

The 9th International Conference on Agricultural and Biological Sciences (ABS 2023) & (ABB 2023) The 6th International Conference on Applied Biochemistry and Biotechnology

Conference Program

July 4th-7th, 2023 Macao, China | Online via MS TEAMS





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Part I Conference Schedule

Tuesday, July 4th, 2023		
Time	Schedule	Location/Link
09:00-18:00	Physical Registration	Lobby of Regency Art Hotel
14:00-19:00	MS Teams Testing	http://www.academicconf.com/teamslink?confname=ABS2023

Notice (for offline participants):

- 1. Please show us the acceptance letter or paper ID for registration;
- 2. Please take the name card during conference, Macao Pass¹ for meals and field visit tickets while joining the field visit.

and Ballroom III, Regency Art Hotel

MS Teams Link: http://www.academicconf.com/teamslink?confname=ABS2023

Welcome and Plenary Speeches are chaired by:

Prof. Moniruzzaman Khondker, University of Dhaka, Bangladesh **Prof. Xuqiao Feng**, Bohai University; Institute for Science and Technology of Fruits and Vegetables,

China

09:00-09:10	WELCOME SPEECH
	Prof. Xuqiao Feng , Bohai University; Institute for Science and Technology of Fruits and Vegetables, China
09:10-09:50	Plenary Speech 1: Improving Food Security and Safety Through High Throughput Phenotyping and Genotyping
	Prof. Shuyu Liu, Texas A&M University and AgriLife Research, USA
09:50-10:30	Plenary Speech 2: Anti-inflammatory and Gut Microbiota Modulatory Effects of Structurally Modified Polysaccharides from Edible Mushroom Auricularia auricula in DSS-induced Colitis Mice
	Prof. Baojun (Bruce) Xu, BNU-HKBU United International College, China
10:30-10:50	Group Photo & TEA BREAK
10:50-11:30	Plenary Speech 3: Comparative Analysis of Genetic Diversity and PopulationGenetic Structure of an Important Medicinal Plant, Grewia Nervosa fromGazipur and Cumilla Sal Forests, BangladeshProf. Ashfaque Ahmed, University of Dhaka, Bangladesh
11:30-12:00	Poster Presentations and Best Poster Awarding
12:00-14:00	LUNCH BREAK (A Pousada Café 玲瓏閣餐廳)

¹Macao Pass will be provided during registration for dinner on July 6th and Lunch on July 7th. Macao Pass can be used in Public Transit, Convenience Store, Supermarket, Café and Self-service Vending Machine in Macao.

14:00-17:40	Oral Session 1: Applied Biochemistry and Biotechnology
17:45-18:00	Gather at the Lobby of Regency Art Hotel (Set off on time at 18:00)
18:30-20:20	Buffet Dinner at Macao Tower (With Buffet Dinner Ticket)
20:20-20:30	Gather at the Ground Floor of Macao Tower (Set off on time at 20:30)
20:30-21:00	Back to Regency Art Hotel

 Thursday, July 6th, 2023
 Grand Ballroom III, Regency Art Hotel

 MS Teams Link: http://www.academicconf.com/teamslink?confname=ABS2023

09:00-12:25

12:25-14:00 LUNCH BREAK (A Pousada Café 玲瓏閣餐廳)

Oral Session 2: Food and Veterinary Science

14:00-18:10 Oral Session 3: Modern Agriculture, Climate Change, Diseases and Pesticides

Friday, July 7th, 2023Macao City, China		
08:15-08:30	Gather at the Lobby of Regency Art Hotel (Set off on time at 8:30)	
08:30-16:00	One Day Field Visit of Macao City (with Field Visit Ticket)	
16:00-16:10	Gather at the Ground floor of Venetian Macao (Set off on time at 16:10)	
16:10-16:30	Back to Regency Art Hotel	

Part II Plenary Speeches

Plenary Speech 1: Improving Food Security and Safety through High Throughput Phenotyping and Genotyping

Prof. Shuyu Liu



Texas A&M University and AgriLife Research, USA

Biography: Dr. Shuyu Liu is a professor in wheat genetics and genomics with Texas A&M AgriLife Research-Amarillo and Dept. of Soil and Crop Sciences of Texas A&M University. He worked as a visiting fellow at Agriculture Agri-Food Canada and a research scientist at Virginia Tech before he joined TAMU in 2010. He got his M.S. from Colorado State University and Ph.D. from University of Missouri-Columbia. He leads the wheat genetic program at Amarillo center and mainly focuses on genetic and genomic studies on important traits of wheat in the US Great Plains. Target traits include drought and heat tolerance, resistance to diseases (leaf, stem and stripe rusts, wheat streak mosaic virus), and arthropods (greenbug, Hessian fly, and wheat curl mite) as well as superior end-use quality for bread making. Both traditional and molecular breeding techniques are being used to develop germplasm lines with multiple target traits. Genomic techniques including gene/QTL mapping, target molecular marker identification, validation and utilization, diagnostic high throughput KASP SNP screening, gene cloning, and gene functional analysis are used to understand and improve those target traits. The established doubled haploid development is integrated to the traditional and molecular breeding pipelines in Texas. He got the research faculty award from Soil and Crop Science and a major member of a collaboration team from Vice Chancellor award in 2019 and Dean's excellence award in 2015. He is leading a USDA-NIFA project as a PD and one as a Co-PD. He completed a USDA-NIFA-IWYP (International Wheat Yield Partnership) WheatCAP project as a co-PD and leads a collaborative project with hard winter wheat regional breeders and geneticists on doubled haploid development project funded by US wheat and Barley Scab Initiative. He also a co-PI for a subaward of WheaCAP in 2022-2027. He has secured \$3.2M for his wheat genetic research and involved with \$25M funding as a team member. He has published 93 peer reviewed publications and presented 112 oral and 136 posters. He has trained 15 Ph.D. and 13 M.S. students, and 20 undergraduate students. He has chaired 6 committees including plant genetic resources in the ASA-CSSA-SSSA tri-societies and joined 9 committees as a member. He is an ambassador of scientists engaging and educating decision makers and joined the virtual congressional visiting day in 2022. He has been an associate editor of five journals and reviewed >25 journal articles per year. He also got the outstanding reviewer award from the editor board of the Plant Genome in 2021.

Abstract: This oral keynote presentation will use wheat as an example by summarizing the research results from the last decade in the US Great Plains hard winter bread wheat in studying resistance to major diseases and pests, yield and its components, and end-use quality to illustrate how food security can be achieved through improving wheat production and crop resilience to climate change. QTL mapping, genome-wide association analyses, and genomic prediction and selection using SNPs from

genotyping-by-sequencing and other sequencing platforms will be discussed. Major Alleles in popular wheat cultivars for improving wheat production and bread-making quality under both dryland and irrigated fields will be presented. High throughput phenotyping using UAS will be shown. In addition, the improvement of food safety, such as using host plant resistance to reduce vomitoxins and aflatoxins in wheat and corn will be discussed.

Plenary Speech 2: Anti-inflammatory and Gut Microbiota Modulatory Effects of Structurally Modified Polysaccharides from Edible Mushroom Auricularia Auricula in DSS-induced Colitis Mice



Prof. Baojun (Bruce) Xu

Department Head, Department of Life Sciences, BNU-HKBU United International College, China

Biography: Dr. Xu is a Chair Professor in Beijing Normal University-Hong Kong Baptist University United International College (UIC, a full English teaching college in China), Zhuhai Scholar Distinguished Professor, Department Head of Department of Life Sciences, Program Director of Food Science and Technology Program, author of over 290 peer-reviewed papers. Dr. Xu received Ph.D. in Food Science from Chungnam National University, South Korea. He conducted postdoctoral research work in North Dakota State University (NDSU), Purdue University, and Gerald P. Murphy Cancer Foundation in USA during 2005-2009. He did short-term visiting research in NDSU in 2012, and University Georgia in 2014, and followed by visiting research during his sabbatical leave (7 months) in Pennsylvania State University in USA in 2016. Dr. Xu is serving as Associate Editor-in-Chief of Food Science and Human Wellness, Associate Editor of Food Research International, Associate Editor of Food Frontiers, and the editorial board member of around 10 international journals. He received inaugural President's Award for Outstanding Research of UIC in 2016, President's Award for Outstanding Service of UIC in 2020. Dr. Xu has been listed in the world's top 2% scientists by Stanford University in 2020, 2021, 2022, and has been listed in the Best Scientist in the world in the field of Biology and Biochemistry at Research.com in 2023.

Abstract: Auricularia auricula-judae (Jew's ear) is a popular edible and medicinal mushroom. Fungal polysaccharides have taken great attention due to their diverse biological activities. However, the biological potential remains unknown due to the structural complexity and high molecular weight of fungal polysaccharides. This study aims to investigate structurally modified Jew's ear polysaccharides' anti-inflammatory effects, gut microbiota regulatory effects, and their underlying mechanisms in DSSinduced colitis mouse model. AP-1 polysaccharide was isolated from Jew's ear and then structurally modified by ultrasonic cell disruptor to AP-2 and AP-3. Furthermore, AP-1, AP-2, and AP-3 polysaccharides were administered to the DSS-induced colitis mice to investigate their antiinflammatory effects and gut microbiota-regulatory effects. The histological changes in the colon were observed by hematoxylin and eosin (H&E), and alcian blue staining. Enzyme-linked immunosorbent assay (ELISA) analysed a series of pro-inflammatory cytokines. Cyclooxygenase-2 (COX-2), inducible nitric oxide synthase (iNOS), and nuclear factor kappa B (NF-kB) signalling proteins were analyzed by western blot, while zonula occludens-1(ZO-1) protein expression was analysed using immunofluorescence. 16s rRNA gut microbiota sequences were performed in mice fecal samples. The results showed that DSS treatment significantly reduced body weight, increased disease activity index (DAI), shortened colon length, increased diarrhea, bleeding diffuse infiltration of the mucosa, submucosa, and crypt, and decreased mucins expression in the colon, while APs treatments effectively ameliorated the above symptoms of inflammation induced by DSS. TNF- α , IL-1 β , and IL-6 secretion were significantly reduced in groups treated with APs polysaccharides, while AP-3 HD treatment group showed the best protective effects. Furthermore, COX-2, iNOS, and NF- κ B signalling proteins (p-p65 and p-I κ B α) were significantly downregulated, while ZO-1 protein expression was significantly upregulated in AP-3 treatment groups. AP-3 relatively suppressed unhealthy gut microbiota (Gammaproteobacteria and Enterobacteriaceae) and enhanced healthy gut microbiota (Allobaculum and Alloprevotella) in DSS-induced colitis mice. These findings demonstrate that ultrasonic is an effective method for modifying biopolymers, and structurally modified Jew's ear polysaccharides could be a great source of anti-inflammatory therapeutic and functional food products after further extensive research into the molecular mechanism and clinical trials.

Plenary Speech 3: Comparative Analysis of Genetic Diversity and Population Genetic Structure of an Important Medicinal Plant, Grewia Nervosa from Gazipur and Cumilla Sal Forests, Bangladesh



Prof. Ashfaque Ahmed

Department of Botany, University of Dhaka, Bangladesh

Biography: Professor Dr. Ashfaque Ahmed has completed his B.Sc. (Hons.) and M.Sc. in Plant Ecology from the Department of Botany, University of Dhaka, Bangladesh. He completed his MS in Natural Resource Management from Norway and PhD in Coastal Zone Ecology from the Department of Botany, University of Dhaka, Bangladesh. He has been working on different aspects including species diversity, genetic diversity, phytoplankton diversity, soil and water quality assessment, Ecosystem health, C-sequestration and C-reserves of plants and soils, and soil respiration of different forest ecosystems of Bangladesh namely Sundarban mangrove forests and Deciduous forests, and uses of GIS techniques and Satellite images in resource assessment, forest health, change detection of land use patterns of different ecosystems including Bangladesh, India and Nepal. He has supervised more than 20 MS and MPhil students and 1 PhD student. Currently he is supervising 4 MS and 3 PhD students. He has published more than 35 articles in different renowned journals published from Bangladesh, India, Pakistan, Nepal and Spain. He has been as the Executive Editor of Bangladesh Journal of Botany since 2021. He is currently holding the position of Secretary General of Bangladesh Botanical Society and Joint-General Secretary of Dhaka University Botany Alumni Association (DUBAA).

Abstract: The study was carried out to determine the genetic diversity and population structure of a medicinal plant Grewia nervosa (Lour.) Panigrahi from two different regions of Sal forest, where one region (Cumilla) showed more abundance of G. nervosa than Sal plant and another region (Gazipur) showed relatively less abundancet. Coupled with these intents we were also interested to find out the best genotypes which can be chosen for breeding program. With these purposes 10 RAPD and 7 ISSR loci were used in the present investigation. We found populations from Cumilla Sal forest showed significantly higher polymorphism and comparatively higher heterozygosity than that of Gazipur, very low gene flow and high differentiation among the populations of Gazipur Sal forest but moderate gene flow and less differentiation of the populations of Cumilla Sal forest. Absence of pollinators, seed dispersal agents and difference in pollinating system are assumed to be the probable reason behind these types of population differentiation.

Part III Poster Session

Materials Provided by the Conference Organizer:

- ♦ X Racks & Base Fabric Canvases (60cm×160cm, see the figure)
- ♦ Adhesive Tapes or Clamps

Materials Provided by the Presenters:

- ♦ Home-made Posters
- ♦ Posters printed by ABS 2023 Committee

Requirements for the Posters:

- ♦ Materials: not limited, can be posted on the Canvases
- ♦ Size: 60cm×160cm
- ♦ Horizontal Head: please make the conference name 'ABS 2023/ABB 2023' and the paper number 'ABS****/ABB****' as the head of the poster in order to make all the posters unified

Best Poster Presentation Selection Procedure

Selection Criteria:

- Research Quality
- Presentation Skill
- > Design

Selection Procedure:

The conference general chair will invite 10 volunteers from invited speakers, professors and experienced researchers to serve as the judges to review the posters (Note: A judge would not have a poster or know the participant exhibiting a poster)

- 2 red stickers and 2 green stickers will be provided to the judges. The red sticker stands for "Research Quality" with a value of 2 points; the green sticker stands for "Presentation Skill and Design" with a value of 1 point
- Each judge will go around the poster session and give the stickers to the poster which he/she thinks is of high quality or well designed and well presented, please be noticed that the judge cannot give 2 red or 2 green stickers to the same poster (one red and one green sticker are acceptable)
- After the poster session, the Chair will count the points from each poster and select one best poster presentation with more points. If there is a tie, the one with more red (Research Quality) stickers wins; if there is still a tie, the Chair will make the final decision

Nature of the Award

- > This award consists of free registration to the ABS/ABB2024 and a certificate
- One Best Poster Presenter will be selected after session finishes with certificate issued onsite and results demonstrated on ABS/ABB2023 website



Samples of Stickers



Poster Presentations

Time: 11:30-12:00, July 5th, 2023 Location: Grand Ballroom III, Regency Art Hotel **Chairs:** Prof. Moniruzzaman Khondker University of Dhaka, Bangladesh Bohai University; Institute for Science and Technology of Fruits and Vegetables, **Prof. Xuqiao Feng** China Potential impact of pre-cropping with rice alternative crops on flour quality of ABS4249 winter wheat (Triticum aestivum L.) in the paddy fields Dr. Seo Young OH, National Institute of Crop Science, Republic of Korea Selection of mungbean [vigna radiata (l.) wilczek] cultivars favorable for ABS4250 mechanical harvesting in southern paddy field Dr. Seo Young OH, National Institute of Crop Science, Republic of Korea Effect of herb supplementation on the egg production performance and egg quality of laying hens during late phase **ABS4288** Prof. Jianhua He, Hunan Agricultural university, China N-fertilizer application and nitrogen species in the soil during sorghum growing ABS4290 season on marginal land in Ontario, Canada Prof. Julia Lu, Toronto Metropolitan University, Canada Chemical characteristics according to aging period in Cheongtaejeon ABS4329 Ms. Mijin Jeong, Tea Industry Institute, Republic of Korea Improvement of quality attributes of canned 'Campbell Early' grape pulp by 2-ABS4351 step pasteurization Ms. Ka-Yeong Kim, Ewha Womans University, Republic of Korea Energy-budget modelling for predicting the thermal comfort for visitors of ABS4353 healing forest in the summer season Prof. Bum-Jin Park, Chungnam National University, Republic of Korea Enhancement of exercise capacity in d-galactose-induced oxidative aging mice ABS4357 by lactobacillus delbrueckii subsp. bulgaricus KSFY08 Prof. Xin Zhao, Chongqing University of Education, China A bacteriophage-resistant Enterotoxigenic *Escherichia coli* is resensitized to ABS4362 antibiotics Prof. Yan Zhou, Jiangsu Academy of Agricultural Sciences, China Evaluation of heading date of paddy rice from slanted and nadir view images ABS4274 using classification deep learning models Dr. Sang Wangyu, National Institute of Crop Science, Republic of Korea Study of rice seed recognition and classification algorithm development using ABS4276 deep learning Ms. Woo-Jin Im, National Institute of Crop Science, Republic of Korea Structural and functional insights into a lysine deacylase in the cyanobacteria ABB1301 Prof. Feng Ge, Institute of Hydrobiology, Chinese Academy of Sciences, China

ABB1311	Effect of microplastics on antibiotic resistance genes during anaerobic digestion of civil sludge Prof. Min Gou, Sichuan University, China
ABS4368	A study on the infection dynamics and prevention of gastrointestinal nematosis in yaks in Qinghai Province Prof. Jinzhong Cai, Qinghai Provincial Academy of Animal Husbandry and Veterinary Sciences, China
ABS4275	A method for diagnosing nitrogen fertilization level through spectroscopic and molecular analysis of rice leaves Dr. Jung-Il Cho, National Institute of Crop Science, Republic of Korea
ABS4369	Study on functional efficacy and underlying mechanism of 7-Geranyloxycoumarin by network pharmacology and experimental verification <i>Prof. Mi Hye Kim, Woosuk University, Republic of Korea</i>

Abstracts of Poster Presentations

ABS4249: Potential impact of pre-cropping with rice alternative crops on flour quality of winter wheat (Triticum aestivum L.) in the paddy fields

Seo Young Oh^{1,*}, Jisu Choi¹, Tae Hee Kim¹ and Seong Hwan Oh¹

¹ Paddy Crop Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, Miryang 50424, Republic of Korea

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Abstract. Double cropping is beneficial for diversifying the rotation, maximizing crop production, and increasing the profit potential of a cropping system. The objective of this study was to compare the quality and baking applicability of flour of winter wheat (Triticum aestivum L. cv. 'Jokyung') harvested under double cropping systems linked to three rice alternative crops (black soybean, sesame, and perilla) in the paddy fields of the southern part of Korea. The color value (L*, a*, and b*) and the whiteness index of the flour changed according to the physical and chemical properties of the soils changed by pre-cropping rice alternative crops. Macro- and micro-nutrient content of wheat flour was generally higher in the wheat grown in rice alternative pre-cropped fields than in the wheat grown in the rice pre-cropped field. Particularly, the P, Mg, Zn and Cu contents were higher in wheat harvested from the black soybean pre-cropped field. Crude protein content of the wheat flour was higher in wheat harvested from rice alternative pre-cropped fields than from rice pre-cropped field, and total starch was higher in wheat harvested from the black soybean and perilla pre-cropped fields. In addition, the dry gluten content of flour from rice alternative pre-cropped fields was significantly higher than from rice pre-cropped field. Among the mixograph parameters, the midline peak time (MPT) was shorter in wheat grown in black soybean and perilla pre-cropped fields than in wheat in rice pre-cropped field. The decrease of protein content causes mixing time longer, resulting that the greater effort should be required to develop the dough. Based on these results, it is concluded that pre-cropping of the rice alternative crops in the crop rotation is expected to have a significantly positive impact on improvement of flour quality of wheat, even though it is possible that it makes the bakery product slightly dark.

Keywords: Double-cropping systems, Flour quality, Paddy field, Rice alternative crops, Winter wheat

Acknowledgements: This work was carried out with the support of 'Research Program for Agriculture Science (Development of cropping systems related to mung bean in paddy field of southern area, PJ016987012023)', Rural Development Administration, Republic of Korea.

ABS4250: Selection of mungbean [*vigna radiata* (l.) wilczek] cultivars favorable for mechanical harvesting in southern paddy field

Seo Young Oh^{1, *}, Jisu Choi¹, Tae Hee Kim¹ and Seong Hwan Oh¹

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Abstract. Legume seeds constitute an essential part of the human diet as they are excellent sources of proteins, bioactive compounds, minerals, and vitamins, in comparison with cereals. Mungbean [Vigna radiata (L.) Wilczek] is a crop belonging to the leguminosae family, and one of the most important pulse crops next to soybean (Glycine max L.) and red bean (Phaseoulous vulgaris L.) in Korea. Moreover, its characteristics of relatively drought-tolerant, low-input chemical fertilizer, and short growth cycle (70~80 days), the mungbean is widely cultivated in many Asian countries including China, India, and Korea. In this study, growth characteristics and yield amongst four cultivars of mungbean were checked to select cultivars suitable for mechanical harvesting in paddy fields in the southern region. When four cultivars of mungbean ('Dahyun', 'Sanpo', 'Areum', and 'Dado') were cultivated in rice fields, the flowering time was around 50 days after sowing, although it was 3 days earlier in 'Dahyun' than in other cultivars. Plant height was greater than 55cm in 'Dahyun' and 'Sanpo', and was less than 50 cm in 'Dado'. The number of pod per plant was the highest 36.8 in 'Dado', 28 in 'Dahyun' and 'Areum', and the lowest 23 in 'Sanpo'. The pod height was as high as 11.2 cm in 'Sanpo', and as low as 5.0 cm or less in 'Dado' and 'Dahyun'. The 100-seeds weight was the heaviest with 5.06g in 'Areum', while 4.3~4.4g in other three cultivars. 'Areum' was a cultivar with high starch content, and its seed size was medium to large. However, it was not suitable for cultivation in paddy fields because it lodged easily by rain or weak wind. On the other hand, 'Dado' and 'Sanpo' showed strong in paddy field. In particular, 'Dado' has a high yield compared to other cultivars because it has a lot of pods. Despite the weak characteristics of the lodging, 'Dahyun' seems advantageous for combine harvesting due to its large plant height and pod height, and favorable for high yields due to the rapid flowering and large number of pods.

Keywords: Dahyun, Mechanical harvest, Mungbean (Vigna radiata Wilczek), Paddy field

Acknowledgements: This work was carried out with the support of 'Research Program for Agriculture

Science (Development of cropping systems related to mung bean in paddy field of southern area, PJ016987012023)', Rural Development Administration, Republic of Korea.

ABS4288: Effect of herb supplementation on the egg production performance and egg quality of laying hens during late phase

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Abstract. The purpose of this investigation is to study the effect of traditional Chinese medicine ultrafine powder on laying performance and product quality of laying hens in the later stage of laying, A total of 288 Xinyang black laying hens at 43 week old were randomly divided into four groups with 8 replicates in each group and 9 birds in each replicate. The Laying hen of control group was fed with basic diet, and the experimental group was supplemented with 0.5% motherwort or 0.25% privet seed or 0.25% dandelion. The trial was lasted for 120 days. Collect egg samples every 30 days to determine the egg quality. The results show that the experimental treatment had no significant effect on the egg laying production (P > 0.05), but had a significant effect on the average daily feed intake and feed egg ratio from 1 to 30 days (P < 0.05). Compared with the control group, the average feed intake and feed egg ratio of dandelion group were significantly lower (P < 0.05). The experimental treatment had significant effects on albumin height, haugh unit, egg yolk colour, eggshell strength and eggshell thickness (P < 0.05). Compared with the control group, on the 30th day of the experiment, the proportion of egg yolk, the height of protein in motherwort group was significantly increased (P <0.05); On the 60th day of the experiment, the protein height, ha unit and eggshell strength of motherwort group was significantly increased (P < 0.05). The content of egg yolk cholesterol in dandelion group decreased significantly on the 60th day of the experiment (P < 0.05). In conclusion, the ultra-fine powder of traditional Chinese medicine can improve the feed conversion rate of laying hens to a certain extent. and improve the laying performance by decreased feed cost, improve the egg quality by the index of the albumin height, haugh unit, eggshell strength and yolk ratio, and it also reduced the content of yolk cholesterol.

Keywords: Laying performance, Egg quality, dandelion, motherwort, privet seed

ABS4290: N-fertilizer application and nitrogen species in the soil during sorghum growing season on marginal land in Ontario, Canada

Julia Lu^{*} Toronto Metropolitan University, Canada *Corresponding author: julialu@torontomu.ca **Abstract.** Nitrogen can take various forms as it cycles through the environment. Fertilizer application is one of the most common agricultural practices that helps plant growth and increase crop yields. Plants, however, take up only a fraction of the fertilizer applied and the unused N can be released into the surface environment with unintended consequences for water and emitted to air, as nitrous oxide, contributing to global warming. This research focuses nitrogen species in soils during the sorghum growing season. Soil samples were collected from agricultural and marginal land fields at three different times during a growing season: Before Planting (BP), After Fertilizer Application (AFA), At Harvest (AH). Plant usable (as water leachable nitrogen species) and unusable nitrogen species in the soil samples were analyzed using calorimetric and Kjeldahl methods. The results show that the plant-usable nitrogen in the soil and that, for the plant-usable nitrogen, the concentration in the soils varies with the land type and collection time; the level in the soils increased after N-fertilizer application but the increase was as not proportional to the rate of fertilizer application and it decreased to that in the soil before fertilizer application at harvest. Data analysis shows that heavy precipitation affects the loading of plant usable nitrogen in the soils, especially in those from marginal land.

Keywords: Nitrogen species, Soil, Marginal land, nitrogen fertilizer, Sorghum

ABS4329: Chemical characteristics according to aging period in Cheongtaejeon

Mijin Jeong^{1*}, Eunhye Kim¹, AhYoung Jeong¹, Gwangyeon Gi1, Seul Lee¹, Hyunseok Park¹, Soojin Jeong¹, Jeong-Yong Cho², Sook Joo Ko¹

¹Tea Industry Institute, Jeollanamdo Agriculture Research and Extension Services, Republic of Korea ² Department of Integrative Food, Bioscience and biotechnology, Graduate School Chonnam National University

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Abstract. *Cheongtaejeon*, a traditional Korean tea, registered as a national important agricultural heritage systems in 2018, is known as a coin-shaped posted-fermented tea. Several studies indicated that this tea is fermented during aging to enhance taste with flavor and aroma. However, studies on fermention characteristics of *Cheongtaejeon* during aging are limited. In this study, morphological and physicochemical characteristics of *Cheongtaejeon* according to the aging period were investigated. Various *Cheongtaejeon* having different aging period (2021~2015, aging 0 to 6 years) were collected from five manufacturers located in Jangheung County. The morphological results indicated that the weight of *Cheongtaejeon* decreased in 1 year of aging and then did not change significantly. The average diameter of *Cheongtaejeon* was 4.0 cm and the thickness was 1.1 cm, and these factors did not change significantly during the aging. During the aging of *Cheontaejeon*, Hunter L and b values of tea leaves decreased and Hunter a value increased, which was similar to the color values of infused tea. The soluble solid content in *Cheongtaejeon* was similar, although it was slightly differed according to different aging period and manufacturers. However, the total amino acid content was observed depending on the manufacturer and the aging period. The total phenolic and total flavonoid content

tended to decrease as the aging period increases, suggesting that the content decreases by inanimate or biological oxidation during the aging of *Cheongtaejeon*. The caffeine and gallic acid contents different on the manufacturer and the aging period, but did not trend according to the aging period. The contents of total catechins and non-ester type catechins such as EC, EGC tended to decrease by increase of the aging period before *Cheongtaejeon*. In variable importance in projection (VIP) result, Hunter L value, Hunter a value, and GC, EGC, and EC were analyzed as the main factors that distinguish from the aging period, the better the color, taste, aroma, and overall preference, but the lower the tea leaves after the rainforest. These results indicated that several physicochemical characteristics of *Cheongtaejeon* changed during the aging. However, a systematic studies on the chemical, biochemical, and microbial properties of *Cheongtaejeon* during the aging should be further performed. The results of this study are expected to be used as basic information for quality improvement along with the establishment of a standardized manufacturing process of *Cheongtaejeon*.

Keywords: *Cheongtaejeon,* aging period, Chemical characteristics, PLS-DA, variable importance in projection (VIP)

ABS4351: Improvement of quality attributes of canned 'Campbell Early' grape pulp by 2-step pasteurization

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Abstract. Retort processing is an essential technique in the food industry to achieve food safety and extend shelf life. However, optimization of processing conditions should be considered to minimize the heat damage to food materials. In this study, 2-step pasteurization, a method of heating at a relatively low temperature and then heating at a higher temperature, was applied for canning 'Campbell' Early' grape pulp and the impacts on the quality characteristics were observed. The grape pulp was processed with various pasteurization conditions by different treatment temperatures (81°C, 91°C, and 101°C) at the same P-value ($P = 0.2 \text{ min at } T_{ref} = 85^{\circ}C$ and $z_c = 7.9^{\circ}C$) with two processing methods (1-step and 2-step pasteurization). After pasteurization, the quality attributes of the canned grape pulp were assessed including the berry hardness, color differences, pH, total soluble solids, and L-ascorbic acid retention. Also, the slowest heating zone, showing the lowest P-value at the center of a berry among different positions in the cylindrical can, was determined to be at 1/6 of the height (1.83 cm from the bottom) along the vertical axis. The canned grape pulp with high temperatures showed relatively poor physical properties such as berry hardness and color difference, but higher L-ascorbic acid retention. It was observed that 2-step pasteurization can decrease the differences in P-values between canned products in the retort chamber without increasing the P-value in the first pasteurization step. However, increasing heating time in the 2-step pasteurization may contribute to causing adverse chemical changes in the products, such as loss of vitamin C.

Keywords: Steam-air retort, Canned grape, 2-step pasteurization

ABS4353: Energy-budget modelling for predicting the thermal comfort for visitors of healing forest in the summer season

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Abstract. This study was conducted from June to August 2022 to validate the performance of the Healing Forest thermal comfort model and predict the thermal comfort of individuals visiting the Healing Forest in summer through energy-budget modeling. Moreover, this study demonstrates a strategy to improve thermal comfort by quantifying the potential heat stress in the Healing Forest using the comparative molecular field analysis (COMFA) model. The performance of the thermal comfort prediction model for the COMFA of the Healing Forest is evaluated by performing a field test on 177 subjects in the Healing Forest. The predicted COMFA energy budget (EB) is compared with the subject's thermal sensation vote, showing a high positive correlation (Spearman's $\rho = 0.705$). The proposed prediction model indicates that the EB tended to be high throughout June. Furthermore, it highlighted that extreme caution should be exercised at points and times in the 120–200 Wm⁻² range. In July, the best scenario was a cloudy morning, and other times were included in the range of caution. Overall, August was similar to June and July. However, August exhibited a wider range of thermal comfort compared to July. The average thermal comfort in August was determined to be higher than that in July. Measures were proposed to improve the thermal environment in relation to space management and visitors to the Healing Forest by providing the EB information based on the Healing Forest thermal comfort prediction model. Visitors can prevent thermal diseases by preparing for heat stress in advance. In addition, the prediction model can contribute to the improvement of forest operations and visitor satisfaction by identifying the main space according to space use and increasing the thermal comfort of the space when planning a forest.

Keywords: COMFA, Heat stress, Human health, Outdoor thermal comfort, Thermal diseases

Acknowledgements: This study was carried out with the support of 'R&D Program for Forest Science Technology (Project No. 2021386B00-2323-0101) provided by Korea Forest Service (Korea Forestry Promotion Institute).

ABS4357: To avoid repeatability issues, this abstract will be available after the full paper is published in the conference proceedings.

ABS4362: A bacteriophage-resistant enterotoxigenic *escherichia coli* is resensitized to antibiotics Yan Zhou^{*}, Hui Zhang, Qiyang Wan and Hongduo Bao

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Abstract. Previously we characterized a bacteriophage vB_EcoM_JS09, against clinical isolates of Enterotoxigenic *Escherichia coli* (ETEC) and established that the bacterial lipopolysaccharide (LPS) is the receptor for these phages. Phage-resistant mutant harboured loss-of-function mutations in genes responsible for LPS biosynthesis, resulting in LPS loss and disruption of phage adsorption. The phage-resistant strain was resensitized to antibiotics including ampicillin, penicillin and cephalothin. Altogether, our data revealed the potential of phage JS09 as a candidate for phage therapy against ETEC and further supports that even though the use of phages would subsequently lead to the emergence of phage resistant bacteria, an evolutionary trade-off would make them more sensitive to antibiotics.

Keywords: Lytic bacteriophage, Phage resistance, Enterotoxigenic e. coli, Antibiotics susceptibility

ABS4274: Evaluation of heading date of paddy rice from slanted and nadir view images using classification deep learning models

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Abstract. The evaluation of the heading date of paddy fields is an essential task in precision agriculture as it helps farmers make informed decisions about crop management practices such as fertilization, irrigation, and harvesting. In recent years, remote sensing and image processing techniques have become an important tool for monitoring crop growth and development, including the heading date of paddy fields.

In this study, we investigate the feasibility of using deep learning models to evaluate the heading date of paddy fields from slant and nadir images. Six classification deep learning models, including VGGNet, ResNet, InceptionV3, DenseNet, Xception, and MobileNet, were trained and tested on a dataset consisting of 1,497 slant images and 11,391 nadir images, each with 700+ images for each heading date class.

The experimental results demonstrate that all six models achieve high classification accuracy for both slant and nadir images. The highest overall f1-score achieved was 0.95 for nadir images using the InceptionV3 model, while the highest overall f1-score achieved for slant images was 0.98 using the

same model.

The results show that deep learning models are a promising approach for accurately evaluating the heading date of paddy fields from slant and nadir images. The study also highlights the effectiveness of the InceptionV3 model in this task, which outperformed the other models.

Overall, this study provides valuable insights into the use of deep learning models in precision agriculture and remote sensing applications. The results suggest that deep learning models can provide an accurate and efficient way to monitor the growth and development of crops, including the heading date of paddy fields, which can ultimately lead to improved crop management practices and increased crop yields.

Keywords: Rice, Deep learning, Heading date, Image

Acknowledgements: This work was funded by the Rural Development Administration (PJ016759032022).

ABS4276: Study of rice seed recognition and classification algorithm development using deep learning

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Abstract. Rice is a staple food crop that many people consume, especially in Asia. In order to predict the yield of rice, it is essential to investigate the number of grain per panicle, which is one of the major quantity components and has a high correlation with the yield. But estimating Grain number per panicle is high-intensive and time-wasting labor, because it should be counted in person. Therefore, this study proposes grain seed counting model based on YOLOv5. YOLO(You Only Look Once) is an object detection method based on CNN(Convolutional Neural Network), which is deep learning algorithm that is trained using the collected dataset. Conventional CNN consists of numerous iterations of matrix, so each calculation is very simple, but it takes time because it passes through several layers. But onestage-detector like YOLO is fast and accurate, and enable to perform real-time object detection. The purpose of the study is to improve the accuracy and efficiency of the seed recognition and classification process, which is essential for ensuring the quality and yield of rice crops. The study proceeds to collect and reprocess large dataset of grain images to train and evaluate the proposed algorithm. Grain images, which are not threshed from panicle, acquired with black background. Since there are many overlapping parts in not spread-not threshed images, three types of images are used to clear annotation: (1) not spread-not threshed(6~8 panicles), (2) not spread-not threshed(one panicle), (3) spread-not threshed(one panicle). Acquired grain images are randomly separated into training, validation, test sets in 8:1:1 ratio. The results show that the proposed algorithm outperforms existing methods in terms of accuracy, speed, and robustness, and also shown to be capable to make it suitable for practical

applications in the agricultural industry.

Keywords: Rice grain, Object detection, Deep learning, Agriculture

Acknowledgements: This work was supported by Rural Development Administration (Project No. PJ016759), Republic of Korea.

ABB1301: Structural and functional insights into a lysine deacylase in the cyanobacteria Feng Ge

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Abstract. Lys deacylases are essential regulators of cell biology in many contexts. Here, we have identified CddA (cyanobacterial deacetylase/depropionylase), a Lys deacylase enzyme expressed in the cyanobacterium Synechococcus sp. PCC 7002 that has both deacetylase and depropionylase activity. Loss of the gene cddA led to slower growth and impaired linear and cyclic photosynthetic electron transfer. We determined the crystal structure of this depropionylase/deacetylase at 2.1 Å resolution and established that it has a unique and characteristically folded a/b structure. We detected an acyl binding site within CddA via site-directed mutagenesis and demonstrated that this site is essential for the deproprionylase activity of this enzyme. Through a proteomic approach, we identified a total of 598 Lys residues across 382 proteins that were capable of undergoing propionylation. These propionylated proteins were highly enriched for photosynthetic and metabolic functionality. We additionally demonstrated that CddA was capable of catalyzing in vivo and in vitro Lys depropionylation and deacetylation of Fru-1,6-bisphosphatase, thereby regulating its enzymatic activity. Our identification of a Lys deacylase provides insight into the mechanisms globally regulating photosynthesis and carbon metabolism in cyanobacteria and potentially in other photosynthetic organisms as well.

Keywords: Lysine deacylase, Cyanobacteria, lysine propionylation, lysine deacetylase

ABB1311: Effect of microplastics on antibiotic resistance genes during anaerobic digestion of civil sludge

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Abstract. Civil sludge is widely regarded as a reservoir for emerging pollutants such as microplastics (MPs) and antibiotic resistance genes (ARGs). As one of the important ways of civil sludge treatment, anaerobic digestion (AD) has been reported with the ability of ARGs reduction. It has been found that

the MPs presence in sludge can affect the performance of mesophilic AD for civil sludge via changing the microbial community structure. Moreover, ARGs enrichment and spread by MPs are frequently found in various water and soil environments. However, the effects of MPs on ARGs during AD of civil sludge are rarely reported. In this study, four AD reactors for treating civil sludge were constructed under mesophilic (35°C) and thermophilic (55°C) conditions, respectively. After adding different single MPs (PVC, PE and PS), these reactors were operated continuously with changed MPs concentration (low stress treatments: 0~1~10 mg/g TS; high stress treatments: 0~100~10 mg/g TS), and their performances were compared. Then, the effects of MPs on microbial community structure and ARGs in all reactors were investigated by 16S rRNA gene and metagenomic high-throughput sequencing techniques, respectively. The results showed that MPs with different concentrations had little effect on the thermophilic AD, but significantly inhibited the methane production in all mesophilic reactors. PVC in low stress treatments and PS in high stress treatments had the strongest inhibition on methane production of mesophilic AD, respectively, with reduction rate of 10.14~17.32% and 6.95~16.14%. Compared with the blank reactor, the presence of MPs significantly reduced the α diversity of microbial community in mesophilic reactors. The composition of dominated genera was similar in MPs reactors but their relative abundances were significantly different, which was affected by the type and concentration of MPs. Under the low concentration stress, different MPs had similar effects on the total abundance of ARGs in mesophilic and thermophilic reactors, showing the change trend of first decreasing (1 mg/g TS) and then increasing (10 mg/g TS). However, there were different changes of ARGs abundance between mesophilic and thermophilic reactors under high concentration stress of MPs. With the addition of 100 mg/g TS MPs, the total abundance of ARGs decreased in all thermophilic reactors. But when the concentration of MPs was further reduced to 10 mg/g TS, the total abundance of ARGs both in PE and PVC reactors rebounded significantly, while no change was observed in PS reactor. For all mesophilic reactors, the total abundance of ARGs exhibited the similar change trend of first increasing (100 mg/g TS) and then decreasing (10 mg/g TS). In addition, there were significantly different changes in the relative abundance of ARGs types, which depended on the digestion temperature, MPs type and MPs concentration. Correlation analysis further showed that ARGs were highly correlated with mobile genetic elements (MGEs) in each reactor, and horizontal gene transfer (HGT) induced by the presence of MPs might be the main cause of ARGs changes. This study may help to understand the effects of MPs on ARGs in AD and to limit the release of ARGs from the civil sludge into the environment.

Keywords: Mesophilic AD, Thermophilic AD, MPs stress, Microbial community, Antibiotic resistance genes, Horizontal gene transfer

Acknowledgements: This work was supported by the National Natural Science Foundation of China (No. 52070135).

ABS4368: A Study on the infection dynamics and prevention of gastrointestinal nematosis in yaks in Qinghai Province

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Abstract. Objective To investigate the infection dynamics of nematode disease in grazing yaks in Qinghai Province, and to provide a basis for formulating and optimizing prevention and cure technologies. Methods The fecal examination method, Parasitology complete dissection method and water bath method were used to isolate the parasitic stage larvae; We conducted clinical efficacy trials and prevention technology research on new prevention and treatment drugs using fecal examination and dissection methods. Result (1) Ostertagia spp., Trichostrongylus spp., Nematodirus spp., spp., Cooperia spp., Capillaria spp., Bunostomum spp., Trichuris spp., Marshallagia. Oesophagostomum spp., Chabertia spp. The overall pattern of 10 dominant genera of digestive tract nematodes in yaks is as follows: during the parasitic stage, the larval load gradually increases from August to December, and the parasitic peak appears from December to February of the following year, reaching its peak from December to January of the following year; During the period from January to June, as the larval load during the parasitic stage decreases month by month, the adult load increases month by month, and reaches its peak throughout the year from April to June, with a clear spring peak. There is a significant larval parasitism climax in the host during winter, an adult parasitism climax in spring, and a secondary climax in autumn. The overall infection dynamics of yak nematodes in Dari and Zhiduo areas are similar to those in Qilian, but the spring peak maintenance time of adult nematodes in Qilian area is longer than that in Dari and Zhiduo areas. The peak maintenance time of adult insects in Dari and Zhiduo regions is relatively short. (2) Established a technique for eliminating parasitic larvae of yak nematodes in winter; Observation on the effect of different control schemes on yak Parasitic disease and weight gain; High efficiency and low residue control technology for main Parasitic disease of yaks was established. Conclusion The research results indicate that using the same method to study the infection dynamics of adult and parasitic stage larvae of yak digestive tract nematodes in different regions of Qinghai Province has confirmed the causal relationship between the end of larval development obstruction (stagnation) and spring adult climax, clarified the major theoretical issue of the origin of spring adult climax, and laid a reliable theoretical foundation for formulating effective prevention and control strategies. According to the results of epidemiological studies, the goal is to control the spring death of grazing yaks caused by Parasitic disease and to curb the climax of adults in spring; The clinical evaluation and prevention experiments of different antiparasitic drugs on yak nematode disease provide solid support for the prevention and treatment of yak nematode disease. It is feasible to adopt timely prevention and control measures to drive away the dominant parasitic stage larvae in the host body. During January and February of each year, the use of highly effective drugs to carry out planned pest control for yaks in winter and the application of highly effective and low residue control new technology can effectively curb the emergence of the peak of Parasitic disease in spring, significantly reduce the death of released yaks in spring, Significant ecological, social, and economic benefits can be achieved, which is an important technical measure to ensure the healthy, green, and sustainable development of grassland animal husbandry.

Keywords: Gastrointestinal nematodes, Infection dynamics, Yak, Larvae, Prevention and control measures

ABS4275: A method for diagnosing nitrogen fertilization level through spectroscopic and molecular analysis of rice leaves

Jung-Il Cho^{1,*}, Dong-Won Kwon¹, Wan-Gyu Sang¹, Hyeok-Jin Bak¹, Sung-Yul Chang¹, Woo-Jin Im¹ ¹ National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

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Abstract. Applying the appropriate amount of nitrogen fertilizer required for rice cultivation is essential to achieve optimal growth, quality and yield and to reduce greenhouse gas emissions in paddy fields. Therefore, it is necessary to develop a technology that can check whether an appropriate amount of fertilizer is applied in paddy fields. In this study, we tried to derive a method for diagnosing nitrogen fertilization level using spectroscopic diagnosis, physiological analysis, and molecular indicator genes. Nitrogen fertilization treatment was performed in a greenhouse by dividing into five treatment conditions: no fertilization (N0), low fertilization (N0.5), standard fertilization (N1.0), excessive fertilization (N1.5), and double fertilization (N2.0), respectively. Growth characteristics analysis was investigated by nitrogen fertilization levels and growth stages, and the height of the canopy was analyzed using a laser scanner. Physiological and spectroscopic analyses were performed by analyzing chlorophyll and sugar contents and measuring SPAD and leaf spectrometer on rice leaves. In addition, real-time PCR experiment was performed to check the relative expression levels of several known nitrogen metabolism-related genes. These results suggest that spectroscopic techniques can be helpful in diagnosing the level of nitrogen fertilization in rice paddy fields.

Keywords: Rice, Nitrogen, Fertilization level, Spectroscopic diagnosis

Acknowledgements: This work was carried out with the support of "R&D Agenda Agriculture and Technology Development Program (Project No. PJ0160342023)" of the Rural Development Administration, Republic of Korea.

ABS4369: Study on functional efficacy and underlying mechanism of 7-Geranyloxycoumarin by network pharmacology and experimental verification

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Abstract. Applying the appropriate amount of nitrogen fertilizer required for rice cultivation is essential to achieve optimal growth, quality and yield and to reduce greenhouse gas emissions in paddy fields. Therefore, it is necessary to develop a technology that can check whether an appropriate amount of fertilizer is applied in paddy fields. In this study, we tried to derive a method for diagnosing nitrogen fertilization level using spectroscopic diagnosis, physiological analysis, and molecular indicator genes. Nitrogen fertilization treatment was performed in a greenhouse by dividing into five treatment conditions: no fertilization (N0), low fertilization (N0.5), standard fertilization (N1.0), excessive fertilization (N1.5), and double fertilization (N2.0), respectively. Growth characteristics analysis was investigated by nitrogen fertilization levels and growth stages, and the height of the canopy was analyzed using a laser scanner. Physiological and spectroscopic analyses were performed by analyzing chlorophyll and sugar contents and measuring SPAD and leaf spectrometer on rice leaves. In addition, real-time PCR experiment was performed to check the relative expression levels of several known nitrogen metabolism-related genes. These results suggest that spectroscopic techniques can be helpful in diagnosing the level of nitrogen fertilization in rice paddy fields.

Keywords: Rice, Nitrogen, Fertilization level, Spectroscopic diagnosis

Acknowledgements: This work was carried out with the support of "R&D Agenda Agriculture and Technology Development Program (Project No. PJ0160342023)" of the Rural Development Administration, Republic of Korea.

Part IV Oral Sessions

General Guidelines

- ♦ All presentation times are shown in China Standard Time (GMT+8:00);
- ♦ Duration for Invited Oral Presentation: 25 Minutes of Presentation including 3-5 Minutes of Q&A;
- ♦ Duration for Regular Oral Presentation: 15 Minutes of Presentation including 2-3 Minutes of Q&A;
- ♦ All presenters are requested to reach the Session Room prior to the schedule time and complete their presentation on time;
- ♦ Presenters should prepare Power Pointer or PDF Files for Presentation with Paper ID (ABS****/ABB****) marked in the last page;
- ♦ Signed and stamped electronic presentation certificate would be issued after presentation.

Offline Oral Presentation Guidelines

Devices Provided by the Conference Organizer:

- ♦ Laptops (with MS-Office & Adobe Reader) & Projectors & Screen
- ♦ Laser Sticks
- \diamond Microphones
- Please send us the PowerPoint once it is ready and have the PPT back up in a U-disk. For presenters who do not send the PowerPoint, please save it in the laptop of the corresponding session 15 min in advance. Kindly tell the Session Chair (before the start of your session) that you are present.

Online Oral Presentation Guidelines

- ♦ Online Oral Presentation will be conducted via Microsoft Teams Meeting.
- ☆ If a presenter is not able to show up via Teams, the session chair / conference secretary will play the pre-recorded video presentation during his/her scheduled presentation time, if listeners have questions about the presentation, please contact the conference secretary to forward the questions.
- ☆ If a presenter cannot show up on time or has problem with internet connection, the session chair has the right to rearrange his/her presentation, and let the next presentation start.

Best Oral Presentation Selection Procedure

ONE best presentation will be selected from EACH session based on the following criteria:

- ✓ Research Quality
- ✓ Presentation Performance
- ✓ Presentation Language
- ✓ PowerPoint Design
- ✓ Effective Communications

Selection Procedure

- An assessment sheet (see picture) will be delivered to listeners before the session starts;
- When the session finishes, each listener is required to fill the sheet (he/she can vote for two excellent presentations) and give it to the Session Chair;
- For the online presenters, the assessment sheet would be sent in advance via e-mail. Kindly send us the filled form in electronic version within ONE HOUR after the session completed;

The Session Chair will count the votes and select one best oral presentation with more votes. If \geq there is a tie, the Session Chair will make the final decision.

Best Oral Presentations Award

The Best Oral Presenter from each session will receive an official certificate and a free registration to the ABS/ABB2024.

Samples of Assessment Sheet

ABS/ABB2023 Oral Presentation Assessment

Dear participants,

Thanks for your support. Kindly read the instructions below for best oral presentation selection:

- You could select two best oral presentations with this form, and kindly fill in the form when all the • speakers finish the presentations;
- 3 Best Oral presentation would be selected separately from Session 1 to Session 3;
- To ensure the fairness of the selection, one person could fill in only one form, kindly fill in the form by yourself and fill in your paper/abstract ID;

You can refer to the following criteria for best oral selection:

Items	Assessment
Content	Right, Logical, Original, Well-Structured
Language	Standard, Clear, Fluent, Natural
Performance	Spirited Appearance, Dress Appropriately, Behaves Naturally
PowerPoint	Layout, Structure, Typeset, Animation, Multimedia
Reaction	Build a Good Atmosphere, Speech Time Control Properly

Please write down the paper ID and give reasons for your recommendation:

Paper ID	Reasons
	Evoluted by (Denen ID)

Evaluated by _____ (Paper ID: _____)

Note: Please fill it out and give it to the Session Chair or assistant so that the Best Oral could be selected.

Session 1_ Applied Biochemistry and Biotechnology

Time: 14:00-17:40July 5th, 2023(China Standard Time (UTC/GMT+8:00)Online Room Link: http://www.academicconf.com/teamslink?confname=ABS2023Offline Location:Grand Ballroom III, Regency Art HotelSession Chairs:14:00-15:30Prof. Huamin Wang, Hainan Vocational University of Science and Technology, China15:45-17:40Prof. Fufeng Liu, Tianjin University of Science & Technology, China

14:00-14:15	ABS4218	Robust and recyclable cross-linked enzyme aggregates of sucrose isomerase for isomaltulose production <i>Prof. Fufeng Liu, Tianjin University of Science & Technology, China</i>
14:15-14:30	ABS4261	Suppressor analysis of essential genes by using suicide plasmid-based conditional alleles in <i>Pseudomonas aeruginosa</i> <i>Prof. Jianhua Liu, Zhejiang Ocean University, China</i>
14:30-14:45	ABS4337	Bioprotection by secretion of pulcherriminic acid Dr. Matthias Sipiczki, University of Debrecen, Hungary
14:45-15:00	ABS4269	Effects of spray drying and freeze drying on the structure and emulsifying properties of yam soluble protein: a study by experiment and molecular dynamics simulation <i>Prof. Youlin Xue, Liaoning University, China</i>
15:00-15:15	ABB1300	Engineering tolerance to stresses for improved bioproduction: yeast as a case study <i>Dr. Xin-Qing Zhao, Shanghai Jiaotong University, China</i>
15:15-15:30	ABS4347 (Online)	Application of attenuated lactic acid bacteria in kombuchaproductionDr. Seng Joe Lim, Universiti Kebangsaan Malaysia, Malaysia
15:30-15:45		TEA BREAK
15:45-16:10	ABS4359 (Online)	Metabolic engineering glycogen structure by OsGBSSI expression in Escherichia coli. Prof. Kimiko Itoh, Niigata University, Japan
16:10-16:25	ABB1315	Rice straw addition improves the stability and efficiency of high-solids anaerobic digestion of dewatered sludge via creating balanced function microbial community Dr. Zhao-Yong Sun, Sichuan University, China
16:25-16:40	ABB1307	Response mechanism of acetate- and propionate-degradation microbial community to ammonia stress in continuous methanogenic reactors <i>Prof. Yue-Qin Tang, Sichuan University, China</i>
16:40-16:55	ABB1310	Effect mechanisms of ENA5, ASP3, and CRZ1 on high temperature and high salt tolerance in <i>Saccharomyces cerevisiae</i> <i>Dr. Caiyun Xie, Sichuan University, China</i>

16:55-17:10	ABB1302	NanoconfinedliquidphasenanoextractionbasedoncarbonnanofibersDr. Yilin Zou, Sun Yat-Sen University, China
17:10-17:25	ABB1297 (Online)	Oncometabolites fuel cancer progression and metastasis: Mimetic of metabolites (MOM) as anticancer drugs Prof. Nilesh Kumar Sharma, Dr. D.Y. Patil Biotechnology & Bioinformatics Institute, India
17:25-17:40	ABS4306	Altered gut microbiota associated with hemorrhage in chronic radiation proctitis Dr. Liangzhe Liu, Guangdong Pharmaceutical University, China

Abstracts of Oral Session 1

ABS4218: Robust and recyclable cross-linked enzyme aggregates of sucrose isomerase for isomaltulose production

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Abstract. A novel cross-linked enzyme aggregates (CLEAs) catalyst was produced by precipitation and cross-linking sucrose isomerase (SIase) for isomaltulose production. The effects of precipitants and cross-linkers on the catalytic performance of the CLEAs were first evaluated. Then, bovine serum albumin (BSA) and trehalose (Tre) were used as additives and three immobilized enzymes, cross-linked SIase aggregates (CLSIAs), CLSIAs-BSA and CLSIAs-Tre were obtained. All the immobilized preparations exhibited superior thermal stability, pH tolerance, and storage stability compared to the soluble SIase, and showed excellent reusability. These samples still retained more than 61% of their initial activity after ten reuse cycles, with CLSIAs-BSA retaining up to 91.7%. The conversion ratios of sucrose into isomaltulose using CLSIAs-BSA reached 88.4% and 81.2% with sucrose and sugar cane juice as substrate, respectively. Therefore, CLSIAs are a highly effective biocatalyst for the preparation of isomaltulose with great potential for industrial applications.

ABS4261: Suppressor analysis of essential genes by using suicide plasmid-based conditional alleles in *Pseudomonas aeruginosa*

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Abstract. *Pseudomonas aeruginosa* is a Gram-negative bacterium that is an opportunistic pathogen in immunocompromised patients and causes life-threatening lung infections in individuals with cystic

fibrosis. Lipopolysaccharide (LPS) is a major cell wall component that plays a critical role in drug resistance, infection, and host inflammatory response. LPS is composed of three structural domains, namely the lipid A, core oligosaccharide, and O-antigen. Lipid A anchors the LPS in the outer portion of the outer membrane. Core oligosaccharide bridges the lipid A and O-antigen. O-antigen is dispensable: LPS with and without O-antigen is known as smooth and rough LPS, respectively. On the other hand, lipid A and core oligosaccharide are essential for cell growth. Essential genes involved in LPS biosynthesis are potential targets for novel drug development. LpxA and LpxC are the first two enzymes in lipid A biosynthetic pathway, which are essential for viability. They have been the focus of target-directed antibiotic discovery projects in many pharmaceutical and academic groups for decades. However, no inhibitor has been currently approved for therapeutic use. This is partly because inhibition of LpxA and LpxC is found be suppressed by a mutation in FabZ. This result indicates that suppressible essential genes are less favorable targets for drug development. Tn-seq analysis has identified ~350 essential genes in P. aeruginosa PAO1. However, systematic suppressor analysis of these genes has not been done, owing largely to conditional alleles of most of these essential genes are not available. Genome-wide suppressor analyses of essential genes in yeast have concluded that at least 17% - 27% essential genes are suppressible. Systematic suppressor analysis of essential genes not only provides insight into strategies adopted by cells to restore target gene functions, but also identifies the insuppressible or hard to be suppressed essential genes as suitable targets for novel drug development. For construction of conditional allele of essential genes suitable for suppressor analysis in P. aeruginosa, we have developed a three-step protocol. Two plasmids are used in this method: a deletion plasmid that contains a deletion allele of target genes cloned in an integration plasmid with positive and negative selection markers of Gm^R and sacB and a rescue plasmid that bears a native promoter controlled complementing copy of the target genes in a plasmid with a *ts*-replicon and Tc^{R} . The three steps of the ts-mutant strain construction include: (1) Electroporation transformation of deletion plasmid into *P. aeruginosa* and selection of single-crossover integrants on LB gentamycin plate; (2) Introduction of rescue plasmid into the resulting integrants and selection of transformants on tetracycline plate at permissive temperature; and (3) Counter-selection of the resulting transformants on LB sucrose plate via sacB marker for deletion plasmid loop-outs. As a result, half of the loop-outs contain a deletion allele on chromosome that would exhibits *ts* phenotype due to the complementary copy on ts-plasmid. By using this three-step protocol, we have constructed a ts-allele of gmhB gene essential for heptose synthesis in P. aeruginosa (Yang et al 2022 Appl Environ Microb 88:e84022). We show that gmhB(Ts) fails to assemble heptose-containing core oligosaccharide and ceases growth at restrictive temperature. Suppressor analysis indicates that overexpression of *fbp* rescues the growth defect of gmhB(Ts) with a heptose-less inner core. To ensure that this method is applicable to many essential genes of interest in *P. aeruginosa*, we are performing suppressor analysis of *fabA*, *lpxH*, etc. In this occasion, I will present you the results that we obtained recently and hope to convince you that this method is suitable for systematic deletion and suppressor analysis of essential genes in P. aeruginosa.

Keywords: Essential gene, Conditional allele, Suppressor, Lipopolysaccharide, Pseudomonas aeruginosa

ABS4337: Bioprotection by secretion of pulcherriminic acid

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Abstract. Pulcherriminic acid is a cyclic dipeptide. Its hydroxamic acid group chelates Fe3+ to form a reddish brown complex referred to as pulcherrimin. The reaction can take place within the cytoplasm of the producer (its cells turn red) or in the environment (extracellularly), if the pulchrimic acid is secreted. Since the complex is insoluble, its production immobilises the free iron in the environment and makes it inaccessible for other microorganisms. The lack/low concentration of free iron adversely affects the growth of many microbes or even kills their cells/hyphae and spores. Many strains of the yeast genus Kluyveromyces and the species of the pulcherrima clade (recently merged in one species) of Metschnikowia can secrete pulcherriminic acid. Due to their antimicrobial antagonism, these yeasts can be used as biological agents against fungi causing plant diseases and/or postharvest decay (e.g. Botrytis, Penicillim, Mucor). The antagonistic Metschnikowia strains have two or more heterogeneous sets of a cluster of four genes (the PUL genes) that encode the enzymes required for the synthesis and secretion of pulcherriminic acid. In spite of the presence of multiple copies of the PUL genes, the strains are prone to segregate (resulting in segregants producing no or low amounts of pulcherrimin), but the segregation is usually reversible (bidirectional). The antagonistic activity can be increased by selecting stable highly pigmented (highly antagonistic) segregants and hybridisation.

Keywords: Antagonistic yeasts, Bioprotection, Plant pathology

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ABS4269: Effects of spray drying and freeze drying on the structure and emulsifying properties of yam soluble protein: a study by experiment and molecular dynamics simulation

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Abstract. This study focused on the effects of freeze drying (FD) and sprays drying (SD) on the structure and emulsifying properties of yam soluble protein (YSP). The results showed that the surface hydrophobicity (Ho) value, free sulfhydryl group (SH) content, turns content, denaturation temperature

and enthalpy value of spray-dried YSP (SD-YSP) were higher than freeze-dried YSP (FD-YSP), but the apparent hydrodynamic diameter (Dh) value of SD-YSP was smaller. The smaller Dh, higher Ho and free SH led to higher percentage of adsorbed proteins and stronger binding between protein and oil droplet in emulsions. Thus, the emulsifying properties of SD-YSP were better, and the SD-YSPstabilized emulsion had better dynamical rheological properties. Molecular dynamics (MD) simulations suggested that some intramolecular disulfide bonds and hydrogen bonds of dioscorin were broken, and some helices transformed into turns during the SD process. These structural changes resulted in better thermal stability and emulsification properties of SD-YSP.

Keywords: Dioscorin, Drying method, Emulsifying property, Molecular dynamics simulations

ABB1300: Engineering tolerance to stresses for improved bioproduction: yeast as a case study

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Abstract. Microbial fermentation has great potential for sustainable bioproduction. To improve fermentation efficiency, it is highly desired that microbial strains are tolerant to various stress conditions that are commonly encountered. These stressors include high temperature, low pH, toxic products, high osmotic stress, among others. Engineering stress tolerance is critical for sustainable bioproduction. In this talk, I will introduce how we improve yeast stress tolerance by both process engineering and metabolic engineering. We demonstrated the beneficial effect of zinc sulfate in yeast stress tolerance, and we further improve yeast stress tolerance by metabolic engineering using the targets discovered by multi-omics analyses. Further prospects on sustainable production using robust microbial cell factories are also provided, especially using lignocellulosic biomass as feedstock.

Keywords: Stress Tolerance, Microbial Cell Factories, Yeast Fermentation, Sustainable Bioproduction, Biomass

ABS4347: Application of attenuated lactic acid bacteria in kombucha production

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Abstract. Kombucha is a beverage made from fermentation of tea (Camellia sinensis) and sugar, using a symbiotic culture of bacteria and yeast (SCOBY). Consumption of kombucha is believed to be beneficial in human health due to its antioxidant properties and organic acid content. Attenuated lactic acid bacteria as a supplement brings about various health benefit, however, the effect of its application in kombucha production has not been determined. Therefore, this study optimised the supplementation

of attenuated lactic acid bacterial types (three types: LAB 1, LAB 2 and LAB 3) and their concentrations (1.0, 2.0 dan 4.0 g/L) in kombucha production using a 3×3 factorial experimental design. The physicochemical properties include pH, colour, sugar content, reducing sugar content, ethanol content and organic acid content in the produced kombucha were determined and its antioxidant activity was studied through DPPH free radical scavenging activity, ferric reduction antioxidant power (FRAP) and ABTS free radical scavenging activity. pH value of the control kombucha (without attenuated LAB) and kombucha supplemented with 3 different types of attenuated LAB at different concentrations showed a small range of differences. The colour of control kombucha showed the lowest lightness (L*) and the highest a* and b* values compared to kombucha supplemented with attenuated LAB. The changes in sugar and reducing sugar content were inconsistent according to the increase in the concentration of attenuated LAB. The results of the ethanol content were in the range of 0.051 to 0.081%. The highest acetic acid and lactic acid content was found in kombucha supplemented with 4.0 g/L LAB 1, comparing with other samples. The antioxidant activity of kombucha supplemented with attenuated LAB exhibited a decrease as the concentration increased. DPPH and ABTS free radical scavenging activity of control kombucha was the highest compared to other kombucha samples. Kombucha supplemented with 1.0 g/L LAB 1 was selected for sensory evaluation due to the highest content of acetic acid and lactic acid compared to other attenuated LAB and at concentration of 1.0 g/L as well as the highest antioxidant activity compared to other concentrations. In short, control kombucha was the favourite choice of most of the panellists.

Keywords: Kombucha, Attenuated lactic acid bacteria, Probiotic, Physicochemical properties, Antioxidant activity

ABS4359: Metabolic engineering glycogen structure by OsGBSSI expression in *Escherichia coli*. Kimiko Itoh¹*

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Abstract. Glycogen is a storage polysaccharide commonly found in bacteria and animals, consisting of a linear chain of α -1,4 glycosidic linkages of glucose with many branches due to α -1,6 glycosidic linkages. In recent years, glycogen has been studied not only as a nutritional source but also for its functional properties. Various changes in the structure of glycogen may enable the development of new uses of glycogen and novel application.

Glycogen metabolism in *Escherichia coli* is mediated by GlgC (ADP-Glucose pyrophosphorylase), which synthesizes ADPG, a substrate of glycogen, from glucose-1-phosphate (G1P), GlgA (Glycogen Synthase, GS), GlgB (Glycogen Branching Enzyme), which transfers one glucan chain to the C6 position of another, GlgX (Glycogen Debranching Enzyme), which is responsible for hydrolysis of the α -1,6 glycosidic linkage, and α -1 4 glycosidic linkages at the non-reducing end, and GlgP (Glycogen Phosphorylase), which catalyzes the hydrolysis of α -1,4 glycosidic linkages at the non-reducing end. On the other hand, the rice GBSSI (Granule-Bound Starch Synthase I) is an enzyme that catalyzes α -

1,4 glycosidic linkages using ADPG as a substrate, similar to GS, to synthesize linear chains of amylose and amylopectin of storage starch.

In this study, the OsGBSSI was introduced into *E. coli* BW25113 and various mutant strains $\Delta glgA$, $\Delta glgX$, and $\Delta glgP$ to investigate changes in the structure of the glycogen and metabolic profile of the modified glycogen producing *E. coli*. Glycogen from BW25113 expressing GBSSI showed a slight reduction in mean particle size, while OsGBSSI expressing $\Delta glgP$ showed a significant increase in mean particle size. Anion exchange-pulsed amperometric high-performance chromatography (HPAEC-PAD) was used to analyze the chain length distribution of the constituent unit chains. The results showed that in BW25113+GBSSI, the Degree of Polymarization (DP) 3-4 unit chains decreased and the DP5-11 unit chains clearly increased compared to BW25113. This suggests that GBSSI may elongate DP3-4. These results indicated that the OsGBSSI can modified particle size of glycogen, and changes in distribution of unit chains in *E. coli*.

Keywords: Glycogen, Granule-bound starch synthase, Escherichia coli, glgX, glgP, glgA

ABB1315: Rice straw addition improves the stability and efficiency of high-solids anaerobic digestion of dewatered sludge via creating balanced function microbial community

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Abstract. Sewage sludge (SS) is the main by-product eluted from wastewater treatment plants (WWTPs). Anaerobic digestion (AD) is widely used to stabilize SS by transforming organic matter into biogas, making SS a potential bioenergy source instead of solid waste requiring disposal. In this study, thermophilic high-solids anaerobic co-digestion of dewatered sludge (DS) and rice straw (RS) was conducted at a constant C/N ratio of 10 (hereafter called C/N ratio-adjusted DS); the long-term reactor performance and microbial community dynamics were compared with DS mono-digestion. The co-digestion allowed stable performance for 952 days, and biogas evolution was 402 ml/g-VTS with methane content of approximate 50% at a higher VTS loading rate of 8.0 g/kg-sludge/d. In contrast, the performance of DS mono-digestion was negatively influenced by the varied properties in DS even at a low VTS loading rate of 1-2 g/kg-sludge/d. Interestingly, the deteriorated DS mono-digestion performance was recovered and promoted by adding RS. Beta-diversity analyses revealed significant differences in the microbial community between co- and mono-digestion. The stable performance of co-digestion was attributed to more balanced function microbes in protein and cellulosic matter degradation, as a result, leading to alleviation of ammonia inhibition.

Keywords: Dewatered sludge, Thermophilic anaerobic digestion, High-solids, Microbial community, Co-digestion

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ABB1307: Response mechanism of acetate- and propionate-degradation microbial community to ammonia stress in continuous methanogenic reactors

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Abstract. Methanogenic microbial communities in anaerobic digestion (AD) are easily affected by ammonia. Previous studies have revealed ammonia inhibition on microbial flora by AD performance, but the influential mechanism of ammonia on microbial community metabolism remains poorly understood. In this study, we constructed reactors fed with acetate (AR) or propionate (PR) as the sole carbon source and gradually increased the total ammonia nitrogen (TAN) concentration during the operation to investigate the effect of TAN on methane production and the structure and metabolism of microbial communities. For AR, even at the TAN of 6 g/L, the biogas production was approximately 92% of that at the TAN of 1 g/L, suggesting the strong TAN tolerance of the acetate-degrading community enriched. Methanothrix predominated in methanogens but the dominant species was gradually replaced from M. soehngenii to M. harundinacea with the increased TAN. Dominant bacterial species changed and Proteiniphilum showed a significant positive correlation with increased TAN. The dominant microorganisms at TAN of 6 g L-1, M. harundinacea and Proteiniphilum, highly expressed genes for peroxides elimination. M. harundinacea and the second dominant methanogen Methanosarcina highly expressed both acetate cleavage and CO2 reduction pathways. Proteiniphilum and some other species in Firmicutes and Synergistetes highly expressed genes for syntrophic acetate oxidization, H2 generation, and electron transfer, suggesting they were likely acetate oxidizing bacteria (AOB) in the community. The results suggested that both acetate cleavage and CO2 reduction pathways were active in AR under high TAN stress. For PR, the propionate fed was accumulated in the reactor and the biogas production was seriously repressed when the TAN was increased to 3 g/L. The population and the activity of syntrophic POBs, Syntrophobacter fumaroxidans and Smithella, significantly decreased at the TAN of 3 g/L. The syntrophic AOB Tepidanaerobacter was the dominant AOB in all operation stages while another SOB Mesotoga increased with the increased TAN. Other candidate AOBs were detected and some of them had both acetate- and propionate oxidation activities which are worthy of further study in the future. Combined with changes in methanogens, it could be deduced that the serious repression of TAN on PR was first because of the sensitivity of propionateoxidation bacteria (POB) to TAN stress. The achievements of the study would contribute to a deeper understanding of the mechanism of microbial ammonia response and the regulation and management of the AD process.

Keywords: Anaerobic digestion, Ammonia stress, Acetate oxidation, Propionate oxidation, Meta omics

ABB1310: Effect mechanisms of *ENA5*, *ASP3*, and *CRZ1* on high temperature and high salt tolerance in *Saccharomyces cerevisiae*

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Abstract. Saccharomyces cerevisiae encounters a variety of stress conditions including high salt, high temperature, high sugar, and high ethanol during fuel ethanol production. Our previous study found that functional genes ASP3, ENA5 and transcription factor Crz1p may affect the tolerance of S. cerevisiae to multiple stresses. In this study, the expression of ASP3, CRZ1, and ENA5 was regulated in a flocculent industrial S. cerevisiae strain and the fermentation performance was evaluated under high-salt and high-temperature conditions, respectively. The tolerance mechanisms of the recombinant strains were revealed through comparative transcriptomic analysis. The results showed that the overexpression of ENA5 and/or CRZ1 or knockout of ASP3 improved the salt tolerance of the strains. Among them, the strain overexpressing ENA5 and CRZ1 produced 46.17 g/L ethanol from 137.51 g/L glucose under the high-salt condition of 1.25 M NaCl, with 99.39% higher ethanol production than the original strain. Comparative transcriptomic analysis revealed that amino acid biosynthesis such as tyrosine and tryptophan, thiamine metabolism, and MAPK signalling pathway may be closely related to high salt tolerance. In contrast, ASP3 knockout or combined with CRZ1 overexpression improved the high-temperature tolerance of the strain. Under the high-temperature condition of 44°C, ASP3 and CRZ1 dual-regulated strain produced 48.02 g/L ethanol using 105.37 g/L glucose, with 15.18% higher ethanol production than the original strain. Comparative transcriptomic analysis showed that genes involved in ribosome biogenesis and translation were significantly repressed in the recombinant strains under high-temperature stress, while heat shock protein genes as well as genes involved in the biosynthesis of NADH, purine, glycerol, and proline were significantly induced. These responses may collectively lead to the enhanced high-temperature tolerance of the recombinant strains. This study provides excellent strain resources and the theoretical basis for the subsequent construction of stresstolerant S. cerevisiae strains.

Keywords: *Saccharomyces cerevisiae*, High-temperature tolerance, High-salt tolerance, Ethanol production, Comparative transcriptomic analysis

ABB1302: Nanoconfined liquid phase nanoextraction based on carbon nanofibers

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Abstract. The point of the *in-vivo* and *in-situ* testing lies in the research and development of the pretreatment technology of innovative samples. Experimental results have proved in fact that with CNFs/CFs, it is possible to extract and preconcentrate polar (phytohormones), medium polar (ginsenosides), and nonpolar (pesticides) analytes with high recoveries and short adsorption times depending on the NCS (nanoconfined solvents) used. A needle-tip device has been realized to allow direct extraction procedures and minimally invasive testing in ripening vegetable and fruit samples, accomplishing fast and minimally invasive analyte extractions. The NLPNE technology is strong in simple operation, high stability and high extraction efficiency, besides the advantages of both SPME and the LPME. Its original phase separation technology breaks new ground in mutual-soluble two-phase extraction. In the application promotion research, the LPNE part can be regarded as a "docker", and the SPME part a "storage room". The joint efforts of LPNE and SPME will set a new trend in pollutant treatment and control.



Figure 1. Nanoconfined liquid phase nanoextraction

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ABB1297: Oncometabolites fuel cancer progression and metastasis: Mimetic of metabolites (MOM) as anticancer drugs

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Abstract. Cancer cells are highly adaptive to cellular and non-cellular factors in their microenvironment. In other way, cancer cells develop distinctive choice-based metabolites pathways that allow using of some metabolites for their advantages in terms of proliferation and migration. However, approaches that can reveal the nature of pro-tumors metabolites at intracellular and

extracellular levels are highly limited. At the same time, avenues to use mimetic of metabolites (MOM) that can interfere with the pro-growth and progression pathways of cancer cells are not explored to the extent.

Because of such problems and needs, we have developed a concept of metabopsy of conventional and non-conventional biological samples and materials including nails, milk teeth, and tears for the early detection of cancer. The metabopsy of biological samples and materials is assisted by an in-house and novel VTGE tool. We have also shown the relevance of key oncometabolites such as sphinganine, CDP-DG, and N1-acetylspermidine using cell culture models at intracellular and extracellular levels. Furthermore, data generated during the metabopsy of biological samples and materials was extended to understand the protein targets of these oncometabolites that support the progression and invasiveness of cancer cells using molecular docking and molecular dynamics (MD) simulations. Furthermore, we have designed a metabolite mimetic that potentially acts as an inhibitor of key oncoproteins such as c-Src kinase, AP-1, c-Raf kinase, and c-Ras. Taken together, the relevance of metabopsy of conventional and non-conventional biological samples and materials is promising in diagnostic and prognostic approaches for cancer patients. Furthermore, exploration of various MOM as a new safer class of anticancer drugs is warranted and needs detailed preclinical and clinical studies in the future.

ABS4306: Altered gut microbiota associated with hemorrhage in chronic radiation proctitis

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Abstract. Pelvic cancer radiotherapy may cause chronic radiation proctitis (CRP) that adversely affects patient's quality of life, especially in patients with prolonged hematochezia. However, previous studies of radiation enteropathy mainly focused on acute irradiation hazards, and the detailed pathogenesis process and mechanism of prolonged hematochezia associated with radiation-induced toxicity remain unclear. In this study, we characterized the gut microbiota of 32 female CRP patients with or without hematochezia. Differential patterns of dysbiosis were observed. The abundance of Peptostreptococcaceae, Eubacterium, and Allisonella was significantly higher in CRP patients with hematochezia, while the compositions of the Lachnospiraceae, Megasphera, Megamonas, and Ruminococcaceae were lower in the microbiota of non-hematochezia patients. Functional prediction suggested significant difference in the expression of mineral absorption and the arachidonic acid metabolism proteins between hematochezia and non-hematochezia patients, possibly interdependent on radiation-induced inflammation. This study provides new insight into the altered composition and function of gut microbiota in patients with hematochezia, implying the potential use of probiotics and prebiotics for assessment and treatment of CRP.

Keywords: Chronic radiation proctitis, Hematochezia, Gut microbiota, Peptostreptococcaceae, Lachnospiraceae

Session 2_ Food and Veterinary Science

Time: 09:00-12:25July 6th, 2023(China Standard Time (UTC/GMT+8:00)Online Room Link: http://www.academicconf.com/teamslink?confname=ABS2023Offline Location:Grand Ballroom III, Regency Art HotelSession Chair: Prof. Ruimin Fu, Henan Finance University, China

09:00-09:25	ABS4242	Fluorescence imagings for non-destructive inspecting strawberry (Fragaria × ananassa) in postharvest stage Dr. Zichen Huang, Kyoto University, Japan
09:25-09:40	ABS4330 (Online)	An ultrasensitive ratiometric aptasensor based on the dual-potential electrochemiluminescence of Ru(bpy) ₃ ²⁺ for detection of Patulin in fruit products Dr. Liangrui Lv, Southeast University, China
09:40-09:55	ABS4331 (Online)	Ultrasensitive multicolor electrochromic sensor built on closed bipolar electrode: Application in the visual detection of <i>Pseudomonas</i> <i>aeruginosa</i> Dr. Wei Yuan, Southeast University, China
09:55-10:10	ABS4303	Mulberry leaf extract reduces abdominal fat deposition via AMPK/SREBP-1c/ACC signaling pathway in female Arbor Acre broilers Dr. Manhu Cao, Hunan Agricultural University, China
10:10-10:25	ABS4319	A broad-spectrum phage endolysin (LysCP28) able to remove biofilms and inactivate Clostridium perfringens strains on food Prof. Hui Zhang, Jiangsu Academy of Agricultural Sciences, China
10:25-10:40	ABS4354	Study on Standardization of Manufacturing Method inCheongtaejeonDr. Eunhye Kim, Tea Industry Institute, Republic of Korea
10:40-10:55		TEA BREAK
10:55-11:10	ABS4332 (Online)	Goat semen production and sperm cell viability as influenced by lysine supplementation Dr. Balbin, Aubrey Joy M, Isabela State University, Philippines
11:10-11:35	ABS4367	Improving the nutrient value of feedstuff using characterized novel microbial fermentation <i>Prof. Julang Li, University of Guelph, Canada</i>
11:35-12:00	ABS4243	The dual role of the black soldier fly: food waste recycler and new animal feed: risks and opportunities Prof. Olivier Andre Sparagano, City University of Hong Kong, China
12:00-12:25	ABS4339 (Online)	Air breathing induced hypoxia and its effects on oxidative stress, antioxidant defenses and respiratory chain enzyme activities in breathing organs of the stinging fish Heteropneustes fossilis Dr. Biswaranjan Paital, Odisha University of Agriculture and Technology, India

Abstracts of Oral Session 2

ABS4242: Fluorescence imagings for non-destructive inspecting strawberry (Fragaria × ananassa) in postharvest stage

Zichen Huang^{*} Laboratory of Bio-Sensing Engineering, Graduate School of Agriculture, Kyoto University, Japan *Corresponding author: huang.zichen.22c@kyoto-u.jp

Abstract. As one of the most popular fruits in the world, the strawberry (Fragaria × ananassa) is a fruit with a sweet and distinctive flavour, but with a soft texture that spoils quickly. A low-cost method is needed to distinguish perishable strawberries from normal fruit in a non-destructive way, as well as the deterioration of strawberries during storage. In this study, a machine vision system is presented for inspecting the quality of strawberries using ultraviolet (UV) light. Related experiments in postharvest stage validated the effectiveness of the proposed method. The results show that UV fluorescence imaging can be used as a fast, non-destructive and low-cost method to classify perishable and normal strawberries at an early stage, as well as to detect the deterioration of strawberries during storage. These findings suggest that strawberries are prone to rapid postharvest deterioration and can be sorted using UV-fluorescence imaging, which is a realtime, non-destructive, and low-cost sensing method. Meanwhile, the proposed method can be used for non-destructively estimate the deterioration level of a strawberry.

Keywords: Strawberry, Fluorescence imaging, Non-destructive, Postharvest

ABS4330: An ultrasensitive ratiometric aptasensor based on the dual-potential electrochemiluminescence of Ru(bpy)₃²⁺ for detection of Patulin in fruit products Liangrui Lv, Chunyang Jing, and Xiaoying Wang^{*} Nutrition and Food Hygiene, School of Public Health, Southeast University, China *Corresponding author: wxy@seu.edu.cn

Abstract. Mycotoxins are secondary metabolites produced by fungi. Patulin (PAT) is a common mycotoxin and widely found in various fruits and their products, which has multiple toxicological effects such as fertility, carcinogenicity, immunotoxicity, and neurotoxicity. It can enter the body through food ingestion, skin exposure and other means, which poses a great threat to food quality and human health. Moreover, PAT is highly stable during food processing. And heat treatment and UV-irradiation can't remove it completely. Therefore, the sensitive monitor of PAT is an effective means to prevent its harm. Standard PAT detection methods such as high-performance liquid chromatography (HPLC) or high-performance liquid chromatography mass spectrometry (HPLC-MS) can provide accurate detection results, but are expensive, time-consuming and require specialist technicians. Attractively, electrochemiluminescence (ECL) biosensor has the merits of simple operation, excellent sensitivity, and wide measuring range. However, ECL biosensor based on single-signal strategies will

inevitably have false positive or false negative errors due to the influence of variable external environment. With the continuous development, the ratiometric ECL biosensor (ECL_R-biosensor) for mycotoxins was established, where an internal calibration mechanism is introduced to further improve the accuracy, reproducibility, and sensitivity. Herein, an ultrasensitive PAT ratiometric aptasensor based on the dual-potential ECL of $Ru(bpy)_3^{2+}$ was first proposed. $Ru(bpy)_3^{2+}$ -doped trimetallic nanocube (Ru@Tri) innovatively integrated the luminophore and cathode coreaction accelerator (CCA), which could generate strong cathodic ECL. Simultaneously, anthocyanin-derived carbon quantum dots (anth-CQDs) prepared from purple potato skins was first served as a green anodic coreactant. And SiO₂-coated anth-CQDs (anth-CQDs@SiO₂) exhibited excellent performance for enhancing anodic ECL of Ru@Tri. Based on this, a novel ternary ECL system was established. In the presence of PAT, the ECL intensity ratio of anode to cathode (I_{ECL-A}/I_{ECL-C}) was significantly increased, and a low detection limit of 0.05 pg mL^{-1} was obtained. Moreover, when proposed method was applied to 18 samples of fruit products, two preserved fruit samples and one fruit vinegar sample were tested positive for PAT, and the obtained results were completely consistent, reflecting its outstanding practicability. Noteworthily, compared with HPLC method, the proposed aptasensor with features of no requirement of complex pretreatment, low-cost and fast analysis, is a potential in-site analysis method. This is also a universal strategy of ratiometric ECL sensor for the detection of other small molecular contaminants, which holds great significance to ensure food security.

Keywords: Food security, Ratiometric, ECL aptasensor, Fruits, Patulin

Acknowledgements: This work was supported by the Postgraduate Research & Practice Innovation Program of Jiangsu Province (KYCX21_0163).

ABS4331: Ultrasensitive multicolor electrochromic sensor built on closed bipolar electrode: Application in the visual detection of *Pseudomonas aeruginosa*

Wei Yuan, Xiaoying Wang*

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Abstract. *Pseudomonas aeruginosa* (*P. aeruginosa*) is an opportunistic infection-causing pathogen that threatens human health. Accordingly, a rapid and ultrasensitive analytical method is required urgently. Inspired by ECL–ratiometry and closed BPE, a novel visualized multicolor biosensor was designed for *P. aeruginosa* determination. Prussian blue (PB), the blue spot that can be easily electrodeposited, was selected as an electrochromic indicator at the closed BPE cathode. Integrating with the anodic emitter, Ru(bpy)₃²⁺, which emitted optical red light, visualized multicolor electrochromism was achieved on closed BPE. Particularly, physical separation between the positive and negative poles of the closed BPE greatly prevented mutual interference between Ru(bpy)₃²⁺ and PB. Consequently, the sensitivity and accuracy of the proposed biosensor considerably improved. Notably, owing to magnetic-separation technology, the closed BPE surface required no modification.

Without any complex pretreatment, the entire experiment time could be greatly shortened because the PA@MBs completely captured *P. aeruginosa* in food matrix within only 20 min. Ultimately, the colors changed at the anode (bright red to dark red) and cathode (light blue to deep blue) with increased *P. aeruginosa* concentration from 1 to 10^8 CFU mL⁻¹, which were equipped with self-calibration. In order to better determine the concentration of *P. aeruginosa*, the suspected samples can also be accurately detected by electrochemical impedance method. In addition, the inner- and inter-assay shows a good stability and accuracy of the proposed biosensor. The concept of this proposed multicolor electrochromic biosensor could be extended to determine other spoilage organisms in the food sector, thereby providing a new perspective on microbial analysis.

Keywords: *Pseudomonas aeruginosa*, Bipolar electrode-electrochromic, Ru(bpy)₃²⁺, Prussian blue (PB), Visualization

ABS4303: Mulberry leaf extract reduces abdominal fat deposition via AMPK/SREBP-1c/ACC signaling pathway in female Arbor Acre broilers

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Abstract. This experiment was carried out to investigate the mechanism of action of mulberry leaf extract (MLE) in reducing abdominal fat accumulation in female broilers. A total of 192 one-day-old female Arbor Acres (AA) broilers were divided into four diet groups, with each group consisting of 8 replicates with 6 birds per replicate. The diets contained a basal diet and three test diets with supplementation of 400, 800, or 1200 MLE mg/kg, respectively. The trial had two phases that lasted from 1 to 21 days and from 22 to 56 days, respectively. The growth performance, abdominal fat deposition, fatty acid composition, serum biochemistry and mRNA expression of genes related to fat metabolism in liver were determined. The results showed that, 1) dietary supplementation with MLE had no significant impact on broilers final body weight, average daily gain (ADG), or feed to gain ration (F/G) (P > 0.05), but linearly reduced abdominal fat accumulation in both experimental phases (P < 0.05); 2) the total contents of MUFA (monounsaturated fatty acids) and PUFA (polyunsaturated fatty acids), such as palmitoleic acid, oleic acid, and eicosadienoic acid, were increased quadratically as a result of dietary supplements of 400, 800, and 1200mg/kg MLE (P < 0.01), while the total contents of SFA (saturated fatty acids), such as teracosanoic acid were decreased (P < 0.01); 3) the addition of 800 or 1200 MLE mg/kg to the diet linearly reduced total cholesterol (TC) in the serum and liver (P <0.05). Adenosine-activated protein kinase (AMPK) mRNA expression in the liver was quadratically increased by the addition of 800 or 1 200 MLE mg/kg to the diet (P < 0.05), and the mRNA expression of sterol regulatory element binding protein-1c (SREBP-1c), acetyl-CoA carboxylase (ACC), and acetyl-CoA carboxylate), fatty acid synthase (FAS) were linearly decreased (P < 0.05).

In conclusion, MLE can be employed as a viable fat loss feed supplement in fast-growing broiler diets since it reduces abdominal fat deposition in female AA broilers via the AMPK/SREBP-1c/ACC

signaling pathway. MLE can also be utilized to modify the fatty acid.

Keywords: Mulberry leaf extract, Abdominal fat deposition, AMPK/SREBP-1c, Broilers

ABS4319: A broad-spectrum phage endolysin (LysCP28) able to remove biofilms and inactivate *Clostridium perfringens* strains on food

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Abstract. *Clostridium perfringens* is a gram-positive, anaerobic, spore-forming bacterium capable of producing four major toxins which cause disease symptoms and pathogenesis in humans and animals. *C. perfringens* strains carrying enterotoxins can cause food poisoning in humans and are associated with meat consumption. An endolysin, named LysCP28, is encoded by orf28 from *C. perfringens* bacteriophage BG3P. This protein has an N-terminal glycosyl-hydrolase domain (lysozyme) and a C-terminal SH3 domain. Purified LysCP28 (38.8 kDa) exhibited a broad spectrum of lytic activity against *C. perfringens* strains (77 of 96 or 80.21%), including A, B, C and D types, isolated from different sources. Moreover, LysCP28 (10 µg/mL) showed a high antimicrobial activity able to lyse 2×10^7 CFU/mL C. perfringens ATCC 13124 and *C. perfringens* J21 (animal origin) within 2 h. Due to this pathogen bacteria form biofilms, LysCP28 (18.7 µg/mL) was successfully evaluated as anti-biofilm agent in both biofilm removing and formation inhibition. Finally, to confirm the efficacy of LysCP28 in a food matrix, duck meat was contaminated with *C. perfringens* and treated with endolysin (100 µg/mL and 50 µg/mL), which reduced viable bacteria by 3.2 and 3.08 units-log in 48 h at 4°C, respectively. Overall, the endolysin LysCP28 could potentially be used as a bio-preservative to reduce *C. perfringens* contamination during food processing.

Keywords: Clostridium perfringens, Phage, Endolysin, Biofilm, Antimicrobial, Duck meat

Acknowledgements: This work was supported by the National Key Research and Development Program of China (No. 2018YFE0101900), the National Foreign Expert Project (No. G2022014149L) and the Key Research and Development Program of Jiangsu Province (No. BE2022361).

ABS4354: Study on standardization of manufacturing method in Cheongtaejeon

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Abstract. Cheongtaejeon is named after the fact that E. linza or moss gets stuck in the coin-shaped tea, and it has historicality as a traditional Korean fermented tea. The name also varies depending on the shape of the Ddeok Cha, lump tea, Cheongtaejeon, and the manufacturing process, product shape and size are established and produced and sold. The manufacturing process of cheongtaejeon was made in the following order: withering in sunlight, steaming, mashing, molding, drying, punching and final drying & storage. Therefore, process of processing Cheongtaejeon is currently being carried out by hand, making it difficult to industrialize. In this study aims to manufacture Cheongtaejeon using a wet grinder as a method for industrialization of Cheongtaejeon. There was no significant difference in the redness, total phenol, and catechin content of the mechanized manufacturing process and the results of the sensory evaluation did not show a significant difference. The standardized manufacturing process of Cheongtaejeon manufactured using a wet grinder can commercialize and industrialize products that replace food processing materials.

Keywords: Korean traditional tea, Cheongtaejeon, processing technology, mechanization

ABS4332: Goat semen production and sperm cell viability as influenced by lysine supplementation

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Abstract. The study was conducted to evaluate the effect of lysine supplementation to the semen production of Boer breeder goats at age 3-4 years and to assess the viability the sperm cells in raw and frozen forms. The different levels of lysine supplementation evaluated are Treatment 1 (without lysine), Treatment 2 (1.75%), Treatment 2 (2.45%) and Treatment 4 (3.15%). Data gathering and analysis were divided into Period 1 (Day 1 to 21) and Period 2 (Day 22 onwards). The study was laid-out in Completely Randomized Design. The results show that in terms of production, a positive effect of levels of lysine (p < 0.05) and the concentration of sperm cells was observed. The amount of semen collected increased as the inclusion of the lysine progresses; while no significant differences were observed on concentration of the sperm cells. On the viability of fresh sperm cells, no positive effect of the sperm cell population is observed in the levels of lysine; however, a positive effect is observed on rate of immotile (p < 0.01) and velocity of the sperm cells (p < 0.05) as lysine supplementation

progresses. Moreover, on the viability of frozen-thawed sperm cells, there is a positive effect on motility, fast progressive motility, slow progressive motility and velocity (p < 0.05) of the sperm cells was observed as the lysine supplementation continuous. Considering all parameters, Treatment 2 lysine supplementation has resulted to higher viability of sperm cells in both fresh and frozen-thawed state. It is therefore concluded that low lysine supplementation improves viability of sperm cells in fresh and frozen-thawed condition. Thus, 1.75% of lysine is recommended for inclusion to daily dietary of breeder bucks. To further verify the results, the same experiment should be conducted during off-during season and a detailed study on testosterone level in relation to lysine supplementation is also recommended to determine the direct effect of nutrient absorption on spermatogenesis of Boer bucks.

Keywords: Goat, Boer, Sperm cell viability, Lysine supplementation

ABS4367: Improving the nutrient value of feedstuff using characterized novel microbial fermentation

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Abstract. Dietary protein is one of the most expensive nutrients in feed. The rising feed cost, and the increased human consumption of plant-based food which competes for protein with the animal together have posed challenges to high-quality protein supply for animal production. These call for using innovative feed processing technologies to improve feed nutrient value to sustain the livestock industry. We aimed to use a fermentation approach to improve the feed nutrient value. We have screened from different sources and identified bacterial strains that secrete cellulase, xylanase and proteinase as candidates for feedstuff fermentation. Further studies revealed that a few of them are capable of breakdown glycinin and beta-conglycinin, the major proteins in SBM that are difficult to digest and often result in intestinal upset in monogastric animals. Molecular characterization revealed that isolate 9 is a Bacillus subtilis strain (B. subtilis 9) that secreted high levels of cellulase, xylanase, and proteinase compared to the ATCC control strain and other isolates. It grew significantly faster than the control strain. In addition, it also survived a wide range of concentrations salts and pH. When used for SBM fermentation, protein profiling of fermented SBM revealed a significant reduction of high molecular weight proteins, especially those of glycinin and beta-conglycinin, to small peptides. On a dry matter basis, neutral detergent fibre (NDF) of the fermented SBM was decreased by 34%; crude protein content was increased from 49 to 57%. Pigs fed with a diet formulated with the fermented SBM as the sole source of crude protein had significantly higher apparent ileal digestibility (AID) of dry matter, ash, crude protein, NDF, and acid detergent fibre compared with the control pigs fed with unfermented soybean meal.

Keywords: Fermentation, Feed nutrient value, Bacteria, Animal production

ABS4243: The dual role of the black soldier fly: food waste recycler and new animal feed: risks and opportunities

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Abstract. In Hong Kong, food waste constitutes about one-third of total municipal solid waste which is mostly landfilled (Environmental Protection Department, 2017). Landfilling leads to problems like loss of biomass, and contamination of underground water and soil (Melikoglu et al., 2013). Circular economy not only brings huge economic gains by transforming waste into by-products such as new food protein sources but is almost a necessity in Hong Kong when space is at a premium. HK has one of the highest human density and therefore has also one of the highest food waste density. Hermetia illucens, also known as the black soldier fly (BSF) has been successfully used to reduce manure waste (Miranda et al, 2021), faecal sludge management (Lalander et al, 2021) or plant-based waste (Singh et al, 2021) or to feed different animal species such as fish (Abdel-latif et al, 2021), Chinese soft-shelled turtles (Li et al, 2021) or pigs (Kar et al, 2021). To avoid filling the landfill sites up with food waste which could be recycled, black soldier flies are already used by very successful HK SMEs. BSF larvae meal is well suited as feed component for aquaculture and poultry nutrition because of its high protein, fat, and mineral content (Surendra et al., 2020). The protein and fat composition of the larvae depends on the substrate they are fed (Ewald et al., 2020). Under experimental conditions, a blend of silkworm pupae and wheat bran substrate yielded the highest (56%) crude protein content (El-Dakar et al., 2021), while fruit waste substrate yielded the highest (47.4%) fat content (Meneguz et al., 2018). Furthermore, the fatty acid composition of the larvae also depends on the fatty acid composition of the substrate (Makkar et al., 2014) and plays an important role in future industrial development in the insect feed sector (Giannetto et al., 2020). Particularly, BSF larvae can accumulate various omega-3 fatty acids, such as docosahexaenoic acid (DHA), eicosapentaenoic acid (EPA) and α -linolenic acid (ALA) from microalgae residual, silkworm pupae, and fish offal substrates (El-Dakar et al., 2021, 2020; St-Hilaire et al., 2007). These polyunsaturated fatty acids (PUFA), especially the omega-3 fatty acids, are known for beneficial health effects such as anti-inflammatory properties, reduced cholesterol levels, and prevention of cardiovascular diseases (Ander et al., 2003). The working hypothesis is that the choice of waste substrate fed to the larvae determines the fatty acid composition of the meal made of the larvae. There are various waste sources potentially available for insect rearing in Hong Kong and our objective is to identify the waste substrate that yields the highest PUFA content of the meal. This will support further progress in the insect meal production industry by adding beneficial health effects to the final products (fish or egg for instance).

Keywords: Black soldier fly, Edible insects, Food waste recycling, Insect-based agriculture

ABS4339: Air breathing induced hypoxia and its effects on oxidative stress, antioxidant defenses and respiratory chain enzyme activities in breathing organs of the stinging fish Heteropneustes fossilis

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Abstract. The effects of air exposure (0, 3, 6, 12, and 18 hours) induced hypoxia on H2O2, oxidative stress (OS), redox regulatory and respiratory complex enzymes (RCE) in breathing organs such as accessory respiratory organ (ARO) and gill of the cat fish Heteropneustes fossilis was investigated. The magnitude of H2O2 and the reduced glutathione (GSH) was higher in the gill than in the ARO, whereas, the level of protein carbonyl (PC), lipid peroxidation and ascorbic acid (AA), the activities of superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPx) had shown the opposite trend. The activity of glutathione reductase (GR) and RCE was comparable in both tissues. These tissues experience OS as evident by the rise in H2O2, LPx and PC under air exposure induced hypoxia state (AEHS). The activities of CAT, GPx, and GR in ARO and SOD and GR in gill, the level of GSH in gill and ARO and AA in gill were alleviated under AEHS. The activities of SOD in ARO and CAT in gill and the level of AA in ARO were elevated under AEHS. The activity of complex II enzyme was elevated whereas the rest of the RCE had negative correlation with the AEHS. Discriminant function analyses indicate clear contribution of the variables to influence the OS physiology of the fish under AEHS. Results indicate that the fish clearly adapts to a separate OS physiology strategy in ARO than gills, which may be an evolutionary adjustment to cope with its airbreathing nature under the AEHS.

Keywords: Accessory respiratory organs, Air-breathing organs, Antioxidant system, Respiratory chain complex enzymes, Aerial exposure induced hypoxia, Heteropneustes fossilis

Session 3_ Modern Agriculture, Climate Change, Diseases and Pesticides

Time: 14:00-18:10July 6th, 2023(China Standard Time (UTC/GMT+8:00)Online Room Link: http://www.academicconf.com/teamslink?confname=ABS2023Offline Location:Grand Ballroom III, Regency Art HotelSession Chairs:14:00-15:35Prof. Moniruzzaman Khondker, University of Dhaka, Bangladesh15:50-18:10Prof. Ahmed Ashfaque, University of Dhaka, Bangladesh

14:00-14:25	ABS4214	The spread of fusarium wilt of banana TR4 and its comprehensive management Prof. Sijun Zheng, Yunnan Academy of Agricultural Sciences, Alliance of Bioversity and CIAT, China
14:25-14:40	ABS4346	Study on fruiting body types traits formation molecular mechanism of <i>auricularia heimuer</i> Dr. Lixin Lu, Jilin Agricultural University, China
14:40-15:05	ABS4236	Photopharmacological ligands for Pesticides <i>Prof. Xusheng Shao, East China University of Science and Technology, China</i>
15:05-15:20	ABS4356 (Online)	Effect of volatile compounds from Shiitake fungi-beds of different ages as Biostimulants on growth and biomass in rice seedlings <i>Dr. Clever Nkhokwe Kanga, Niigata University, Japan</i>
15:20-15:35	ABS4247 (Online)	Comparative efficacy of various plant extracts against cotton whitefly (<i>bemisia tabaci</i>) and thrips (<i>thrips tabaci</i>) Dr. Abid Mahmood Alvi, Ghazi University, Pakistan
15:35-15:50		TEA BREAK
15:35-15:50 15:50-16:05	ABS4313	TEA BREAK Integration of barley yield estimation results into a cross-platform application for implementation of precision farming elements in Kazakhstan Ms. Zhanna Alexandrovna Assylkhanova, D. Serikbayev East Kazakhstan Technical University, Kazakhstan
15:35-15:50 15:50-16:05 16:05-16:20	ABS4313 ABS4348	TEA BREAKIntegration of barley yield estimation results into a cross-platform application for implementation of precision farming elements in KazakhstanMs. Zhanna Alexandrovna Assylkhanova, D. Serikbayev East KazakhstanMs. Zhanna Alexandrovna Assylkhanova, D. Serikbayev East KazakhstanOptimization research of agricultural supply chain finance based on blockchain technology: evidence from Chinese industry Dr. Zhen Chen, Lingnan Normal University, China
15:35-15:50 15:50-16:05 16:05-16:20 16:20-16:35	ABS4313 ABS4348 ABS4241	TEA BREAK Integration of barley yield estimation results into a cross-platform application for implementation of precision farming elements in Xazakhstan Ms. Zhanna Alexandrovna Assylkhanova, D. Serikbayev East Kazakhstan Optimization research of agricultural supply chain finance based on Slockchain technology: evidence from Chinase industry. Dr. Zhen Chen, Lingnan Normal University, China Practices, problems and policies of climate-smart agriculture in China. Dr. Wanling Hu, Huazhong Agricultural University, China

16:50-17:05	ABS4291 (Online)	Characteristics of high-quality rice varieties and taste sensoryevaluation values in ChinaDr. Dawei Zhu, China National Rice Research Institute, China
17:05-17:20	ABS4251 (Online)	Effect of biochar on physiological, molecular and architecture root of two wheat cultivars under non-irrigation conditions <i>Dr. Mariapina Rocco, University of Sannio, Italy</i>
		Connection between environmental and agricultural policies
17:20-17:45	ABS4361 (Online)	promoted by European green deal Dr. Cristian Gheorghe Popescu, University of Pitesti, Romania

Abstracts of Oral Session 3

ABS4214: The spread of Fusarium wilt of banana TR4 and its comprehensive management Sijun Zheng^{1,2*}

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Abstract. Double cropping is beneficial for diversifying the rotation, maximizing crop production, and increasing the profit potential of a cropping system. The objective of this study was to compare the quality and baking applicability of flour of winter wheat (Triticum aestivum L. cv. 'Jokyung') harvested under double cropping systems linked to three rice alternative crops (black soybean, sesame, and perilla) in the paddy fields of the southern part of Korea. The color value (L*, a*, and b*) and the whiteness index of the flour changed according to the physical and chemical properties of the soils changed by pre-cropping rice alternative crops. Macro- and micro-nutrient content of wheat flour was generally higher in the wheat grown in rice alternative pre-cropped fields than in the wheat grown in the rice pre-cropped field. Particularly, the P, Mg, Zn and Cu contents were higher in wheat harvested from the black soybean pre-cropped field. Crude protein content of the wheat flour was higher in wheat harvested from rice alternative pre-cropped fields than from rice pre-cropped field, and total starch was higher in wheat harvested from the black soybean and perilla pre-cropped fields. In addition, the dry gluten content of flour from rice alternative pre-cropped fields was significantly higher than from rice pre-cropped field. Among the mixograph parameters, the midline peak time (MPT) was shorter in wheat grown in black soybean and perilla pre-cropped fields than in wheat in rice pre-cropped field. The decrease of protein content causes mixing time longer, resulting that the greater effort should be required to develop the dough. Based on these results, it is concluded that pre-cropping of the rice alternative crops in the crop rotation is expected to have a significantly positive impact on improvement of flour quality of wheat, even though it is possible that it makes the bakery product slightly dark.

Keywords: Greater mekong subregion (GMS), Spread of Fusarium wilt of banana, Tropical race 4 (TR4), Somaclonal selection, Biological control

ABS4346: Study on fruiting body types traits formation molecular mechanism of *auricularia heimuer*

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Abstract. Auricularia heimuer is a gelatinous fungus widely cultivated in China, with a total output of 7,064,300 tons (fresh) by 2020, making it the second largest edible mushroom in China. Our research team conducted several years of cultivation experiments on hundreds of strains with different methods of A. heimuer, and used quantitative taxonomy to divide the fruiting body types into cluster type (CL) and the chrysanthemum type (CH). The CL strains produce a fruiting body with a veined segmented appearance on the upper surface, while the CH strains produce a fruiting body with undifferentiated organization at the base. The fruit-body type trait is an important agronomic trait and breeding index. With the change of the cultivation method, the CL strains are easily induced to produce fruiting bodies by punching a small hole in the surface of existing fruiting bodies. This method allows producers to meet the consumer market and requires minimal labor input. In this study, we found that the locus controlling fruiting type trait was located in the range of 220267bp-239189bp on genome Scaffold39 through the positioning of fruiting body type trait locus, anchoring and encryption of linkage groups, and comparison of fruiting body type marker SCL-18 to genome, etc. Through gene annotation, it was found that there were three protein coding genes, namely g7217, g7218 and g7219. Further transcriptomic analysis and qPCR verification of tufted strain "Qihei 1" and compositae strain "Qihei 2" found that g7219 had significant differences between the two strains, and other genes had no significant differences. By functional comparison, it was found that g7219 affected the development of fruiting body types by regulating the secretion of cytokinin. The nucleotide and protein characteristics of the coding region of g7219 gene of the two strains were compared. There was no nonsense mutation of the nucleotide in the coding region and no significant difference in the protein characteristics. Genomic comparison and PCR verification of the nucleotides in the promoter region of g7219 gene of the two strains revealed that the TATA-box sequence of the promoter core of the tufted variety was CATAA, and the TATA-box sequence of the composite variety was TATAA. In summary, gene g7219 is the controlling gene for the fruiting body type. The difference of the ciselement TATA-box of the promoter core leads to different transcription levels of the controlling gene g7219, which ultimately affects the fruiting body type of A. heimuer.

Keywords: *Auricularia heimuer*; Fruiting body type; Genetic linkage map; Collineation of genome; Cis type element

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ABS4236: Photopharmacological ligands for Pesticides

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Abstract. Photopharmacological ligands provide a powerful way for optical control of the activity of a molecule, which will facilitate better understanding of toxicological mechanism. By blending of photoswitch with pesticides, we prepared series of photochromic ligands acting on various receptors or enzymes, such as nAChR, GABAR, sodium channel, Ryanodine receptor. Some PCLs showed different activity before and after light irradiation. These PCLs were then used to optically control over the enzyme, neuron and insect behavioral responses.

Keywords: Photopharmacology, Pesticide, Photoswitch, Activity

ABS4356: Effect of volatile compounds from Shiitake fungi-beds of different ages as Biostimulants on growth and biomass in rice seedlings

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Abstract. Biostimulants are the emerging solution for achieving sustainable agriculture productivity in the context of the changing climate. Recent studies have reported volatile compounds (VCs) emitted by fungi as potential Biostimulants. However, current technologies and techniques for culturing fungi mycelium to extract VCs are still complex. In contrast, fungi-beds used for cultivating edible fungi, which consist of wood chips mixed with rice straw and inoculated with rice spawn, are readily available with a reliable supply chain. In this study we investigated the effect of VCs from Shiitake fungi-beds of colonized with the fungi mycelium at varying ages (young, mature, and waste) on growth and biomass of rice seedlings (*Oryza sativa* L). To do this, we cultivated rice seedlings in a non-contact exposure manner to Shiitake fungi-beds of the different ages for a period of 14 days under 27°C/13hr/light and 23°C/11hrs/night conditions. We assessed the effect of the VCs on the growth and biomass by measuring plant height, root growth and dry weight. The results of the study revealed that VCs from Young, Mature and Waste Shiitake fungi-beds had a positive effect on the growth and biomass accumulation of the rice seedlings. Seedlings exposed to VCs from young Shiitake fungi-beds exhibited the most pronounced growth, including a notable increase in plant height (164.5%), root length (111%), and biomass measured by dry weight (180%) compared to the control group. These

findings are proof positive that Shiitake fungi-beds of different ages are a practical and accessible resource that can be harnessed into a sustainable source of Biostimulants for enhancing rice crop growth and productivity.

Keywords: Biostimulants, Volatile compounds, Fungi, Shiitake fungi-beds, Growth, Biomass

Acknowledgements: This study was made possible with funding the Japan Science and Technology under the ASTEP pilot project (JPMJTM22CA) and Industry collaboration from Hokken Corporation and Yairo Shiitake Farmers' Cooperative Association

ABS4247: Comparative efficacy of various plant extracts against cotton whitefly (*bemisia tabaci*) and thrips (*thrips tabaci*)

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Abstract. The most of the cotton-producing countries in the world, including Pakistan, focus mainly on the cultivation of cotton as a source of fabric. The yield of cotton reduced over the years due to many factors, insect pests is one of them. Due to the attack of sucking and chewing pests the production of cotton crop is alleviated approximately 50-60%. Generally, to eradicate insect pests, synthetic pesticides are used. High doses of pesticides provided the selection pressure on the pests and caused development of pest resistance. Moreover, it extremely damaged the ecosystem and also caused harmful impact on human health. To overcome these issues, the main strategy of the present study is to improve management techniques and control harmful insect with environment friendly technique such as phytochemicals. The study was designed to know the efficacy of four plants' water extracts i.e., Kortumma (Citrullus colocynthis), Akk (Calotropis procera), Neem (Azadirachta Indica) and Tobacco (Nicotiana tobacium) against cotton whitefly and thrips in the climatic conditions of Districts Rajanpur Punjab, Pakistan. Randomized Complete Block Design (RCBD) was used to conduct the experiment (plot size 20×20 sq: ft). The standard agronomic practices and fertilizer dosage were used. The plant extracts were prepared according to the field recommendations of dose/acre. Crude extracts of Kortumma fruit 600g/acre, Akk 600g/acre, Neem 600g/acre and Tobacco 600g/acre were mixed with 100 liters water for application, twice in 15 days' interval. The data regarding the whitefly and thrips population before 24 hours of plant extracts application were noted from 5 randomly selected plants from each plot. Similarly, the data were also collected after 24 hours, 72 hours and 120 hours of the plant extracts application using 5 randomly selected plants. Our results suggested that tobacco indicated the highest efficacy and showed more toxicity to the population of whitefly which persisted upto 1 week. Neem showed minimum toxic persistency followed by kortumma and akk. However, against thrips, all four plants extracts were highly effective and toxicity persisted upto 2 weeks for the population of thrips. This data would be useful for future research and development of biopesicides.

Keywords: Insect pests, Integrated pest management, Plant extracts, Citrullus colocynthis, Azadirachta indica, Whitefly, Thrips

ABS4313: Integration of barley yield estimation results into a cross-platform application for implementation of precision farming elements in Kazakhstan

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Abstract. Based on the conducted analysis of software and hardware methods and functionality of various applications for development of precision farming elements toolkit, the authors developed a cross-platform application "Agronomist Tablet". The research and yield analysis was carried out on the example of barley crops on rainfed land in the sharply continental climate of eastern Kazakhstan for the period 2017 - 2022. It is of interest to integrate the results of barley yield estimation into a cross-platform application for implementation of precision farming elements for further replication in Kazakhstan. A mathematical model using classification and regression algorithms has been developed based on the collected data using machine learning.

The application provides the user with barley yield estimates for each field, as well as recommendations for optimum fertiliser doses and other measures to improve yields. A distinctive component of this cross-platform is the ability to adapt the barley yield estimation function to the soil and climatic features of eastern Kazakhstan. The use of deep learning library TensorFlow and PyTorch in the architecture of the environment on the back-end allows the construction of more complex models. The developed models, in turn, have the ability to handle non-linear dependencies and reveal more complex patterns. The above features are an important addition to this platform which makes it suitable for replication in smart crop production in Kazakhstan.

Thus, the successful integration of barley yield estimation results into a cross-platform application for the implementation of precision farming elements in Kazakhstan requires a comprehensive approach and several steps, including data collection and analysis, model development, integration with other systems, implementation of additional features, user training and service improvement.

Keywords: Precision farming, Software, Cross-platform application, Yield analysis, Barley crops, Machine learning

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ABS4348: To avoid repeatability issues, this abstract will be available after the full paper is published in the conference proceedings.

ABS4241: Practices, problems and policies of climate-smart agriculture in China

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Abstract. Climate smart agriculture is a new concept of agricultural system transformation in the context of climate change. It aims to achieve three goals: adapting to climate change, improving agricultural production and reducing greenhouse gas emissions. A lot of practices and researches have been carried out in many countries. As a large agricultural country, China is also a pioneer to adopt climate smart agriculture, and has carried out a series of practical activities to cope with climate change. In order to promote the healthy and rapid development of climate smart agriculture in China, this paper summarized the current situation of the practices of climate smart agriculture in China in recent years and the measures implemented responding to climate change, pointed out the existing problems, and finally gave the corresponding countermeasures for the problems.

Keywords: Climate change, Climate adaptability, Climate smart agriculture, China practice

ABS4273: To avoid repeatability issues, this abstract will be available after the full paper is published in the conference proceedings.

ABS4291: Characteristics of high-quality rice varieties and taste sensory evaluation values in China

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Abstract. In order to clarify the quality characteristics of high-quality *japonica* rice in north and south China and high quality *indica* rice, and explore the physical chemical indexes related to rice taste quality, this study investigated the differences of quality and taste sensory evaluation value of high-quality rice in China. It would provide theoretical basis for quality evaluation and improvement of high-quality rice varieties in China. A total of 122 high quality rice grain varieties from 30 provinces of China in the third national high-quality rice variety taste quality evaluation activities were used as

materials. According to suitable planting area, all the samples were divided into three types as northern japonica, southern japonica and indica rice with the sample numbers of 38, 15 and 69, respectively. To clarify the relationship between physical chemical parameters and taste sensory evaluation value, rice appearance quality, rice flour pasting properties, protein content and taste sensory evaluation value were measured. According to the taste sensory evaluation value, each type of rice was divided into three categories as high (\geq 90), medium (80-90) and low taste (<80). The differences of rice qualities among different types and taste categories were analyzed. Northern *japonica* rice could be divided into high and medium taste categories. The length-width ratio, protein content, setback viscosity and hardness of high taste category rice were lower than those of medium taste category rice, by 0.2, 0.32 g/100 g, 134 cP, 16 g, respectively ($P \le 0.05$). However, the peak viscosity, stickiness and spring value of high taste category rice were higher than those of medium taste category rice, by 145 cP, 70 g and 0.04%, respectively ($P \le 0.05$). Southern *japonica* rice could be divided into high, medium and low taste categories. The chalkiness degree, peak, and breakdown viscosity, and stickiness of high taste category rice were higher than those of low taste category rice, by 0.65%, 314 cP, 259 cP, 261 g, respectively ($P \le 0.05$). However, the apparent amylose content, protein content, final and setback viscosity of high taste category rice were lower than those of low taste category rice, by 4.0 g/100 g, 9.2 g/100 g, 260 cP and 574 cP, respectively ($P \le 0.05$). Indica rice could be divided into high, medium and low taste categories. The high taste category rice had a longer and thinner grain shape and a better appearance quality than the low taste category rice ($P \le 0.05$). The protein content, setback viscosity and hardness of high taste category rice were higher than those of low taste category rice, by 0.45 g/100 g, 157 cP, 46 g, respectively ($P \le 0.05$). However, the breakdown viscosity and stickiness of high taste category rice were lower than those of low taste category rice, by 115 cP and 107 g, respectively $(P \le 0.05)$. Northern *japonica* rice type with high taste sensory evaluation value had a crystal-clear appearance (chalkiness degree was less than 1%), low protein content (about 6 g/100 g), moderate hardness, and high elasticity (about 0.6%). Southern *japonica* rice type with high taste sensory evaluation value had a good appearance quality, low apparent amylose content (about 13 g/100 g) and setback viscosity (about -250 cP), and high cooked rice stickiness (about -1200 g). Indica rice type with high taste sensory evaluation value had a long and thin grain (length-width ratio about 4.0) and crystal-clear appearance, and low ratio of hardness to stickiness (about 0.25).

Keywords: High quality rice, Quality evaluation, Taste sensory evaluation value, Northern *japonica* rice, Southern *japonica* rice, *Indica* rice

ABS4251: Effect of biochar on physiological, molecular and architecture root of two wheat cultivars under non-irrigation conditions

Ilva Licaj¹, Maria Chiara di Meo¹, Mauro Marra² and Mariapina Rocco^{1,*} ¹Department of Science and Technology, University of Sannio, Benevento, Italy ²Department of Biology, University of Tor Vergata, Rome, Italy *Corresponding author: rocco@unisannio.it Abstract. Due to global climate change, the earth is facing severe droughts that adversely affect the growth and development of grain crops. Biochar addition has been explored in the last few years as a way to mitigate global warming by improving soil production. In addition, with advances in wheat varieties, in this study we aim to provide new insights into the great drought response mechanisms among two wheat seedling cultivars, the ancient one Saragolla and the modern Svevo, which can be helpful even for future drought tolerant breeding programs of grain. The root system is the first organ that perceives soil water deficiency as triggering to respond to drought through a variety of adaptation strategies that enable them to avoid and tolerate stress by doing root architecture remodeling. Therefore, roots of both wheat seedling cultivars were selected as materials to explore the physiological, molecular and architectures root responses to soil drought and Biochar+soil drought. The root architecture consists of several structural features, which were characterized by the number and length of main and lateral roots along with the density of root hairs. Under biochar+soil drought stress Saragolla possibly revamped greater its root architecture, by significantly increasing the root length, the lateral root and hair density compared to the other cultivar, enhancing thus the total surface area for water acquisition. Furthermore, as the water deficit is strictly associated with the accumulation of ROS, we evaluated a better performance of the hydrogen peroxide production, the electrolyte leakage, the membrane lipid peroxidation and the proline synthesis of both cultivars under biochar+soil drought condition, and specifically more in Saragolla wheat. Molecular investigations were focused on the transcription analysis of genes belonging to the main classes of TFs known to be potentially exploitable for the improvement of drought tolerance, demonstrating an up-regulation in both varieties after 10 days of water deficit. Even though, this up-regulation was generally higher in the Saragolla cultivar with the presence of Biochar, particularly concerning WRKY12, WRKY34 and DREB2 genes. Performing proteomic analysis of changes in the protein repertoire of roots from the two cultivars, allowed us to ascertain that after 10 days of water stress treatment, we found an alteration in the expression of several proteins belonging to the abiotic stress, oxidative stress, energy/carbon metabolism and amino acid/nitrogen metabolism functional classes, in both soil conditions for each cultivar. Nevertheless, these findings point to the agronomic relevance of biochar addition in these crops.

Keywords: Climate change, Drought stress, Biochar, Saragolla cultivar, Svevo cultivar

ABS4361: Connection between environmental and agricultural policies promoted by European green deal

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Abstract. The European Green Deal is the most important vision and strategy of the vision of the European Union related to sustainability, green technologies and high environmental standards. Agriculture is one of the most important sectors of the European Union that interferes a lot with

European policies, exceptionally environmental policies. According to Europe's new strategy, the most important strategies and policies connected with environmental and agricultural policies are:

- —— EU Farm to Fork Strategy;
- —— EU soil strategy for 2030;
- ------ EU Climate Law;
- 2030 Climate Target Plan;
- —— EU Biodiversity Strategy for 2030;
- ------ EU's Circular Economy Action Plan.

Keywords: Sustainability, Environmental policy, Organic farming, Agricultural policy, European green deal

ABS4366: Investigation of multidrug resistant Enterococcus spp. from hospital wastes and aquatic habitats in Dhaka, Bangladesh

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Abstract. The emergence of multidrug resistant bacteria is a global problem and major obstacle for the treatment of many infectious diseases. Indiscriminate, unnecessary, and unwise use of antibiotics boosts up this antibiotic resistance giving rise to multidrug-resistant (MDR) bacteria in the environment. The role of the hospital environment as a reservoir of multidrug-resistant Enterococcus spp. in Dhaka has been poorly investigated; however, it could be responsible for the transmission of multidrug-resistant bacteria. Enterococci are indicators of the presence of fecal material in water and, therefore, of the possible presence of disease-causing bacteria, viruses, and protozoa. Enterococci are organisms with remarkable ability to adapt to the environment and acquire antibiotic resistance determinants. It is now a global concern as the innocent, easily treatable bacteria are slowly making changes resistant to antimicrobial agents because of careless, rapid, and widespread use. Freshwater environments are a well-recognized system for the dissemination and evolution of antibiotic resistance. Water bodies are sites of genetic exchange where environmental bacteria interact with microbes originated from humans and other animal sources, through horizontal gene transfer. Enterococci are indigenous flora of the gastro-intestinal tracts of animals and humans. Recently, interest in two major species, Enterococcus faecium and Enterococcus faecalis, has heightened because of their ability to cause serious infections and their intrinsic resistance to antimicrobials. So, the aim of the present study was performed to see the status of hospitals in Dhaka city and aquatic habitats as the global concern of rising antibiotic resistance Enterococcus spp. which has become a threat to humans. Enterococci are ubiquitous. The origins of Enterococcus species vary from environmental to animal and human sources. Enterococcus faecalis and E. faecium are the predominant, gram positive cocci in human stools. Animals like poultry, cattle, and pig, E. faecium is the prevalent species, but other species occur like E. faecalis, E cecorum, E. gallinarum, and E. durans. Because of unusual use of antibiotics, these

bacteria grow high level resistance among them against multiple drugs. The present study aimed to enumerate, isolate, and characterize antibiotic resistant Enterococcus spp. from freshwater habitats. Fifty-one samples were collected from ten different hospitals and 90 samples were collected from nine different freshwater habitats in Dhaka city. The pH of the collected samples ranged 7.18 - 8.45. Enterococcus agar medium was used to enumerate, isolate, and characterize bacteria. In Enterococcus agar, the bacterial load ranged $1.10 \times 101 - 3.71 \times 102$ cfu/g. Out of initial 177 bacterial isolates, finally 21 isolates were selected for detail studies considering their growth pattern, morphological and physiological characteristics. All the selected isolates were facultative anaerobic, gram positive, cocci shaped and non-spore former. Enterococcus were phenotypically identified considering their colonial morphology and physiological and biochemical characteristics. Out of eleven isolates nine were E. faecium and two were E. faecalis. The antimicrobial resistant pattern of the selected isolates to eight antibiotics were determined using disk diffusion method. E. faecium (60.52%) were more resistant to most of the antibiotics than E. faecalis (56.25%). All the isolates were shown to be resistant to antibiotics viz; Erythromycin, Tetracycline, Amoxycillin, Penicillin, Gentamycin, Chloramphenicol, Ciprofloxacin and Vancomycin. Enterococcus faecalis showed resistance to all 8 antibiotics tested as Erythromycin (78.57%), Tetracycline (21.43%), Amoxycillin (50%), Penicillin (57.14%), Gentamycin (28.57%), Chloramphenicol (92.86%), Ciprofloxacin (71.43%) and Vancomycin (42.86%). Furthermore, Enterococcus faecium exhibited resistance to Erythromycin (98.41%), Tetracycline (41.27%), Amoxycillin (36.51%), Penicillin (73.02%), Gentamycin (20.63%), Chloramphenicol (84.13%), Ciprofloxacin (82.54%) and Vancomycin (47.62%). Remarkable multiple antibiotic resistances to the classes of antibiotic tested were observed between two species. An active sustainable program should be carefully developed to prevent the emergence of these multidrug resistant bacteria. If antimicrobial resistance continues to increase from current levels, it is estimated that by 2050 ten million people would die every year due to lack of available treatment and the world's GDP would be reduced to 2-3.5%. More study needs to be formulated to find out the mechanism of multidrug resistant activities with possible preventive measures.

Keywords: Enterococcus, Hospitals, Aquatic habitats, MDR

Part V Conference Venue

Regency Art Hotel 麗景灣藝術酒店

Website: www.regencyarthotel.com.mo/index.php/ Address: 2 Estrada Almirante Marques Esparteiro, Taipa, Macao Tel.: 853 2883 1234

Brief Introduction





The Regency Art Hotel offers a 6 meters high ballroom with a total area of 349 square meters pillarless design and 4 multi-purpose function rooms equipped with audio-visual equipment. Chinese and Western or buffet menus are available to cater to all functions. Our experienced banquet team will go the extra mile to ensure the success of your event. It is the ideal venue for business meetings and private events from 10 to 300 persons.

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Hotel Macao

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- Approx. 8 minutes by taxi
- Approx. 20 30 minutes by bus No. MT1

2. Border Gate Terminal (澳门关闸)(注:大陆方向为拱北口岸)— Regency Art Hotel Macao

- About 10 KM
- Approx. 20 30 minutes by taxi
- Approx. 45 60 minutes by bus No. 25B or No. 25.

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Macao

- About 16 KM
- Approx. 30 35 minutes by taxi

• Approx. 40 - 50 minutes. Take bus No.102X, get off at Chun Lai Garden (泉澧花园), walk about 380m to Regency Art Hotel Macao.

4. Cotai Frontier Post (路氹边检大楼) (莲花口岸) — Regency Art Hotel Macao

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Part VI Acknowledgements

On behalf of the ABS/ABB 2023 Organizing Committee, we would like to take this opportunity to express our sincere gratitude to our participants. Without their support and contributions, we would not be able to hold the conference successfully in this special year. We would also like to express our acknowledgments to the Technical Program Committee members who have given their professional guidance and valuable advice as reviewers. Below are the lists of the Technical Program Committee members. For those who contribute to the success of the conference organization without listing their names here, we would love to say thanks as well.

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