11th ICBB & 5th ICAFS

2021 International Conference on Biotechnology and Bioengineering

2021 International Conference on Agricultural and Food Science

Conference Program & Abstract Book

Virtual (Online Video)

October 27th - 30th, 2021

Content

1. Welcome Message

Welcome message

Dear Friends and Colleagues,

On behalf of the Organizing Committee, it is our great pleasure to welcome you to participate in the 2021 International Conference on Biotechnology and Bioengineering (11th ICBB, 2021), jointed with the 2021 International Conference on Agricultural and Food Science (5th ICAFS, 2021), to be held Virtual Online.

The ICBB Conference aims to provide an innovative and comprehensive overview of BIOTECHNOLOGY and BIOENGINEERING, a focus will be given to major research advances including: Microbiology, Virology, Cytology and Immunology; Biological macromolecules, proteins and nucleic acids; Biomaterials, biopolymers and bioenergy; Biomedicine, Pharmacology and Toxicology; Agricultural and Food Science; Applications in Bioengineering and Biotechnology, and other related fields.

The ICAFS has been designed to provide an innovative and comprehensive overview of agricultural and food science. Various disciplines are contributing to agricultural and food sciences. Merging interdisciplinary is the stew in which creativity and innovation thrive. In this conference, we intended to present and discuss various themes from the aspect of fundamental as well as application parts.

Over the last one year, it felt as though the world around us has changed massively - so many things are now operating so differently and life, at least for the near future, isn't quite how we expected it to be. This is, of course, due to the ongoing Coronavirus pandemic, under this special situation, our conference has to be held as a virtual conference online.

Through the network, we can keep in contact with each other since many have taken to using video meeting software and apps, a significant amount of people experiencing video conferencing. Hope we can all meet face by face at the conference of next year.

With best regards,

ICBB 2021 Organizing Committee
Email: icbb@apaset.org
https://www.icbb.apaset.edu.pl/

ICAFS 2021 Organizing Committee
Email: icafs@apaset.org
https://www.icafs.apaset.edu.kg/

2. Introduction for Organizers

Asia-Pacific Association of Science, Engineering and Technology

The Asia-Pacific Association of Science, Engineering and Technology (APASET) is a scientific organization. APASET organizes, co-organize and technical support to multidisciplinary international conferences, workshops, summits, conferences and workshops, with a focus in the fields of biology and medicine science.

APASET aims to provide a platform for academic exchange and cooperation opportunities by organizing international workshops and conference with many of the academies and scholars all over the world. For now, APASET has hundreds of members throughout the world, including research scientists, professors, engineers, postdoctoral appointees and doctoral students, etc.

The goals of APASET are to promote the co-operation between the professionals in various fields of science and engineering, and to cultivate an environment for the advance and development of the technology. Our objective includes: Encouraging regional and international communication and collaboration; promoting professional interactions between the scholars; advancing the application of science and engineering techniques from the academics to the industry; facilitating the exchange of information and ideas among the scientists and scholars freely. For potential collaborations to organize a conference, please contact at icbb@apaset.org.

Institute of Bioorganic Chemistry, Polish Academy of Sciences

The Institute of Bioorganic Chemistry, Polish Academy of Sciences is one of the leading scientific units in Poland. Its exceptionality across Europe and even the whole world is proven by multi-faceted activities at the interface of three sciences: chemistry, biology and informatics. It is a place where interdisciplinary studies encompassing such fields as bioorganic chemistry, biochemistry, molecular biology, systems biology, synthetic biology and bioinformatics are conducted; and in particular – research on the synthesis, structure and function of nucleic acids, and proteins along with their components, as well as their mutual interactions in model and cellular conditions.

The Institute's history dates back to 1969 when the Department of Stereochemistry of Natural Products within the Institute of Organic Chemistry, PAS was established. Subsequently in 1980, it was transformed into an independent Department of Bioorganic Chemistry, PAS and finally in 1988, reorganized into the Institute of Bioorganic Chemistry, PAS.

Together with Poznań Supercomputing and Networking Center, affiliated to IBCH PAS, the Institute currently hires over 550 employees, including ca. 100 scientists (22 full professors and 25 associate professors). There are more than 100 Ph.D. students participating in the Partnership-based Doctoral Program of IBCH PAS, accomplishing their dissertations at IBCH PAS and other institutes of the PAS. The Institute is authorized to confer PhD and DSc (habilitation) degrees in chemistry, within two disciplines: chemistry and biochemistry.

IBCH PAS is comprised of 30 research departments, supported by 10 specialized laboratories offering high-class infrastructure. Other significant components within the Institute's framework are the PAS Center for Science, Scientific Publishers, Guest Rooms and the Library. Moreover, jointly with the Institute of Computing Science, Poznań University of Technology, the Institute created the European Center for Bioinformatics and Genomics, which is a unique initiative in our country.

Chinese Journal of Biologicals

Chinese Journal of Biologicals, hereinafter referred to as Journal, is under the leadership of Ministry of Health of the People's Republic of China and sponsored by China Preventive Medicine Association. It mainly reports information of China biologicals, important R&D achievements and latest progresses of biologicals, as well as the status of worldwide biological and biotechnology products. The main readers of it are production, research and management personnel who come from biological and biotechnology products enterprises, clinician, and government officials who take charge of verification, disease surveillance and control.

1988 is the inaugural year of the Journal. As a carrier for academic exchange, it has faithfully and objectively reported 20 years' development history of China biological course and has a widespread impact on the biological and biotechnology field. Readers and authors of the Journal are home and abroad and increasing year by year. Worldwide biological workers may have a thoroughly understanding of the development history and current situation of China biologicals and may undertake academic exchange and cooperation with Chinese biological production and scientific research persons by it, thereby to stimulate the development of world biological course.

In recent years, the Journal was included by many international retrieval systems, in which include *Chemical Abstracts (CA), Biological Abstract (BA), Cambridge Scientific Abstracts (CSA), BIOSIS Previews (BP), Ulrich's Periodicals Directory, Abstract Journal (AJ), Excerpta Medica (EM), Scopus, Index Copernicus (IC),* and *international center for agricultural and biological sciences research (*CABI), etc.

In Collaboration With

South-Central University for Nationalities, China (SCUN)

Zoological Society of Pakistan (ZSP)

3. Conference Information

General Introduction of ICBB

The 2021 International Conference on Biotechnology and Bioengineering (11th ICBB) will be held online during October 27-29, 2021. ICBB2021 is co-organized by Asia-Pacific Association of Science, Engineering and Technology, in collaboration with multiple academic affiliations.

Conference Themes of ICBB

The conference aims to provide an innovative and comprehensive overview of BIOTECHNOLOGY and BIOENGINEERING, with topics ranging from: 1. Microbiology, virology, cytology and immunology; 2. Biological macromolecules, proteins and nucleic acids; 3. Biomaterials, biopolymers and bioenergy; 4. Biomedicine, biopharmaceuticals, pharmacology and toxicology; 5. Agricultural & food science and industrial biotechnology; 6. Applications in bioengineering, biomedical engineering & technology and other related fields. More details please check Themes and Topics.

ICBB is designed to promote interactive discussions at both the talks and poster sessions, and will feature a mix of invited speakers drawn from a wide variety of backgrounds and experiences. The conference is therefore purposely broad to cover all aspects of biotechnology and bioengineering, a unique combination that is highly appreciated by the participants. Given the excellent line up of speakers and the meeting's outstanding reputation, this is a 'must' attend for anyone interested in cutting edge research in biotechnology and bioengineering.

Conference History

Previously conferences were successfully held online (webinar, 2020); in Poznan, Poland (2019); Budapest, Hungary (2018); Offenburg, Germany (2017); Lahore Pakistan (2017, agriculture aspect); Bangkok, Thailand (2016); Singapore (2015); Hong Kong (2014); China (2013 & 2012).

For more details about previous conferences, please visit conference archives at https://www.icbb.apaset.edu.pl/about/archive.html

Conference website: https://www.icbb.apaset.edu.pl/

General Introduction of ICAFS

The 2021 The 5th International Conference on Agricultural and Food Science (5th ICAFS2021), organized by Asia-Pacific Association of Science, Engineering and Technology, in cooperation with multiple academic affiliations, will be held in video online as a webinar during Oct. 28-30, 2021.

Aims and Scope of ICAFS

It has been designed to provide an innovative and comprehensive overview of agricultural and food science. A focus will be given on: Plant sciences; Agronomy and Agricultural sciences; Soil & Environmental Science; Food Science and Technology; Agricultural Environment, Ecology and Resources, etc. The aim of the conference is to provide worldwide specialists, scholars, and researchers that are engaged in related filed a chance to exchange the latest research results and advances, study the latest technology and establish international friendship.

Conference History

Previous ICAFS were successfully held webinar online (ICAFS2020), Kuala Lumpur, Malaysia (ICAFS2019), Istanbul, Turkey (ICAFS2018) and Lahore, Pakistan (ICAFS2017 & 7thICBB).

For more details about previous ICAFS conferences, please visit conference archives at https://www.icafs.apaset.edu.kg/about/archive/

Conference website: https://www.icafs.apaset.edu.kg/

Call for Proposals to Co-Organize ICBB 2022

ICBB is pleased to announce this Call for Proposals for individuals or universities / institutes who are interested in co-organizing the next ICBB conference, slated for the third quarter of 2022.

If you are not personally interested but know of someone else who could do an excellent job of organizing this event, please feel free to forward this information.

I. An overview of ICBB

Previously conferences were successfully held online (webinar, 2020); in Poznan, Poland (2019); Budapest, Hungary (2018); Offenburg, Germany (2017); Lahore Pakistan (2017, agriculture aspect); Bangkok, Thailand (2016); Singapore (2015); Hong Kong (2014); China (2013 & 2012). For more details about previous conferences, please visit conference archives at https://www.icbb.apaset.edu.pl/about/archive.html

With the aim of continuing these successful conferences, ICBB is now soliciting applications for the co-organization of our next meeting in the year 2022.

II. The details of the proposal requirements

Having co-organised the ICBB conference with multiple universities and institutes, ICBB now looks to continue expanding its network of affiliations by seeking proposals from other universities or institutions, or by working with a group that has a similar interest in organising a new biotechnology meeting.

Proposals should be submitted via email to icbb@apaset.org.

4. Conference Program

2021 International Conference on Biotechnology and Bioengineering

2021 International Conference on Agricultural and Food Science (5th ICAFS 2021)

11th ICBB & 5th ICAFS 2021 Virtual Conference (Webinar Online)

Oral Presentation List

Wednesday Oct. 27, 2021

Session 1: Pharmacology & Drug Delivery, Biomedicine and Natural Product

Please check-in 15 minutes in advance. Check-in time is in is in parentheses.
UTC+0200 Cairo / Warsaw (Check-in: 8:45) 9:00~11:00AM UTC+0300 Moscow / Istanbul (9:45) 10:00 ~12:00 AM
UTC+0530 New Delhi (12:15) 12:30 ~14:30PM UTC+0800 Beijing/Kuala Lumpur (14:45) 15:00~17:00PM
~ about 2 hours

11461-S1-O1

Mohamed Mahmoud El-Shazly Shedding light on the cytotoxic activity and mechanism of action of heteronemin, a marine sesterterpenoid-type natural product, against LNcap and PC3 prostate cancer cells

11524-S1-O2

Intan Safinar Ismail Evidence-based traditional medicinal-plant as biomedicines source

11516-S1-O3

Mohmad Farooq Shaikh Zebrafish As An Alternative Animal Model for Anticonvulsant Drug Discovery

11514-S1-O4

Saroj Kumar Evolving role of exosomes in neurodegenerative diseases

Wednesday Oct. 27, 2021

Session 2: Biomolecules in Complex Biological and Biochemical Systems

Please check-in 15 minutes in advance.
UTC+0200 Cairo / Warsaw 12:00~14:00 PM UTC+0300 Moscow / Istanbul 13:00~15:00 PM
UTC+0530 New Delhi 15:30~17:30 PM UTC+0800 Beijing / Kuala Lumpur 18:00~20:00PM
~ about 2 hours

11523-S2-O1

Ahmed Shihab Ahmed Al-bahri Growth of Data Science Roles and Decision-Theory for Shaping the Future of Biotechnology and Bioengineering Applications

11567-S2-O2

Salam Lateef Babatunde Elucidation of the CYPome of the Prokaryotic and Eukaryotic Communities of a Chronically Polluted Soil

11531-S2-O3

Livia Alexandra DINU Metallic nanoparticles-graphene nanohybrids as artificial enzymes for environmental and biomedical electrochemical applications

11563-S2-O4

Om Prakash Gupta Integrative physiological, biochemical and transcriptomic analysis of hexaploid wheat roots and shoots provides new insights into the molecular regulatory network during Fe & Zn starvation

11548-S2-O5

Naveen Vankadari Molecular interplay between SARS-CoV-2 and Human proteins for viral activation and entry, potential drugs and scope for new therapeutics

Thursday Oct. 28, 2021
Session 3: Application of Agricultural Biotechnology

Please check-in 15 minutes in advance.
UTC+0200 Cairo / Warsaw (Check-in: 8:45) 9:00~11:00AM UTC+0300 Moscow / Istanbul (9:45) 10:00 ~12:00 AM
UTC+0530 New Delhi (12:15) 12:30 ~14:30PM UTC+0800 Beijing/Kuala Lumpur (14:45) 15:00~17:00PM
~ about 2 hours

	11014-S3-O1
Rachel Amir	Evidence of metabolic competition between methionine and glutathione biosynthetic pathways
	11153-S3-O2
Luca Giupponi	Plant agro-biodiversity is a resource for the sustainable development of mountain areas: the case of Italy
	11039-S3-O3
Amir Mirzadighohari	Investigation on the role of phenolic compounds in Zymoseptoria tritici -wheat interaction
	11034-S3-O4
Md Sayeedul Islam	Roles of Myosin XI-i in Mitochondrial Movement in *Arabidopsis thaliana* Leaf Mesophyll Cells
	11460-S3-O5
Bülent Bülbül	Some reproductive traits in Central Anatolian Merino sheep under breeder conditions

Thursday Oct. 28, 2021
Session 4: Comprehensive Application of Natural Products and Food

Please check-in 15 minutes in advance.
UTC+0200 Cairo / Warsaw 12:00~14:00 PM UTC+0300 Moscow / Istanbul 13:00~15:00 PM
UTC+0530 New Delhi 15:30~17:30 PM UTC+0800 Beijing / Kuala Lumpur 18:00~20:00PM
~ about 2 hours

	11727-S4-O1
Louiza Belkacemi	Blanching effect on physicochemical and functional properties of flours processed from peeled and unpeeled white‐fleshed sweet potato Algerian cultivar
	11098-S4-O2
Amelia Martins Delgado	Can bakery products be tasty healthy and sustainable? Clues for SMEs
	11489-S4-O3
Maria Vinas	Polyphenols of common beans (Phaseolus vulgaris L.) as possible compounds for mycotoxin resistance
	11552-S4-O4
Cristina Mihaela ACHIM	Photoacoustic spectroscopy in the detection of volatile organic compounds with applications in life science
	11040-S4-O5
Champa Wijekoon	Bioactive molecules and fungal endophytes in table grape berries

Friday Oct. 29, 2021

Session 5: Agronomy and Environmental Biotechnology

Please check-in 15 minutes in advance. Check-in time is in is in parentheses.

UTC+0200 Cairo / Warsaw (Check-in: 8:45) 9:00~11:00AM UTC+0300 Moscow / Istanbul (9:45) 10:00 ~12:00 AM

UTC+0530 New Delhi (12:15) 12:30 ~14:30PM UTC+0800 Beijing/Kuala Lumpur (14:45) 15:00~17:00PM

~ about 2 hours

11117-S5-O1

Jawwad A. Qureshi — Managing global pest threats to citrus production

11212-S5-O2

James T. Vogt — Pest status of the invasive Callery pear tree (Pyrus calleryana Decne.) in the Unites States, and herbicide options for management and control

11739-S5-O3

Lirong Han — A Polysaccharide ECS66A From Streptomyces mauvecolor Inducing Plant Defense Response Against Black Shank of Tobacco

11586-S5-O4

Marine Bezhuashvili — Change of vine leaves (Vitis vinifera L.) phytoalexin stilbenoids under Downy mildew infection

Session 6: Young scholars session (Part 1)

11444-S6-O1

Maciej Prusinowski — Protein interaction research with dedicated biosensors using Blitz technology

11271-S6-O2

Syeda Fahria Hoque Mimmi — Prospects of Milk Protein-Lactoferrin as a Potential Alternative of Natural Antibiotic

11606-S6-O3

Małgorzata Ponikowska — Lytic bacteriophage proteins fused with a binding domain as an antimicrobial preparation

11343-S6-O4

Małgorzata Witkowska — Towards biohydrogen production: high-throughput cloning methods for robust hydrogenase biosynthesis

Friday Oct. 29, 2021

Session 7: Young scholars session (Part 2)

Please check-in 15 minutes in advance. Check-in time is in is in parentheses.

UTC+0200 Cairo / Warsaw 12:00~14:00 PM UTC+0300 Moscow / Istanbul 13:00~15:00 PM

UTC+0530 New Delhi 15:30~17:30 PM UTC+0800 Beijing / Kuala Lumpur 18:00~20:00PM

~ about 2 hours

11187-S7-O5

Peiru Gao — Microplastics and mesoplastics in commercial fish from Kota Kinabalu, Malaysia

11289-S7-O6

Parya Kheyri — Description of included systematic reviews on isolated compounds on the anti-trichomonas activities of medicinal plants

11554-S7-O7

A.A. Asanka Udaya Aberathna — Fungal species as rock phosphate solubilizing agents to use as biofertilizers

11650-S7-O8

Shenjin Huang — Recognizing Zucchinis Intercropped with Sunflowers in UAV Visible Images Using an Improved Method Based on OCRNet

11691-S7-O9

Jianyi Ao — Assimilation of LAI Derived from UAV Multispectral Data into the SAFY Model to Estimate Maize Yield

11638-S7-O10

Haipeng Chen — Estimating fractional vegetation cover of maize under water stress from UAV multispectral imagery using machine learning algorithms

Poster Presentation List

Poster Session 1

Khaled Trabelsi	Production and purification of recombinant SARS COV-2 receptor binding domain in different expression system for human IgG/IgM ELISA	11758-SP1-1.
Souad Akroum	The ability of some moulds to degrade condensed tannins of Punica granatum fruits	10970-SP1-2.
Vladimir Safonov	Enzymes of the Antioxidant Support Network in Cows During Pregnancy Formation	11500-SP1-3.
Laura Darie Ion	An optimized ultrasound-based protein determination in maize seeds	11671-SP1-4.
Joanna Żebrowska	Biomicropolymers as a new therapeutic protein delivery system	11206-SP1-5.
Olga Marchut-Mikołajczyk	Bioremediation of soil contaminated with creosote oil PAHs enhanced with Mucor racemosus enzymatic preparation	11725-SP1-6.
Katarzyna Struszczyk-Świta	Biodegradation of creosote oil in the soil environment with the use of immobilized cells of Bjerkandera adusta DSM no. 3375	11726-SP1-7.
Qiulin He	“All-in-one” gel system for whole procedure of stem cell amplification and tissue engineering	11216-SP1-9.
Patrycja Laszuk	Biosynthesis and purification of the recombinant major capsid protein derived from TP-84 bacteriophage	11311-SP1-10.
Anna Struck	A rapid universal mini-scale method for the isolation of TP-84 genomic DNA devoid of bacteriophage particles	11335-SP1-11.
Tao Sun	HnRNP H/F promote TLR4-mediated inflammatory response by activating NF-KB and MAPK signaling pathway in macrophages	11645-SP1-12.
Shuanglong Lu	Metformin alters intestinal flora and ameliorates immune-mediated bone marrow failure in mice	11648-SP1-13.
Shuaijie Li	A Novel Biodegradable Bone Wax with Antibacterial Property for Bone Hemostasis	11649-SP1-14.
Thomas A. Strong	Recombinant Human ACE2 Surface Functionalized Cell-Mimetic Microparticles Restrict SARS-CoV-2 Spike Protein Binding to Cellular Targets	11672-SP1-15.
Akitsu Masuda	Artificial trimerization of coronavirus spike proteins improves their productivity in silkworm-baculovirus expression vector system and is effective for eliciting neutralizing antibodies	11678-SP1-16.
Ziqun Zhou	Morphology extraction of fetal electrocardiogram by slow-fast LSTM network	11701-SP1-17.

11723-SP1-18.

Sikozile Ncembu THERAPEUTICALLY TARGETING CD64 IN ACUTE MYELOID LEUKEMIA VIA SINGLE-CHAIN BASED ANTIBODY IMMUNOTOXIN

11724-SP1-19.

Piotr Drożdzyński Bioremediation of soil contaminated with hydrocarbons enhanced by biosurfactants produced by endophytic Bacillus pumilus 2A

11748-SP1-20.

Nouran Hassan Tantawy Farag Tackling COVID-19 pandemic with natural products: Evaluation of Tamarix nilotica phytochemical constituents as potential coronavirus-2 major protease inhibitors

11757-SP1-21.

Yuhua Wei FAK inhibitors suppress the proliferation and improve the immune microenvironment of HCC in mice

Poster Session 2

11099-SP2-22.

Edison Jacinto Mazón Paredes Bromatological composition of palm kernel meal according to its origin and production periods potential use of palm kernel meal in animal feed

11391-SP2-23.

Hernán Eduardo Rodríguez-Ríos Amaranthus cruentus L. as a food alternative in laying hens to reduce cholesterol in eggs.

11594-SP2-24.

YuanYu Lin Effect of Mesobiliverdin IXα-enriched microalgae on intestinal morphology, inflammatory cytokines and antioxidant enzymes activity of weaning piglets

11627-SP2-25.

Jianmei Zheng Analysis of Flavor Substances in Potato Instant Vermicelli Seasoning

11647-SP2-26.

Kuotai Yang Preliminary study of citrus extract supplement in cecum microbiota fluctuation in laying hens

11652-SP2-27.

Sheng-Yao Wang Effects of calcium ions on physicochemical properties and stability of preserved eggs

11655-SP2-28.

Monika Pliszka Angiotensin-converting enzyme inhibitory and anti-diabetic properties of oat proteins hydrolysates

11740-SP2-29.

Davide Pedrali Quality traits of saffron produced in Italy from 2015 to 2020

11592-SP2-30.

Lyndsay Priscilla Arthur Gut bacterial communities in the commercially valuable polychaete worms (*Annelida Polychaeta*) from the east coast of India with implications to aquaculture

11679-SP2-31.

Le Van Dang Impact of Animal Manures on Pummelo Leaf Nutrient Status and Fruit Quality

11675-SP2-32.

Daniel Asfaw Kitessa Improving nutritional quality of food products through fermentation and formulation

11753-SP2-33.

Hamida Akli An Optimized Enzymatic Hydrolysis of Bovine Whey Protein with Chymotrypsin, Trypsin, and Pepsin Using a Full Factorial and a Surface Response Methodology

Poster Session 3

11518-SP3-34.

Vinod Scaria Genomes - from Personal to Populations and Back

11519-SP3-35.

Fabiola Vilaseca Application of biotechnology for the production of bacterial cellulose

11247-SP3-36.

Kalandarov Palvan Iskandarovich THE EFFECT OF BIOMASS MOISTURE ON THE INTENSITY OF THE FERMENTATION PROCESS IN THE PRODUCTION OF BIOGAS

11309-SP3-37.

Che Azurahanim Che Abdullah Encapsulation of Anti-cancer Drug (Tamoxifen Citrate) conjugated with Magnetite Nanoparticle for Targeted Drug Delivery

11309-SP3-38.

Che Azurahanim Che Abdullah Encapsulation of Anti-cancer Drug (Tamoxifen Citrate) conjugated with Magnetite Nanoparticle for Targeted Drug Delivery

11620-SP3-39.

Mohammad Rabbani Khorasgani Probiotic Potential of Bacillus subtilis strains Isolated from Camel milk In Iran

11703-SP3-40.

Yun Chen Recipe Adaption Methods for Sugar Content and Sweetness Taste Balance of Homemade Fresh Drinks

11595-SP3-41.

Xia Hu A quantitative peptidomic approach and bioinformatic analysis reveals immunological biomarkers and antimicrobial peptides from Hermetia illucens L.

11452-SP3-42.

Yu Yuan A Hematocyte Detection System Based on YOLOv4

11357-SP3-43.

Min Wang Effect of Catgut Embedding with Acupuncture of Moxibustion in Traditional Chinese Medicine on Human Obesit.

11268-SP3-44.

Hongchao Liu Gene expression profile of glioblastoma in response to temozolomide

11170-SP3-45.

Yi Xu Deep Integration of Information Technology and Nursing Education: a Case Study of Education Informatization

11057-SP3-46.

Xu Yang Physicochemical properties and antioxidant activities in vitro of water- soluble compound polysaccharides from Chinese herbal medicines

10898-SP3-47.

Yaping Zhao Research on the connotation structure of fitness literacy and its influence on fitness behavior

17919-SP3-48.

Yujiao Wang Design and Implementation of Medical Information Resource System Based on Intelligent Recommendation

11683-SP3-49.

Jianying Tian Involement of Gut microbiota-brain axis in protection of Lycium barbarum polysaccharides against D-galactose induced aging

Poster Session 4

		10997-SP4-50.
Sonia Mbari	Fractionation of Heavy Metals in Multi-Contaminated Soil Treated with Biochar Using the Sequential Extraction Procedure	
		11207-SP4-51.
Roksana Nazari	Salicylic acid priming before and after accelerated aging process increases seedling vigor in aged soybean seed	
		11046-SP4-52.
Karlina Sari, M.A.	Innovation Path and Business Development Strategy: The Case of Indonesian Functional Food Firm	
		11222-SP4-53.
AmanELmi Tufa	Rating and Modeling Oilseeds Extractability in Mechanical Press	
		11210-SP4-54.
Jonathan Proctor	Atmospheric opacity has a nonlinear effect on global crop yields	
		11269-SP4-55.
Karidiatou GNANKAMBARY	Assessment of Cowpea (Vigna unguiculata (L.) Walp.) Mutant Lines for Drought Tolerance	
		11417-SP4-56.
Ahliddin Rahmonov	Study of the effect of fungicides in field conditions from vegetable crops against tomato disease	
		11132-SP4-57.
Latifah Omar	Ammonia volatilization following application of urea and rice husk compost	
		11168-SP4-58.
Jacob Lisuma	Nicotine release at the tobacco rhizosphere and their adsorption capacities in different soil textures	
		11037-SP4-59.
Vijaya Juturu	Functional ingredient Collagen and Joint Health	

5. Abstracts

Oral Session 1

11461-S1-O1

Shedding light on the cytotoxic activity and mechanism of action of heteronemin, a marine sesterterpenoid-type natural product, against LNcap and PC3 prostate cancer cells

Mohamed El-Shazly

Pharmacognosy Department, Ain-Shams University, Cairo, Egypt

Biology Department, Faculty of Pharmacy and Biotechnology, The German University in Cairo

Abstract

Marine environment is the richest form of life on earth. It provided humanity with food, jewelry, and medicine. Marine sponges represent a rich source of potent therapeutics with thousands of biologically active compounds isolated from these magnificent creatures. One interesting example of the isolated class of secondary metabolites is heteronemin, which was isolated from the marine sponge *Hyrtios* sp. It is a marine sesterterpenoid-type natural product that exhibited potent cytotoxic activity against several cancer cell lines including prostate cancer cell lines. The importance of finding new therapeutic entities against prostate cancer encouraged us to evaluate the cytotoxic activity of heteronemin and its mechanism of action. Heteronemin exhibited potent cytotoxic effect against LNcap and PC3 prostate cancer cells with IC_{50} 1.4 and 2.7 μM after 24 h, respectively. In the xenograft animal model, the tumor size was significantly suppressed to about 51.9% in the heteronemin-treated group in comparison with the control group with no significant difference in the mice body weights. Heteronemin inhibited topoisomerase II (topo II) as demonstrated by the cell-free system assay. Heteronemin induced apoptosis by 20.1–68.3%, disrupted mitochondrial membrane potential (MMP) by 66.9–99.1% and promoted calcium release by 1.8-, 2.0-, and 2.1-fold compared with the control group in a dose-dependent manner, as demonstrated by annexin-V/PI, rhodamine 123 and Fluo-3 staining assays, respectively. The pretreatment of LNcap cells with an inhibitor of protein tyrosine phosphatase (PTPi) diminished growth inhibition, oxidative and Endoplasmic Reticulum (ER) stress, as well as activation of Chop/Hsp70 induced by heteronemin, indicating that PTP activation played a crucial rule in the cytotoxic activity of heteronemin. Using molecular docking analysis, heteronemin exhibited more binding affinity to the N-terminal ATP-binding pocket of Hsp90 protein than 17-AAG, a standard Hsp90 inhibitor. It promoted autophagy and apoptosis through the inhibition of Hsp 90 and topo II as well as PTP activation in prostate cancer cells. These multiple targets render heteronemin as an interesting candidate which can be further developed into an antiprostatic agent.

11524-S1-O2

Evidence-based traditional medicinal-plant as biomedicines source

Intan Safinar Ismail*[1, 2] and Xia Hong[1, 3]

[1]Natural Medicine and Products Research Laboratory, Institute of Bioscience, Universiti Putra Malaysia, 43400, Serdang, Selangor, Malaysia

[2]Department of Chemistry, Faculty of Science, Universiti Putra Malaysia, 43400, Serdang, Selangor, Malaysia

[3]Hebei Key Laboratory of Research and Development for Traditional Chinese Medicine, Chengde Medical University, 067000, Chengde, Hebei, P.R. China.

Abstract

The current study is to evaluate anti-inflammatory activity of *Scurrula ferruginea* (Jack) Danser as well as determine the metabolite differences of this plant parasitizing on three different hosts. The potential anti-inflammation of aqueous extracts of air-dried and freeze- dried leaf and stem samples along with their selected partitions of different solvents was assessed. The anti-inflammatory activity was determined via inhibition of nitric oxide (NO) production in lipopolysaccharide (LPS) and interferon-γ (IFN-γ) induced RAW 264.7 macrophage cells. Whereas the mechanism was deciphered through reverse transcriptase and real time quantitative polymerase chain reactions (RT-PCR and qPCR). The metabolite variation was examined using proton nuclear magnetic resonance (1H NMR) combined with multivariate data analysis (MVDA). The results showed that *S. ferruginea* stems parasitizing on *Tecoma stans* and *Vitex negundo* which were freeze dried exhibited higher anti- inflammatory activity with IC50 values 114.47 ± 2.96 and 118.87 ± 2.31μg/mL, respectively. The mid-polar ethyl acetate fraction of *T. stans* displayed the highest NO inhibition with 84.78 ± 1.45% at 200 μg/mL. This bioactivity was observed to exert the anti-inflammation via inhibition of iNOS and IL-1β mRNA expression. Principal component analysis (PCA) indicated notable and clear discriminations among the different plant parts and host plants based on the identified metabolites. Furthermore, partial least square regression (PLS) model suggested the anti-inflammatory bioactivity might be associated to the presence of choline, isoleucine, catechin, leucine, and chlorogenic acid. This study suggests *S. ferruginea* could serve as a potential anti-inflammatory agent, highlighting the importance of *T. stans* as the host plant in exploiting its medicinal value.

Keywords: *Scurrula ferruginea* (Jack) Danser, Anti-inflammatory activity, 1H NMR Metabolomics, Host plant, PCR

11516-S1-O3

Zebrafish As An Alternative Animal Model for Anticonvulsant Drug Discovery

Mohd. Farooq Shaikh

Neuropharmacology Research Strength, Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, Selangor, Malaysia.

Abstract

Epileptic seizures are the manifestation of several signs and/or symptoms due to heightened brain activity, causing a variety of disturbances such as motor and cognition dysfunction. In contrast, epilepsy is characterised by a chronic tendency to spawn these epileptic seizures. One way of studying epilepsy or seizures is to induce either acute seizures or epilepsy in animals via chemoconvulsants such as pentylenetetrazol (acute seizures) or kainic acid (chronic seizures), though pentylenetetrazol can also produce chronic seizures via kindling. Zebrafish are of great utility as an animal model as they have a high breeding rate and are genetically similar to humans. Seizure-like behaviour are induced using chemoconvulsants in adult zebrafish, seizures can be scored to determine severity. By recording this behaviour, the resulting locomotion pattern and parameters can also be tracked via software analysis. To investigate the cognitive decline comorbidity of epileptic seizures, mazes such as the T-maze and three-axis maze can be used to evaluate the learning and memory ability of the zebrafish via operant conditioning. This is done by comparing and contrasting the time taken for a zebrafish to reach the location of a reward over successive trials. Zebrafish also allow to study action potential/EEG, neurotransmitters, gene and proteins involved in cognitive functioning.

11514-S1-O4

Evolving role of exosomes in neurodegenerative diseases

Saroj Kumar

Department of Biophysics, All India Institute of Medical Sciences, New Delhi, India

Abstract

BACKGROUND: Alzheimer's Disease (AD) and Parkinson's Disease (PD) are the most common neurodegenerative diseases. Cognitive impairment (CI) is the common accomplice of dementia and the majority of dementia cases are dictated by AD pathology, whereas, the progressive loss of dopaminergic neurons leads to PD. The hallmark pathological features of both diseases are amyloid plaques in AD and Lewy bodies in PD. Predominantly, amyloid-beta (Aβ) in AD and alpha-synuclein (α-Syn) in PD are involved in respective disease pathologies. Diagnosis of both neurodegenerative diseases is primarily done by scaling of physical signs and symptoms which suffer from subjective variation and appear in late stages. Also, there is no biomarker exist and the use of neuroimaging techniques are expansive and not being used routinely. There is a lack of proper diagnostic tools to detect these diseases with high sensitivity or specificity, especially in the early stages which creates an urgent need for new and cost-effective screening and diagnostic methods. In recent years, extracellular vesicles like exosomes are a widely researched role in the pathogenesis of various diseases as they carry signals of disease pathology in their protein cargos. In this study, we have demonstrated a novel method, i.e. nanoparticle tracking analysis (NTA) to investigate how salivary exosomes can be exploited to correlate these neurodegenerative diseases and that could open a new way for early and cost-effective screening of these diseases. **METHODOLOGY:** A total of 10 CI, 5 AD and 18 PD patients, as well as 12 HC for AD and PD were recruited using proper inclusion and exclusion criteria. Unstimulated whole saliva was taken as clinical samples from patients of CI, AD and PD with age-matched healthy controls (HC). The exosomes were isolated from saliva using chemical precipitation method. Total salivary exosomes concentration was measured by nanoparticle tracking analysis (NTA) followed by exosomal cargo protein validation by western blot using antibodies of CD63 (exosome biomarker), L1CAM (Neural Cell Adhesion Molecule L1). Total protein abundance was calculated for and p-tau for both neurodegenerative disease whereas Aβ oligomer and monomer antibodies were used for AD, and phospho-α-Syn (Ser-129) antibody was used for PD. Statistical analysis was done using Graph-Pad Prism. **RESULT:** We observed changes in the concentrations of salivary exosomes by NTA that is correlated with the disease. Significantly higher concentration of exosomes (p=0.0001) was reported in PD patients (1.44×10^8 particle/ml) than HC (2.94×10^7 particle/ml). We also observed a significant difference in exosomes concentration (p=0.0023) in CI (1.884×10^{11} particle/ml) and AD (1.905×10^{11} particle/mL) patients comparing with HC (4.333×10^{10} particle/ml). The exosomes were validated using exosomal surface marker CD63 and to validate its neuronal presence L1CAM was used. Also, there is a significantly higher abundance of L1CAM (p<0.0001), and phospho-α-Syn (p<0.0004) in PD comparing with HC; whereas, the protein abundance of p-tau (p=0.0325), Aβ oligomer/fibril (p=0.0291), and Aβ monomer (p=0.0198) were significantly high in AD and CI patients in

comparison to the HC. **CONCLUSION:** We demonstrated that the exosome concentration as well as the expression levels of hallmark proteins for both the neurodegenerative diseases, which were significantly higher in PD as well as CI and AD than age-matched healthy controls which is in accordance with the disease severity staging. This study has the potential to be used for the development of a cost-effective screening method for the detection of both neurodegenerative diseases in early stages.

11523-S2-O1

Growth of Data Science Roles and Decision-Theory for Shaping the Future of Biotechnology and Bioengineering Applications

Ahmed Shihab Ahmed Al-bahri

Affiliation: IIPS Institute, University of Information Technology and Communications,

Iraq

Abstract

Data science has attracted a lot of attention, promising to turn vast amounts of data into useful predictions and insights. The goal of data science is to improve decision-making through the analysis of data where it is an essential tool that can be applied to medical fields and solve clinical problems. Along with its rising importance in biology, Multi-criteria decision making (MCDM) shows an increasing and broader presence in the scholarly discourse, and this presence has affected many fields, and MCDM is now researched from a more holistic perspective, with different fields (Microbiology, virology, cytology, Biomedicine, and immunology) to profit from MCDM methods. MCDM is 'an extension of decision theory that covers any decision with multiple objectives for assessing alternatives on the individual, often conflicting criteria, and combining them into one overall appraisal'. The technique involves various processes including structuring, planning, and solving different decision problems with the use of many criteria. The new paradigm, often called "Biological Data Science" has developed advanced techniques that can be applied toward understanding biological data. Recently, challenges outlined from various biological perspectives when using data science tools in terms of "*data issues and how to avoid them?*" may require a novel design solution. This claim is supported by a different type of biological data issues such as ***multiple criteria*** decision-making problems need to be considered in the evaluation, ***criteria importance*** to determine criteria weights which is the most important task, ***data variation*** in which the variability describes how far apart data points lie from each other and from the center of a distribution with respect to each criterion, ***trade-off*** one criteria against another, and ***conflict*** among criteria. These issues are a complex multi-attribute decision-making problem that falls under multicriteria decision making (MCDM), in particular, MCDM methods often require decision-makers (DMs) or experts to provide qualitative and/or quantitative assessments to determine the performance of any alternative with respect to each criterion. Thus, the integration between 'Biological Data Science' and 'MCDM' is a new branch of study which deals with scientific methodologies, processes, and techniques drawn from different biological fields to extract knowledge from structured data and unstructured data and can solve any data issue for different biological perspectives. In conclusion, emerging data science applied probability and statistical tools committed to biological fields can change the entire face of biotechnology and bioengineering applications development by integrating decision theory and especially for MCDM methods, however, it is expected to take it to an innovative level in near future. Accordingly, the transfer of knowledge among data science, decision-making theory, and biology is considered a multidisciplinary field, and complex problems or open challenges can be solved to produce district methodology solutions towards biotechnology and bioengineering techniques for different assessments.

Keywords: Biological Data Science, data science, MCDM, data issues, Biotechnology and Bioengineering Applications, biology

11567-S2-O2

Elucidation of the CYPome of the Prokaryotic and Eukaryotic Communities of a Chronically Polluted Soil

Salam Lateef Babatunde[1], Obayori Oluwafemi Sunday[2]

[1]Department of Biological Sciences, Microbiology unit, Elizade University, Ilara-Mokin, Ondo State, Nigeria

[2]Department of Microbiology, Lagos State University, Ojo, Lagos State, Nigeria

Abstract

Cytochrome P450 monooxygenases (CYPs) are exciting biocatalysts found in the three domains of life and catalyzes diverse regio- and stereoselective reactions of a broad range of substrates. The CYPome of a chronically polluted soil (3S) was deciphered via functional annotation of putative ORFs (open reading frames). Functional annotation of 3S metagenome ORFs for cytochrome P450 proteins (CYPome) was conducted using KEGG KofamKOALA, PHMMER, the Cytochrome P450 Engineering Database CYPED v6.0, and the NCBI Batch Web CD-Search tool. Annotation revealed the detection of ninety-four (94) cytochrome P450 proteins cutting across the three domains of life with 72 and 21 CYP families for the domains Bacteria and Eukarya while Archaea has 1 CYP family. In the prokaryote CYPome, the domain Archaea was represented by CYP119A1 while the phylum *Proteobacteria* and the genera *Streptomyces, Mycobacterium* and *Bacillus* with 17, 16, 24 and 5 CYP families dominated the prokaryote CYPome in 3S metagenome. The detected prokaryote CYPs are responsible for biodegradation of camphor, hydroxylation of monoterpene alcohols, biosynthesis of secondary metabolites, and hydroxylation of fatty acids and steroidal compounds. Animal and plant CYPome constitute 31.5% and 60% of the eukaryote CYP families in the metagenome. Animal CYPome dominated by CYP4 family are involved in metabolism of fatty acids, eicosanoids, steroids, xenobiotics, therapeutic drugs, leukotrienes and prostanoids. The plant CYPome recovered from 3S metagenome are involved in oxidative degradation of abscisic acid and salt tolerance response, triterpenes hydroxylation and carboxylation, secologanin biosynthesis and plant defense mechanism, brassinosteroid biosynthesis and inactivation, taxol biosynthesis, and gibberellin biosynthesis. Fungi CYPs involved in biosynthesis of secondary metabolites, hydroxylation of fatty acids, dissimilatory nitrate reduction and denitrification were also detected. This study has established the diverse roles played by CYPs in soil and its implication for soil health and resilience as well as its potentials for industrial application.

11531-S2-O3

Metallic nanoparticles-graphene nanohybrids as artificial enzymes for environmental and biomedical electrochemical applications

Livia Alexandra DINU

National Institute for Research and Development in Microtehnologies (IMT-Bucharest), Bucharest, Romania

Abstract

In the last years, more and more nanomaterials have been studied as artificial enzyme, due to their high catalytic activity towards the determination of various organic compounds, and biomarkers. In the last years, electrochemical techniques have been developed for the detection of various compounds because they bring important advantages, such as high sensitivity, fast response time, low cost and the possibility for point-of-care (PoC) and on-site monitoring, through miniaturization. Electrochemical sensors with high sensitivity and selectivity are desired. Enzyme-based sensors represent one of the most selective electrochemical sensors, but they have several weaknesses, such as complex immobilization procedure (crosslinking and stabilizing reagents) that may cause loss of activity and signal reproducibility, special storage conditions (2-8o C), low sensitivity and less stability in time1. Also, they are losing ground for the development of a stable, reliable, sensitive, and selective sensor for commercial use2. Likewise, cost effectiveness is another concern that can decisively affect sensor application due to the huge implementation scale and volume in environmental monitoring. Low-cost materials, which also benefit from unique physico-chemical properties, are the nanosized materials. The findings from 20073 broke the conventional idea that inorganic materials are bio-inert, and inspired researchers to explore nanomaterials as catalyst or artificial enzymes (nanozymes) in electrochemical applications. The nanozymes' scientific field embodies an incipient research area, which has generated massive scientific enthusiasm due to their superior properties in terms of 'refined' response to external incentives, self-assembly ability, large surface area, size-dependent catalytic activities, and, most important the structural tunability4. Nanozymes based on graphene functionalized with metallic nanoparticles, as sensitive material for the development of electrochemical sensors, were exploited in biomedical and environmental applications. Carbon paste and screen-printed electrodes have been chemically modified with several nanohybrid materials based on graphene or graphene quantum dots modified with gold and silver nanoparticles, for the non-enzymatic detection of i) bisphenol A and ii) quercetin from biological samples, and iii) catechol and iv) glyphosate from water samples. These nanozyme-based sensors showed very low detection limits, high sensitivity and selectivity for the analysis of selected analytes. This research integrates the newest ideas and features of the next generation of artificial enzymes, with the miniaturized and portable screen-printed electrodes, by bringing aside biology, chemistry, electronics and materials science. This research has high impact in several scientific domains, such as electrochemical, environmental, agricultural and biomedical fields and opens new research pathways that make nanozyme-based electrochemical sensors to be used as reliable analytical tools.

11563-S2-O4

Integrative physiological, biochemical and transcriptomic analysis of hexaploid wheat roots and shoots provides new insights into the molecular regulatory network during Fe & Zn starvation

Om Prakash Gupta[1*], Vanita Pandey[1], Ritu Saini[1], Tushar Khandale[1], Ajeet Singh[1], Vipin Kumar Malik[1], Sneh Narwal[1$], Sewa Ram[1], Gyanendra Pratap Singh[2]

[1]Division of Quality and Basic Sciences, ICAR-Indian Institute of Wheat and Barley Research (IIWBR), Karnal, 132001, Haryana, INDIA

Abstract

In plants, iron (Fe) & zinc (Zn) uptake and transportation from the rhizosphere to the grain is a critical process regulated by complex transcriptional regulatory networks. However, understanding the combined effect of Fe & Zn starvation on their uptake and transportation and the molecular regulatory networks that control them lack in wheat. Here, we performed a comprehensive physiological, biochemical and transcriptome analysis in two bread wheat genotypes, *i.e.* Narmada 195 and PBW 502, differing in inherent Fe & Zn content to understand the mechanism of Fe & Zn homeostasis. Compared to PBW 502, Narmada 195 exhibited increased tolerance to Fe & Zn withdrawal by an increased level of antioxidant enzymes and DPPH radical scavenging activity along with less malondialdehyde (MDA), H_2O_2 level, increased PS accumulation and lower reduction of root and shoot Fe & Zn content and length, leaf chlorosis, and leaf area. By integrating physiological and biochemical data along with co-expression & functional genome annotation and gene expression analysis, we identified 25 core genes associated with four key pathways, *i.e.* Met cycle (10), PS biosynthesis (4), antioxidant (3) and transport system (8) that were significantly modulated by Fe & Zn withdrawal in both the genotypes. Genes of these four pathways were more considerably up-regulated in Narmada 195, allowing better tolerance to Fe & Zn withdrawal and efficient uptake and transportation of Fe & Zn. Chromosomal distribution and sub-genome wise mapping of these genes showed a contribution from all the chromosomes except group 5 chromosomes with the highest number of genes mapped to chromosome 4 (24%) and sub-genome D (40%). Besides, we also identified 26 miRNAs targeting 14 core genes across the four pathways. Together, our work provides a crucial angle for an in-depth understanding of regulatory cross-talk among physiological, biochemical and transcriptional reprogramming underlying Fe & Zn withdrawal in wheat. Core genes identified can serve as valuable resources for further functional research for genetic improvement of Fe & Zn content in wheat grain.

Key Words: Wheat (*Triticum aestivum* L.), Fe & Zn withdrawal, transcriptome, phytosiderophore biosynthesis, methionine cycle, antioxidant enzymes, transporters, miRNAs

11548-S2-O5

Molecular interplay between SARS-CoV-2 and Human proteins for viral activation and entry, potential drugs and scope for new therapeutics

Naveen Vankadari[1*]

[1]Monash Biomedicine Discovery Institute and Department of Biochemistry and Molecular Biology, Monash University, Victoria 3800, Australia.

Abstract

The pandemic Coronavirus Disease 2019 (COVID19) caused by SARS-CoV-2 is a serious public health concern with global mortality reaching 1 million. Whilst the search for a vaccine is underway, there a several antiviral and antibody treatment being clinically evaluated to fill the "therapeutic gap". The development of potential drugs requires an understanding of SARS-CoV-2 pathogenicity and mechanism of action. Thus, it is essential to understand the full repertoire of viral proteins and their interplay with host factors. Here, we show how the SARS-CoV-2 spike protein undergoes 3 stages of processing to allow virion activation and host cell infection. We also conduct pre-clinical and cohort studies and found effective viral clearance by Arborol drug treatment inpatients. Our comprehensive structural studies reveal why COVID19 is hypervirulent and the reason for the failure of several antibody treatments to date. We demonstrate via molecular dynamics and functional studies how the host proteins CD26, Furin and TMPRSS2 process the viral spike glycoprotein and assist in the viral entry in addition to ACE2. These results cognize the detailed mechanism of spike glycoprotein and reveal new avenues for potential therapeutics to block different stages of viral entry and new pathways for vaccine development.

11014-S3-O1

Evidence of metabolic competition between methionine and glutathione biosynthetic pathways

Rachel Amir[1,2 *], Yael Hacham[1,2]

[1]Migal-Galilee Research Institute, Israel

[2]Tel Hai College, Israel

Abstract:

Cysteine, the first organic sulphur-containing metabolite, serves as a precursor for the synthesis of glutathione and methionine, two metabolites that are central to plant growth and survival. Glutathione plays a crucial role in the defence against a diverse environmental stresses due to its antioxidant function, while methionine is a protein constituent, and through its first metabolite, *S*-adenosylmethionine, regulates essential processes required for plant growth. To reveal the relations between glutathione and methionine, we used tobacco plants overexpressing the regulatory enzyme of methionine biosynthesis pathway, cystathionine γ-synthase (CGS) (FA plants). FA plants were significantly more sensitive to oxidative stress than wild-type (WT) plants. Measuring the levels of glutathione in WT plants exposed to oxidative stress (6 h of 150 mM H_2O_2) shows that its level significantly increased, while the level of methionine significantly decreased, compared to untreated plants. Such significant differences were not observed in FA plants. Feeding and metabolic profiling analyses indicated the existence of metabolic competition between the biosynthesis pathways of methionine and glutathione on their common precursor, cysteine, and that this competition is more crucial under oxidative conditions. Immunoblot and transcript analyses had shown that the protein expression level of CGS was significantly reduced, unlike its transcript, when the level of glutathione increased in plants. Further studies have shown that glutathione covalently binds CGS and then reduces its stability. This reduction in CGS and thus in the flux towards methionine and its associated metabolites leave more cysteine that required for the synthesis of glutathione during oxidative stress.

11153-S3-O2

Plant agro-biodiversity is a resource for the sustainable development of mountain areas: the case of Italy

Luca Giupponi, Valeria Leoni, Davide Pedrali, Annamaria Giorgi
Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas–CRC Ge.S.Di.Mont., University of Milan, Via Morino 8, 25048 Edolo (BS), Italy

Abstract

The loss of plant agro-biodiversity is a global problem with repercussions on both humans and agro-ecosystems. In the past, there were many more landraces, understood as dynamic populations of cultivated plants that have a historical origin and distinct identity and lack formal crop improvement, as well as often being genetically diverse, locally adapted, and associated with traditional farming systems. Landraces constitute unique genetic resources for genetic crop improvement programs and a source of food diversity available to humans and other living beings. The Food and Agriculture Organization of the United Nations (FAO) estimates that about 75% of global agrobiodiversity has been lost over the last century and that three quarters of food worldwide is produced by only 12 plant species and five animal species. This loss represents a serious problem that has prompted governments at global and local levels to take immediate action. Italy is legislating to counteract the problem of landrace loss by following EU guidelines: with the law of 1st December 2015 n. 194 ("Provisions for the conservation and enhancement of biodiversity of agricultural and food interest"), Italy recognized the principles for the establishment of a national system of conservation and enhancement of biodiversity of agricultural and food interest. This protection system provides for the creation of an Agrobiodiversity National Register which was set up in December 2019. In recent years, researchers from the University of Milan (Ge.S.Di.Mont. Research Centre) have carried out research aimed at implementing the data of this register. Ours research investigated the situation for Italian herbaceous landraces preserved on farms (*in situ*) by merging and analyzing data contained in the main databases on plant agrobiodiversity in Italy. A total of 1615 herbaceous landraces were found: Poaceae, Fabaceae, and Solanaceae together comprise 70% of all herbaceous landraces and are mostly preserved/grown in areas between 150 and 800 m a.s.l. Some hilly and sub-mountain areas of the Apennines and the Alps are hotspots of herbaceous landraces and some of them ("Nero Spinoso" maize, "Grano Siberiano Valtellinese" Tartary buckwheat and "Copafam" bean) were characterized from an agronomic, nutritional/ phytochemical and/or genetic point of view. The results of the analyzes conducted on these landraces will be shown as well as the methods to protect them and promote local and sustainable agri-food chains.

11039-S3-O3

Investigation on the role of phenolic compounds in *Zymoseptoria tritici* -wheat interaction

Mojtaba Emami[1], Amir Mirzadi Gohari*[1], Mohammad Javan-Nikkhah[1], Mohsen Farzaneh[2]

[1] Department of Plant Protection, Faculty of Agriculture Science & Engineering, College of Agriculture & Natural Resources, University of Tehran

[2] Medicinal Plants and Drugs Research Institute, Shahid Beheshti University

Abstract

Zymoseptoria tritici is the causal agent of septoria tritici blotch (STB), a devastating foliar wheat disease worldwide. It is responsible for significant yield losses occurring annually in all main wheat-growing areas and threatens global food security. STB management is mainly achieved through fungicide applications and growing commercial cultivars carrying *Stb* resistance genes. However, the efficacy of both strategies is limited as strains resistant to fungicides frequently develop and progressively dominate natural populations. Therefore, there is a need for discovery research to understand better the molecular basis of the host-pathogen interaction enabling breeders to identify and deploy new *Stb* genes, which will eventually contribute to more sustainable disease control. This study aimed to investigate the phenolic compounds of cv. Shafir carrying the *Stb6* resistance gene once infected by the *Z. tritici* IPO323 containing the AvrStb6 effector. To this aim, wheat seedlings were infected by the applied isolates, and the inoculated leaves were harvested at 2, 4, 8, 12, 16, and 20 days post-inoculation (dpi). Subsequently, the samples were immediately transferred to a -80 freezer, and finally, the harvested samples were crushed and grinned with liquid nitrogen. The quantity of phenolic compounds was measured at the mentioned time courses using a high-performance liquid chromatography (HPLC) device. Our analysis demonstrated that the quantity of phenolic compounds was significantly different between both interactions at $P < 0.001$. We observed an increase in the quantity of phenolic compounds in the incompatible interaction deriving from the infection of cv. Shafir by the *Z. tritici* IPO323 compared to that of compatible one resulting from the infection of cv. Shafir by IPO323*ΔAvrsStb6#33*. We concluded that probably phenolic compounds in *Z. tritici*-wheat interaction play an important role in mediating resistance response against *Z. tritici*.

Keywords: Septoria tritici blotch, wheat, phenolic compounds, Stb6, AvrStb6

11034-S3-O4

Roles of Myosin XI-i in Mitochondrial Movement in *Arabidopsis thaliana* Leaf Mesophyll Cells

Md Sayeedul Islam*[1], Atsuki Onishi[1], Yuuko Miyatake[2], Motoki Tominaga[2], and Shingo Takagi[1]

[1]Department of Biological Sciences, Graduate School of Science, Osaka University, Japan

[2]Department of Biology, Faculty of Education and Integrated Arts and Science, Waseda University, Japan

Corresponding author: islam@bio.sci.osaka-u.ac.jp

Abstract

Mitochondria are one of the most dynamic cell organelles. Using *Arabidopsis thaliana* stably expressing mitochondrion-targeted-GFP, we examined whether mitochondria in leaf mesophyll cells change their intracellular positions under different light conditions. In darkness, mitochondria were distributed almost uniformly throughout the cytoplasm. The pattern of light-dependent redistribution of mitochondria was essentially identical to that of chloroplasts, i.e. mitochondria occupied the periclinal regions under weak blue light (470 nm, 4 μmol $m^{-2}s^{-1}$) and the anticlinal regions under strong blue light (100 μmol $m^{-2}s^{-1}$). Genetic approaches identified phototropin as the photoreceptor involved in blue-light-dependent redistribution of chloroplasts. There are two phototropins in *A. thaliana*, termed phototropin 1 (phot1) and phototropin 2 (phot2). We semi-quantitatively analyzed the mode of movement of individual mitochondria in the outer periclinal region by time-lapse fluorescence microscopy. Within 30 min of weak blue light illumination, mitochondria movement was accelerated, whereas gradually decelerated, resulting in colocalization with chloroplasts. Using phototropin mutants, we demonstrated that phot1 and phot2 were non-redundantly involved in the early acceleration of mitochondrial movement, while phot2 predominantly regulated the late immobilization of mitochondria, causing colocalization with chloroplasts. We were further interested in factors involved in the regulation of mitochondrial movement. Mitochondria move along actin filaments with motor protein myosin. Among the 13 *A. thaliana* myosin XI isoforms, gene knockout studies revealed that myosin XI-k and XI-1 mainly function for mitochondrial movement in leaf cells. These myosin isoforms belong to the medium-velocity group. On the other hand, myosin XI-i is a unique isoform that has very low actin-activated ATPase activity, high affinity for actin filaments, and very low actin-sliding velocity. In darkness, the velocity of mitochondrial movement appeared to be normal in the myosin XI-i mutant, whereas blue-light-induced acceleration of mitochondrial movement was hampered. We also demonstrated the presence of myosin XI-i-GFP in the mitochondrion-enriched fraction prepared from complementary lines as well as the colocalization of myosin XI-i with mitochondria in cultured Alex cells. Considering the unique properties of myosin XI-i, we propose that myosin XI-i works as a "tether" to inhibit the dissociation of mitochondria from actin filaments under blue light, leading to continuous mitochondrial movement driven by the medium-velocity group myosin isoforms.

Keywords: *Arabidopsis thaliana*, Blue light, Phototropin, Mesophyll cell, Mitochondrial movement, Myosin XI.

11460-S3-O5

Some reproductive traits in Central Anatolian Merino sheep under breeder conditions

Mesut Kırbaş[1], Bülent Bülbül[2], Yavuz Kal[1]

[1]Bahri Dağdaş International Agricultural Research Institute, TR42020, Konya, Turkey

[2]Dokuz Eylül University Veterinary Faculty, TR35890, İzmir, Turkey

Abstract

In the presented study, the reproductive characteristics of birth and multiple birth rates, fecundity, fecundity at weaning, litter size and litter size at weaning of 21505 sheep between 2017 and 2020 were investigated in the Project of "Breeding of the Central Anatolian Merino Sheep in Karaman-I (70OAM2011-01)" carried out within the project "Nationwide Genetic Improvement of Small Ruminants in Farm Condition". Statistical analyses were performed by x^2 test for birth and multiple birth rates, and by ANOVA for fecundity, fecundity at weaning, litter size and litter size at weaning. In the study, overall birth and multiple birth rates, fecundity, fecundity at weaning, litter size and litter size at weaning were 86.9%, 28,9%, 1.12, 1.03, 1.29 and 1.19, respectively. In the study, birth rate was 85.3%, 88.0%, 86.8% and 87.5%, multiple birth rate was 26.5%, 30.7%, 32.7% and 26.3%, fecundity was 1.08, 1.14, 1, 15 and 1.11, fecundity at weaning was 0.98, 1.05, 1.07 and 1.02, litter size was 1.27, 1.29, 1.33 and 1.27, and litter size at weaning was 1.14, 1.20, 1.24 and 1.16 in 2017, 2018, 2019 and 2020, respectively. In the study, it was determined that the year effect was significant in terms of all the examined features ($p<0.01$). As a result, it has been concluded that an increase in fertility can be achieved over time with the breeding studies carried out in Central Anatolian Merino sheep, but the effect of the year is important.

Keywords: Central Anatolian Merino, reproductive traits, breeder condition

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11727-S4-O1

Blanching effect on physicochemical and functional properties of flours processed from peeled and unpeeled white‐fleshed sweet potato

Algerian cultivar

Louiza Belkacemi[1,2], Nadia Hamaizi[1]

[1]Higher School of Agriculture of Mostaganem, Bp Mostaganem 27000 Ex Hall de Technologie-Kharrouba, Mostaganem, Algeria

[2] Laboratoire de technologie alimentaire et nutrition, Ex-INES, AbdELhamid Ibn Badis University, Mostaganem.

Abstract

Backgrounds: White sweet potato has high potential for flour production whose using in food preparations depends on its functional characteristics which in turn depend on variety, pretreatment methods and processing steps. This study investigated the effect of unpeeling and blanching on the chemical composition and functional properties of flour produced from white fleshed sweet potato Algerian cultivar; (2) Methods: Sweet potato tubers were divided into two batches: a manually peeled (P) batch and the unpeeled one (U), which were trimmed and soaked in water during 15 min. Each batch was then divided into two equal parts: one part was blanched (B) in water at 100 °C for 5 min, the second part remained non-blanched (NB). All samples were dried at 60 °C during 24 hours. The four flours (FPB, FPNB, FUB, FUNB) were analyzed for proximate composition, polyphenol and tannin content, and functional properties; (3) Results: Flour processed from unpeeling sweet potato exhibited higher ($p<0.001$) lipid (0.75 ± 0.05% and 0.8 ± 0.1% in FUB and FUNB, respectively), fibers (1.29 ± 0.48% and 1.63 ± 0.3% in FUB and FUNB, respectively), polyphenol and tannin content. Blanching decreased significantly polyphenol about 39% and 30% and tannin about 48% and 63%, respectively in unpeeled and peeled blanched SP-based flours. Sweet potato flour has a significant water absorption capacity, especially those processed from unpeeled sweet potato (FUB: 237.10 ± 1.7% and FUNB: 182.70 ± 0.30%). The FUNB demonstrated the highest swelling power (3.49 ± 0.01 g/g). However, the FPB displayed the highest bulk density (0.77 ± 0.0 g/cm^3) and oil absorption capacity (136.2 ± 0.20%); (4) Conclusion: Combination of both unpeeling and blanching resulted in better nutritional and nutraceutical values of sweet potato flour with interesting functional properties for various food products especially those for gluten intolerant consumers.

Keywords: Sweet potato Algerian cultivar; blanching; unpeeling; flour; chemical composition; functional properties.

11098-S4-O2

Can bakery products be tasty, healthy and sustainable? Clues for SMEs (Centered, Bold, Times New Roman, Size 14)

Amélia Delgado[1], Manel Issaoui[2]

1. MED, University of Algarve Edf 8, Campus de Gambelas 8005-139 Faro, Portugal;
2. Lab-NAFS Nutrition - Functional Food & Vascular Health, Faculty of Medicine, University of Monastir, Tunisia

Abstract

Food is more than a daily source for energy and nutrients, also bringing pleasure and playing a central role in social events and traditions. Food habits, once commanded by local features and lifestyles became controlled by marketing machines. Wheat-based bread and bakery became staple foods worldwide, mostly ultra-processed, and blamed for obesity, non-communicable diseases, environmental problems, and the erosion of sustainable food cultures. To tackle such issues, top-down and bottom-up changes are now transforming food systems, driven by SDG-based policies and by consumer's concerns about environmental and health impacts of their lifestyles. Bakery products are illustrative on how deleterious foodstuffs can be and on how market tendencies can be swiftly reverted. We investigated two different approaches to mild processing formulations: one consisting in enriching wheat flour with fruit's zests and/or spices (e.g. fruit processing by-products) and the second approach consisting in testing wheat and carob flour blends. In both cases, we measured technological parameters, performed composition analysis, hedonic studies, and taking environmental aspects into consideration. Our results revealed that the texture of new products was poorer than that of white bread, but formulations well accepted by naïve consumers, were richer in aroma compounds (aldehydes, short-chain fatty acids), minerals and fibres. Simultaneously, we show that the healthier and sustainable breadmaking options preserved higher radical scavenging activity while accumulating less furan derivatives than with white bread. In short, by removing non-sustainable ingredients (as palm derivatives and additives) and adjusting formulations, it is possible to please the consumer, lowering the carbon footprint of bread (namely imported CO_2), decreasing salt and sugar contents, eliminating harmful ingredients and contaminants, and improving health-protective features. Our findings support changes towards healthier and more sustainable foodstuffs by food processors, including small-holders, especially if encouraged by dissemination actions and by green policies, as in the EC, USA and beyond.

Keywords: Sustainable bakery products; bioactive ingredients; nutrient-dense foods; climate action;

11489-S4-O3

Polyphenols of common beans (*Phaseolus vulgaris* L.) as possible compounds for mycotoxin resistance

Ricardo Quesada Grosso, Andrea Irías Mata*, María Viñas Meneses*
Centro para Investigaciones en Granos y Semillas (CIGRAS), Universidad de Costa Rica,
11501-2060, San Pedro, Costa Rica.

Abstract

Mycotoxins are secondary metabolites produced by mycotoxigenic fungi such as *Aspergillus*, *Fusarium* and *Penicillium*. These compounds are toxic to humans and animals and are mainly produced on cereal-grains such as beans, maize, rice, or wheat. The production of toxins depends on many factors including the type of substrate, thus, even when the fungi is present, not always there is a mycotoxin contamination. Based on preliminary experimental results, we have hypothesized that *P. vulgaris* produced some species-specific compounds that inhibits mycotoxin production in some fungi such as *F. verticillioides.* To demonstrate this hypothesis, mycotoxin-free grains were used as substrates to induce the production of toxins by *F. verticillioides.* Grains were inoculated with known quantities of fungal spores in optimal conditions for mycotoxin production (26oC and > 0.98 Aw) for two weeks. Interestingly, even when the fungal growth was similar on each grain (common beans, rice or maize), statistical analysis showed that toxins were not produced when the fungus was cultivated on twelve Costa Rican common bean genotypes, while high concentrations of toxins were produced when maize or rice was employed as substrates. On parallel we have extracted and analysed polyphenols from all common beans genotypes and have observed that some polyphenols are present in common beans but not in rice or maize, meaning that they could be related to the mycotoxin - resistance observed in common beans. Based on the results, we proposed that *P. vulgaris* (common beans) produced some species-specific polyphenols that inhibit mycotoxin production in *F. verticillioides*. This might contribute to develop novel approaches for mycotoxin management, aiming in the future to ensure food security.

Keywords: Polyphenols, Common beans, Mycotoxins, Fusarium

11552-S4-O4

Photoacoustic spectroscopy in the detection of volatile organic compounds with applications in life science

C.M. Achim (Popa)[1], A.M. Bratu[1], M. Bercu[1],

[1]National Institute for Laser Plasma and Radiation Physics, Laser Department, Magurele, Romania

Abstract

Infrared gas spectroscopy is becoming most widely used in many life science applications. In this paper we present a type of trace gas detection system based on a continuous wave (cw) CO_2 laser in combination with photoacoustic spectroscopy. Examples are included to expose the suitability of CO_2 laser system (over the last few years) to monitor in real time gases emission from various dynamic processes in: fruits [1], plants [2] and human respiration [3-7]. Relationships between the photoacoustic signal and gas pressure, laser power and gas concentration were measured and discussed in detail, respectively [1-7]. The combination of photoacoustic spectroscopy and the CO_2 laser has resulted in simple, robust and easy to maintain designs which are giving photoacoustic spectroscopy a competitive advantage over other sensitive techniques [7]. Applications from different field of life sciences demonstrate their potential for laboratory and field experiments, respectively. For detecting a single species, the CO_2 laser remains a powerful source especially in combination with photoacoustic spectroscopy.

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References

[1] C. Popa, M. Petrus, A.M. Bratu, M. Patachia, S. Banita, Optoelectronics and Advanced Materials - Rapid Communications, vol. 11, pp: 262-266 (2017).

[2] C. Popa and M. Petrus, Microchemical Journal, Vol. 134, pp. 390-399, (2017).

[3] C. Popa, M. Petrus, A.M. Bratu, Microchemical Journal 139, DOI 10.1016/j.microc.2018.02.030 (2018).

[4] M. Petrus, A. M. Bratu, C. Popa, Optical and Quantum Electronics, 49:2, doi: 10.1007/s11082-016-0837-y b (2017).

[5] Ana M. Bratu, Mioara Petrus, Cristina Popa, Microchemical Journal, Volume 138, pp. 203- 208, https://doi.org/10.1016/j.microc.2018.01.014 (2018).

[6] D. C. Dumitras, D. C. Dutu, C. Matei, A. M. Magureanu, M. Petrus and C. Popa, Journal of Optoelectronics and Advanced Materials, Vol 9, No. 12, pp: 3655-3701 (2007).

[7] C. Popa, M. Petrus, A. Bratu ", Journal of Biomedical Optics 20(5), 057006 - 057006-8 [DOI: 10.1117/1.JBO.20.5.057006], (2015).

11040-S4-O5

Bioactive molecules and fungal endophytes in table grape berries

CHAMPA WIJEKOON[1], ALI SABRA[1], ZOE QUILL[2]

[1]Agriculture and Agri-Food Canada, Canadian Centre for Agri-Food Research in Health and Medicine, Winnipeg, MB, R2H 2A6. Canada. [2] University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.

Abstract

Grape (*Vitis vinifera*) is a rich source of bioactive molecules including flavonoids, anthocyanins and stilbene compounds. In addition to their nutritive values, these compounds possess antioxidant, antimicrobial, anti-inflammatory, and anticarcinogenic activities and have wide applications in food and nutraceutical industries. Endophytes are systematically distributed asymptomatically in plant tissues such as roots, stems, leaves, seeds and fruits. In the last decade, endophytes have sparked a great deal of interest with their immense diversity and unique features that show potential in being useful tools in agricultural, industrial, and pharmaceutical applications. Interestingly, recent evidence showed few strains of fungal endophytes producing polyphenol compounds in grapes as well. Grape phytochemical and fungal endophyte community studies are more focused on wine grapes whereas documented endophyte research on table grapes are limited. The objective of this study is to show the composition of bioactive phytochemicals and fungal endophytes of table grapes in Winnipeg market to identify their potential interactions. Grape polyphenols were extracted and analyzed using high performance liquid chromatography (HPLC) in cultivars such as Flame, Autumn Royal, Sweet Scarlet and Red Globe. Amplicon ITS (internal transcribed spacer) metagenomics approach was used to profile the fungal communities of the table grape endophyte microbiome. This study showed containing bioactive compounds and fungal endophyte diversity in commercial table grapes found in market. However, further research is needed to develop a deeper understanding of bioactive-endophyte-host relationships and the metabolic contributions given through this exchange.

11117-S5-O1

Managing global pest threats to citrus production

Jawwad A. Qureshi

University of Florida/IFAS, Department of Entomology and Nematology, Southwest, Florida Research and Education Center, Immokalee, FL 34142, USA

Abstract

Citrus is an economically important crop in several regions of the world. It is attacked by a wide range of pests including Asian citrus psyllid, citrus leafminer, thrips, mites, aphids, scales, weevils, etc. However, Asian citrus psyllid (ACP) *Diaphorina citri* is the most serious threat due to its role as a vector of the pathogen responsible to cause huanglongbing (HLB) or citrus greening disease which is established in most citrus-producing regions of the world. Cultural, biological, and chemical methods of pest control using reflective mulches, predators, parasitoids, and insecticides have been shown to reduce ACP populations between 80-100% in the citrus crops grown under the traditional orchard system. However, increased chemical control is resulting in ACP resistance to some important insecticides as well as negative effects on the biological control and environment. The integrated pest management programs have shown promising results against ACP. Additionally, the judicious use of insecticides to target multiple pests helps with reducing the unnecessary use of insecticides. The advanced production systems providing a physical barrier against ACP-HLB colonization such as Citrus Under Protective Screen (CUPS) and Individual Protective Covers (IPCs) have shown promising results and are becoming common. Significant advantages of these advanced systems have been documented to show protection from ACP-HLB and improved plant health and yield. However, the occurrence of other pests is reported from these systems. Successes and challenges from the traditional and advanced systems will be discussed.

11212-S5-O2

Pest status of the invasive Callery pear tree (*Pyrus calleryana* Decne.) in the Unites States, and herbicide options for management and control

James T. Vogt[1] and David R. Coyle[2]

[1]US Department of Agriculture, Forest Service, Southern Research Station, Athens, GA, USA

[2]Forest Health and Invasive Species, Clemson University, Department of Forestry and Environmental Conservation, Clemson, SC, USA

Abstract

Early transcontinental movement of plants for horticulture and new sources of plant material for forage, food, and industry have resulted in several benign or beneficial introductions around the globe. Some species, however, have become invasive and economically and ecologically detrimental. The history of Callery pear (*Pyrus calleryana* Decne.) in the United States began in the early 1900s when Frank N. Meyer, plant explorer with the US Department of Agriculture, brought seeds from China into the US in an effort to find germplasm to improve fire blight resistance in commercial European pear (*Pyrus communis* L.). Additional introductions ensued over the years. The original Callery pear selection is self-incompatible; however, additional *Pyrus* species or cultivars can cross-pollinate and produce viable seed, with the resulting progeny forming sexually reproducing populations. Grafting can also result in viable seed if the rootstock is allowed to sprout, flower, and cross-pollinate with the scion. Over 25 cultivars of Callery pear have been developed and released in the US since the initial introduction; wherever these cultivars are able to cross-pollinate wild progeny may then be available to spread across the landscape. Callery pear is now present throughout the entire eastern US (with the exception of Maine and Vermont), much of the central US, and Colorado, Utah, Idaho and California. It began attracting the attention of researchers and forest health specialists in the 1990s, when wild populations became apparent along roadsides and in abandoned fields. Since then it has been noted as a concern in production forestry areas, longleaf pine restoration stands, and naturally regenerating pine stands. Callery pear exhibits reproductive plasticity, sprouting from underground tissue when cut or top-killed by fire. It produces large numbers of fruits which contribute to bird- and mammal-mediated spread. Evidence is mounting to indicate that Callery pear is an effective ecosystem engineer. Problems associated with Callery pear include outcompeting and shading out understory plants (with potential direct and indirect effects on pollinators and other arthropods), and interference with management operations due to the large, strong thorns present on many wild individuals. In this presentation we review the global distribution of Callery pear, its pest status in the US, efficacy of commonly available herbicides for control of smaller trees and shrubs (< 7.6 cm diameter at breast height), and preliminary data on herbicide efficacy for management of larger trees (> 7.6 cm diameter at breast height) using cut-stump, hack-and-squirt, and soil applications.

11739-S5-O3

A novel Polysaccharide ECS66A From *Streptomyces mauvecolor* triggers plant defense against Black Shank of Tobacco

Yubo Sun, Hao Wu, Peibing Geng, Jianjun Hao, Lirong Han*
College of Forestry, Northwest A&F University, Yangling, Shaanxi 712100, China

Abstract

ECS66A is a polysaccharide derived from *Streptomyces mauvecolor* strain HL-66 and potentially suppresses plant pathogens. In this study, we investigated the effect of ECS66A on inhibiting black shank caused by *Phytophthora nicotianae* on tobacco, which is an economically important disease tobacco crop. In vitro tests showed that ECS66A highly inhibited mycelial growth, sporangiogenesis and zoosporogenesis of *P. nicotianae* on agar plates. In vivo tests showed that, when applied to tobacco, ECS66A inhibited *P. nicotianae*, and induced plant resistance against black shank, which was indicated by reduced infection area, significantly increased activities of enzymes related with defense responses and significant growth much more than the non-treated control in fresh weight, dry weight, seedling height and leaf area. The mechanism of ECS66A was studied by examining changes in ultrastructure and respiratory metabolism of *P. nicotianae*. Scanning electron micrographs showed that ECS66A-treated *P. nicotianae* mycelia were swollen with excessive branching. Observation of transmission electron microscopy and detection for enzymatic activities showed that ECS66A reduced the content of cell soluble protein, destroyed cell membrane, and affected mitochondria and metabolism enzymes of NAD-MDHase and ATPase of *P. nicotianae.* Thus, ECS66A had combined mechanisms of producing antimicrobial activities and producing molecules in inducing plant resistance against tobacco black shank.

Keywords: *Phytophthora nicotianae*, GC-MS, ultrastructure of mycelia, enzymatic activities

11586-S5-O4

Change of vine leaves(*Vitis vinifera* L.) phytoalexin stilbenoids under Downy mildew infection

M.Bezhuashvili[1], L.Bavaresco[2], M.Surguladze[1], L. Tskhvedadze[1], G.Shoshiashvili[1], L.Gagunashvili[1],P.Vashakidze

Abstract

In this work, the variability of phytoalexin stilbenoids in the leaves of Georgian vine grape varieties under the condition downy mildew infection was studied. It is investigated healthy and downy mildew -diseased vine leaves stilbenoids of Rkatsiteli (white), Saperavi (red) and Tsolikouri (white) vine variety in eastern (kakheti region) and western(Racha-Lechkhumi) part of Georgia. Healthy and naturally diseased leaves of Tsolikouri are harvested from a 10-year vineyard cultivated on Brown Forest Acid type of soil. Healthy and infected leaves of Rkatsiteli are taken from meadow cinnamonic type of soil and from 40 year old vineyard. Saperavi is taken from meadow cinnamonic type of soil and from 16 year old vineyard. Stilbenoids containing fractions were isolated from each sample and analyzed by HPLC / MS method. Based on the stilbenoid profiles of healthy and diseased vine leaves, the variability of physiological concentrations of individual stylbenoids have been established and the stress-metabolite stilbenoids have been identified. The obtained results are an important data for determining the correlation of immunity for the vine varieties with fungal diseases against phytoalexin stilbenoids.

Key words: vine, stilbenoids, phytoalexins, downy mildew

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11444-S6-O1

Protein interaction research with dedicated biosensors using Blitz technology

Maciej Prusinowski[1], Żebrowska Joanna[1], Krefft Daria[1], Ponikowska Małgorzata[1], Prusinowska Marta[1], Klaudia Jędryś, Natalia Górecka, Piotr Skowron

[1]Department of Molecular Biotechnology, University of Gdansk, Gdansk 80-309, Poland

E-mail of the corresponding author: maciej.prusinowski@ug.edu.pl

Abstract

Proteins perform very important and diverse functions. They are major compounds in most of cellular processes. Whereas their functions often depend on interactions with other proteins or different molecules. Therefore, the development of accurate methods of studying these interactions in cells is extremely important. We present results series of the kinetic mesurements of recombinant proteins interactions with selected molecules and biomolecules. Kinetic measurements of protein-ligand interactions have made by using the Label-free Assays in a Drop technique using the Blitz® apparatus from ForteBio. The main advantages characterizing the selected technique is the possibility of real-time measurements, a wide range of measurements, without the use of dangerous labels such as radioisotopes, only 4 µl of the sample is sufficient for measurements, and the possibility of analysing various interactions, including protein-protein, protein-antibody guaranteed by using specialized biosensors. For the measurements were used recombinant proteins, which were overexpressed in *Escherichia coli* expression system after designed, codon-optimized and expressed synthetic genes. The proteins were purified by affinity chromatography methods. Obtained proteins showing the selective properties of interactions with different biomolecules. One of this proteins is the hTRF1 from the Shelterin complex, which binding to telomeric DNA. In the kinetic interactions between protein-DNA were used a linear DNA fragment of 165 bp containing 2 telomeric repeats. Because all of obtained proteins had a His tag, for interaction measurement was used His1k biosensors which are selected to immobilize the proteins on the sensors. The ability of the obtained, recombinant proteins to bind selectively to a specific molecules for example telomeric DNA was confirmed. The rate and affinity constants for binding interactions (k_a, k_d, K_D) were determined.

Keywords: protein interactions, kinetic, biolayer interferometry, binding affinities

11271-S6-O2

Prospects of Milk Protein-Lactoferrin as a Potential Alternative of Natural Antibiotic

Syeda Fahria Hoque Mimmi[1*], Md. Aminul Haque[2]

[1]Department of Mathematics and Natural Sciences, Brac University, Dhaka 1212, Bangladesh

[2]Department of Pharmacy, Brac University, Dhaka 1212, Bangladesh

Abstract

Many new and promising treatments for reducing or diminishing the adverse effects of microorganisms are being discovered day by day. On the other hand, dairy industry is accelerating the economic wheel of Bangladesh. Considering all these facts, new thoughts were developed to isolate milk proteins by the present experiment for opening up a new era of developing natural antibiotics from milk. Lactoferrin, an iron-binding glycoprotein with multifunctional properties is crucial to strengthening the immune system and also useful for commercial applications. The protein's iron-binding capacity makes it undoubtedly advantageous to immune system modulation and different bacterial strains. For fulfilling the purpose of isolating lactoferrin, 4 of raw and 17 of commercially available milk samples were collected from different farms and stores in Bangladesh. Protein quantification by NanoDrop technology has confirmed that raw milk contains higher amount of protein than the commercial ones. Further, SDS-PAGE confirmed the presence of lactoferrin in 5 of the total milk samples. Lactoferrin observed in goat milk and Milk Vita commercial milk was recovered from SDS-PAGE gel and purified using dialysis method. Then the purified lactoferrin was tested for its antimicrobial activity against 18 bacterial strains. Interestingly, *Vibrio cholera, Bacillus cereus, Pseudomonas aeruginosa, Staphylococcus aureus, Klebsiella pneumonia, Enterococcus faecali* and *Streptococcus pneumonia* significantly displayed sensitivity against lactoferrin extracted from aforementioned milk samples. This study suggests that lactoferrin has the potential to be used as an alternative of antibiotics for many diseases and also can be used to reduce microbial deterioration in food and feed industry.

Keywords: Natural antibiotics, Lactoferrin, NanoDrop technology, Bacterial strains, SDS-PAGE gel electrophoresis, Dialysis.

11606-S6-O3

Lytic bacteriophage proteins fused with a binding domain as an antimicrobial preparation

Małgorzata Ponikowska[1], Joanna Żebrowska[1], Maciej Prusinowski[1], Daria Krefft[1], Piotr Skowron[1]
[1]Department of Molecular Biotechnology, Faculty of Chemistry, University of Gdańsk, Gdańsk 80-309, Poland

Abstract

Background: Increasing antibiotic resistance and emergence of multidrug resistant bacterial strains challenge pharmaceutical industry worldwide to search for new treatment options of wound infections. Endolysins are enzymes naturally found in bacteriophages and they play key role in degradation of the peptidoglycan wall in host bacteria. Endolysin TP84_28 is such a protein produced in a lytic cycle of thermophilic TP-84 bacteriophage. It could be used to fight against bacteria resistant to antibiotics, however, it is a challenge to produce a formulation keeping the protein stable and enzymatically active at a wound site. A fusion protein consisting of the endolysin and a binding domain of a fusion partner protein could be a promising compilation of antimicrobial activity of an endolysin and ability to adhere to medical dressings via a binding domain.

Methods: DNA encoding TP84_28 endolysin was obtained from original TP-84 bacteriophage using PCR with mutagenic starters. The starters introduced restriction sites for restriction endonucleases to allow for directional cloning, inserting the endolysin-coding gene into a plasmid between its binding domain gene and a sequence encoding for His^_tag. *Escherichia coli* was then transformed with the recombinant plasmid DNA, cultivated and subsequently plasmid DNA was isolated and transformed into expression strain *Escherichia coli* BL(DE3) Gold. Protein overproduction was achieved through cultivation of the bacteria and stimulating gene expression through IPTG induction. Protein purification was performed using Ni-NTA affinity media. Diffusion assay with host of TP-84 bacteriophage - *Geobacillus steratothermophilus* was used to test the enzyme activity.

Results: Fusion TP84_28_His protein overproduction was efficient: in SDS-PAGE electrophoresis a overproduced band of expected size was clearly visible after IPTG induction of gene expression from T7-lac promoter. Purification on Ni-NTA media allows isolation of the recombinant protein. Diffusion test proves the enzyme activity on the host bacterium, *Geobacillus stearothermophilus* and other Gram positive bacteria from *Bacillus* family.

Conclusions: Fusion TP84_28_His protein is an interesting candidate to be combined with medical dressings.

Keywords: lytic protein, endolysin, antimicrobial activity

11343-S6-O4

Towards biohydrogen production: high-throughput cloning methods for robust hydrogenase biosynthesis

Malgorzata Witkowska[1], Piotr Skowron[1], Agnieszka Zylicz-Stachula[1]

[1]Dept. of Molecular Biotechnology, Faculty of Chemistry, University of Gdansk, Wita Stwosza 63, 80-308 Gdansk 80-308, Poland

Abstract

Hydrogenases (H2ases) are abundant in all different kingdoms of life and can be found in a vast array of environments: from hydrothermal vents to the human gut. Even though hydrogenases were first described in the early 1930s, their maturation mechanism and catalytic pathways are still widely disputed. Very few of these enzymes were successfully produced in easy to handle, accessible organisms. This is due to the complicated structure of H2ases, which includes several inorganic ligands, as well as Fe-S clusters and metal ions in the active center. Another drawback is their vulnerability to oxygen species, causing partial or irreversible inactivation of the active site. To exploit the potential of H2ases, it is necessary to design a fast and easy method of robust, active enzyme production. Here, we describe the employment of high-throughput cloning methods for the efficient production of recombinant *Dmb* hydrogenase. This H2ase is originally derived from a strict anaerobe *Desulfomicrobium baculatum* and was never produced as an enzymatically active recombinant enzyme. By determining the minimal H2ase operon, remodelling of operon layouts, and site-directed mutagenesis, we have developed a recombinant *Dmb* construct suitable for an *E. coli* expression system. We have also performed successful site-directed mutagenesis to alter selenocysteine to cysteine in the active site of the enzyme. This exchange allows the smooth translation in *E. coli* while preserving enzyme activity. The resulting proteins were purified as soluble multimers displaying an activity towards hydrogen evolution even in semi-anaerobic conditions.

Keywords: hydrogenase, high-throughput cloning, biohydrogen, metalloenzymes

11187-S7-O5

Microplastics and mesoplastics in commercial fish from Kota Kinabalu, Malaysia

Peiru Gao[a], Nor Qhairul Izzren Mohd Noor[a] and Sharifudin Md. Shaarani[b]

[a]Faculty of Food Science and Nutrition, Universiti Malaysia Sabah, Jalan UMS, 88400 Kota Kinabalu, Sabah, Malaysia;

[b]Food Biotechnology Programme, Faculty of Science and Technology, Universiti Sains Islam Malaysia, Nilai, Negeri Sembilan, Malaysia

dn1911002a@student.ums.edu.my

Abstract

Plastic pollution in marine environment becomes a hot issue of global concern. In the present study, plastic pollution was investigated using a microscope with 40-100 magnification in 4 marine fish species (*Epinephelus coioides, Atule mate, Nemipterus bipunctatus, Priacanthus macracanthus*) which are the most consumable fish in Kota Kinabalu, Malaysia. A total of 25 plastic particles, including 23 pieces of microplastics and 2 pieces of mesoplastics, were found in all fish samples with an occurrence rate of 83.33% within 10 of the total 12 individuals. Microplastics were detected in all of fish species and two fish species (*Atule mate* and *Priacanthus macracanthus*) were found to ingest mesoplastics. The abundance of plastics ranged from 1.33 – 2.67 items individual^{-1}, with an average of 2.08 ± 0.69 items individual^{-1}. There was no significant difference in the content of plastics among different species and between the gill and gastrointestinal tract (GIT) of fish. The plastics were dominated by fiber in morphotype and black in colour. Overall, in this study, plastic pollution was widespread in gill and GIT of marine commercial fish samples, and detection should be further explored to better understand the situation of plastic pollution in fish.

Keywords: Microplastic; Commercial fish; Ingestion

11289-S7-O6

Description of included systematic reviews on isolated compounds on the anti-trichomonas activities of medicinal plants

Faham Khamesipour[1*], Parya Kheyri[2]

[1]Shahid Beheshti University of Medical Sciences, Tehran, Iran

[2]Young Researchers and Elite Club, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran

Abstract

The parasitic diseases represent the most important health risk, especially in underdeveloped countries where they have a deep impact on public health. Trichomoniasis is a prevalent non-viral sexually transmitted disease, and a significant number of new cases are identified each year globally. Furthermore, the infection is linked with serious concerns such as pregnancy outcomes, infertility, predisposition to cervical and prostate cancer, and increased transmission and acquisition of HIV. The therapy is restricted, adverse effects are often observed, and resistance to the drugs is emerging. Based on this, a new treatment for trichomoniasis is necessary. Natural products represent a rich source of bioactive compounds, and even today, they are used in the search for new drugs. Additionally, natural products provide a wide variety of leadership structures that can be used by the pharmaceutical industry as a template in the development of new drugs that are more effective and have fewer or no undesirable side effects compared to current treatments. This review focuses on the medicinal plants that possess anti-trichomonal activity *in vitro* or *in vivo*. An electronic database search was carried out covering the last three decades, i.e., 1990–2020. The literature search revealed that almost a dozen isolated phytoconstituents are being explored globally for their anti-trichomonal activity. Simultaneously, many countries have their own traditional or folk medicine for trichomoniasis that utilizes their native plants, as a whole, or even extracts. This review focuses mainly on the human parasite *Trichomonas vaginalis*. However, at some points mention is also made to *Tritrichomonas foetus* that causes trichomoniasis in animals of high veterinary and economical interest. We will focus on the plants and plant-based compounds and their anti-trichomonal activity. The literature search highlighted that there are abundant compounds that possess anti-trichomonal activity; however, in-depth *in-vivo* evaluation of compounds and their clinical evaluation has not been undertaken. There is a critical need for new anti-trichomonal compounds, and focused research on phytoconstituents can provide the way forward.

Keywords: Trichomoniasis, Anti- *trichomonas* activity, Medicinal plants, Natural products, Compounds

11554-S7-O7

Fungal species as rock phosphate solubilizing agents to use as biofertilizers

A.A.A.U. Aberathna[1], D.A. Satharasinghe[2], A.P. Jayasooriya[2], R.N. Jinadasa[3], Manopriya S.[1], B.P.A. Jayaweera[1], W.A.D.V. Weerathilake[1], G.A. Prathapasinghe[1], C.A.N. Fernando[4], J.A. Liyanage[5] and J.M.K.J.K. Premarathne[1]

[1] Department of Livestock and Avian Sciences, Faculty of Livestock, Fisheries and Nutrition, Wayamba University of Sri Lanka, Makandura, Gonawila,60170, Sri Lanka.

[2] Department of Basic Veterinary Sciences, Faculty of Veterinary Medicine and Animal Science, University of Peradeniya, Peradeniya, 20400, Sri Lanka.

[3]Department of Veterinary Pathobiology, University of Peradeniya, 20400, Sri Lanka.

[4] Department of Nano Science Technology, Faculty of Technology, Wayamba University of Sri Lanka, 60200, Kuliyapitiya, Sri Lanka.

[5]Department of Chemistry, Faculty of Science, University of Kelaniya, 11600, Sri Lanka.

Abstract

Phosphorus (P) is the second most required nutrient of plants, which frequently provides for crops through fertilizers. Nevertheless, the bioavailability of phosphate is relatively low and the cost for phosphate fertilizers is high relative to the harvest. Natural phosphate deposits are the source of P, which cannot be renewable. The largest phosphate deposit in Sri Lanka, located at Eppawala is underutilized due to low solubility of phosphate. Phosphate solubilizing fungus (PSF) plays an important role in plant nutrition through the increase in phosphate uptake by plants. This study was conducted to isolate PSF species in North Central province in Sri Lanka and evaluate the phosphate solubilizing ability. Two fungal species were isolated using National Botanical Research Institute's Phosphate (NBRIP) growth media containing insoluble calcium phosphate. The key feature to identify PSF is forming clear halo zones around the fungal growth. Morphological identification confirms the PSF as *Aspergillus sp.* and *Fusarium sp.* Quantitative evaluation of phosphate solubilizing ability of fungi was done by using UV visual spectrophotometer according to the molybdenum blue method. Three replicates were used for each control and inoculated samples. None inoculated control sample of High graded Eppawala Rock Phosphate (HERP) reported 2.82% phosphate solubilization while samples inoculated with *Aspergillus sp.* and *Fusarium sp.* reported 4.93% and 5.57% phosphate solubilization, respectively. This potential of PSF can be used to formulate biofertilizers.

Keywords: *Aspergillus, Fusarium,* Phosphate, Solubilization, Eppawala

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11650-S7-O8

Recognizing Zucchinis Intercropped with Sunflowers in UAV Visible Images Using an Improved Method Based on OCRNet

Shenjin Huang [1,2], Wenting Han [1,2,3,*], Haipeng Chen [1,2], Guang Li [1,2] and Jiandong Tang [4]

1. College of Mechanical and Electronic Engineering, Northwest A&F University, Xianyang 712100, China; 2. Key Laboratory of Agricultural Internet of Things, Ministry of Agriculture, Yangling 712100, China; 3. Institute of Soil and Water Conservation, Northwest A&F University, Yangling 712100, China; 4. College of Water Resources and Architectural Engineering, Northwest A&F University, Yangling 712100, China

Abstract

An improved semantic segmentation method based on object contextual representations network (OCRNet) is proposed to accurately identify zucchinis intercropped with sunflowers from un-manned aerial vehicle (UAV) visible images taken over Hetao Irrigation District, Inner Mongolia, China. The proposed method improves on the performance of OCRNet in two respects. First, based on the object region context extraction structure of the OCRNet, a branch that uses the channel attention module was added in parallel to rationally use channel feature maps with different weights and reduce the noise of invalid channel features. Secondly, Lovász-Softmax loss was in-troduced to improve the accuracy of the object region representation in the OCRNet and optimize the final segmentation result at the object level. We compared the proposed method with extant advanced semantic segmentation methods (PSPNet, DeepLabV3+, DNLNet, and OCRNet) in two test areas to test its effectiveness. The results showed that the proposed method achieved the best semantic segmentation effect in the two test areas. More specifically, our method performed better in processing image details, segmenting field edges, and identifying intercropping fields. The proposed method has significant advantages for crop classification and intercropping recognition based on UAV visible images, and these advantages are more substantive in object-level evaluation metrics (mIoU and intercropping IoU).

Keywords: intercropping identification; UAV remote sensing; semantic segmentation; OCRNet

11691-S7-O9

Assimilation of LAI Derived from UAV Multispectral Data into the SAFY Model to Estimate Maize Yield

Xingshuo Peng, Wenting Han, Jianyi Ao, Yi Wang

Abstract

In this study, we develop a method to estimate corn yield based on remote sensing data and ground monitoring data under different water treatments. Spatially explicit information on crop yields is essential for farmers and agricultural agencies to make well-informed decisions. One approach to estimate crop yield with remote sensing is data assimilation, which integrates sequential observations of canopy development from remote sensing into model simulations of crop growth processes. We found that leaf area index (LAI) inversion based on unmanned aerial vehicle (UAV) vegetation index has a high accuracy, with R 2 and root mean square error (RMSE) values of 0.877 and 0.609, respectively. Maize yield estimation based on UAV remote sensing data and simple algorithm for yield (SAFY) crop model data assimilation has different yield estimation accuracy under different water treatments. This method can be used to estimate corn yield, where R 2 is 0.855 and RMSE is 692.8kg/ha. Generally, the higher the water stress, the lower the estimation accuracy. Furthermore, we perform the yield estimate mapping at 2 m spatial resolution, which has a higher spatial resolution and accuracy than satellite remote sensing. The great potential of incorporating UAV observations with crop data to monitor crop yield, and improve agricultural management is therefore indicated.

11638-S7-O10

Estimating fractional vegetation cover of maize under water stress from UAV multispectral imagery using machine learning algorithms

Haipeng Chen

College of Mechanical and Electronic Engineering, Northwest A&F University, Yangling, Shaanxi 712100, China

Abstract

Crop water stress is an inevitable and increasing challenge for agriculture. To improve crop water use efficiency, management of water stress and accurate estimation of crop traits were required. Among crop traits used to detect crop growth status and predict yield, fractional vegetation cover (FVC) is of great significance. We conducted studies in a maize field located in Inner Mongolia, China with different irrigation levels during 2018 and 2019 growing seasons. UAV RGB imagery was captured to investigate the effect of image sensors on thresholds obtained by the fixed-threshold method (proposed in our recent study), and to provide reference FVC (FVC_{UAV_R}) for FVC models based on UAV multispectral imagery. Five vegetation indices (VIs), calculated from UAV multispectral imagery, and three regression algorithms (RF: random forest, ANN: artificial neural network, and MLR: multivariate linear regression) were used to build the FVC model suitable for different growing seasons, growth stages, and crop water stress. The results showed that there was a change in thresholds obtained using the fixed- threshold method based on different image sensors, but this change did not make a big difference on the accuracy of FVC_{UAV_R}, with the R^2 difference of 0.01 and the RMSE difference of 0.01. As for the three FVC regression models, RF model was the most suitable model when these models established in 2018 were used to estimate maize FVC in 2019 for different growth stages and water stress. The low estimation accuracy for high FVC levels was the reason why MLR model could not be used in the other maize growing season. This study provides a low cost and easy way to estimate maize FVC and its inter-field variability under various water status in different maize growing seasons or growth stages.

Keywords: Threshold method； Regression algorithms； UAV RGB images； Model suitability； FVC maps

11758-SP1-1

Production and purification of recombinant SARS COV-2 receptor binding domain in different expression system for human IgG/IgM ELISA

Khaled Trabelsi, Dana Ashoor, Ali Nairouz, Sondos Almubayedh, Ahmed Rasmy, Noureddine Ben Khalaf, and Mohamed-Dahmani Fath Allah

Life Science Department, King Fah Chair for Health Biotechnology, College of Graduate Studies, Arabian Gulf University, Manama 26671, Bahrain

Abstract

The outbreak of SARS-CoV-2 (COVID-19) pandemic warranted a large number of multidisciplinary studies focused on the development of medical treatment and vaccines. To understand the immune response to Sars-CoV2 and to detect potential donors for convalescent plasma therapy among patients who developed strong protective immunity against the virus, it is essential to develop efficient serological test to estimate the prevalence of past viral infection, in addition to measure the immune responses in the vaccinated persons in large populations. Toward this end, the commonly used antigen was the receptor-binding domain (RBD) of the spike S1 protein of SARS-CoV2. In this work, we developed the expression of recombinant his-tagged RBD in two expression systems: *Pichia Pastoris* and the mammalian cell line (HEK293). We investigated different culture conditions for each system respectively (Time of induction, concentration of Methanol, Time of harvest) and (Transfection reagent, Amount of DNA, Medium, Time of harvest) to maximize the productivity of the process. The recombinant protein was purified on Ni+ column and collected fractions were analysed by SDS-PAGE, silver stain gels and Western blot. The recombinant RBD produced in *Pichia* showed a diffused band of ~45 kDa compared to the one expressed in HEK293 was around 37kDa. This difference in molecular weight being probably due to the different glycosylation pattern. The two purified recombinant RBDs were evaluated by ELISA,

The protein produced in mammalian cells demonstrate a high reactivity (specificity and sensitivity) compared to that produced in Pichia. We are currently carrying out the validation steps necessary to approve the clinical use of the recombinant SARS-CoV-2 RBD we've produced in HEK293 cells in tracking anti-SARS-C0V-2 humoral immunity.

Keywords: SARS-COV-2 receptor binding domain; Recombinant protein; ELISA test

10970-SP1-2

The Ability of Some Moulds to Degrade Condensed Tannins of *Punica granatum* Fruits.

Souad Akroum[1], Dounya Achwak Chemmam[1].

[1] Molecular and cell biology laboratory. Faculty of natural and life sciences. University of Jijel. BP 98 Ouled Aissa. Jijel 18000. Algeria.

Abstract

(1) Background: Condensed tannins are non-biodegradable polyphenols. They cause malnutrition when they are present in big quantity in alimentation. (2) Methods: In the current study, we tested the ability of moulds to degrade condensed tannins extracted from *Punica granatum*. So, we extracted and separated these molecules form the peels and seeds of the fruit, than we quantified them and determined their type. In the other hand, we isolated some moulds and identified them; then we tested their ability to degrade hydrolysable and condensed tannase. The tannase activity was measured of the most performing species. (3) Results: The results indicated that the fruits of *Punica granatum* contained principally polymeric tannins and more precisely procyanidins. Thirteen moulds were isolated from the soil surrounded this plant but only two had a tannase that degrade procyanidins. *Trichoderma viride* was the best producer of tannase and had the best enzyme activity, followed by *Aspergillus niger*. (4) Conclusions: *Trichoderma viride* and *Aspergillus niger* could be used to produced tannase and reduce the problem of malnutrition caused by condensed tannins.

Keywords: *Punica granatum*, condensed tannins, quantification, moulds, tannase activity.

11500-SP1-3

Enzymes of the Antioxidant Support Network in Cows During Pregnancy Formation

Vladimir Safonov[1a]

[1]Voronezh State Agrarian University named after Emperor Peter the Great, 394087, Russia, Voronezh, Michurina str.1

Abstract.

Changes in the physiological state of the body can, as it is known, lead to an increase in the intensity of free-radical oxidation. In this investigation, we studied the indicators of the oxidant-antioxidant status of black-and-white cows kept in the conditions of the Druzhba stud farm in Voronezh region of Russia, during the formation and development of pregnancy. The content of malondialdehyde (MDA), the activity of superoxide dismutase (SOD), catalase, glutathione peroxidase (GPO), glutathione reductase (GR), the content of vitamin E and A, carotene, stable metabolites of nitric oxide and S-nitrosothiols were determined in blood samples of non-pregnant cows and cows at 2, 5, 8.5 months of pregnancy. It was revealed that the intensity of free-radical oxidation processes increases with the development of pregnancy in cows, as evidenced by an increase in the concentration of MDA by 83.0%, the activity of glutathione peroxidase – by 68.1%, glutathione reductase – by 22.9%, superoxide dismutase – by 63.9%, catalase – by 49.4% in comparison with the value in non-pregnant cows. The number of stable nitrogen metabolites (NO 2+NO 3) increases by 3.0 times amid the decomposition of S-nitrosothiols, the number of which decreases by 20.9% by the end of pregnancy.

11671-SP1-4

An optimized ultrasound-based protein determination in maize seeds

Laura Darie Ion[1], Monica Iavorschi[2], Ancuta Veronica Lupaescu[2], Marius Zaharia[3], Brindusa Alina Petre[1,4]

[1]Chemistry Department, Faculty of Chemistry, Alexandru Ioan Cuza University of Iasi, Iasi, Romania;

[2]Faculty of Medicine and Biological Sciences, "Stefan cel Mare" University, Suceava, Romania

[3]Petru Poni Institute of Macromolecular Chemistry, Iasi, Romania

[3]Regional Institute of Oncology, Center for Fundamental Research and Experimental Development in Translation Medicine – TRANSCEND, Iasi, Romania;

Abstract

Zein proteins belong to the prolamin class proteins from maize which represent more than 60% of the total endosperm protein. Zeins are classified into four different zein structures (α, β, γ, δ) based on their molecular weight, sequence and solubility. The lysine and tryptophan content of the primary maize seed storage proteins, zeins, contributes to corn's poor nutritional quality. As a result, we provide an innovative and novel procedure that involves sequential grinding and sifting of corn seeds to produce several maize flours with variable chemical compositions and protein concentrations depending on particle hardness. Moreover, zeins extracted from corn have a wide range of applications, including: (i) refining food products such as candies and nuts; (ii) microspheres filled with pesticides are made from zein proteins for controlled release of biologically active substances to provide a safer working environment or (iii) “zein films” are used as a controlled release matrix of active components such as salicylic acid and lysozyme. Furthermore, zein proteins greatest distinguishing feature is their insolubility in water and strong solubility in aqueous high-percentage alcoholic solutions, such as 65 to 95 % ethanol. The consistency of the "zein product" varies significantly due to the vast genetic polymorphism of the starting material and the extraction conditions, therefore, analysis of protein compositions in biological samples of high complexity necessitates a combination of the most recent and modern analytical methods, such as SDS-PAGE electrophoresis, and mass spectrometry. In this report, we've looked into zein extraction from dry-ground whole corn and meals with various grain sizes utilizing 65 and 95 % aqueous ethanol under ultrasonic conditions. UV-Vis spectrophotometry was used to determine the protein concentration and the extracted zein was characterized by mass spectrometry, electrophoresis and FT-IR spectroscopy. Our results show a high yield in zein extraction using eco-friendly solvent in comparison with previous reports in the literature.

Keywords: zein, ultrasound, extraction, SDS-PAGE electrophoresis, FT-IR spectroscopy

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11206-SP1-5

Biomicropolymers as a new therapeutic protein delivery system

Joanna Żebrowska[1], Daria Krefft[1], Maciej Prusinowski[1], Małgorzata Ponikowska[1], Piotr Skowron[1]
[1]University of Gdansk, Faculty of Chemistry, Department of Molecular Biotechnology, Gdansk 80-309, Poland

Abstract

Nanotechnology is the new interdisciplinary a department of science and technology dealing with design and the formation of structures called nanoparticles, which the size is in the range 5-100 nm. It belongs to one of the most popular fields of science today and its development is of great importance in pharmacy and medicine. The binding domain (BD) is useful in developing unique products based on bio-immobilization of biologically active molecules to biomicropolymers. Applications of BD technology include: BD-fusion vectors for production and isolation of different recombinant BD-fusion proteins such as enzymes, hormones, growth factors vaccines and antibodies. The extremely low non-specific protein binding to matrices, together with the novel BD-technology enable us to develop sensitive diagnostic tools. We designed the appropriate vectors from the binding domain, which we intended for cloning in the appropriate places of genes encoding proteins with therapeutic effect. Thus, the obtained new plasmid constructs were used for gene expression in the *Escherichia coli* system. The fusion protein was biosynthesized and purified using the NiNTA resin. The nanoparticles of the new carrier biopolymer were prepared to study the interaction with the obtained fusion proteins. The interaction between the biomolecules was investigated with the Blitz analyzer and by scanning and transmission microscopy. We obtained pure fusion proteins, which we combined with a biomaterial as a protein carrier. It turned out that washing with the detergent buffer the matrix with the attached proteins still retains its structure and therapeutic properties. The results clearly show that the preparation we have created is an ideal matrix for the attachment of proteins with different biological properties on one surface.

Keywords: biomolecules interactions, biomicropolymers, Blitz analysis,

11725-SP1-6

Bioremediation of soil contaminated with creosote oil PAHs enhanced with *Mucor racemosus* enzymatic preparation

Olga Marchut-Mikołajczyk[1], Piotr Drożdżyński[1], Katarzyna Struszczyk-Świta[1]
[1]Institute of Molecular and Industrial Biotechnology, Faculty of Biotechnology and Food Sciences, Lodz University of Technology, Stefanowskiego 2/22, 90-537, Lodz, Poland

Abstract

One of the main strategies of contamination elimination is bioremediation. The technology uses degradative abilities of some microorganisms (mainly bacteria) to decompose hydrocarbons. Hydrocarbons, including polyaromatic hydrocarbons (PAH), are toxic, mutagenic, teratogenic and cancerogenic, and due to that fact, it is crucial to remove them from the environment as soon as it is possible.

During few past years the attention of the scientists is focused on the solutions that will greatly intensify purification of the environment. It is possible due to application of enzymes, mainly hydrolases and oxidoreductases, which are involved in decomposition of xenobiotics in nature. The aim of the research was the development of technology supporting the microbial degradation of aromatic hydrocarbons with the use of the multi-enzyme preparation *Mucor racemosus*. Optimal conditions for the cultivation of the *Mucor racemosus* mold were developed, the mycelium of which, after being washed with the hexane:acetone mixture (3: 1) thrice, became a multienzyme biopreparation immobilized in mycelium. The obtained multi-enzymatic preparation was used to conduct bioremediation of soil contaminated with age-old polycyclic aromatic hydrocarbons at the premises of Nasycalnia Podkładów S.A. in Koźmin Wielkopolski, Poland. It was found that the use of the preparation at a concentration of 0.3-0.6 g / kg of pollutant is the most effective concentration, at which the efficiency of the process was increased by over 20-60%. Moreover, application of that preparation reduces significantly time of the purification process.

The technology may be applied not only for bioremediation of old-aged PAHs, but many others hydrocarbons and organic compounds.

Keywords: *Mucor racemosus,* mulit-enzymatic biopreparation, biodegradation, PAHs, bioremediation

Acknowledgement: This research was funded by grant No POIR.04.01.02-00-0057/17-00 “Modern technology of bioremediation of soils contaminated with creosote oil in the area of Nasycalnia Podkładów Spółka Akcyjna in Koźmin Wielkopolski” (“Nowoczesna technologia bioremediacji gruntów zanieczyszczonych olejem kreozotowym na terenie Nasycalni Podkładów Spółka Akcyjna w Koźminie Wielkopolskim (BIOREM)”) of the National Centre for Research and Development, Poland

11726-SP1-7.

Biodegradation of creosote oil in the soil environment with the use of immobilized cells of *Bjerkandera adusta* DSM no. 3375

Katarzyna Struszczyk-Świta, Piotr Drożdżyński, Olga Marchut-Mikołajczyk
Institute of Molecular and Industrial Biotechnology, Faculty of Biotechnology and Food Sciences, Lodz University of Technology, Stefanowskiego 2/22, 90-537, Lodz Poland

Abstract

Creosote oil is a product of coal distillation and consists mainly of aromatic compounds, including polycyclic aromatic hydrocarbons and phenolic compounds, as well as N-, S- and O-heterocyclic compounds. It is a highly toxic substance and its presence in the environment is undesirable. Creosote is widely used as a wood preservative, especially for railway sleepers, power line poles, ship hulls to prevent rotting. Its fungicidal, insecticidal and sporicidal properties are used. One of the European plants dealing with the protection of railway sleepers with creosote oil is the Nasycalnia Podkładów Kolejowych in Koźmin Wielkopolski, located in Poland. The soil on the site has been heavily contaminated with this toxic substance. As part of the conducted experiments, a preparation of *Bjerkandera adusta* DSM no. 3375 mycelium immobilized in polyurethane foam (PUF) was obtained. It contained mold cells in the amount of 0.613 ± 0.065 g (DW)/g carrier. These enzymes preparation was used in the bioremediation process of soil (moisture content 20% w/w) contaminated with creosote oil (2% w/w). 10 g (WW) of PUF-immobilized mycelim was introduced per 1 kg of soil. The effectiveness of this process was measured by determining the loss of creosote in soil samples (oil extraction using the Soxhlet method) after 5 weeks. The obtained results confirmed that the use of PUF-immobilized mycelium of *B. adusta* DSM no. 3375 allows the removal of 31% (w/w) creosote oil from the soil.

Keywords: *Bjerkandera adusta*, creosote oil, bioremediation

Acknowledgement: This research was funded by grant No POIR.04.01.02-00-0057/17-00 "Modern technology of bioremediation of soils contaminated with creosote oil in the area of Nasycalnia Podkładów Spółka Akcyjna in Koźmin Wielkopolski" ("Nowoczesna technologia bioremediacji gruntów zanieczyszczonych olejem kreozotowym na terenie Nasycalni Podkładów Spółka Akcyjna w Koźminie Wielkopolskim (BIOREM)") of the National Centre for Research and Development, Poland.

11216-SP1-9.

"All-in-one" gel system for whole procedure of stem cell amplification and tissue engineering

Qiulin He[1,2,3], Youguo Liao[2,3,6], Jingwei Zhang[2,3], Xudong Yao[1,2,3], Wenyan Zhou[1.2.3], Yi hong[*1,2,3], Hongwei Ouyang[*1,2,3,4,5]

1. Department of Orthopaedic Surgery, Second Affiliated Hospital & Zhejiang University-University of Edinburgh Institute & School of Basic Medicine, Zhejiang University School of Medicine, Hangzhou 310058, China.

2. Dr. Li Dak Sum & Yip Yio Chin Center for Stem Cells and Regenerative Medicine, Zhejiang University School of Medicine, Hangzhou 310058, China.

3. Key Laboratory of Tissue Engineering and Regenerative Medicine of Zhejiang Province, Zhejiang University School of Medicine, Hangzhou 310058, China.

4. Department of Sports Medicine, Zhejiang University School of Medicine, Hangzhou 310058, China.

5. China Orthopedic Regenerative Medicine Group (CORMed), China.

6. Guangxi Collaborative Innovation Center for Biomedicine, Guangxi Medical University, Nanning 530021, China.

Abstract

Gel Microsphere (MS)-based system provides great advantages for cell expansion and transplantation due to high surface to volume ratio and biomimetic environment. However, a MS-based system includes cell attachment, proliferation, passage, harvest, cryopreservation and tissue engineering all in one MS has not been realized yet. Herein, an "all-in-one" gel MS-based system is established for human adipose-derived mesenchymal stem cells (hADSCs), realizing real 3D culture with enhanced expansion efficiency and simplified serial cell culture operations, as well as construction of macro-tissues with uniform cell distribution and specific function. A 3D digital light processing (DLP) technology is developed to fabricate gel MSs in an effective way. The printed MSs present suitable environment with rough surface architecture and soft tissues' mechanical property, leading to high cell viability, attachment, proliferation, activity and differentiation potential. Further, convenient standard operation procedures, including cell passage, detachment and cryopreservation, are established for cell culture on the gel MSs. At last, hADSCs-loaded gel MSs form macro-tissues through a "bottom-up" approach, which demonstrates the potential applications for tissue engineering. The findings exhibit the feasibility and beauty of "all-in-one" stem cell culture and tissue engineering system.

Keywords: microspheres, hydrogel, stem cells, 3D printing

11311-SP1-10.

Biosynthesis and purification of the recombinant major capsid protein derived from TP-84 bacteriophage

Patrycja Laszuk[1], Małgorzata Witkowska[1], Aneta Szymańska[2], Piotr Skowron[1], Agnieszka Żylicz – Stachula[1]

[1]Department of Molecular Biotechnology, University of Gdansk Faculty of Chemistry, Gdansk 80-306, Poland

[2]Department of Biomedical Chemistry, University of Gdansk Faculty of Chemistry, Gdansk 80-306, Poland

Abstract

Many viral structural proteins have self-assembling ability and can form nanostructures, named virus-like particles (VLPs). VLPs resemble native virus particles, but through lack of viral genome they are neither infectious nor able to replicate. VLPs have wide applications in biotechnology and medicine. They are used as elements of the recombinant vaccines or as carriers enabling precise delivery of bioactive molecules. However, to date no such structures have been obtained based on bacteriophage proteins. The purpose of this study was to purify and characterise one of the bacteriophage TP-84 structural proteins, potentially useful for developing thermostable, bacteriophage-derived VLPs.

A bioinformatic analysis of the TP-84 genome was performed to identify a gene, encoding major structural capsid protein. Its DNA sequence was optimized for heterologous gene expression. The designed gene was chemically synthesized, cloned and expressed in *Escherichia coli*. A purification procedure of the recombinant protein was developed, and the protein was purified to homogeneity.

Initial conformation analysis of the recombinant protein was performed by circular dichroism. Stability of the protein at 4 and -80^{o}C was investigated and its melting temperature was established by differential scanning calorimetry (DSC).

The recombinant major capsid protein is soluble and stable during storage. The protein contains several helical structures. No protein aggregation was observed during the purification process. In the future, the resulting protein, along with other TP-84 capsid proteins, will be tested for their ability to form bacteriophage VLPs.

Keywords: virus-like particles, major capsid protein, TP-84 bacteriophage, recombinant gene expression

11335-SP1-11.

A rapid, universal, mini-scale method for the isolation of TP-84 genomic DNA devoid of bacteriophage particles

Anna Struck[1*], Katarzyna Adamowicz [1], Piotr M. Skowron[1], Agnieszka Żylicz-Stachula[1], Ireneusz Sobolewski[1]

[1]Dept. of Molecular Biotechnology, Faculty of Chemistry, University of Gdansk, Wita Stwosza 63, Gdansk 80-308, Poland

Abstract

Thermophilic bacteriophages are a rare object of research but are interesting because of their potential applications in molecular biology. They have been isolated from hot springs, hydrothermal vents, soils near volcanic activity, compost heaps and wastewaters. TP-84 is an example of a thermophilic bacteriophage first isolated in 1952 from greenhouse soil. Its host range is rather narrow – it only infects a few *Geobacillus stearothermophilus* strains.

Our aim is to construct a new phage-display system, based on the thermophilic bacteriophage TP-84, with a potential use in protein engineering, drug discovery and diagnostics. Such a new thermostable phage-display system could be used in the pharmaceutical and medical industry (production of new drugs, vaccines), in the protection of the environment (plant protection products, elimination of pollution) and other applications. The main advantage is that TP-84 is a thermophilic phage, which broadens the potential applications of the system. To construct the phage-display system, the isolation of high-quality genomic DNA from TP-84 phage is necessary for further genetic manipulations. There are several methods for the purification of bacteriophages, such as density gradient ultracentrifugation, pelleting viruses by centrifugation, ultrafiltration, or chromatography.

Our newly designed DNA purification protocol was originally developed for TP-84. However, it can be used for other thermophilic bacteriophages. It enables the fast and efficient isolation of bacteriophage genomic DNA from concentrated phage preparations without the time-consuming removal of concentrated CsCl solutions. The method is universal – different silica mini-columns can be used to conduct the procedure. Purified DNA is ready for further manipulations and is free from infectious bacteriophage particles. This is particularly important for thermophilic phages that can survive standard isolation procedures and contaminate the final product.

Keywords: bacteriophage, TP-84, phage-display, genomic DNA isolation

11645-SP1-12.

HnRNP H/F promote TLR4-mediated inflammatory response by activating NF-KB and MAPK signaling pathway in macrophages

Tao Sun[1], Xiaohua Mao[1,2,*]

[1] School of Life Science and Technology, Southeast University, Nanjing 210096, China

[2] Department of Biochemistry and Molecular Biology, School of Medicine, Southeast University, Nanjing 210009, China

Abstract

(1) Background: Heterogeneous nuclear ribonucleoproteins (hnRNPs) represent a large family of RNA-binding proteins (RBPs) that contribute to multiple aspects of nucleic acid metabolism including alternative splicing, mRNA stabilization, and transcriptional and translational regulation. With further exploration of the biological functions of hnRNP family proteins, multiple hnRNPs (such as hnRNP K, hnRNP U, hnRNP M and hnRNP L) have been confirmed to be involved in the innate immune response. Therefore, we investigated the effect of hnRNP H/F on LPS-induced proinflammatory cytokines production and TLR4 activation in macrophages. (2) Methods: qPCR analysis was used to determine the proinflammatory cytokines mRNA abundance. Firefly luciferase assay was performed to measure the activity of proinflammatory cytokines promoter. Western blotting was carried out to detect the expression of proinflammatory cytokine proteins and the key molecules in NF-κB and MAPK signaling pathways. (3) Results: The knockdown of hnRNP H or/and F significantly decreased TNF and IL-6 mRNA and protein expression in LPS-stimulated mouse peritoneal macrophages. In addition, hnRNP H/F silencing attenuated LPS-induced luciferase activity driven by either *Tnf* or *Il6* promoter, indicating that hnRNP H/F affect proinflammatory cytokine expression at least at the transcriptional level. Consistently, the absence of hnRNP H or F compromised the phosphorylation of IκBα, JNK and p38 in LPS-treated RAW264.7 macrophages. (4) Conclusions: hnRNP H and F promote LPS-induced proinflammatory response in macrophages by upregulating the activation of NF-κB and MAPK signaling pathway.

Keywords: hnRNP H/F, cytokine, TLR4, NF-κB, MAPK

11648-SP1-13.

Metformin alters intestinal flora and ameliorates immune-mediated bone marrow failure in mice

Lu Shuanglong, Zhou Ning, Qiao Xiaohong*

Department of paediatrics, Tongji hospital affiliated to Tongji University, Shanghai (200065) China

Abstract

Background: Metformin is an effective hypoglycaemic drug, which can reduce hepatic glycogen synthesis. However, in addition to its impact on metabolism, its impact on intestinal microorganisms and blood system is still being explored. **Methods**: The intestinal flora of metformin fed mice and conventional fed mice were compared by 16S rRNA sequencing. Then the two groups of mice were irradiated and received allogeneic lymphocyte infusion to construct immune- mediated bone marrow failure. The severities of bone marrow failure were compared by peripheral blood examination and bone marrow pathological examination. **Results**: Metformin feeding changed the α Diversity and β Diversity of intestinal flora in mice, increased the abundance of akkermansia muciniphila in the intestinal flora. Meanwhile, metformin improved the blood cells and ameliorated bone marrow failure in immune-mediated bone marrow failure mice. **Conclusions**: Metformin can increase the diversity of intestinal flora, increase the abundance of beneficial bacteria, and ameliorate immune-mediated bone marrow failure.

Keywords: Metformin, Intestinal microorganism, 16S rRNA sequencing, bone marrow failure.

11649-SP1-14.

A Novel Biodegradable Bone Wax with Antibacterial Property for Bone Hemostasis

Shuaijie Li[1], Chunyu Liu [,2],Xu Cui[2] ,Feng Yuan[1*], Haobo Pan[2*]

[1]Department of orthopedic, Tongji Hospital, School of Medicine, Tongji University, Shanghai, China .

[2]Center for Human Tissues and Organs Degeneration, Shenzhen Institutes of Advanced Technology, Chinese Academy of Science, Shenzhen, China

Abstract

Background: As a material that physically blocks bone capillary bleeding, bone wax is a classical hemostatic agent in orthopedic surgery. Bone wax plays a crucial role in controlling hemorrhage. Still, it is found difficult to be degraded by the body. After implantation, it will remain in the body as a foreign matter for an extended period of time. As the accompanying risk of bone wax implantation, the ability of tissue anti-infection is decreased, and the risk of postoperative infection is increased. Besides, complications around formation of granuloma and impaired osteogenesis are commonly seen.

Objective: In this study, The NGO and NGO-HA bone wax was used to mitigate the shortcomings of traditional bone wax. A novel bone wax was designed with degradation and anti-infection ability, accompanying the miantian ability of bone tissue hemostasis.

Methods: A new degradable bone wax with good hemostatic and antibacterial properties was designed. The main component was Low-carbon chain lipids (NGO), hydroxyapatite (HA) and vancomycin. Respectively, the NGO, NGO-HA and bone wax was implanted into a 2.5 mm diameter circular bone defect of the femur of SD rats to evaluate the hemostatic performance (*n=4*). And the non implanted material group was set as the blank control group. Finally, these materials was mixed with Gram-positive Staphylococcus aureus in vitro to evaluate its antibacterial activity.

Results: The loss weight of blood of NGO and NGO-HA was no statistically significant difference between bone wax, indicating that the hemostatic performance of the NGO and NGO-HA was comparable to that of the bone wax. The results of bacteriostatic circle showed that the NGO and NGO-HA present obviously anti-infection performance better than that of bone wax.

Conclusion: The NGO and NGO-HA bone wax overcomes the shortcoming of traditional bone wax and provides a new way for cancellous bone hemostasis.

Keywords: bone wax, NGO, hydroxyapatite, antibacterial

11672-SP1-15.

Recombinant Human ACE2 Surface Functionalized Cell-Mimetic Microparticles Restrict SARS-CoV-2 Spike Protein Binding to Cellular Targets

Thomas A. Strong[1,3], Daniel Pelaez[1,2,3*]

[1]Bascom Palmer Eye Institute, Department of Ophthalmology, University of Miami, Miami 33136, United States of America

[2]Department of Biomedical Engineering, University of Miami College of Engineering, University of Miami, Coral Gables 33146, United States of America

[3]Department of Cell Biology, University of Miami Miller School of Medicine, University of Miami, Miami 33136, United States of America

Abstract

The development of novel clinical countermeasures to aid in the prevention and propagation of SARS-CoV-2 infections is critical to manage the current health crisis brought about by COVID-19. Here we present a proof-of-concept study on the use of respiratory epithelial cell-mimetic microparticles (Cytomimetics) for the interference and sequestration of virions away from the cellular surfaces required for infection, replication, disease manifestation, and propagation. For this application, recombinant human ACE2 was functionalized onto the surface of 1μm diameter beads to generate rhACE2-Cytomimetic microparticles resembling the respiratory epithelial cell surface. The functionalized rhACE2 on the surface of the cytomimetic microparticles binds the receptor binding domain (RBD) of recombinant SARS-CoV-2 spike protein with higher affinity than soluble rhACE2, demonstrating a stoichiometric advantage over the use of soluble rhACE2. Inhalable delivery of rhACE2-Cytomimetic microparticles to mice prior to their exposure to aerosolized spike RBD protein demonstrated the applicability of these cytomimetic microparticles particles in preventing viral protein uptake in respiratory epithelial cells. Mice receiving inhaled rhACE2-Cytomimetic microparticles had significantly less spike RBD protein recovered from their nasal epithelium, and virtually undetectable levels of the viral protein in their oropharynx and trachea, whereas those that did not receive the particles, had high levels of the viral protein throughout the epithelial lining of the airway tree. This project demonstrates the great potential of an easily deliverable and highly modular technology, cytomimetic microparticles, for the control of viral infections and propagation which can complement other prophylactic countermeasures and aid in suppressing pathogenic outbreaks.

Keywords: “COVID-19”, “SARS-CoV-2”, “Cytomimetics”, “Countermeasures”, “Angiotensin I Converting Enzyme (ACE2) carboxypeptidase”

11678-SP1-16.

Artificial trimerization of coronavirus spike proteins improves their productivity in silkworm-baculovirus expression vector system and is effective for eliciting neutralizing antibodies

Akitsu Masuda[1], JaeMan Lee[1], Takeshi Miyata[2], Hiroaki Mon[1], Takahiro Kusakabe[1*]

[1]Department of Bioresource Sciences, Graduate School of Bioresource and Bioenvironmental Sciences, Kyushu University, Fukuoka 819-0395, Japan

[2]Department of Food Science and Biotechnology, Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima 890-0065, Japan

Abstract

The spike (S) protein of coronaviruses is essential for attachment to and entry into host cells, making it a vulnerable target for vaccine development. Therefore, to develop protein-based subunit vaccines against coronaviruses, a powerful recombinant protein expression system capable of producing the S protein with high efficiency is needed. However, the expression efficiency of the coronavirus S protein as a recombinant protein is low due to its large molecular weight and complex structure that forms homotrimers. In this study, we attempted to improve the productivity of the S protein using the silkworm-baculovirus expression vector system (silkworm-BEVS), a baculovirus expression system that uses the silkworm as a host to produce recombinant proteins, and evaluated its immunogenicity in mice. To stabilize S protein as a homotrimer, we genetically fused chicken cartilage matrix protein (CMP) as a trimerization motif to the S ectodomain of porcine epidemic diarrhea virus (PEDV), a highly infectious coronavirus in pigs. As a result, the expression of the S protein fused with CMP (S+CMP) in silkworm serum was greatly increased compared to that without CMP. In addition, we screened 25 silkworm strains conserved at Kyushu University to further improve the S protein productivity. Among these strains, several strains expressed relatively high levels of S+CMP protein in their sera, achieving a yield of about 2 mg from 10 mL of larval serum. In an immunogenic analysis in mice, the S protein elicited strong antigen-specific antibodies and neutralizing antibodies that prevented PEDV infection. These results indicate that a strategy to stabilize the trimeric form of the S protein is very effective in improving its expression, and its productivity can be further increased by using suitable silkworm strains. Furthermore, the results of the immunological experiment indicate that a stable S trimer might be a promising subunit vaccine candidate against PEDV.

Keywords: subunit vaccine, silkworm-baculovirus expression vector system, coronavirus, silkworm strain

11701-SP1-17.

Morphology extraction of fetal electrocardiogram by slow-fast LSTM network

Ziqun Zhou[1], Kejie Huang[1*], Yue Qiu[1], Haibin Shen[1], Zhaoyan Ming[2]

[1]Department of Information Science and Electronic Engineering, Zhejiang University, Hangzhou 310027, People's Republic of China

[2]Institute of Computing Innovation, Zhejiang University, Hangzhou 310027, People's Republic of China

Abstract

Background: Fetal electrocardiogram (FECG) morphology plays an essential role in the early diagnosis of fetal health conditions. However, it is intractable to extract the clean morphology of FECG signals, which are usually contaminated by maternal ECG (MECG) and various noises. **Methods:** To extract the clean morphology of FECG signals from non-invasive abdominal ECG records, a high-performance and high-efficient two-stage slow-fast long short-term memory (SFLSTM) based architecture is proposed. The MECG elimination and the FECG enhancement are realized by the elaborately designed slow LSTM and fast LSTM to filter out the MECG and the residual noise components. **Results:** Qualitative and quantitative experiments are conducted on the records from two public datasets. The experimental results reveal that our designed scheme achieves the best performance in kSQI, signal-to-noise ratio, and root mean square error. The MECG elimination and the FECG enhancement improve SNR by 3.09 and 1.81 dB, respectively. The proposed fast LSTM reduces computation cost by approximately 50%, without any degradation in performance. **Conclusions:** Our method may leverage non-invasive FECG monitoring for the early detection of fetal heart diseases.

Keywords: Adaptive filter, Fetal electrocardiogram, FECG extraction, FECG enhancement, Long short-term memory, Recurrent neural network

11723-SP1-18.

Therapeutically targeting CD64 in acute myeloid leukemia via single-chain based antibody immunotoxin

Sikozile Ncembu[1], Siew Tai[1], Stefan Barth[2], Susan Harisson[1*]

[1]Centre for Bioprocess Engineering Research (CeBER), Department of Chemical Engineering, Faculty of Engineering and the Built Environment, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa

[2]Institute of Infectious Disease and Molecular Medicine (IDM), Department of Integrative Biomedical Sciences, Faculty of Health Sciences, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa

Abstract

Cancer immunotherapy is a promising innovative and effective treatment for many forms of cancer. Among hematologic malignancies, acute myeloid leukemia (AML) remains an unmet medical need as it is primarily treated with chemotherapy, which is characterised by severe side effects. H22(scFv)- ETA' is an immunotoxin comprised of a truncated toxin moiety; *Pseudomonas* exotoxin A (ETA') that is linked to a humanised single-chain variable fragment (scFv) targeting CD4. H22(scFv)- ETA' has been shown in this study to be highly effective in selectively destroying CD64-positive dysfunctional myeloid tumour cells in AML. CD64 is highly expressed on monocytic blast cells in patients with AML and not in normal hematopoietic stem cells or non-hematopoietic tissues. The overexpression of CD64 and its rapid internalization make it a suitable target antigen for antibody-based targeted therapies. H22(scFv)- ETA' has only been produced in shake flasks, a scale that does not provide sufficient quantity to conduct preclinical and/or clinical studies. Therefore, the current phase of this study is focused on optimizing the productivity of H22(scFv)- ETA' and conducting a scale-up production from the shake flask to a 5 L stirred tank reactor (STR). This will enable us to conduct further preclinical studies. H22(scFv)- ETA' is recombinantly expressed in *E. coli* Bl21 (DE3) and purified by metal ion affinity chromatography and size exclusion chromatography. The volumetric mass transfer coefficient (k_La) is used as a scale-up criterion to achieve effective batch and fed-batch fermentation processes. The therapeutic efficacy of H22(scFv)- ETA' is evaluated by several biological assays, including binding assays using flow cytometry and cytotoxicity using Annexin-V bioassay. The development of successful scale-up production of H22(scFv)- ETA' is critical as it will provide insight into a process that can be established at pilot scale and eventually at commercial scale in the context of biopharmaceutical manufacturing.

Keywords: Acute myeloid leukemia, Immunotherapy, immunotoxin, process development, scale-up

11724-SP1-19.

Bioremediation of soil contaminated with hydrocarbons enhanced by biosurfactants produced by endophytic *Bacillus pumilus* 2A

Piotr Drożdżyński[1], Katarzyna Struszczyk-Świta[1], Olga Marchut-Mikołajczyk[1]
[1]Institute of Molecular and Industrial Biotechnology, Faculty of Biotechnology and Food Sciences, Lodz University of Technology, Stefanowskiego 2/22, 90-537, Lodz, Poland

Abstract

The continuous development of civilization, apart from the undoubted benefits related to the production of useful products, also generates large amounts of waste and contaminate the environment. The metabolic activity of microorganisms in a polluted environment is extremely important in the processes of microbiological environmental purification. The innovative solution is application of endophytic microorganisms witch usually have a number of unique abilities i.e. degradation of xenobiotics or biologically active compounds. The endophytic *Bacillus pumilus* 2A strain isolated from *Chelidonium majus* L., has a great degradation activity and ability for biosurfactants production, and it was used for biosurfactants production and bioremediation of soil contaminated with diesel oil. Firstly, the biosurfactants production was performed in shaken conditions, then the scale of the process was upgraded to quarter-technical scale in bioreactor Infors Techfors HT 30l. Post-culture fluid was centrifuged at 10 000 rpm for 30 minutes, acidified with HCl to pH 2, and left for 24 hours for crude biosurfactant precipitation. Then obtained biosurfactants were centrifuged again in the same conditions and the precipitate was dissolved in 0,1M sodium bicarbonate and lyophilized.

Produced biosurfactants were applied as an enhancer of bioremediation of soil contaminated with hydrocarbons. The biosurfactant was introduced into the soil contaminated with hydrocarbons in order to support its biodegradation using the 2A strain, thanks to which the biodegradation increased by 56%.

The application of biosurfactants to the bioremediation process greatly induced metabolic activity of introduced microorganisms (soil dehydrogenases activity), and lowered the toxicity of the contaminated soil (catalase activity, phytotoxicity tests). The endophytic biosurfactant obtained as part of the work can be widely used in environmental protection for the degradation of hydrocarbons and, at the same time, soil reclamation for the purpose of its re-development.

Keywords: endophytes, *Bacillus pumilus* 2A, biodegradation, hydrocarbons, bioremediation

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11748-SP1-20.

Tackling COVID-19 pandemic with natural products: Evaluation of *Tamarix nilotica* phytochemical constituents as potential coronavirus-2 major protease inhibitors

Nouran Hassan Tantawy Farag[1], Sally I. Hassanein[2], Mohamed El-Shazly[3,4]

[1]Pharmaceutical Biotechnology, College of Biotechnology, Misr University for Science & Technology (MUST), 6th October, Egypt.

[2]Biochemistry Department, Faculty of Pharmacy and Biotechnology, German University in Cairo (GUC), New Cairo City, Egypt.

[3]Department of Pharmacognosy, Faculty of Pharmacy, Ain-Shams University, Cairo, Egypt

[4]Department of Pharmaceutical Biology, Faculty of Pharmacy and Biotechnology, German University in Cairo, Cairo, Egypt

Abstract

COVID-19 pandemic, which results in high mortality and morbidity rate around the globe, enforced the scientific community to search for biologically active agents either synthetically or with natural origin to stop the spread and replication of coronavirus-2 (SARS-CoV-2). In this study, we used a bioinformatics approach to examine the possible inhibitory effect of *Tamarix nilotica* phytochemical compounds against the main protease (M^{pro}) of severe acute respiratory syndrome SARS-CoV-2. The pharmacokinetics, pharmacodynamics, and toxicological profiles of the compounds were also tested using the pkCSM server. All phytochemicals showed good binding affinity to the binding pocket of PDB ID 6LU7. It was observed that "1,3-di-*O*-galloyl-4,6-*O*-(*S*)-hexahydroxydiphenoyl-beta-D-glucose" exhibited the highest binding affinity in comparison with remdesivir, hippomanin A, kaempferol 3-glucuronide, isorhamnetin 3-sulfate, and tamarixetin. The amino acids GLU166, GLN189, CYS145, HIS41, GLY143, ASN142 were the key residues for 1,3-di-*O*-galloyl-4,6-*O*-(*S*)-hexahydroxydiphenoyl-*β*-D-glucose binding to human SARS-COV2 major protease, where the 6LU7 residues Cys145 and His164 played a significant role in replication and are essential for the survival of 2019-nCOV hence this phytochemical compound could inhibit the replication and proliferation in the host. The pharmacokinetics and pharmacodynamics results suggested that all tested phytochemicals showed significant drug-likeness properties, and they could be absorbed through the human intestine. Moreover, all tested phytochemicals were not hepatoxic and showed no or relatively low toxic effects in humans. According to this study, the results indicated that all tested phytochemicals are potential putative inhibitors of SARS-COV2 major protease with no or low toxic effects. Further experimental and clinical studies are needed to examine their activities and justify their mode of action against COVID-19.

Keywords: COVID-19, *Tamarix nilotica*, main protease (M^{pro}) of SARS-CoV-2, bioinformatics approaches, pharmacokinetics, pharmacodynamics.

11757-SP1-21

FAK inhibitors suppress the proliferation and improve the immune microenvironment of HCC in mice

Yuhua Wei[1], Nanbin Liu[1],Ran Qi[1], Xiuyan Wang[2*], Baomin Shi[1*]

1Department of General Surgery, Tongji Hospital, Tongji University Medical School, Shanghai 200065, China

2Department of Ultrasonography, Tongji Hospital, Tongji University Medical School, Shanghai 200065, China

Abstract

Background: In recent years, studies have shown that focal adhesion kinase (FAK) inhibitors have therapeutic effects on some tumor and improves the immune microenvironment of tumor. However, the effect of FAK inhibitors on the immune microenvironment of hepatocellular carcinoma (HCC) has not been studied.

Objective: This study observed the efficacy of FAK inhibitors (VS4718) in the treatment and the immune microenvironment of HCC in mice.

Methods: We used the C-Met /β-catenin plasmid to induce a primary HCC model in C57BL/6J mice with complete immune function. We then randomly assigned the mice to FAK inhibitors group or placebo group for drug treatment. After two weeks, the mice were sacrificed for sampling. The liver weight and the ratio of liver weight to the body weight of mice were analyzed. Then, we observed the proliferation, fibrosis, and immune cell infiltration of HCC in mice by immunohistochemistry or immunofluorescence.

Results: Compared to the placebo group, the liver weight and the ratio of liver weight to the body weight of mice in the FAK inhibitors group were lower. At the same time, the infiltration of Tregs and macrophages was decreased and the infiltration of $CD8^+$ T cells was increased in the FAK inhibitors group.

Conclusion: Our study suggests that FAK inhibitors suppress the proliferation of HCC in mice. At the same time, it can reduce the immunosuppression of HCC in mice and improve the immune microenvironment of HCC in mice.

Keywords: FAK inhibitors, Hepatocellular carcinoma, Immune microenvironment

11099-SP2-22.

Bromatological composition of palm kernel meal according to its origin and production periods potential use of palm kernel meal in animal feed

Edison Mazón Paredes[1], Marcelino Herrera Rodríguez[2], Carlos Mazón Paredes[1], Antón García Martínez[3], Manuel Delgado Pertiñez[4] and José Luis Guzmán Guerrero[5]

[1] School of Zootechnical Engineering, Faculty of Livestock Sciences, Quevedo State Technical University, Km 6½ via a El Empalme cruce a Mocache, 120501 Quevedo, Los Rios, Ecuador. [2] Department of Aquaculture, Agricultural and Fisheries Research and Training Institute (IFAPA), Km 4, Carretera El Rompido-Punta Umbria, 21450 Cartaya, Huelva, Spain. [3] Faculty of Veterinary Medicine, University of Cordoba,Campus de Rabanales, s/n 14071 Cordoba, Spain. [4] Department of Agroforestry Sciences, Higher Technical School of Agronomic Engineering, Sevilla University, 41013 Sevilla, Spain. [5] Department of Agroforestry Sciences, University of Huelva, Campus de la Rabida, 21819 Palos de la Frontera, Huelva, Spain.

Abstract

Ecuador has a variety of agroindustrial by-products, which can be used in animal feed, although their nutritional values are often unknown. The objective of this study was to evaluate bromatological composition of palm kernel cake (PKC) in samples from two palm oil extraction plants in two areas (Quevedo and Santo Domingo) and two production periods (August and September). Random samples were taken weekly with two repetitions for a total of 64 samples. Dry matter (DM), ash, organic matter (OM), crude protein (CP), ether extract (EE), crude fibre (CF), nitrogen-free extract (NFE), neutral detergent fibre (NDF), acid detergent fibre (ADF), acid detergent lignin (ADL), calcium, phosphorus, crude energy (CE) and metabolisable energy (ME) were determined. OM (62.92%) and EE (10.10%) content were higher at the Quevedo plant, while CF (23.84%) and ADL (24.66%) were higher at the Santo Domingo plant. The sampling period affected DM (98.58%), CF (23.98%) and ADL (23.78%) content, which were higher in September, while EE (10.87%) and phosphorus (0.44%) were higher in August. For CP, NFE, NDF, ADF, ash, calcium, CE and ME, interaction was observed between the two factors studied. It was concluded that most of the parameters analysed depend on the place of origin or the extraction season, or interaction between the two factors.

Keywords: *Elaeis guineensis* Jacq 1763 L, agroindustrial by-products, proximal analysis, production period, Ecuador.

11391-SP2-23.

Amaranthus cruentus L. as a food alternative in laying hens to reduce cholesterol in eggs.

Hernán Rodríguez-Ríos[1] , Jorge Campos-Parra[1] , Rita Astudillo-Neira[2] , Jesús Grande-Cano[3] , Silvia Carrillo-Domínguez[4] , Fernando Pérez Gil- Romo[4]

[1] University of Concepción, Faculty of Agronomy, Department of Livestock Management, Avenida Vicente Méndez 595, Chillán, Chile.

[2] University of Concepción, Faculty of Veterinary Medicine, Department of Animal Science, Avenida Vicente Méndez 595, Chillán, Chile.

[3] Independent Metropolitan University Iztapalapa, Department of Agricultural Production Systems, Av. San Rafael Atlixco No. 186, Col. Vicentina, Delegación Iztapalapa, C. P. 09340, Ciudad de México.

[4] Salvador Zubirán National Institute of Medical Science and Nutrition, Avenida Vasco de Quiroga No.15, Colonia Belisario Domínguez Section XVI, Tlalpan Delegation C.P.14080, México.

Abstract

Amaranth (*Amaranthus cruentus* L.) is a food high in protein and lysine content, and has a wellbalanced amino acid composition. In addition, it has shown to be efficient in lowering egg cholesterol. The objective of this study was to evaluate the effect of different inclusion levels of Amaranthus cruentus L. in the diet of laying hens, on egg cholesterol content and production parameters. 200 laying hens of 30 weeks of age were fed on diets that included 0, 15, 30 and 45% (dry matter basis) of A. cruentus. For 2 months, weekly feed intake per hen, egg production per week, egg mass and feed conversion ratio were evaluated. 480 eggs were analyzed to determine cholesterol content by high performance liquid chromatography. The results were analyzed by analysis of variance for a randomized block design. The inclusion of 15% of A. cruentus seeds in the diet decreased egg yolk cholesterol content without significantly affecting the main production parameters.

Keywords: *Amaranthus cruentus*, amaranth, laying hens, egg, cholesterol, nutrition

11594-SP2-24.

Effect of Mesobiliverdin IXα-enriched microalgae on intestinal morphology, inflammatory cytokines and antioxidant enzymes activity of weaning piglets

Tz-Shian Liao, Chen-Yi Chen, Yuan-Yu Lin

Department of Animal Science and Technology, National Taiwan University, Taipei city, 106, Taiwan

Abstract

Weaning is a critical period in pig industry. Novel animal feed additives that promote gut health and regulate immune function of piglets without antibiotics are needed. In this study, we intended to broaden the application of mesobiliverdin IXα-enriched microalgae to piglets. A total eighty 28-day-old weaned piglets were randomly allocated to four groups with 4 replicate pens and 5 piglets per pen. The dietary treatments comprised a basal diet as control (CON), basal diet plus 0.05% tylosin (PC), basal diet plus 0.1% and 0.5% MBV-enriched microalgae as low and high dose respectively (MBV-SP1 and MBV-SP2).

All treated animals showed no significant differences in live weight, average daily gain and feed efficiency compared to control animals. Histological examination showed that MBV-SP1 and particularly MBV-SP2 increased the ratio of villus height to crypt depth in the jejunum and ileum compared to CON ($P < 0.05$). Similarly, tylosin treatment also increased villi lengths and the ratio of villus height to crypt depth in the jejunum and ileum compared to the control ($P < 0.05$). From the studies of immune-regulatory effects, we observed that MBV-SP and particularly MBV-SP2 can reduce the inflammatory cytokines like IL-6 and TNF-α in small intestine. Moreover, lipid peroxidation marker MDA showed MBV-SP2 have a similar effect as antibiotic which effectively reduce the TBARS value in duodenum and ileum. MBV-SP improves the intestinal morphology and has anti-inflammation function via down-regulated secretion of inflammatory cytokines of piglets. In conclusion, MBV-SP could be an important asset in promoting gut health and regulate immune function of piglets, and has the potential to replace the use of antibiotic in pig industry.

Keywords: Mesobiliverdin IXα, microalgae, weaning piglets

11627-SP2-25.

Analysis of Flavor Substances in Potato Instant Vermicelli Seasoning

Huishan Shen, Guoquan Zhang, Jianmei Zheng*

College of Food Science and Engineering, Northwest A & F University, Yangling 712100, China

Abstract Instant vermicelli is a pre-packaged convenience food made from potatoes, beans, and cereal starch, with or without added ingredients, and processed into dry, no-cooking vermicelli and then flavored with seasonings. Instant vermicelli has been widely consumed in Asian countries because of its nutrition profile and sensory properties. Seasonings play a key role in determining sensory attributes of instant vermicelli. The flavor profile of five different brands of instant vermicelli seasonings (seasoning powder, seasoning mixture sauce and the mixture of powder and sauce) were identified by headspace solid-phase micro-extraction coupled with gas chromatography–mass spectrometry (HS-SPME/GC–MS), electronic nose (e-nose) and electronic tongue (e-tongue). GC–MS showed that the volatile compounds of instant vermicelli seasonings were significantly different. A total of 70, 92 and 98 volatile compounds were identified through GC–MS in the instant vermicelli seasoning powder, seasoning mixture sauce and the mixture of powder and sauce, respectively. Alkenes, alcohols, aldehydes and sulfur containing compounds were the major volatile compounds in instant vermicelli seasonings. The seasonings could be classified via PCA of the GC–MS results. The overall volatiles profiles were also analyzed by e-nose and e-tongue. Feature-level fusion for the integration of the signals was introduced to integrate the e-nose and e-tongue signals, aiming at improving the performances of identification and prediction models. Principal component analysis (PCA) of the individual e-nose and e-tongue data discriminated all samples. The combination of e-nose and e-tongue had much better discrimination than either alone. This work demonstrated that in combination e-nose and e-tongue provided more comprehensive information about the seasonings compared to each individual dataset. The volatile compounds showed good correlation with e-nose and e-tongue sensors according to cluster analysis. Combining GC–MS, e-nose and e-tongue with multivariate statistical analysis is a useful technique for evaluating and distinguishing variation among instant vermicelli seasonings.

Keywords instant vermicelli seasoning;· volatile compounds;· gas chromatography-mass spectrometry;· electronic nose; ·electronic tongue· principal component analysis

11647-SP2-26.

Preliminary study of citrus extract supplement in cecum microbiota fluctuation in laying hens

Hsin Chen, Yun-Jing Li, Tz-Yih Huang, Kuo-Tai Yang
Department of Animal Science, National Pingtung University of Science and Technology, 1, Shuefu Road, Neipu, Pingtung 91201, Taiwan

Abstract

The purpose of this study was to describe the cecum microbiota composition in supplemented with powder and liquid feed additive of citrus extract (CE) in laying hen using 16s rRNA metagenomics analysis. A total of 90 Lohmann laying hens in high egg production period were random divided into 5 treatment groups, with 3 replicates per treatment and 6 hens per pen. Five treatments were fed ad libitum with basal diet (C), basal diet / 0.5ml/L (W0.5) and basal diet / 1ml/L (W1) of liquid CE in drinking water, basal diet / 0.5g/kg (P0.5) and basal diet / 1g/kg (P1) of powder CE for 5 weeks. The cecum contents were collected from randomly selected 3 hens per treatment and isolated total bacteria nucleic acids for 16s rRNA gene sequencing. The results showed that the operational taxonomic units (OTUs) were significantly increase with increasing dosage of powder or liquid citrus extract supplemented as 6765 OTUs in group P1 and 6105 OTUs in group W1 compare to 4417 OTUs in control. Beta-diversity metrics showed significant difference among treatments. Further species annotation pointed that the *Bacteroidaceae*, *Ruminococcaceae*, *Lachnospiraceae*, and *Lactobacillaceae* were the most abundant family in all experimental groups. The metabolic pathways and predicted function of cecum microbiota need to advance investigation. These preliminary results provide important information of cecum microbiota distribution and fluctuation after dietary additive with either powder or liquid of citrus extract.

Keywords: cecum microbiota, citrus extract, laying hens, metagenomics analysis

11652-SP2-27.

Effects of calcium ions on physicochemical properties and stability of preserved eggs

Pin-Chun Tseng, Yi-Chen Chen, Sheng-Yao Wang*

Department of Animal Science and Technology, National Taiwan University, No. 50, Lane 155, Sec. 3, Keelung Rd., Taipei 106, Taiwan, R. O. C.

Abstract

Preserved egg is an Asian duck egg product processed with strong alkali. However, liquefaction will occur due to a continuous reaction under alkali conditions. To improve the quality of preserved eggs by regulating the penetration of alkali, heavy metal ions (lead or copper) are added to the pickling solution in the traditional process; however, these heavy metals can cause health problem and environmental pollution. The purpose of this study was to investigate the mechanism of calcium chloride ($CaCl_2$) on physicochemical properties and stability of preserved eggs. By attempting a switch-process, which pickles duck eggs in two different solutions for different stages. This process involves pickling in strong alkali for three days and subsequently in 0.0% to 4.0% (w/w) $CaCl_2$ aqueous solution for 24 hours, and then switching back to strong alkali and pickling for 6 weeks. The results indicated that the hardness, cohesiveness value, and disulfide bonds content of preserved egg white were significantly higher than the control duck eggs ($p < 0.05$), and the free thiol group content was significantly lower than the control group by applying 2.0% $CaCl_2$ switch-process ($p < 0.05$). Additionally, the hardening ratio of preserved egg yolk of 2.0% and 4.0% $CaCl_2$ switched groups was significantly higher than the ratio of the control group and copper sulfate group ($p < 0.05$), indicating the switch-process contributed to the better formation of preserved egg yolk. Interestingly, we also found preserved eggs quality may be affected by penetration of strong alkali regulated via plugs formed on egg shell pores. In summary, $CaCl_2$ appears to be beneficial to the formation and stability of preserved eggs. Therefore, this innovative switch-process should be capable of replacing the use of heavy metals, producing preserved eggs with spotless appearance and stable quality.

Keywords: egg processing, preserved eggs (pidan), calcium ions, heavy metal

11655-SP2-28.

Angiotensin-converting enzyme inhibitory and anti-diabetic properties of oat proteins hydrolysates

Monika Pliszka, Małgorzata Darewicz
Department of Food Biochemistry, University of Warmia and Mazury in Olsztyn, Poland

Background: Peptides derived from plant proteins have been attributed to different prophylactic and even therapeutic effects. Oat may be the valuable source of proteins and represents a promising source of peptides with biological activity, including peptide inhibitors of dipeptidyl peptidase-IV (DPP-IV), α-glucosidase (AG) and angiotensin-converting enzyme (ACE). The study aimed to characterize and identify anti-diabetic and anti-hypertensive bioactive peptides generated upon in vitro digestion of oat kernels proteins.
Methods: In in silico part of the study computer tools available in UniProt database (www.uniprot.org), BIOPEP-UWM database (www.uwm.edu.pl/biochemia/), Fragment Ion Calculator (www.db.systemsbiology.net:8080/proteomicsToolkit/FragIonServlet.html) and METLIN database (www.metlin.scripps.edu) were used. The in vitro digestion method according to the INFOGEST protocol (www.cost-infogest.eu) consisted of the following steps: "oral" - 2 min, pH = 7, "gastric" – 2 hours, pH = 3.0, "intestinal"- 2 hours, pH = 7.0. Hydrolysates were characterized for their anti-diabetic properties via inhibition of DPP-IV and AG, and anti-hypertensive property via inhibition of ACE. Amino acid sequences were identified using LC-Q-TOF-MS/MS method based on in silico systematic screening for DPP-IV, AG and ACE inhibitory peptides.
Results: Hydrolysates of oat kernels proteins showed DPP-IV, AG and ACE inhibitory activities. The intestine hydrolysate demonstrated the highest degree of DPP-IV inhibition (91.65%; IC_{50} = 0.04 mg/ml), AG inhibition (51.29%; IC_{50} = 1.55 mg/ml) and ACE inhibition (87.76%; IC_{50} = 0.82 mg/ml). The DPP-IV, AG and ACE inhibitory fragments, selected based on the results of in silico studies were identified in the "intestinal" hydrolysate via LC-Q-TOF-MS/MS method.
Conclusions: In conclusion, oat proteins were identified as potential sources of bioactive hydrolysates and peptides with inhibitory properties towards key enzymes involved in the control of type 2 diabetes and hypertension.

Keywords: oat proteins, bioactive peptides
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11740-SP2-29.

Quality traits of saffron produced in Italy from 2015 to 2020

Davide Pedrali[1], Luca Giupponi[1], Valeria Leoni[1], Marco Zuccolo, Alessia Rodari, Tiziana L. Zendrini[1], Annamaria Giorgi[1,2]

[1]Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas – CRC Ge.S.Di.Mont., University of Milan, Via Morino 8, 25048 Edolo (BS), Italy; [2]Department of Agricultural and Environmental Sciences - Production, Landscape and Agroenergy, University of Milan, Via Celoria 2, 20133 Milan, Italy.

Abstract

Saffron (*Crocus sativus* L) is considered the most expensive spice in the world. This plant is an autumn-flowering geophyte and is believed to have originated in Greece, Asia Minor and Persia. It is mainly produced in Iran but also in some European countries such as France, Greece, Spain and Italy. The increasing interest in *Crocus sativus* cultivation and production in Italian Alpine area could increase revenues for rural farming economy.

This research is the first to investigate the quality of saffron produced in Italy and georeferenced the producers. Quality analysis was performed according to ISO 3632 1,2:2010-2011. In particular, moisture content and the amount of picrocrocin (flavour strength), safranal (aroma strength) and crocins (colouring strength) of about 741 samples collected from throughout Italy were evaluated using spectrophotometric methodology. Qualitative analysis was carried out from 2015 to 2020 considering about 100 samples per year.

The map of farms producing saffron showed a homogeneous distribution in all Country. More than 89% of samples belong to the first quality category, about 4.7% belong to the second quality category, approximately 1.3% belong to the third quality category and the rest of the samples are outside all categories. Exclusion of samples from the first category was mainly due to high moisture content (>12%) and lower coloring strength (crocin < 200 $A^{1\%}_{1\,cm}$ $A^{1\%}_{1\,cm}$). This research shows that high quality saffron can be produced all over Italy from plain to mountain areas. Some good practices for the production of this precious spice are provided to further improve the quality of Italian saffron.

Keywords: *Crocus Sativus*, picocrocin, crocin, safranal, food quality

11592-SP2-30.

Gut bacterial communities in the commercially valuable polychaete worms (Annelida, Polychaeta) from the east coast of India with implications to aquaculture

Lyndsay Priscilla [1], Meora Rajeev [2], Shunmugiah Karutha Pandian [2] and Malathi E [1]

1Department of Zoology, Queen Mary's College (Autonomous), affiliated to the University of Madras, Chennai - 600 004, Tamil Nadu, India.

2Department of Biotechnology, Alagappa University, Science Campus, Karaikudi - 630 003, Tamil Nadu, India.

Abstract

Polychaetes are used as crucial maturation feed for shrimp broodstock in captive culture. The Indian aquaculture sector meets the dietary requirements of shrimp broodstock by using wild captured worms as supplemental feed, but the bacterial community structure and composition in the polychaetes are not well known. In the present study, two polychaete species *Namalycastis* sp. and *Marphysa madrasi*, used as maturation feed by shrimp brooders, were analysed for the culturable gut microbiota. Based on colony characteristics, 39 bacterial isolates were selected, which were grouped into 23 phylotypes using amplified ribosomal DNA restriction analysis (ARDRA) profiling. 16S rRNA gene sequencing of the 23 isolates revealed that the predominant bacteria in the gut of polychaetes belonged to the phyla Firmicutes, Actinobacteria, and Proteobacteria. Of the 23 isolates screened for the presence of proteolytic, lipolytic, amylolytic, and cellulolytic activities, fourteen (60.87%) isolates expressed at least one of the enzymes tested. The diversity index showed that *M. madrasi* had higher species abundance and diversity ($p < 0.05$) than *Namalaycastis* species. Phylogenetic analysis revealed human and shrimp pathogens such as *Bacillus Cereus* and nosocomial human pathogens such as *Staphylococcus epidermidis*, *Microbacterium paraoxydans*, *Gordonia terrae*, and *Staphylococcus gallinarum* in the guts of both the polychaete species. 50% of the gut isolates (*B. altitudinis*, *B. halotolerans*, *B. subtilis*, *B. megaterium*, *B. pumilus*, *B. licheniformis*, *Penaebacillus dendritiformis*, *Pediococcus pentosaceus*, and *Shewanella algae*) have established probiotic applications in shrimp aquaculture. The gut colonizing bacteria in polychaetes have human and shrimp disease implications along with bacteria with the known probiotic application.

Keywords: Polychaeta; Maturation feed; Gut bacterial community; Culture dependent; Probiotic bacteria; Aquaculture.

11679-SP2-31.

Impact of Animal Manures on Pummelo Leaf Nutrient Status and Fruit Quality

Le Van Dang, Ngo Phuong Ngoc, Ngo Ngoc Hung

Abstract

Nam Roi Pummelo (*Citrus grandis*) is considered a vital plant in poverty alleviation programs in the Vietnamese Mekong Delta (VMD) due to its high economically and commercially valuable. However, fruit yield and quality severely declined in recent years because of decrease soil fertility, soil pH, and poor nutrient management. The continuous 3–year field experiments were carried out in the three orchards in Chau Thanh district, Hau Giang Province, Vietnam. The objectives of the study aimed to evaluate the effects of animal manures on nutritional status of pummelo leaves and fruit quality. The treatments include control (NPK fertilizer), chicken manure (10 ton per ha per year + NPK fertilizer), and cow dung (10 ton per ha per year + NPK fertilizer). Results revealed that the concentrations of N, K, Ca, Fe, and Mn in leaves was greatly improved by cow dung (CD) or chicken manure (CM) application. Organic manures application also enhanced total soluble solids (TSS) by 1.0 Brix comparison with mineral fertilizer. In addition, the content of titratable acidity (TA) was declined by applying poultry or cattle manure. The use of CD or CM is considered a beneficial measure for improving pummelo leaf nutrient uptake and fruit quality.

Keywords: cow dung, chicken manure, fruit quality, pummelo leaf nutrient

11675-SP2-32.

Microbial dynamics of *Shameta*: Ethiopian cereal-based fermented porridge

Daniel A. Kitessa[1,3], Ketema Bacha[2], Yetenayet B. Tola[3], Mary Murimi[4]

[1]Department of Food Science and Nutrition, Wollega University, Shambu Campus, P.O. Box: 38 Shambu

[2]Department of Biology, College of Natural Science, Jimma University, P.O. Box: 378

[3]Department of Postharvest Management, College of Agriculture and Veterinary Medicine, Jimma University, P.O. Box: 307, Jimma

[4]Department of Nutritional Sciences, College of Human Science, Texas Tech University, and P.O. Box: 41270 Texas

Abstract

Across the world, lactic acid fermentation has attracted attention in reducing pathogenic contamination because of the ability to produce organic acids and antimicrobial products. The aim of this study is to determine the microbial quality of *shameta* samples collected from home of lactating mothers. Also to investigate the growth dynamics, and identify and characterize dominant microorganisms during *shameta* fermentation in laboratory. Results showed that the LABs were the only dominant microbes in *shameta* samples. The highest mean counts was in laboratory prepared sample (8.33 logcfu/g) and lowest in BM (5.88 logcfu/g) sample. Present results showed that the counts of AMB and Enterobacteriaceae in all samples were >3 logcfu/g. The counts of total coliform in more than half samples were below detectable level (<2), while the counts of *Staphylococcus spp.* in more than half samples were ranged between 2.47-3.28 logcfu/g. Present results investigated that the counts of *Bacillus spp*. in more than half of samples were below detectable level. In both laboratory prepared barley-based and maize-based *shameta*, LAB was dominated followed by counts of yeast. The growths exponential of LABs were 3.41-8.33 and 4.04-6.26 logcfu/g for barley and maize-based, respectively. The isolated strains in these results were dominated by the genera of Lactobacillus (74.85%) followed by Enterococcus (15.79%). Present results indicated that *shameta* collected from home of lactating mothers are safe for consumption due to less contaminated by pathogenic microorganisms. However, as *shameta* is traditional fermented porridge which helps lactating mothers for their rapid recovery and gain strength after delivering babies, it needs further improvement of product quality by starter culture in controlled conditions. Therefore, a dominant genus needs further characterization to identify either potential starter culture for *shameta* fermentation or not.

Keywords: Barley-based shameta, Fermentation, Lactating mothers, Maize-based shameta

11753-SP2-33.

An Optimized Enzymatic Hydrolysis of Bovine Whey Protein with Chymotrypsin, Trypsin, and Pepsin Using a Full Factorial and a Surface Response Methodology.

Hamida Akli [1,2], Spiros Grigorakis [2], Sofia Loupassaki [2], Ioannis Livieratos [3], Dimitris Makris [2,4], Nikolaos Lydakis-Simantiris [2,5*], Abderrahmane Mati [1].

[1] Mouloud Mammeri University, Analytical Biochemistry and Biotechnologies Research Laboratory (LABAB), Tizi Ouzou, Algeria.

[2] Food Quality & Chemistry of Natural Products, Mediterranean Agronomic Institute of Chania (M. A. I. Ch.), International Centre for Advanced Mediterranean Agronomic Studies (CIHEAM), P.O. Box 85, 73100 Chania, Greece.

[3] Plant Virology and Microbiology, Mediterranean Agronomic Institute of Chania (M. A. I. Ch.), International Centre for Advanced Mediterranean Agronomic Studies (CIHEAM), P.O. Box 85, 73100 Chania, Greece.

[4] Green Processes & Biorefinery Group, School of Agricultural Sciences, University of Thessaly, N. Temponera Street, 43100 Karditsa, Greece.

[5] Hellenic Mediterranean University, Department of Agriculture, Heraklion, Crete, Greece.

Abstract

The hydrolysis of bovine whey proteins was optimized using chymotrypsin, trypsin, and pepsin. The aim of this study was to reach the optimal conditions for whey proteins hydrolysis using the digestive enzymes, either separately or combined in order to generate peptides with higher antioxidant activity. The optimum conditions were applied on A full factorial design was employed for the single enzymatic hydrolysis in order to evaluate the effect of two independent factors on the potency of the antioxidant activity of the generated peptides, which were: the sonication time applied on the bovine whey protein concentrate prior hydrolysis and the enzyme-to-substrate ratio (E/S). In addition to these factors, the portion of each enzyme (E1/E2) among the total (E/S) ratio was assessed in the combined enzymatic hydrolysis by implementing a response surface methodology (Box-Behnken design). Regression analysis exhibited more that 90% of the explained variation by the six models; chymotrypsin, trypsin, pepsin, chymotrypsin-trypsin, pepsin-chymotrypsin, and pepsin-trypsin. The hydrolysis conditions were found to have significant effects on the cupric reducing antioxidant capacity value (CUPRAC), which was the response in each model. The optimal conditions of the independent variables were (40 min, 2,81%), (40 min, 3,5%), and (10 min, 5%) for sonication time and the E/S ratio in the case of chymotrypsin, trypsin, and pepsin models, respectively, and it was (10 min, 5%, 49,3%), (10 min, 5%, 30%), and (40 min, 5%, 30%) for sonication time, the E/S ratio and the portion of each enzyme (E1/E2) in the case of chymotrypsin-trypsin, pepsin-chymotrypsin, and pepsin-trypsin models, respectively. Hydrolysis under these optimum conditions provided the highest CUPRAC value with chymotrypsin, which was 815.33 µM cysteine equivalent, and 771.67, 680, 668, 575, and 533 µM cysteine equivalents for chymotrypsin-trypsin, trypsin, pepsin-chymotrypsin, pepsin, and pepsin-trypsin models, respectively. These results suggest the suitability of using chymotrypsin for an optimal antioxidant effect with bovine whey proteins.

Keywords: bovine milk whey proteins, enzymatic hydrolysis, bioactive peptides, optimization.