2026
7TH AFSA CONFERENCE ON "FOOD SAFETY AND FOOD SECURITY"





To launch a Food Safety and Food Security Conference focusing on current trends and needs in Asia

17-18
November 2026
9:30AM - 5PM
Tsukuba Center for Institutes
TSUKUBA, JAPAN

afsa.secretariat@gmail.com

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Conference Program

Day 1: November 17, 2026 (Tuesday)

Time	Program
09:00-09:45	**Guest arrival and Registration**
09:45-09:50	**Welcome remark By** Dr. Yasuhiro Inatsu, Conference Organizing Secretary
09:50-09:55	**Adress by** Dr. Takashi Uemura, Prof. Emeritus, President, Asian Food Safety and Security Association
09:55-10:00	**Remarks by** Prof Hiroko Isoda, ARENA Director
10:00-10:05	**Remarks By** Dr. Yoshikiyo Sakakibara, Director, Institute of Food Research, NARO
10:05- 10:35	**Keynote 1:** **Food Microbiology: Roles in Food Security and Food Safety** By Prof. Dr. Weihuan FANG Zhejiang University, Institute of Preventive Veterinary Medicine, Hangzhou, China Abstract code: K-01 (P-10)
10:35-11:00	**Poster (odd numbers) & Refreshment break**
11:00-11:20	Phenotypic and Genomic Characterization of *Cronobacter sakazakii* Recovered from Powdered Infant Formula and a Child Nutrition Manufacturing Environment in Bangladesh. (O-01) **By Dr. Sangita AHMED, University of Dhaka, Bangladesh**
11:20-11:40	Domestication of Fermented Milk Associated *Rothia kristinae* and *Streptococcus infantarius* through Whole-Genome Sequencing Approach (O-09). **By. Dr. Arafat Al Mamun, University of Dhaka, Bangladesh.**
11:40-12:00	Occurrence of *Legionella pneumophila* in Processed Water Systems of Food Industries: Evidence of Potable Water Contamination **By Dr. Nazmun Naher,** Bangladesh Standard Testing Institute (BSTI), Bangladesh
12:00 - 13:30	**Group Photo1 & Lunch & Poster**
13:30 - 14:00	**Keynote 2:** **Overview of Bacterial Injury Induced by High Hydrostatic Pressure**

	By Dr. Kazutaka Yamamoto Institute of Food Research, NARO, Japan Abstract code: K-02 (P-11)
14:00 - 14:20	Post-treatment deterioration of drinking water quality in Dhaka: Linking redox conditions, microbial contamination, and heavy metal exposure By **Mr. Prince Biswas,** Ministry of Agriculture (MoA), Bangladesh
14:20 - 14:40	Combined effects of rosemary extract and high hydrostatic pressure treatment on the quality and microbiological changes of lemon juice during refrigerated storage. (O-06) **By Ms. Lul Hassan Mohamed, Niigata University, Japan**
14:40 - 15:20	**Poster (even numbers) & Coffee Break**
15:20 - 15:40	Analysis of nucleic acid retention characteristics by cause of death in stored-product insect pests **By Ms. Saki MATSUMOTO, Institute of Food Research, NARO, Japan**
15:40-16:00	Antidiabetic functional food potential of green synthesized nano formulation from the mix of Fenugreek, Nigella sativa, and Momordica charantia in streptozotocin-induced diabetic rats. (O-03) **By Dr. Atiar Rahman, University of Chittagong, Bangladesh**
16:00-16:20	Nutrition and Dietary Support Activities Following the 2026 Kumamoto Prefecture Earthquake—Status of Activities and Future Challenges for the Kochi Prefecture Dietitians Association (O-10) **By Dr. Ikuko Shimada, University of Kochi, Japan**
17:30 - 19:00	**Banquet (Ristrante Tsumu) & Poster Awarding** **End of Technical Session (Day 1)**
Day 2: November 18, 2026 (Wednesday)	
	Technical session 2
09:35-10:05	**Keynote-3:** **The future of food and agriculture research: trends, challenges and mitigation"** Dr. Md. Latiful Bari Center for Advanced Research in Sciences, University of Dhaka Abstract code: K-03 (P-12)
10:05 - 10:25	The Issue of Mycotoxins in Maize and Countermeasures **By Dr. Masayo Kushiro, Institute of Food Research, NARO, Japan**
10:25 - 10:45	Coffee Break
10:45 - 11:05	Deep-Sea Tuna Fisheries Potential in Bangladesh: An Integrated Geospatial and Economic Assessment. (O-07) **By Dr. Syed M Istiak, ACI Agrolink Ltd, Dhaka, Bangladesh**

11:05 - 11:25	Transcriptomic and Network Analyses Reveal Neuronal Functional Adaptation to a Potential Airborne Toxicant in Human iPSC-Derived Autonomic Neurons (O-11). **By Dr. Farhana Ferdousi, University of Tsukuba, Japan**
11:25 - 11:45	Analytical Methods for the Detection of Genetically Modified Organisms (GMOs) for Food Labeling in Japan. **By Dr. Reona TAKABATAKE, Institute of Food Research, NARO, Japan**
11:45 - 13:30	Group Photo & Lunch
13:30 - 14:00	Profiles of antimicrobial resistance in agricultural environment **By Dr. Nobuyuki KIJIMA** **Institute of Food Research, NARO, Japan** Abstract code: K-04 (P-13)
14:00 - 14:20	Effects of Agricultural Antibiotic Application on Soil Microbiota, Antimicrobial-Resistant Bacteria, and Resistance Genes in Vegetable Cultivation. (O-04) **By Dr. Ken-ichi Honjoh, Kyushu University, Fukuoka, Japan**
14:20 - 14:40	Antimicrobial resistance and occurrence of Salmonella spp. and Escherichia coli in Vietnamese poultry across different farming scales. (O-08) **By Dr. Huong Quynh Vu, Vietnam National University of Agriculture**
14:40 - 15:00	Prevalence and Genomic Characterization of Antimicrobial-Resistant *Salmonella spp*. from Fresh Foods in Cambodia. (O-05) **By Dr. Laingshun Huoy,** **Swedish University of Agricultural Sciences, Uppsala, Sweden**
15:00 - 15:30	**Coffee Break & Poster Removal**
15:30 - 16:00	**Closing ceremony and Certificate giving**

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KN-01

Food Microbiology: Roles in Food Security and Food Safety

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Abstract

Food security and safety (FSS) is a critical issue of modern society not only in developed countries but also in developing countries, especially those in Asia. Food microbiology contributes to FSS in multiple ways: food fermentation to extend the shelf-life of agro-products, reduced waste of foods due to food spoilage, and prevention of foodborne pathogens via proactive surveillance and risk management. In this work, the synopsis of the FoodMicro2026 conference that took place in Ljubljana, Slovenia from September 7-10, 2026 will be presented. Also presented will be the continuing research support of major funded projects related to FSS in China from 2000 to 2025 from development of key technologies for identification of major foodborne pathogens, prevalence investigation of foodborne pathogens, processing for food safety, development of important reference materials, control of foodborne pathogens and chemical residues from primary production, demo of comprehensive measures ensuring food safety, risk assessment, integration of Big Data and AI in identification and characterization of important risks as well as risk assessment, risk communication, and risk management. Projects currently in progress include integration of food nutrition and food safety, AI-assisted surveillance and management, logistics for reduced food waste and food safety risk due to microbial spoilage and contamination of foodborne pathogens via cold chain, foods as vehicles of antimicrobial resistant pathogens, and proactive control measures to ensure safe foods and to secure the agricultural farming systems and to safeguard the food industries. There are lessons that could be learned for Asian countries from research findings achieved elsewhere in the world in the past.

Keywords: Food Microbiology, Food safety and Food Security

KN-02

Overview of Bacterial Injury Induced by High Hydrostatic Pressure

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Abstract

High hydrostatic pressure (HHP) has been commercially applied to high-quality food processing since 1990, when Japan introduced the first commercial HHP fruit products, such as jams, jellies, and yogurts. Since that time, the commercial HHP market has experienced continuous growth, with an increasing number of industrial HHP units being installed in the food industry year after year. The primary objective of HHP food processing is microbial inactivation. Above all, bacterial inactivation is of paramount important, given that bacterial pathogens—such as *Escherichia coli* and *Listeria monocytogenes*—account for the majority of foodborne illness-related fatalities, thereby posing a more critical public health threat than parasites or molds. Depending on the intensity of HHP-induced stress, bacterial inactivation is either lethal or sublethal in nature. The stress associated with sublethal inactivation is influenced by the HHP level, holding time, bacterial species or strain, and environmental factors. The sublethal inactivation induces injury of bacteria, and the injured bacteria may recover under suitable conditions. The level of injury can be categorized into slightly-, lightly-/moderately-, and severely-injured states. Furthermore, the recovery behavior is governed by ambient nutrients and storage temperature, among other factors. For the detection of HHP-injured bacteria, selective/differential media and incubation temperatures play pivotal roles. The mechanisms underlying HHP-induced bacterial injury can be elucidated from several structural and physiological viewpoints, such as membrane damage, reactive oxygen species (ROS) accumulation, HHP resistance, ribosome degradation, metabolomic alterations, and colony-forming behavior.

This work was in part supported by JSPS KAKENHI Grant Numbers JP23K05105 and JP24K08779.

Keywords: HHP, high hydrostatic, pressure, bacterial injury, food processing

KN-03

The future of food and agriculture research: trends, challenges and mitigation

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Abstract:

A number of global trends including, population growth, urbanization and aging, economic growth, investment, trade and food prices, natural disasters, migration and employment, among others, are influencing food security, and the overall sustainability of food and agricultural systems. These trends and developments are likely to have an impact on the future of food and agriculture. The future of food and agriculture is likely to be shaped by a combination of technological advancements, sustainability considerations, changing consumer preferences, and global challenges such as climate change. To address these challenges, social, policy, and research and innovation interventions such as climate-smart agriculture, vertical farming and indoor agriculture, water conservation, aquaculture development, biotechnology and genetic editing, alternative protein sources, food processing and preservation technology, and the use of agricultural fossil fuels will be required. Future food and agriculture researchers, scientists, and innovators will need to collaborate across disciplines to develop solutions that are not just technologically advanced but also sustainable, nutritious, and capable of addressing the diversified requirements of the rising population. Additionally, greater international and/or regional collaboration will be required to combat developing transboundary agriculture and food system challenges such as pests and diseases. The trend and challenges, as well as some major priority areas for future research in food and agriculture, will be briefly covered in this keynote address in order to minimize the challenges and improve the quality of life.

Keywords: Food & Agriculture, Research, Trend and challenges

K-04

Profiles of antimicrobial resistance in agricultural environment

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Abstract

The discovery of penicillin in 1928 was a new beginning in the treatment of bacterial infection. Subsequently, several research groups found beneficial compounds in microbial metabolites as human medication. Currently, we use antibiotics in variety of applications, with food production, including meat, egg, fish and crop production, accounting for almost 60 % of total consumption in Japan. It is possible to apply oxalinic acid, streptomycin and oxytetracycline to control pathogens in crop field. Up to this point, we have focused on the prevalence of resistant bacteria to β-lactam, quinolone, aminoglycoside and tetracyclines in soil, irrigation water and crops as agricultural specimens. So, we examined the bacterial resistance to amino-benzyl-penicillin; ABPC, ciprofloxacin; CPFX, streptomycin; SM and oxytetracycline; OTC by the culture dependent methods and genetic analysis of isolated bacteria. The culture dependent methods revealed that population of resistant bacteria to ABPC was approximately the same level as the population of total bacteria and CPFX resistance was relatively low in the environmental specimens, soil and irrigation water. In case of resistance to SM or OTC in the edible parts of lettuce and onion, population size of SM or OTC resistant bacteria was almost same level and significantly lower than resistant population to ABPC. Even without application of β-lactam compound as agricultural chemical, ABPC resistance was higher than resistance to other antimicrobial agents in our experiments. These results suggest that existence of β-lactam resistance is one of common property in agricultural environment. Genetic analysis of SM resistant bacteria in the edible parts of vegetables showed that many isolates possessed phosphorylation enzyme of SM, but rarely had other resistant genes, acetylation or adenylation of SM. These results may suggest that phosphorylation of SM is most common genetic factor to resist to SM in the edible parts of vegetables.

This work was in part supported by Ministry of Agriculture, Foresty and Fisheries, Japan.

Keywords: AMR, β-lactam, streptomycin, oxytetracycline, vegetables

O-01

Phenotypic and Genomic Characterization of *Cronobacter sakazakii* Recovered from Powdered Infant Formula and a Child Nutrition Manufacturing Environment in Bangladesh

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Abstract

Cronobacter sakazakii is an opportunistic foodborne pathogen that can cause severe infections in neonates and is frequently associated with contaminated powdered infant formula (PIF). This study aimed to comprehensively characterize *C. sakazakii* isolates obtained from infant formula products and a child nutrition manufacturing environment through an integrated phenotypic and genomic approach. A total of 112 samples, including 80 infant formula products and 32 environmental samples from a manufacturing facility, were examined for *Cronobacter* spp. Recovered isolates were characterized using culture-based and biochemical methods, PCR, 16S rRNA gene sequencing, and whole-genome sequencing (WGS), followed by assessment of antimicrobial susceptibility, hemolytic activity, biofilm formation, protease production, and tolerance to environmental stresses. Five *Cronobacter* isolates were recovered, representing 4.46% of the tested samples. Four isolates from infant formula products were identified as *C. sakazakii*, whereas one environmental isolate was identified as *Cronobacter dublinensis*. All isolates were positive for the *gluA* gene and confirmed by 16S rRNA sequencing. PCR analysis detected the virulence-associated genes *omp, fli, hly,* and *sip*. Three *C. sakazakii* isolates were assigned to ST83, a sequence type linked to neonatal infections, while one belonged to the uncommon ST789, reported here for the first time in South Asia. WGS identified 19 antimicrobial resistance genes, mainly related to efflux-mediated resistance, with *qacJ* detected uniquely in one isolate. The isolates demonstrated optimal growth at 37°C, limited growth at 45°C, and negligible growth at 4°C. Growth occurred between pH 5 and 9, while increasing lactose concentrations progressively inhibited growth but remained detectable at 12% lactose. Four *C. sakazakii* isolates showed resistance to nitrofurantoin, cefazolin, and fosfomycin, also showed α-hemolytic activity, and moderate biofilm formation, whereas none exhibited proteolytic activity. These findings underscore the importance of integrated phenotypic and genomic surveillance to improve infant food safety and reduce potential neonatal health risks.

Keywords: *Cronobacter sakazakii*, infant formula, infant health, infant food safety

O-02

The Issue of Mycotoxins in Maize and Countermeasures

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Abstract

Maize is one of the most important staple crops worldwide and plays a crucial role in food security, animal feed production, and agricultural economies. However, maize is highly susceptible to contamination by mycotoxins, toxic secondary metabolites produced by certain fungi. Among these contaminants, aflatoxins, mainly produced by *Aspergillus flavus* and related species, are considered one of the most serious food safety concerns due to their potent carcinogenicity and frequent occurrence in tropical and subtropical regions. Mycotoxin contamination in maize causes substantial economic losses by rendering harvested grain unsuitable for human consumption or animal feed. Exposure to aflatoxins poses significant health risks to both humans and livestock, including acute toxicity, impaired growth, and an increased risk of liver cancer. To mitigate these impacts, effective monitoring and early detection of aflatoxin-producing fungi are essential. These technologies provide new opportunities for risk assessment and the implementation of targeted control strategies before toxin accumulation occurs. This presentation will provide an overview of mycotoxins and their significance in maize, discuss the economic and public health impacts of aflatoxin contamination, and introduce recent developments in the detection of aflatoxigenic fungi as a promising approach for improving mycotoxin management and ensuring food safety.

Keywords: aflatoxin, aflatoxigenic fungi, detection

O-03

Antidiabetic functional food potential of green synthesized nano formulation from the mix of *Fenugreek*, *Nigella sativa*, and *Momordica charantia* in streptozotocin-induced diabetic rats

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Abstract

This study investigated the antidiabetic actions of green synthesized MgO-NPs (MgO nanoparticles) from polyherbal extracts of *Fenugreek*, *Nigella sativa*, and *Momordica charantia* in a streptozotocin-induced Wistar Albino model. The bioorganic MgO-NPs were characterized using several methods, including ultraviolet-visible spectroscopy (UV–Vis), X-ray diffraction (XRD), scanning electron microscopy (SEM) with energy-dispersive X-ray diffraction (EDX), transmission electron microscopy (TEM), Fourier-transform infrared spectroscopy (FT-IR), and Zeta potential. The characterization revealed the successful synthesis of nanoparticles, tiny, petal-like nanostructures (nanoflowers) with an average diameter of 4.65 ± 3.04 nm. The green-synthesized NP demonstrated significant amount of total phenolic content (60.9 mg GAE/g) and total flavonoids content (30.81 mg QE/mL), emphasizing strong antioxidant properties as demonstrated in the 2,2-diphenyl-1-picrylhydrazyl (DPPH) (IC_{50}=221.86µg/mL), 2,2-azinobis-(3-ethylbenzothiazoline-6-sulfonate) (ABTS•+) (IC_{50}=373.72µg/mL), and FRAP (Ferric Reducing Antioxidant Power) assays. In the alpha-amylase inhibitory assay and bovine serum albumin denaturation assay, the MgO-NPs were found to display promising potential for glycemic control, along with anti-inflammatory activity, with inhibitory concentrations of 420 µg/mL and 253.38 µg/mL, respectively. Following cytotoxic analysis in the Vero cell lines, in the streptozotocin-induced Wistar albino rat model of seven groups (n=5), with weights ranging from (130-170) g, the administration of NP 30 mg/kg and 70% ETH Extract 100 mg/kg for 21 days improved and alleviated glucose levels and other diabetes related biomarkers (ALT, AST, TG, TC, HDL, LDL, Creatinine, Uric acid, Total glucose and Total protein). In the anti-oxidative and anti-diabetic gene expression, the MgO-NPs upregulated the SOD, CAT, and PFK-1 biomarkers while downregulating the pro-apoptotic marker $_P$53. Histopathological analysis showed improved architecture of the liver, Kidney, and pancreas, which are consistent with biochemical findings. The findings demonstrate that that polyherbal-based nano formulations of MgO-NPs could be used as antidiabetic nano formulations with further evidences.

Keywords: Polyherbal; nanoparticle; green synthesis; glycemic control; streptozotocin.

O-04

Effects of Agricultural Antibiotic Application on Soil Microbiota, Antimicrobial-Resistant Bacteria, and Resistance Genes in Vegetable Cultivation

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Abstract

Antimicrobial resistance (AMR) is projected to cause ten million deaths annually by 2050. Under the One Health concept, agricultural antibiotic use as pesticides deserves attention, yet its impact on soil microbiota remains unclear. Oxytetracycline (OTC) and streptomycin (SM), both used in human medicine, are registered pesticides against bacterial rot of vegetables. We evaluated how their label-compliant application affects soil microbiota, antimicrobial-resistant bacteria (ARB), and resistance genes (ARGs). Lettuce (spring, 25/15°C; autumn, 30/20°C) and onion (28/23°C) were grown in a phytotron in pesticide-free and conventionally managed soils. An Agrimycin 100-based solution (OTC 7.5 µg/mL, SM 94 µg/mL) was applied twice (lettuce) or five times (onion) before harvest. Soils were analyzed by 16S rRNA amplicon sequencing, ARB isolation on R2A agar with 40 µg/mL OTC or SM, PCR-based ARG detection, qPCR, plasmid extraction, genome sequencing, and conjugation assays. Antibiotic application did not alter the dominant phyla or genera, although species diversity decreased significantly in sprayed pesticide-free soil under spring conditions. In contrast, the ARB composition shifted: *Lysinibacillus*, *Stenotrophomonas*, *Dyella*, *Sphingopyxis*, *Agrococcus*, and *Rummeliibacillus* increased after spraying, and resistant fractions were far higher in conventionally managed soil (SM-resistant, 13–16%) than in pesticide-free soil (0.1–0.5%). Notably, no foodborne pathogens were isolated. *aph(3')-IIa* and *smrA* were detected in nearly all isolates, whereas *strA* and *strB* were more frequent in conventionally managed soil. No plasmid was recovered, and genome analysis placed the ARGs on the chromosome rather than adjacent to mobile genetic elements. Consistently, soil ARG abundance did not increase and no transconjugants were obtained. These results suggest that, under the conditions tested, label-compliant antibiotic use enriches certain Gram-negative ARB but does not increase the total soil ARG pool. Continued monitoring of these genera would help refine AMR risk assessment in vegetable production.

Keywords: antimicrobial resistance; One Health; oxytetracycline; streptomycin; soil microbiota; fresh produce

O-05

Prevalence and Genomic Characterization of Antimicrobial-Resistant *Salmonella* spp. from Fresh Foods in Cambodia

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Abstract

Salmonella spp. are important foodborne pathogens and a significant global public health concern. In Cambodia, however, limited information is available on the prevalence of *Salmonella* along the food chain, circulating serotypes, and the occurrence of antimicrobial-resistant (AMR) strains. This study aimed to determine the prevalence, antimicrobial resistance, and genetic characteristics of *Salmonella* spp. isolated from fresh food products collected from local markets in Phnom Penh and nearby farms in Cambodia. A total of 285 fresh food samples, comprising 75 meat, 50 seafood/fish, and 160 leafy green vegetable samples, were collected and examined for *Salmonella*. A total of 138 samples (48.4%) were confirmed positive for *Salmonella*. Among 81 isolates subjected to whole-genome sequencing, 32 serotypes were identified. The most frequently detected serotypes were *S.* Corvallis (7%), *S.* Haifa (6%), *S.* Weltevreden (6%), *S.* Agona (5%), *S.* Kentucky (5%), and *S.* Livingstone (5%). Antimicrobial susceptibility testing showed that 99 of 139 isolates (71%) were resistant to at least one antibiotic, while 32 of 99 resistant isolates (32%) exhibited multidrug resistance. Resistance-associated genes were detected across multiple antimicrobial classes, including macrolides, aminoglycosides, tetracyclines, cephalosporins, phenicols, fluoroquinolones, sulfonamides/trimethoprim, and β-lactams. Multiple antimicrobial resistance mechanisms and genes were identified, highlighting the genetic diversity and complexity of AMR among *Salmonella* isolates from fresh foods. The high prevalence of *Salmonella* and the substantial occurrence of antimicrobial resistance among isolates indicate a potential foodborne public health risk in Cambodia. These findings may reflect the combined effects of antimicrobial use in livestock production and inadequate hygiene and sanitation practices throughout the food value chain. Strengthening *Salmonella* surveillance, antimicrobial stewardship, food hygiene, and sanitation from production through consumption is essential to reduce the burden of antimicrobial-resistant *Salmonella* in Cambodia.

Keywords: *Salmonella* spp.; antimicrobial resistance; antimicrobial resistance genes; multidrug resistance; fresh food; food safety; Cambodia.

O-06

Combined effects of rosemary extract and high hydrostatic pressure treatment on the quality and microbiological changes of lemon juice during refrigerated storage

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Abstract

Fresh juices have a short shelf life due to microbial growth and quality deterioration during storage. Lemon juice generally has a longer shelf life than other fresh fruit juices because of its low pH; however, some microorganisms can still survive and grow during storage. This study aimed to determine whether a combination of high hydrostatic pressure (HHP) treatment and rosemary extract (RE) could inhibit microbial growth and maintain the quality of lemon juice during storage. Fresh lemon juice was prepared by adding 20% (w/v) sugar to freshly squeezed lemon juice, followed by the addition of 0–2% (w/v) commercial water-soluble RE. The samples were treated with HHP at 600 MPa for 5 min at 4°C, then stored at 10°C and evaluated for microbial counts and quality parameters during storage. HHP treatment reduced both total viable counts and yeast and mold counts in lemon juice to below the detection limit (<1 log CFU/mL) immediately after treatment, regardless of RE addition. During storage, microbial growth remained inhibited for 2–3 weeks in HHP-treated juice, whereas microbial counts increased in raw juice. When approximately 4 log CFU/mL was considered an indicator of spoilage, the time to reach this level was extended from 1–2 weeks in raw juice to 3–4 weeks in HHP-treated juice. RE concentration did not affect microbial growth. In contrast, antioxidant activity and ascorbic acid were better retained with increasing RE concentration in both raw and HHP-treated juices, even after 3–4 weeks. These results indicate that HHP effectively reduces initial microbial contamination and delays spoilage, and that RE contributes to maintaining juice quality during storage. Consequently, from the viewpoint of both microbial growth inhibition and quality preservation, their combined use may be beneficial as a means of extending the shelf life of lemon juice in food processing.

Keywords: Rosemary extract, high hydrostatic pressure, microbial quality, lemon juice and refrigerated storage

O-07

Deep-Sea Tuna Fisheries Potential in Bangladesh: An Integrated Geospatial and Economic Assessment

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Abstract

The Bay of Bengal encompasses approximately 118,813 km² of maritime waters, offering substantial opportunities for sustainable offshore and deep-sea fisheries. Despite documented tuna resources and favorable oceanographic conditions, Bangladesh remains a minor participant in the Indian Ocean tuna fishery. This study evaluates Bangladesh's commercial tuna potential by integrating Indian Ocean Tuna Commission (IOTC) statistics, satellite derived oceanographic indicators, scientific survey evidence, spatial hotspot analysis, and preliminary economic assessment. Sea surface temperature (SST), chlorophyll-a concentration, and ocean-front dynamics were analyzed to identify potentially suitable tuna habitats. A simplified habitat framework considered SST of approximately 24–30°C, chlorophyll-a concentrations of 0.1–0.4 mg m^{-3}, deep-water environments, and proximity to thermal fronts and upwelling zones. The Indian Ocean contributes approximately 17% of global tuna catches. Analysis of 2013–2024 catch data indicates that purse-seine operations in the Bay of Bengal's high-seas areas (ABNJ) are largely absent, whereas longline, gillnet, and pole-and-line fisheries are widely used elsewhere in the Indian Ocean. Sri Lanka and India harvested yellowfin, skipjack, bigeye, kawakawa, and albacore, while Bangladesh primarily recorded skipjack, kawakawa, frigate tuna, and Spanish mackerel as bycatch from trawl and gillnet fisheries. Georeferenced catch data were analyzed using catch-weighted Kernel Density Estimation (KDE), identifying statistically significant hotspots at the 90–95% confidence levels in ABNJ. R/V *Dr. Fridtjof Nansen* surveys and IOTC records confirm commercially important yellowfin tuna (*Thunnus albacares*) and skipjack tuna (*Katsuwonus pelamis*) in the region. Preliminary spatial analysis indicates potentially productive fishing grounds around the Swatch of No Ground and deep offshore waters toward the Andaman Sea. For 2026, Bangladesh's IOTC yellowfin allocation is 2,000 MT compared with 33,123 MT for Sri Lanka, a 16.6-fold difference. Sri Lanka reported 112,494 MT of tuna and tuna-like species in 2024. Preliminary economic analysis indicates an approximately five-year payback period and 18.5% IRR for modern longline investment, highlighting opportunities for Bangladesh's sustainable tuna-fishery development.

Keywords: Longline Fisheries; Chlorophyll-a; Sea Surface Temperature; Ocean Fronts; Kernel Density Estimation; Economic Assessment.

O-08

Antimicrobial resistance and occurrence of *Salmonella* spp. and *Escherichia coli* in Vietnamese poultry across different farming scales

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Abstract
Salmonella spp. and *Escherichia coli* are important pathogens for food safety and antimicrobial resistance (AMR) surveillance in poultry production. This study compared the occurrence, AMR, and multidrug resistance (MDR) of *Salmonella* spp. and *E. coli* between large- and small-scale farms in Hai Phong, Vietnam, while minimum inhibitory concentration (MIC) testing was used to further characterize the antimicrobial susceptibility profiles of the isolates. A total of 72 chicken meat and intestinal samples were analyzed. *Salmonella* spp. and *E. coli* were isolated according to ISO 6579-1:2017 and ISO 16649-2:2001, respectively. Antimicrobial susceptibility to eight antibiotics was determined using the disk diffusion method and interpreted according to CLSI M100, while MICs were determined by agar dilution. Differences in bacterial occurrence, AMR, and MDR rates between farming scales were assessed using Fisher's exact test. Detection rates of *Salmonella* spp. in meat and intestinal samples were 2.78% and 25.00%, respectively, whereas those of *E. coli* were 13.89% and 83.33%. No significant differences in bacterial occurrence were observed between farming scales ($P > 0.05$). High resistance rates were primarily observed against amoxicillin, ampicillin, oxytetracycline, trimethoprim, trimethoprim–sulfonamide, and florfenicol. MDR rates for *Salmonella* spp. were 66.7% and 75.0% in large- and small-scale farms, respectively, while those for *E. coli* were 84.2% and 87.5%, with no significant differences between farming scales ($P > 0.05$). Overall, both pathogens were detected more frequently in intestinal than meat samples and exhibited high levels of AMR and MDR. These findings highlight the need for strengthened hygiene monitoring and prudent antimicrobial use in poultry production.

Keywords: antimicrobial resistance, *Escherichia coli*, farming scale, *Salmonella* spp., poultry.

O-09

Domestication of Fermented Milk Associated *Rothia kristinae* and *Streptococcus infantarius* through Whole-Genome Sequencing Approach

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Abstract

Traditionally, fermented milk production has relied on back-slopping, a practice that has been followed for approximately 100 years in Bangladesh. The repeated back-slopping may allow the adaptation and persistence of undesirable microorganisms within the production environment. Therefore, the identification and characterization of efficient and safe starter cultures are important for improving the consistency and safety of the final product. In this study, more than 170 bacterial isolates were obtained from 93 fermented milk samples collected from different regions of Bangladesh. Among the isolates, two strains, designated AAM01 and AAM02, showed highest rate of milk acidification. Whole-genome sequencing and subsequent genomic analysis identified AAM01 as *Rothia kristinae* and AAM02 as *Streptococcus infantarius*. Although both species have been reported in association with opportunistic pathogenicity, genomic assessment indicated that the investigated strains possessed characteristics distinct from known pathogenic strains. In Bioinformatics study, PathogenFinder2 predicted the strains as non-pathogenic, while no known virulence factors were detected using ABRicate-based screening. Phylogenetic analysis further indicated that the isolates belonged to lineages distinct from reported pathogenic strains. The technological suitability of the isolates was further evaluated through milk fermentation. Both strains efficiently fermented milk, lowering the pH below 4.5 within 8 h of fermentation at 37ºC. The fermented products also demonstrated favorable organoleptic characteristics, suggesting their potential as efficient milk-fermenting cultures. Additionally, under optimized culture conditions, AAM01 and AAM02 produced approximately 200 and 170 mg/mL lactic acid, respectively. Notably, co-cultivation of the two strains resulted in a substantially higher lactic acid concentration of approximately 325 mg/mL, indicating a potentially beneficial interaction between the strains and demonstrating their promise for industrial lactic acid production. Collectively, these findings indicate that AAM01 and AAM02 may have potential for further development as domesticated microbial cultures for lactic acid production as food preservative and fermented-food applications. However, comprehensive phenotypic and safety evaluations, including strain-specific toxicological and functional assessments, will be necessary before their application in food production.

Keywords: *Rothia kristinae*; *Streptococcus infantarius*; strain domestication; whole-genome sequencing; food preservation; starter culture.

O-10

Nutrition and Dietary Support Activities Following the 2026 Kumamoto Prefecture Earthquake—Status of Activities and Future Challenges for the Kochi Prefecture Dietitians Association—

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Abstract

On July 28, 2026, a magnitude 7 earthquake struck Kumamoto Prefecture. This major earthquake caused significant damage in Yatsushiro City, Hikawa Town, and Uki City. The Japan Dietetic Association (JDA), in collaboration with the Kumamoto Prefectural Dietetic Association, dispatched JDA-DAT (Japan Dietetic Association Disaster Assistance Team) leaders from the Kyushu, the Chugoku and Shikoku regions. The Kochi Prefecture Dietitians Association also dispatched four support staff; this report details their activities and future challenges. From August 17 to 30, four dietitians of the Kochi Prefectural Dietetic Association, including the author, were dispatched and each worked on-site for two to three days. They conducted rounds of evacuation shelters in Yatsushiro City, Uki City, and Hikawa Town. Their primary tasks were to monitor vulnerable individuals and, when necessary, bring and provide meals tailored to their needs from the special nutritional food station established by the Kumamoto Prefectural Dietitians Association. During the support period, in Yatsushiro City, they visited a total of 14 evacuation shelters and 22 individuals requiring special care; in Uki City, they visited 2 shelters and 1 individual; and in Hikawa Town, they visited a total of 10 shelters and 12 individuals. The needs of those requiring special care varied widely, including chronic conditions (kidney disease, diabetes, gastric ulcers, hypertension, etc.) and constipation. The likelihood of a Nankai Trough earthquake occurring in Kochi Prefecture is high, and urgent countermeasures are needed. Given Kochi Prefecture's east-west orientation, multiple special nutritional food distribution stations are necessary. According to a report from the Kumamoto Prefecture Dietitians Association, there was demand for soft meals for the elderly, baby food, and milk immediately after the disaster; therefore, we believe preparations must be made to ensure these supplies can be provided during the initial response phase following a disaster.

Keywords: Kumamoto Prefecture earthquake, shelter, dietitian, multiple special nutritional food distribution stations

O-11

Transcriptomic and Network Analyses Reveal Neuronal Functional Adaptation to a Potential Airborne Toxicant in Human iPSC-Derived Autonomic Neurons

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Abstract

Airborne chemicals can originate from products and technologies routinely used in daily life for comfort and convenience, raising interest in their potential biological effects on the human nervous system. In this exploratory study, we investigated transcriptomic changes in human induced pluripotent stem cell (iPSC)-derived autonomic neurons following exposure to a potential airborne toxicant to characterize its molecular effects and associated biological pathways. Human iPSC-derived autonomic neurons (201B7) were exposed to Compound A, a potentially airborne chemical, or maintained under non-exposure control conditions, followed by microarray-based transcriptomic profiling. Differential expression analysis, gene set enrichment analysis (GSEA) of Gene Ontology (GO) and KEGG pathways, and protein–protein interaction (PPI) network analysis was performed. A total of 588 differentially expressed genes (DEGs) were identified, comprising 93 upregulated and 495 downregulated genes. Functional enrichment analysis revealed positive enrichment of neuronal and sensory functions, including neuroactive ligand–receptor interaction, glutamatergic and GABAergic synapses, ion-channel and transporter activities, and sensory signaling. Neuronal compartments, including synapses, dendrites, axons, and synaptic vesicles, were also enriched. In contrast, pathways related to PI3K–Akt, TGF-β and TNF signaling, apoptosis, cellular senescence, extracellular matrix remodeling, and stress-related processes showed negative enrichment. PPI analysis further identified downregulated networks associated with inflammatory, TGF-β, extracellular matrix, and stress-related regulation, whereas the upregulated network included genes involved in neuronal regulation, cellular plasticity, intracellular transport, and metabolic adaptation. Despite concerns regarding its potential adverse effects, the transcriptomic response to Compound A under the examined conditions was not predominantly characterized by stress- or inflammation-associated changes. Instead, enrichment of neuronal signaling, synaptic, and sensory functions suggests a potential neuronal functional adaptation to exposure. These exploratory findings provide a basis for further functional and toxicological studies to clarify the biological significance of Compound A exposure.

Keywords: airborne toxicant, human iPSC-derived neurons, transcriptomics, neuronal signaling, functional adaptation

O-12

Occurrence of *Legionella pneumophila* in Processed Water Systems of Food Industries: Evidence of Potable Water Contamination

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Abstract

Legionella pneumophila is an opportunistic waterborne pathogen that colonizes engineered water systems and poses a significant public health risk through aerosol transmission. While cooling towers are recognized as major reservoirs, potable water distribution systems within food processing facilities have received comparatively little attention, particularly in developing countries. This study investigated the occurrence of *Legionella* spp. in processed water systems in the food industry in Bangladesh, with particular emphasis on potable water.

Water and biofilm samples were collected from five food processing industries in Dhaka, Bangladesh, including potable water, cooling towers, chillers, hot water tanks, air-conditioning systems, softener water, and cooling tower basin biofilms. Samples were analyzed using conventional PCR targeting the *L. pneumophila* 16S rRNA (LP-16SrRNA) gene, followed by a highly sensitive nested PCR assay to improve the detection of low bacterial loads. Conventional PCR detected *L. pneumophila* in 5 (20.74%) samples, including potable water, chiller water, and cooling tower water. Nested PCR identified an additional 11 positive samples that were undetected by conventional PCR, demonstrating substantially improved sensitivity. Potable water represented the second largest proportion of positive samples (3, 60%), followed by cooling towers (7, 20%), air-conditioning systems (2, 20%), softener water (1, 10%), hot water tanks (1, 10%), and chiller water (1, 20%). The frequent detection of *L. pneumophila* in potable water highlights the potential for colonization of internal water distribution systems beyond traditionally recognized sources, suggesting that potable water may contribute to occupational and environmental exposures within food processing facilities. The enhanced sensitivity of nested PCR provides evidence that potable water systems in food industries can harbour *L. pneumophila* and should be considered a priority in surveillance for routine environmental monitoring and risk management programs. To minimize the risk of legionellosis in food industry water environments, it is essential to plan comprehensive water safety plans and effective control measures together.

Keywords: *Legionella pneumophila*, Potable water, Food Industry, LP-16SrRNA, Nested PCR

O-13

Post-treatment deterioration of drinking water quality in Dhaka: Linking redox conditions, microbial contamination, and heavy metal exposure

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Abstract

Ensuring the safety of treated drinking water in rapidly expanding megacities requires evaluation beyond treatment efficiency, incorporating distribution network integrity and post-treatment handling. This study assessed the physicochemical quality, microbiological contamination, heavy metal occurrence, and associated human health risks of three widely consumed treated drinking water sources in Dhaka, Bangladesh: reusable jar water, Dhaka Water Supply and Sewerage Authority (DWASA) booth water, and commercially bottled water. A total of 135 samples were collected from ten locations during May–June 2025 and analyzed for physicochemical parameters, indicator microorganisms, and seven priority metals (Cr, Pb, Fe, Mn, Zn, Cd, and Se). Water quality was evaluated using the Water Quality Index (WQI), Heavy Metal Pollution Index (HMPI), Heavy Metal Evaluation Index (HEI), and Entropy-Weighted Water Quality Index (EWQI), while human health risks were estimated following USEPA guidelines. Jar and DWASA booth water frequently contained total coliforms, *Escherichia coli*, *Salmonella* spp., and *Vibrio* spp., whereas bottled water showed no detectable microbial contamination. Selenium concentrations exceeded national and WHO guideline values in most jar and DWASA samples (15.94 ± 4.05 and 22.23 ± 3.74 µg L^{-1}, respectively), while elevated manganese was observed in some municipal supplies. Water quality indices classified a considerable proportion of jar and DWASA samples as poor to unsuitable for drinking, whereas bottled water consistently exhibited superior quality. Although non-carcinogenic risks remained within acceptable limits (HI < 1), risks were higher for children and greatest in DWASA booth water. Total lifetime cancer risk exceeded the acceptable threshold (10^{-4}), primarily due to cadmium exposure, reaching 3.26 × 10^{-4} in DWASA samples. These findings highlight microbial contamination, elevated selenium, and system vulnerabilities, emphasizing the need for risk-based monitoring and improved water safety.

Keywords: Drinking water quality, microbial contamination, heavy metal and Dhaka city

O-14

Analysis of nucleic acid retention characteristics by cause of death in stored-product insect pests

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Abstract

Determining when and how insects contaminate into foodstuff is essential for effective hygiene management, as well as for clarifying responsibility within the supply chain. In the field of forensic science, methods for estimating the time of death based on postmortem nucleic acid degradation have been used; however, whether these methods can be applied to trace insect contamination in food safety aspects has not yet been systematically verified. In this study, adult red flour beetles (*Tribolium castaneum*) were killed under four conditions simulating food manufacturing and distribution: boiling, mechanical impact from a fall, continuous freezing at −20°C, and freezing followed by storage at 15°C to simulate thawing. The amounts of intact RNA and DNA were quantified using three marker genes by RT-qPCR and qPCR, respectively. The patterns of degradation varied depending on the cause of death. Nucleic acids remained stable under continuous freezing, whereas thawing after freezing caused the most rapid loss. Boiling largely preserved nucleic acids beyond day four, and mechanical shock led to a slower, steady decline. DNA persisted longer than RNA, and mitochondrial RNA outlasted nuclear RNA across all treatments. Based on these data, prediction of cause of death and postmortem interval was also attempted. Within the first four days after death, any of the marker tested can indicate insect contamination, while DNA and mitochondrial RNA remain more reliable between 7 and 14 days, offering a practical basis for marker selection in food traceability.

Keywords: Postmortem, nucleic acid degradation, insect pests, and stored-product

O-15

Analytical Methods for the Detection of Genetically Modified Organisms (GMOs) for Food Labeling in Japan

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Abstract

The global area under genetically modified (GM) crops is continually increasing and reached 216 million hectares in 2025. According to the ISAAA database (https://www.isaaa.org/gmapprovaldatabase/default.asp), 30 countries cultivated a range of 11 different GM crops, and 213, 58, and 77 of GM maize, soybean, and cotton varieties have been approved worldwide for use as food, feed, or for cultivation. However, some consumers still express concerns about the utilization of genetically modified organisms (GMOs). Many countries have implemented the labeling system of GMO. In Japan, non-GM maize and soybean are segregated and imported from other countries by an identity-preserved (IP) handling system. However, the unintentional commingling of GM products in non-GM materials is inevitable. In such cases, up to 5% unintentional commingling of approved GM is generally accepted, and foods within this level of GM content can voluntarily be labeled as "handled to prevent commingling of GMO," while non-GMO labeling is permitted when commingled GM contents are not detectable. To enforce the labeling system, it is indispensable to define a practical threshold level of GM content and to develop qualitative and quantitative methods for detection and the estimation of unintentional commingling of GMO. The polymerase chain reaction (PCR) technique is used to detect and quantify GM crops in foods worldwide. We have developed and validated many qualitative and quantitative detection methods for GMOs. I will introduce regulations including labeling system and detection methods using real-time PCR for GM foods in Japan. I will also introduce cost- and time-effective GMO detection using loop-mediated isothermal amplification (LAMP).

This work was in part supported by a Grant from the Consumer Affairs Agency of the Government of Japan.

Keywords: genetically modified (GM), food labeling, analytical method, PCR, LAMP

P-01

Microbial risk and hygiene management in Flexible Intermediate Bulk Containers (FIBC) manufacturing industries intended to use in food

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Abstract

The FIBC are strong polypropylene bags for carrying bulk dry goods, reducing cost, contamination and spills. In this study, risk assessment and management was performed of FIBC bag manufacturing facility was conducted from 2017 to 2025 evaluating the microbial contamination along the production chain and control measures were also taken to improve the condition. A total of 22-34 locations in each year along the production chain were chosen, and samples (total 387 swab and solid samples in eight years) were collected from these locations each year and analyzed for microbial contamination. Total aerobic bacterial count, total coliform count, *E. coli*, Yeast and Mould and *Staphylococcus* spp. was evaluated along the study. The findings revealed that the microbial contaminations were primarily caused by workers' hands or hand gloves due to poor hygiene from inadequate knowledge, poverty, workers migration etc. Other contaminated locations included baling machine surfaces, liner surfaces, and finished product surfaces were also recorded originating from workers activities. Floor surfaces along the production area, on the other hand, were found contaminated due to a lack of routine sanitization. To improve the contaminations, hand gloves were recommended for UV sterilization proper, daily cleaning and sanitization was recommended to the floor and machine surface before starting work, along with UV sterilization of finished products were also recommended. Moreover, preventive control measures were taken by providing soap, paper towels, sanitizers along with awareness training on proper hand-washing practices to the workers and monitoring were undertaken to ensure that the condition remained acceptable.

Keywords: FIBC, Microbial hazard, Risk management, Pathogens

P-02

Selective Predation of Foodborne Pathogens and Seafood Spoilage Bacteria by *Bdellovibrio* and Like Organisms: Potential for Biological Control in Food Safety

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Abstract

Foodborne pathogens and seafood spoilage bacteria remain important challenges to food safety and quality, highlighting the need for sustainable biological interventions. *Bdellovibrio* and like organisms (BALOs) are obligate predatory bacteria that selectively prey on Gram-negative bacteria, including important foodborne, aquatic, and spoilage organisms. This study investigated predator–prey specificity among freshwater and saltwater BALOs and evaluated the potential of marine *Bacteriovorax* against seafood-associated bacteria. Prey-susceptibility patterns of four phylotypes of saltwater *Bacteriovorax* and three genera of freshwater BALOs were assessed against a diverse panel of pathogenic bacteria using broth suspension and soft-agar assays. Additional experiments evaluated marine *Bacteriovorax* OT2 against the seafood spoilage bacterium *Photobacterium phosphoreum* under varying environmental and predator–prey conditions. Distinct prey-range patterns were observed. *Salmonella* isolates and other Enterobacteriaceae, including *Enterobacter aerogenes, Proteus mirabilis*, and *Providencia stuartii*, were generally susceptible to freshwater BALOs but resistant to saltwater *Bacteriovorax*. In contrast, marine-associated bacteria, including *Vibrio vulnificus, Vibrio* sp., and *Vibrio parahaemolyticus* P-5, showed greater susceptibility to saltwater *Bacteriovorax*. Importantly, *Bacteriovorax* OT2 reduced *P. phosphoreum* by 4.5–4.8 $\log_{10}$ within 9 h at 25°C and remained effective across a range of pH, salinity, and temperature conditions. These findings demonstrate ecologically distinct prey preferences among BALOs and substantial predatory activity of marine *Bacteriovorax* against seafood-associated bacteria. The results support further development of predatory bacteria as targeted biological interventions for controlling foodborne pathogens and seafood spoilage.

Keywords: *Bacteriovorax*; BALOs; *Salmonella*; *Vibrio*; *Photobacterium phosphoreum*; seafood spoilage; biological control

P-03

Molecular Characterization and Phylogenetic Diversity of Bacterial Isolates from Integrated Poultry, Dairy and Aquaculture Farms in Bangladesh

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Abstract
Integrated poultry, dairy and aquaculture farms connect animals, humans and the environment, allowing bacteria to circulate across different ecological compartments. However, bacterial diversity in these systems remains poorly characterized in Bangladesh. This study identified bacteria from integrated farms using 16S rRNA gene sequencing and evaluated their phylogenetic relationships, potential relevance to antibiotic resistance and biofilm formation. Seventy representative bacterial isolates obtained from poultry, dairy, aquaculture, and associated environmental samples were analyzed using partial 16S rRNA gene sequencing. Sequences were identified through comparison with the NCBI BLAST database, and phylogenetic relationships were assessed using the Neighbor-Joining method with 1,000 bootstrap replicates. Both Gram-negative and Gram-positive bacteria were identified, with Gram-negative isolates predominating. *Enterobacter hormaechei* was the most frequent species (17.1%), followed by *Proteus mirabilis* (12.9%), *Klebsiella pneumoniae* (10.0%), and *Citrobacter freundii* (7.1%). *Aeromonas hydrophila*, *Enterobacter cloacae*, and *Escherichia coli* each accounted for 5.7%, while *Aeromonas caviae* and *Pseudomonas aeruginosa* represented 4.3% each. Less frequent species included *Providencia rettgeri* and *Vibrio cholerae*. Among Gram-positive isolates, *Mammaliicoccus sciuri* and *Exiguobacterium profundum* were most common (7.1% each). Phylogenetic analysis showed close clustering of isolates with corresponding reference sequences, supporting their species-level identification. Integrated farming systems in Bangladesh harbor diverse bacterial populations, including organisms of potential public health significance. The predominance of Gram-negative bacteria emphasizes the importance of surveillance at the animal-human-environment interface. These findings provide useful baseline data for future One Health studies addressing bacterial transmission, antimicrobial resistance and biofilm-associated risks.

Keywords: 16S rRNA gene sequencing, bacterial diversity, phylogenetic analysis, integrated farming systems, Bangladesh, One Health.

P-04

Food Contamination by Hard Foreign Materials Detected in Commercial Laboratories in Japan, 2015-2019

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Abstract

In Japan, complaints on food contamination by foreign materials (FMs) are reported to the municipal health centers. However, not all FM-contamination events are reported to health centers. As a different information source, complaints detected in commercial laboratories were also aggregated and analyzed. Our previous results indicated that majority (80 - 90%) of health damages were caused by hard FMs. Since hard FMs are considered important in the context of HACCP, we analyzed hard FMs detected in commercial laboratories in this study. Complaints from the consumers on food contamination by FMs were provided by Japanese Consumers' Cooperative Union (period: Fiscal Year 2016 - 2018). We compiled the data for CO-OP by hard FMs, food items, occurrence of health damage, and size of hard FMs. There were 4,299 (CO-OP) complaints on food contamination by FMs during the data collection period. Among 4,299 complaints, 896 (20.8%) were hard FMs. Most frequently reported hard FMs were raw materials (65.0%) followed by plants (11.2%), and plastics (9.9%). Of 818 hard FMs with information available, 81.9% were contaminated at raw materials stage. Frozen foods (26.7%), frozen vegetables (13.2%), and livestock products (11.9%) were the most frequently reported food items. Of 269 hard FMs with size information available, 37.5% for "0 - 9.9 mm", 31.2% for "10.0 - 19.9 mm" and 15.2% for "20.0 - 29.9 mm". During the data period of 3 years, 28 events with injury were reported in CO-OP data. The hard FMs that caused injury were raw materials (25 events), stones (2 events) and plastics (1 event). Among 25 events by raw materials, 20 were caused by "Bone / Shell" category. These data, together with the municipal data, enable us to recognize the situation of food contamination by FMs in Japan, and to guide food business operators in preventing food contamination by FMs.

Keywords: HACCP, Contamination, Hard Foreign Material, Injury, Japan

P-05

Developing Food Safety Culture Based on Case Analyses of Food Safety Incidents and Corporate Misconduct: A Comparative Analysis Using the Five Food Safety Culture Elements of CXC 1-1969

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Abstract

Food safety culture is essential for the effective implementation of hygiene management practices, including HACCP. The 2020 revision of the Codex General Principles of Food Hygiene (CXC 1-1969) identifies commitment, leadership, awareness, open and clear communication, and sufficient resources as key elements of food safety culture. This study compared food safety incidents and corporate misconduct cases in Japan based on these five elements and examined approaches to fostering food safety culture. Ten cases in Japan since 2000 were analyzed using publicly available reports. Each element was classified as having major problems, some problems, or insufficient information for evaluation. Although causes and hazards differed among cases, problems involving multiple elements were identified in many cases. Major problems were most frequently identified in awareness of abnormalities and warning signs as food safety concerns, followed by commitment and leadership. These findings highlight management's important role in preventing food safety incidents. The findings suggest that the five elements should be interconnected to support continuous improvement rather than addressed independently. Accordingly, a PDCA-based model was proposed: management commitment, food safety policy, and leadership in Plan; food safety objectives, leadership, resource allocation, commitment, and awareness in Do; open and clear communication in Check; and workplace improvement in Act. Food safety culture provides an organizational foundation for recognizing and sharing abnormalities and warning signs and translating them into preventive actions. A continuous PDCA cycle initiated by management commitment and leadership may contribute to fostering food safety culture throughout the organization.

Keywords: Food safety culture, incidents, misconduct and culture elements

P-06

Developing a Regional Network of Food Safety Professionals in the Tokai Area

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Abstract

Large-scale food poisoning incidents in Japan have shown notable changes in their causes and patterns over time. These shifts highlight the need for food safety and quality control professionals to continuously update their knowledge and competencies. While many seminars and study groups on food safety are actively organized in major metropolitan areas such as Kanto and Kansai, the Tokai region—located between these two hubs—has lacked comparable opportunities for professional learning and networking. To address this gap, we established a new study group in 2024, led by Professor Hayashi at Meijo University, titled "Meeting to Consider Food Quality Control." The initiative was founded on Meijo University's guiding philosophy of cultivating individuals who are moderate, fair-minded, action-oriented, and trusted by society. The group aims to: 1) Provide up-to-date knowledge and practical insights related to food safety; 2) Offer a platform for information exchange among food safety and quality control professionals; and 3) strengthen collaboration between industry and academia, including opportunities for companies to engage with university students. The study group has been well received by Meijo University alumni and food industry professionals in the Tokai region, becoming recognized as a new source of learning in food safety. At the 8th meeting held in March 2026, more than 50 participants attended, demonstrating growing regional interest and engagement. Moving forward, we aim to further expand this network and enhance its contribution to food safety capacity building in the Tokai area.

Keywords: Food safety, regional network, quality control and Tokai area

P-07

Thirty years activities of NPO Food Safety Network in Japan

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Abstract

The NPO Food Safety Network started its activities in July 1997 and proposed the 7S of food hygiene in 2005. The basic concept of the NPO Food Safety Network (At the time of establishment) is based on the following four points: 1) Aim to be a comprehensive think tank on hygiene and safety in the food industry; 2) Provide consulting for the introduction, guidance, and education of the HACCP system; 3) Offer consulting on hygiene management in food manufacturing; 4) Promote friendship and camaraderie among members and aim to create a network for exchanging information. In order to become a top leader in this field in Japan as a comprehensive think tank on hygiene and safety in the food industry, we carried out activities on multiple fronts. First, recognizing that it is essential not only to acquire basic knowledge but also to understand the actual sites and current states of the food industry, we, since the founding of the association, have observed many food industry sites across Japan, as well as investigated and studied food industry sites in countries like the US and Canada, which are advanced in HACCP, and in many Southeast Asian countries. From the results of such surveys and research activities, the NPO Food Safety Network was the first in Japan to announce that HACCP can maximize its effectiveness only within an organization-wide management system, even before ISO22000 was internationally discussed. Based on that idea and the achievements of company-wide quality control activities in Japan, the 7S for food hygiene proposed from the NPO Food Safety Network has become a major driving force in promoting hygiene and safety activities in the food industry, and it has also become clear that it plays an important role in establishing the recently popular concept of a 'food safety culture'.

Keywords: NPO, Food hygiene and safety, safety network, and food industry

P-08

Packaged Food labels in Bangladesh: Information gaps, Food additives, and Health risk assessment through consumption pattern

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Abstract

Packaged foods label provides information which is a legal requirement for consumers making choices to include the foods in their diet chart. The use of excess additives in processed packaged foods is also an alarming food safety issue for all aged people. The purpose of this research was to assess labels of packaged foods, the prevalence of additives and health risk assessment of children. Label information was collected from 2000 packaged foods from Tangail Sadar, Bangladesh. The artificial color, preservative, and sweetener were measured from selected processed foods by HPLC. A validated, structured questionnaire was used on 2246 children for data collection of health risk assessment. The findings showed that 47.50% packaged foods covered standard labels, whereas 52.50% didn't according to Bangladesh Standard and Testing Institutions (BSTI) labelling requirements. HPLC analysis showed that 38.82% of processed foods contained acesulfame k, 71.60% sunset yellow, and 94.54% potassium sorbate. The health risk analysis results indicated that children consumed a high percentage of artificial color sunset yellow from drinks, juices, biscuits, and cakes and exceeded the hazard quotient index 1. The average daily intake (ADI) of potassium sorbate and acesulfame k from processed foods by children were below the maximum permitted usage level as set by Codex Alimentarius and didn't exceed the hazard quotient 1. However, a few samples had a high concentration of potassium sorbate and acesulfame k, which could be a risk factor for children's health. The study emphasizes maintaining the standard label, particularly for nutritional ingredients and additives with a focus on food safety. Strict law enforcement and regular monitoring are crucial for using additives in processed foods within regulatory limits as they exceeded maximum permitted level in some processed foods and posed health risk for children.

Keywords: Packaged food label, food additives, health risk, and HPLC

P-09

Engineering Multifunctional Plant Growth-Promoting Rhizobacteria for Sustainable Crop Production: Integrating Climate Resilience and Green Nanotechnology

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Abstract

Soil salinity and phytopathogenic diseases remain two of the major abiotic and biotic constraints, respectively, limiting sustainable crop production and food security worldwide. This presentation highlights an integrated microbial biotechnology platform that exploits multifunctional plant growth-promoting rhizobacteria (PGPR) to simultaneously enhance plant resilience against abiotic stress and provide environmentally friendly disease management. Salt-tolerant PGPR isolated from coastal rice-growing regions of Bangladesh were evaluated for plant growth-promoting attributes, stress adaptation, nutrient mobilization, and biocontrol potential. Among these, *Priestia aryabhattai* MS3 emerged as a promising microbial chassis, exhibiting efficient nitrogen metabolism, phosphate solubilization, siderophore-mediated iron acquisition, phytohormone production, and robust tolerance to saline environments. Whole-genome sequencing further revealed an extensive repertoire of genes associated with stress adaptation, biofilm formation, secondary metabolite biosynthesis, ion homeostasis, and root colonization, supporting its broad ecological fitness and agricultural potential. Building upon these genomic and physiological attributes, *P. aryabhattai* was further exploited as a biological nanofactory for the green synthesis of zinc oxide nanoparticles (ZnO-NPs). The biosynthesized nanoparticles, characterized by FTIR and scanning electron microscopy, were predominantly spheroidal with sizes ranging from 20–40 nm. Biomolecule-mediated synthesis was evidenced by characteristic functional groups acting as reducing and stabilizing agents. The ZnO-NPs exhibited marked antifungal activity against several agriculturally important phytopathogenic fungi, demonstrating their potential as eco-friendly alternatives to conventional fungicides while minimizing chemical inputs into agricultural systems. Collectively, these findings establish *P. aryabhattai* as a multifunctional microbial platform integrating plant growth promotion, abiotic stress mitigation, and green nanotechnology for sustainable crop protection. This dual-function strategy provides a promising framework for developing next-generation bioinoculants that simultaneously improve crop productivity and reduce dependence on synthetic agrochemicals, thereby contributing to climate-resilient agriculture, food safety, and long-term food security.

Keywords: Rhizobacteria, sustainable crop production, climate resilience and green nanotechnology

P-10

Lipopeptide Biosurfactants from *Bacillus subtilis* for Sustainable Crop Protection and Food Security

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Abstract

Microbial biosurfactants are promising natural alternatives for sustainable plant disease management and resilient food production. This study evaluated six biosurfactant-producing *Bacillus subtilis* strains for biosurfactant production, functional properties, antifungal activity, and plant-protective potential. The strains were cultivated using six previously reported production media. Minimal salt medium supported the highest biosurfactant production, with strains 1i, 50S, and Leaf 28 yielding 0.121, 0.116, and 0.109 mg/mL, respectively. Oil displacement assays confirmed surface activity, while emulsification assays demonstrated differences among strains, with strain 1i showing the highest emulsification index (58%). Fourier-transform infrared spectroscopy (FTIR) revealed peptide- and lipid-associated functional groups consistent with lipopeptide-containing biosurfactant preparations. Antifungal activity was evaluated against five phytopathogenic fungi using minimum inhibitory concentration assays, dual-culture assays, and contaminated-food assays. *Sclerotium rolfsii*, a soil-borne pathogen associated with poor seedling establishment, was selected for subsequent plant challenge experiments. Among the preparations tested, the biosurfactant from *B. subtilis* Leaf 28 exhibited the strongest overall plant-protective activity. In post-germination challenge assays, treatment with the Leaf 28 preparation improved cucumber seedling survival and protection against disease. Increased phenylalanine ammonia-lyase (PAL) activity suggested that activation of plant defense responses may contribute to this protective effect. These findings identify *B. subtilis* Leaf 28 as a promising source of biosurfactants for biologically based crop protection. Further greenhouse and field validation is warranted to establish its practical potential to reduce disease-related crop losses and support sustainable food production and food security.

Keywords: Biosurfactants, *Bacillus subtilis*, sustainable crop protection and food security

P-11

Valorization of Broken PUD Shrimp into High-Value IQF Foods for Sustainable Seafood Processing

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Abstract

The shrimp-processing industry in Bangladesh faces increasing challenges from rising raw-material costs, international price volatility and strong competition from major shrimp-producing countries. This study explored the valorization of food-grade broken peeled and deveined (PUD) shrimp into high-value individually quick frozen (IQF) foods as an approach to improve raw-material utilization and diversify seafood products. Cooked broken PUD shrimp, with an initial standard plate count (SPC) of 3.3×10^4 CFU/g, coliforms and *E. coli* below 3 CFU/g, and absence of *Salmonella* and *Vibrio*, was converted into standardized shrimp mince. Approximately 40–45% shrimp mince was incorporated with potato, vegetables, herbs, cheese, flour/starch, breadcrumbs, egg and seasonings to develop seven ready-to-cook products: Prawn Rissoise, Shrimp Top, Prawn Cheese Ball, Prawn Finger, Shrimp Momo, Shrimp Cutlet and Shrimp Tempura. Products were manufactured under controlled hygiene, sanitation and cold-chain conditions and individually quick frozen to a core temperature of approximately −18°C, followed by storage at −18°C or below. Sensory evaluation using a 9-point hedonic scale demonstrated good acceptance. Shrimp-ball samples achieved mean scores ranging from 7.36 to 8.00, with an overall mean of 7.67; ANOVA showed no significant difference among panelist scores ($F_{4,50}$ = 1.14, p = 0.349). Another formulation achieved an overall mean score of 7.53, with no significant difference among groups ($F_{4,50}$ = 0.915, p = 0.462). Prawn Rissoise showed significant differences among treatments ($F_{4,50}$ = 12.22, p < 0.001), indicating formulation-dependent sensory responses. Finished products recorded an SPC of 5.18 $\log_{10}$ CFU/g, *E. coli* 5 CFU/g and coliforms 23 CFU/g, with *Salmonella* and *Vibrio* absent. Overall, the study demonstrates the potential to transform lower-value broken PUD shrimp into convenient, protein-rich IQF foods, supporting resource efficiency, product diversification and value creation in Bangladesh's shrimp-processing sector.

Keywords: Broken PUD shrimp; valorization; shrimp mince; value-added foods; IQF; ready-to-cook foods; sensory evaluation; sustainable seafood processing.

P-12

Practical Model of Food Hygiene 7S: Building Food Safety Culture for Small-Scale Food Businesses

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Abstract

This study presents a practical model of the Food Hygiene 7S aimed at building a food safety culture among small-scale food businesses. The 7S begins with Seiri (Sort), which removes unnecessary items, and Seiton (Organize), which arranges tools and equipment efficiently to visibly improve the production environment. This initial stage creates a comfortable and efficient workplace and enhances motivation for improvement among frontline workers. In the next stage, emphasis is placed on scientifically grounded hygiene management. Seiso (Dry Cleaning) and Senjo (Wet Cleaning) are applied appropriately according to food characteristics, soil properties, and equipment design to ensure thorough removal of contaminants. Subsequently, Sakkin (Sanitize) reduces microorganisms to levels acceptable for food safety. Because these processes are invisible activities, maintaining motivation can be challenging; however, visualizing outcomes—such as microbiological test results or complaint trends—plays an important role in sustaining engagement and reinforcing the value of these efforts. The accumulation of these five S activities leads to Seiketsu (Microbiological Hygiene), and Shitsuke (Self-Discipline) enables the maintenance and continuous improvement of hygienic conditions. The collective practice of Shitsuke by individual employees contributes to the establishment of an organizational food safety culture. The Food Hygiene 7S is a system that emphasizes the "soft" aspects of employee behavior and awareness rather than relying on "hard" infrastructure investments, making it particularly suitable for small-scale food businesses in Asia. Based on 30 years of experience within the Food Safety Network (FSN), this study introduces case examples of workplace hygiene improvement and demonstrates that the Food Hygiene 7S is effective in enhancing hygiene and fostering a food safety culture.

Keywords: Food hygiene 7S, practical model, food safety culture and small food businesses

P-13

Development of Distinctive Bread Using Brewing Yeast

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Abstract

With the westernization of dietary habits, consumer demand for bread has increased, along with a growing preference for safe, natural, and clean-label foods. However, conventional mass-produced breads often rely on chemical additives or fail to satisfy diverse consumer preferences. To address this challenge, this study focused on the development of novel bread with distinctive flavor and texture utilizing brewing yeast strains (Saccharomyces cerevisiae). Specifically, we evaluated the application of sake and wine yeasts in grape juice-enriched breadmaking. The physiological performance of commercial baker's yeast, sake yeast, and wine yeast was assessed through dough fermentation kinetics and gas evolution assays. Bread formulations were prepared with grape juice substitution and subjected to evaluations of specific volume, texture profiles, volatile organic compounds, and sensory attributes. Dough fermentation tests indicated that while brewing yeasts required longer fermentation durations than baker's yeast, they attained equivalent maximum dough volumes and exhibited clear utilization of both sucrose and maltose. Notably, brewing yeasts achieved superior loaf expansion, yielding specific volumes of 2.78 mL/g (wine yeast) and 2.41 mL/g (sake yeast) compared to 1.92 mL/g for baker's yeast. Volatile analysis via gas chromatography-mass spectrometry revealed that brewing yeast breads contained approximately two-fold higher concentrations of isoamyl alcohol, contributing to a rich, sweet aroma. In texture profile analysis, baker's yeast bread displayed 2- to 3-fold higher hardness and 10- to 15-fold higher adhesiveness than brewing yeast loaves. Correspondingly, sensory evaluation confirmed that brewing yeast breads received significantly higher scores for crumb softness, smooth mouthfeel, and overall acceptability. Overall, fermenting grape juice with brewing yeasts provides an effective strategy for innovating bakery products with superior physical texture and distinct sensory qualities. Furthermore, utilizing brewing yeasts with a long history of safe food consumption ensures high microbiological safety and consumer trust, highlighting their value as safe, clean-label ingredients in food production.

Keywords: Brewing yeast**,** sensory qualities, microbial safety and bakery products,

P-14

Diet-friendly sugar beet jelly: sucrose level, quality and safety

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Abstract

This study developed a diet-friendly vegetable jelly from sugar beet (*Beta vulgaris* L.) juice and evaluated the effects of sucrose concentration on physicochemical, sensory, and microbiological quality during refrigerated storage. Jelly formulations containing 0, 20, 25, and 30% sucrose (w/w) were prepared with pectin (1–2.5%, w/w) and citric acid (0.5%, w/w), then heated to the desired soluble-solids concentration. The experiment followed a completely randomized design with three replications, and samples were stored at 4 °C for one month. Physicochemical properties, including pH and total soluble solids (TSS), were assessed at regular intervals. Sensory quality was evaluated by 11 semi-trained panelists using a nine-point hedonic scale for appearance, taste, texture, aroma, and overall acceptability. Microbiological safety was determined according to the USFDA Bacteriological Analytical Manual using selective and non-selective media for indicator and pathogenic microorganisms. Sucrose concentration significantly influenced jelly quality. pH decreased from 6.15 in the sugar-free control to 3.83 in the 30% sucrose formulation, while TSS increased from 49.17 to 62.60 °Brix. The 25% sucrose treatment achieved 58.60 °Brix, meeting typical jelly quality requirements while maintaining favorable spread ability. This formulation received the highest sensory scores for appearance (9.00), taste (7.00), texture (8.00), aroma (7.67), and overall acceptability (8.67). In contrast, the sugar free jelly was comparatively fluid, whereas the 30% sucrose jelly was excessively firm and less preferred. Fresh products had microbial loads below detectable limits (<10 cfu/g) for total aerobic bacteria, coliforms, faecal coliforms, yeasts, and moulds; *Escherichia coli*, *Salmonella* spp., and *Staphylococcus* spp., were not detected. These satisfactory microbiological results were maintained after one month of storage at 4°C. Sugar beet juice is therefore a promising raw material for reduced-sugar vegetable jelly, with 25% sucrose providing the best balance of quality, acceptability, and microbiological safety.

Keywords: sugar beet jelly, low-sugar product, physicochemical properties, sensory quality, and microbiological safety

P-15

Indigenous *Bacillus thuringiensis* Strain JSd1 as a Genomically Validated Biopesticide Candidate Against Tephritid Fruit Flies in Bangladesh

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Abstract

In Bangladesh, persistent cucurbit crop damage poses a major and recurring threat to agricultural productivity. One of the causal agents of damage is tephritid fruit flies, most notably the melon fly *Zeugodacus cucurbitae* and the pumpkin fruit fly *Zeugodacus tau*. Regarded as among the most destructive pests, they can cause economic loss and yield reduction, ranging from 30% to 100%. For pest management, farmers are mostly dependent on chemical pesticides, and there have been well-documented environmental and resistance-related costs regarding the use of traditional pest control. This leads to the search for indigenous, field-adapted biological alternatives. In this study, we screened 44 indigenous *Bacillus thuringiensis* (Bt) strains *in vivo* against third-instar larvae of both pest species. Among them, strain JSd1 consistently emerged as the most potent isolate. It caused 95% larval mortality in *Z. cucurbitae* (LC_{50} 0.429 ml/gm; LT_{50} 54.16 h) and 92% mortality in *Z. tau* (LC_{50} 0.472 mg/ml; LT_{50} 55.17 h), performance comparable to the reference strain *Bt kurstaki* HD-73. JSd1 treatment significantly disrupted *Z. tau* development in infested bitter gourd and cucumber. This was observed based on reductions in pupation, adult emergence, sex ratio, wing length, and flight ability relative to untreated controls. To understand the genetic basis of this efficacy, whole-genome sequencing of JSd1 was performed. This resulted in yielding a 5.39 Mb draft genome (5,833 genes, four plasmids, 25 genomic islands). Genome mining helped us identify *cry22A* and *vip3A* homologs, multiple *bmp1*-like metalloproteases, *enhancin*, *cytK*, and *chiA*, alongside biosynthetic gene clusters for petrobactin, bacillibactin, and thuricin CD. This indicated a multi-layered insecticidal and antimicrobial arsenal. Phylogenomic analysis placed JSd1 within the *Bacillus cereus* sensu lato group, closely allied with *B. thuringiensis* serovar konkukian. Together, these bioassay and genomic findings establish JSd1 as a genetically validated and dual-target biopesticide candidate for sustainable tephritid management in Bangladeshi agriculture, with clear potential for field-level formulation and deployment.

Keywords: Biopesticides**,** *Bacillus thuringiensis* Strain JSd1, and tephritid fruit flies

P-16

Isolation and characteristics of phages against multi-drug resistance *Streptococcus agalactiae* in tilapia farms in Mekong Delta, Vietnam

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Abstract

Antibiotics are commonly used as the main prevention and treatment of disease-causing bacteria in both human and animals. In agriculture, antibiotic occupies significant niche in food producing animals and plants. In contrast, the antimicrobial resistance (AMR) is a naturally occurring phenomena of microorganisms through which they become resistant to antimicrobial compounds. In Vietnam, a high antibiotic-resistant rate of pathogenic bacteria has been reported in fish farms. Phages are virus infecting bacteria. The use of lytic phages as a prevention and treatment for bacterial diseases in fishery industry has gained serious attention in the last 40 years, especially due to the widespread evolution of antibiotic-resistant bacteria. We will present some achievements of our research about phage therapy against multi-drug resistance *Streptococcus agalactiae* in tilapia farms in Mekong Delta, Vietnam. The research works are in the terms of bacterial isolation, antibiotic susceptibility test and genome analysis; phage isolation, infection activity, phage genome analysis; phage cocktail strategy to control *Streptococcus agalactiae in vitro* and *in vivo* trial at wet lab.

Keywords: phage therapy, AMR, genome, tilapia, bacterial pathogens.

P-17

Monitoring of *Sitophilus zeamais* adults in low-temperature grain storage warehouses

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Abstract

Adult numbers of the maize weevil, *Sitophilus zeamais* Motschulsky, were investigated using pheromone traps in five low-temperature grain storage warehouses in the Kanto Plain from April 2016 to October 2020, to confirm the effectiveness of the pheromone traps and observe the change in the numbers of adults caught. Pheromone traps and sticky traps were placed in the storage rooms and working areas of each warehouse and replaced with new ones monthly. Bait traps were also used in three warehouses. Large numbers of adult *S. zeamais* were caught in the traps from April to December. The number of adults caught by pheromone traps was greater than that that caught by sticky traps at all the investigation sites in most months. In pheromone traps, up to 427 adults were caught in one trap, while in bait traps, up to 247 adults were caught in one trap. In two warehouses, the number of adults trapped markedly decreased during the investigation period due to improvements made to storage conditions, but no such trend was apparent in the other three warehouses. The efficacy of mass trapping of *S. zeamais* adults by pheromone traps was also tested in two of these warehouses from October 2018 to April 2020.

Keywords: maize weevil, pheromone traps low temperature, and food grains

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Effects of Sodium Chloride and Osmotic Pressure on the Detection of Injured Cells, Injury Rate, and Survival of *Staphylococcus aureus* After High Hydrostatic Pressure Treatment

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Abstract

Staphylococcus aureus is a foodborne pathogen highly resistant to environmental stresses, including salt and pressure. However, the effects of sodium chloride (NaCl) and osmotic conditions on detecting injured cells and their survival after high hydrostatic pressure (HHP) treatment remain unclear. This study aimed to determine how NaCl and osmotic pressure affect injured-cell detection, sublethal injury, and survival of *S. aureus* following HHP treatment. We confirmed that NaCl affected the detection of injured *S. aureus* cells using multiple detection media and examined bacterial injury rates after HHP treatment by adding NaCl or other solutes. *S. aureus* was inoculated into a liquid medium and treated with HHP at 400 MPa for 10 min at room temperature. Bacterial counts were determined and compared using mannitol salt (MS) agar, a selective medium, and non-selective media such as Brain Heart Infusion (BHI) agar and trypticase soy agar. Immediately after HHP treatment, bacterial counts on MS agar were approximately 1 log CFU/mL lower than those on non-selective media but increased to similar levels after 24 h of incubation at 37°C. Similar results were obtained on BHI agar containing 7.5% NaCl and on MS agar, confirming that NaCl, rather than other components of the selective medium, contributed to differences in colony counts during injured-cell detection. Furthermore, we added 7.5–21% NaCl before or after HHP treatment and determined bacterial injury and lethality rates immediately after treatment and after incubation. When NaCl was added before HHP, both rates decreased immediately after treatment as NaCl concentration increased. Similar results were obtained with some solutes other than NaCl when osmotic pressure was adjusted to comparable levels. These results suggest that *S. aureus* is more likely to survive HHP treatment under conditions of high osmotic pressure, regardless of the solute used.

Keywords: Sodium chloride, osmotic pressure, injured cells, *Staphylococcus aureus* and HPP Treatment

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Bacterial contamination in commercial purchased powered or frozen cricket in Japan

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Abstract

Recently, edible insects were getting to be considered as 'eco-friendly' sustainable protein source. The production of edible insects for overseas or foreign domestic travelers may have potential to increase the income of the rural community in the developing countries. *Gryllidae* insects such as *Gryllus bimaculatus* or *Acheta domesticus* have been consumed traditionally consumed and considered as safe. However, we do not have much evidence and therefore, this study was designed under the research project on "Regulatory research projects for food safety, animal health and plant protection (JPJ008617.23812608" funded by the Ministry of Agriculture, Forestry and Fisheries of Japan. We collected commercially available crickets (powder or frozen) in Japan and checked their bacteriological quality. From the 7 collected powered crickets (4 races) purchased from 5 companies in 2024, no fecal coliform, *Salmonella enteritidis*, *Staphylococcus aureus* and *Listeria monocytogenes* were isolated. A 2 log CFU/g order of *Bacillus cereus* was isolated from 3 of 7 (43%) samples. The range of aerobic bacterial count (APC) and coliform bacteria were 2.6 to 3.7 and less than 2.3 log CFU/g, respectively. In the 28 frozen crickets (5 races) purchased from 6 companies from 2023 to 2026, 4 (14%), 11 (39%) and 3 (11%) of the samples were contaminated with *Escherichia coli*, *B. cereus* and *S. aureus*, respectively. No *S. enteritidis* and *L. monocytogenes* were isolated. The range of APC and coliform bacteria were 3.2 to 8.2 log CFU/g and 2.3 to 5.8 log CFU/g respectively. 12 kinds of glucose fermenting Gram-negative lot (GNR) bacteria and 5 kinds of other GNR bacteria were identified by the conventional biochemical tests. *Klebsiella* spp. and *Pseudomonas* spp. were isolated from 10 (36%) and 8 (29%) samples, respectively. The contamination of *S. aureus* had better to be controlled by general hygiene practices in the cricket farms. Even the level of bacterial contamination will be high, most of bacteria will to be killed by heating in the power making process. The possibility of the growth of *B. cereus* spore in cricket powder had better to consider when we use it as a source of food.

Keywords: Edible insect, foodborne bacteria and food safety

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Exploring Genetic Variations and Plasmid Diversity in *Escherichia coli* strains Isolated from Tertiary Care Hospitals

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Abstract:

The multidrug-resistant (MDR) *Escherichia coli*, particularly β-lactamase producing strains, has become a global health challenge, where wastewater systems, specially from hospitals, serve as critical reservoirs for the dissemination of resistance genes. The objectives of the study were to investigate the whole genome sequence diversity and genetic variations focusing on their evolutionary relationships, genetic similarity, and single nucleotide polymorphisms (SNPs) of pathogenic β-lactamase producing *E. coli* strains. A total of four β-lactamase producing *E. coli* strains, from differently located tertiary care hospitals, were included in this study. A heatmap of genetic similarity revealed near-identical genetic makeup among the strains. A number of genes including *AcrAB -TolC*, β-lactamases, and resistance determinants such as *glpT, gyrA, msbA* , and *tet(M)* were identified in these strains. However, the presence of virulence genes of the aerobactin synthesis gene (*iucA , iutA*) and type III secretion systems (*espX1, espX4, espX5*) in the strain has the potential for pathogenicity. These resistance genes were identified at the genomic level; however, their transcriptional expression was not evaluated and the detection of virulence-associated genes suggests that the isolates have the potential to cause disease and pathogenicity. These findings provide insights into the whole genome sequence diversity of *E. coli* in urban based tertiary care hospital wastewater, emphasizing the genetic variation and plasmid diversity in these *E. coli* strains, which may have implications in public health and microbial ecology of the environment.

Keywords: Genetic variation, plasmid diversity, *Escherichia coli* and hospitals

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Assessment of Protective Antibody Responses Against *Streptococcus pneumoniae*

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Abstract

In developing countries, including Bangladesh, an estimated five million children under the age of five years die each year from pneumonia, caused by *S. pneumoniae*. The polysaccharide capsule is the major virulence factor and on the basis of differences in the capsular polysaccharide structure, pneumococci are divided into more than 90 serotypes. The serotype distribution found in Bangladesh is distinctively different from that found in children in other parts of the world. The polysaccharide vaccine was found to be effective against less than 70% of the pneumococcal infections in Asian countries. In contrast, pneumococcal conjugate vaccines are found to be more effective. However, serotype distribution in the pneumococcal protein conjugate vaccines make them specific for any particular region. In this study, we investigated the possibility of introducing a common antigenic protein of *S. pneumoniae* as the protein component of the conjugate vaccine which may allow broader protection against pneumococcal infections. For this, human sera samples from 40 patients, who were suffering from pneumonia or meningitis, were investigated for the presence of protective antibodies against the surface antigens of *S. pneumoniae* serotype 7F. Western blot analysis demonstrated that all antibodies could bind a 74 kDa protein antigen, which also showed antigenic cross reactivity with other serotypes. The 74 kDa antigen demonstrated strong protective efficacy against live *S. pneumoniae* challenge in the immunized mice. All these results suggest that the 74 kDa antigen may be incorporated as a potential candidate for the protein portion of a conjugate vaccine, which may allow broader protection.

Keywords: Antibody Responses, *Streptococcus pneumoniae* and vaccine