation of bioenergy with the Sustainable Development Goals is also highlighted.

Keywords: Bioenergy; Environment; Greenhouse gases; Legal framework; Waste materials

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Most ambitious climate change mitigation pathways indicate multifold bioenergy expansion to support the energy transition, which may trigger increased biomass imports from major bioenergy-consuming regions. However, the potential global land-use change and sustainability trade-offs alongside the bioenergy trade remain poorly understood. Here, we apply the Global Biosphere Management Model (GLOBIOM) to investigate and compare the effects of different increasing bioenergy import strategies in line with the 1.5°C-compatible bioenergy demand in China, which is projected to represent 30% of global bioenergy consumption by the middle of the century. The results show that sourcing additional bioenergy from different world regions could pose heterogeneous impacts on the local and global land systems, with implications on food security, greenhouse gas emissions, and water and fertilizer demand. In the worst cases under strict trade settings, relying on biomass import may induce up to 25% of unmanaged forests converted to managed ones in the supplying regions, while in an open trade environment, increasing bioenergy imports would drastically change the trade flows of staple agricultural or forestry products, which would further bring secondary land-use changes in other world regions.

Nevertheless, an economically optimized biomass import portfolio for China has the potential to reduce global overall sustainability trade-offs with food security and emission abatement. However, these benefits vary with indicator and time and are conditional on stricter land-use regulations. Our findings thus shed new light on the design of bioenergy trade strategies and the associated land-use regulations in individual countries in the era of deep decarbonization.

Keywords: Bioenergy; 1.5°C; International trade; Land-use change; GLOBIOM

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The contribution of bioenergy to the global energy system is substantial and indispensable. Because of the population explosion, global energy demand has increased along with fossil fuel consumption. In this scenario, energy derived from biomass may significantly lower carbon emissions, exclusively in difficult-to-decarbonize industries like manufacturing, heavy transportation, and aviation. However, expanding the use of bioenergy with sustainability in the global energy grid is a great challenge due to the need for cleaner production methods and stakeholder governance. This chapter will provide an overview of sustainable bioenergy with special emphasis to focus on the generation of biodiesel, biogas and bioethanol. The main objectives highlight the advances in various modern techniques for producing economically feasible bioenergy in future. Moreover, this chapter will cover affluences of clean and renewable energy production from non-edible oil seeds for bioenergy (raw materials shouldn't compete with food production). The overview of bioenergy, modern production methods, challenges, prospects, and future work in bioenergy development are all emphasized. These factors should all be taken into account for a smooth transition to a bioenergy economy.

Keywords: Bioenergy; Biofuel; Biowaste; Climate change; Sustainability

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The application of renewable alternatives to the use of petroleum derivatives has faced several challenges, especially regarding high carbon dioxide emissions. Among existing solutions, bioenergy stands out for its high availability of feedstock worldwide and for being CO2 neutral. It produces solid, liquid and gaseous biofuels via a thermochemical or biochemical route. Over the years, the bioenergy industry has shown some difficulties, which has affected industrial productivity worldwide. Nonetheless, prospects are promising considering the advances in research that have enabled the emergence of technologies that can adapt the products to become a viable replacement for fossil resources.

Keywords: Biochar; Biodiesel; Bioenergy; Bioethanol; Biofuels; Biogas; Biomass conversion; Energy; Energy production; Fuel; Renewable energy; Sustainability.

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This paper makes projections of the theoretical and technical potentials of bioenergy supply for 2050. The projections consider changes in available land for bioenergy and food for the global demand and advancements in yield, productivity, expansion of bio-waste recovery, and energy conversion. We present a literature review on projections. We introduced a novel logical and transparent forecasting model. Three future scenarios were established: business as usual (BUS), optimistic trends (OPT), and full adaptation response (FAR). The projection is carried out based on four adjusting factors. An uncertainty analysis was carry-out based on a Monte-Carlo method. Projections of bioenergy production in 2050 were compared with other projections in the literature. The FAR scenario showed that it would be possible to produce twenty-one times the current primary bioenergy supply and to even supply all global primary energy demand in 2050, mostly by energy crops. The assumptions adopted for the BUS and OPT scenarios make their projections more likely. Therefore, the contribution of bioenergy in the global energy matrix is expected to be between 64 and 313 EJ (7.5%–37%) in 2050. There would be a significant change in the composition of the bioenergy supply from today's mostly firewood to energy crops and biowastes. The technical potential for fuel and electric power mostly follow the supply trends for primary bioenergy (theoretical). The potential avoided greenhouse emissions are estimated. The heuristics and the level of transparency of the novel model will allow adjustments and exploration of other scenarios as time passes.

Keywords: Bioenergy; Modeling; Improved scenarios; Biofuel land use; C2050 projections; Energy crops

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Engineering and Sciences, Mapúa University, Metro Manila 1002, The Philippines,[b]Department of Medical Science Industries, College of Health Sciences, Chang Jung Christian University, Tainan 711, Taiwan, [c]Department of Chemical and Materials Engineering, National I-Lan University, I-Lan 260, Taiwan). Unveiling electron-mediating properties of red perilla (shiso) leaves for bioenergy-steered antiviral capabilities, Biochemical Engineering Journal, Volume 197 (2023): 108986

Antiviral herbal medicines with polyphenolics were studied to exhibit effective disease treatment, antioxidant and antiviral capabilities. Prior studies have deciphered synergistic interactions of herbal medicines for disease treatment through electrochemical catalysis. Supplementing TCM to microbial fuel cell (MFC) systems allows herbal medicines to work as electron shuttles (ESs) or electrochemical catalyst, stimulating bioenergy-generating and disease-treating capabilities. ES prevents redox balance damage induced by viruses while bioelectricity-steered antiviral characteristics were triggered. Hence, this feasibility study selected the red variant of perilla leaves to decipher such correlations. This study proceeded by extracting the perilla leaves using water and ethanol. The water and ethanol extracts were subjected to phytochemical analysis and antioxidant activity. Moreover, augmentation of water and ethanolic extracts of red perilla to MFCs was quantitatively assessed for comparative study of bioenergy generation. As TPC and antioxidant activity indicated, water extract exhibited the most significant results. Meanwhile, the ethanolic extracts showed the maximal performance of bioenergy generation. With the findings of this study, it proves that the use of electrochemical approach to screen possible antiviral herbal medicine could be a promising and sustainable technique. Furthermore, deciphering the antiviral characteristics of herbal medicines through bioenergy production could address the current challenges regarding antiviral drugs.

Keywords: Antiviral; Microbial fuel cell; Electron shuttle; Red Perilla frutescens

Maxence Gérard, Pierre-Alain Jayet. (Université Paris-Saclay, INRAE, AgroParisTech, Paris-Saclay Applied Economics, 91120, Palaiseau, France) European farmers' response to crop residue prices and implications for bioenergy policies, Energy Policy, Volume 177 (2023):113561

To achieve the European bioenergy objectives, member states are likely to implement support policies targeting the use of lignocellulosic biomass for advanced bioenergy. Such policies could increase prices. In this study, we argue that with higher prices and new market opportunities for lignocellulosic biomass, farmers will account for crop residues in their choice of production and use of inputs. We test this hypothesis in an economic model of the EU agricultural supply coupled with a crop model to assess the effect of crop residue prices on residue supply, land allocation, yields, fertiliser use, and nitrogen pollution. We find that 120 million tonnes of dry matter (tDM) of crop residues are co-produced when they are unpriced. The price-induced additional supply is elastic to price but limited to 8% at €100/tDM and 13% at €200/tDM of the unpriced production. However, the increase in residue prices induces farmers to increase their crop areas and yields, which leads to significantly higher fertiliser consumption and nitrous oxide emission. These results indicate to policy makers that supporting prices would not substantially increase crop residue potential but could have collateral effects on the environment. They raise issues of coordination between bioenergy and agri-environmental policies in the EU.

Keywords: Bioenergy policy; Renewable energy directive; Biomass supply; Crop residues; Mathematical programming model

Nano Biotechnology

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Nanobiocatalysts, in which enzyme molecules are integrated into/onto multifunctional materials, such as metal-organic frameworks (MOFs), have been fascinating and appeared as a new interface of nanobiocatalysis with multi-oriented applications. Among various nano-support matrices, functionalized MOFs with magnetic attributes have gained supreme interest as versatile nano-biocatalytic systems for organic bio-transformations. From the design (fabrication) to deployment (application), magnetic MOFs have manifested notable efficacy in manipulating the enzyme microenvironment for robust biocatalysis and thus assure requisite applications in several areas of enzyme engineering at large and nano-biocatalytic transformations, in particular. Magnetic MOFs-linked enzyme-based nano-biocatalytic systems offer chemo-regio- and stereo-selectivities, specificities, and resistivities under fine-tuned enzyme microenvironments. Considering the current sustainable bioprocesses demands and green chemistry needs, we reviewed synthesis chemistry and application prospects of magnetic MOFs-immobilized enzyme-based nano-biocatalytic systems for exploitability in different industrial and biotechnological sectors. More specifically, following a thorough introductory background, the first half of the review discusses various approaches to effectively developed magnetic MOFs. The second half mainly focuses on MOFs-assisted biocatalytic transformation applications, including biodegradation of phenolic compounds, removal of endocrine disrupting compounds, dye decolorization, green biosynthesis of sweeteners, biodiesel production, detection of herbicides and screening of ligands and inhibitors.

Keywords: Nanobiocatalysis; Magnetic materials; MOFs; Enzyme immobilization; Biotransformation

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Chemical Corporation, 1-2, Ushikawadori 4-chome, Toyohashi-shi, Aichi, 440-8601, Japan,[c]Technology Section, Performance Separation Materials Unit, Aqua and Infrastructure Sector, Mitsubishi Chemical Corporation, 10th Floor, Gate City Ohsaki East Tower, 11-2, Osaki 1-chome, Shinagawa-ku, Tokyo, 141-0032, Japan). Performance of pilot-scale membrane aerated biofilm reactors integrated with anoxic nano-biotechnological reactor for domestic wastewater treatment. Chemosphere, Volume 319 (2023): 137927

Membrane-aerated biofilm reactors (MABRs) have aroused increasing attention due to their excellent performance in treating wastewater, where the membranes behave as bio-carriers for microorganisms and bubbleless air diffusers. The MABR technology has not been fully commercialized due to reactor design and low total nitrogen (TN) removal efficiency at short hydraulic retention times (HRT). In this study, a hybrid system of MABR 1 integrated with an anoxic nano-biotechnological reactor filled with Granulated Nanoscale Oxyhydroxides of Fe (GNOF) media was evaluated to assess the improvement in nitrogen removal performance at 12, 10, and 4 h of HRTs. At the same time, another MABR (MABR 2) was operated individually at 12, 10, 8, 6, 4, and 2 h of HRTs to assess the influence of HRT on nitrogen removal performance. An enhancement in removal performance was reported in the hybrid MABR-GNOF, achieving the highest removal efficiencies of 74.3 ± 3.1% for ammonium nitrogen (NH4+-N), 69.8 ± 2.1% for total nitrogen (TN), and 90.9 ± 1.7% for chemical oxygen demand (COD), at 12 h HRT. The hybrid MABR-GNOF system attained 18% higher nitrogen removal than the MABR-only system at 12 h of HRT. A simultaneous anoxic nitrification-denitrification and COD oxidation might be developed for the removal of COD, NH4+-N, and TN from domestic wastewater by using GNOF as an electron acceptor in the hybrid MABR-GNOF unit. The findings in this study confirmed the possibility of integration of GNOF and MABR on a pilot scale and are promising for the application of this hybrid system on a full scale.

Keywords: Denitrification; Domestic wastewater; Granulated nanoscale oxyhydroxides of Fe; Membrane aerated biofilm reactor; Nitrification

Biomimicry

Tolulase Olufunmilayo Ajayi. (University of Lagos Faculty of Engineering, Nigeria). Biomimicry: the nexus for achieving sustainability in the people-process-planet relationship. Heliyon, Volume 9, Issue 5 (2023): e16180

Population growth inevitably gives rise to an increase in consumption of products and services. This has the domino effect of more exploitation of already scarce natural resources, with its concomitant pollution from the industries that process these natural resources into products and services for man. At the end of life of these products, they are disposed of as waste to landfills. All these issues threaten the sustainable development of any society. To proffer sustainable solutions to the environmental problems associated with the process industry, it has incorporated the concepts of process intensification via modularization, lean manufacturing, and industrial ecology into its operations. These same concepts are used by nature, though in a different way. As nature has survived for billions of years, looking to nature for inspiration – biomimicry, might be the only sustainable solution to the planet's problem. This paper, reviews nature's strategies that have been tested, and are relevant to the process industry. It highlights biomimicry

as a powerful tool for achieving sustainability in the people-process-planet relationship as it assists to reduce waste, increase process efficiency and reduce reliance on scarce natural resources. As the process industry seeks to reduce its negative impact on the planet, biomimicry offers a promising approach to creating a more sustainable future.

Keywords: Industry; Environment; Sustainable development; Nature; Inspiration

Name of Journals

1. Acta Biotechnologica
2. Aerobiologia
3. Annual Review-Plant Pathology
4. Annual Review- Ecology and Systematics
5. Annual Review-Biochemistry
6. Annual Review-Biomedical Engineering
7. Annual Review-Biophysics and Biomolecular Structure
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