ABERDEEN
SCOTLAND
3–5 May 2023

PROGRAMME

P&J LIVE

International Association for Food Protection®

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Thursday, 4 May

S6 Paving the Avenue for the Application of Natural Antimicrobials

Suite 2B

Organizer and Convenor: Heidy den Besten

8.30 Prenylated Isoflavonoids as Natural Preservatives Against *Listeria monocytogenes*: Application and Mode of Action
ALBERTO BOMBELLI, Carla Araya-Cloutier, Jean-Paul Vincken, Tjakko Abee, Heidy den Besten, Wageningen University and Research, Wageningen, The Netherlands

9.00 Going Viral – Bacteriophages as Biocontrol Agents for Foodborne Pathogens
OLIVIA MCAULIFFE, Teagasc Food Research Centre, Fermoy, Cork, Ireland

9.30 Selection and Evaluation of Natural Antimicrobials – The Industry Perspective
JAN WILLEM SANDERS, Unilever Foods Innovation Centre Wageningen, Wageningen, The Netherlands

10.00 – 10.30 Networking Coffee in the Exhibit Hall

RT2 Responding to Food Safety Crises: Evolving Role of Food Scientists

Suite 3

Organizers: John O'Brien, Purnendu Vasavada
Convenor: Purnendu Vasavada

FRANCOIS BOURDICHON, Università Cattolica Del Sacro Cuore, Cremona, Italy

MICHELLE PATEL, UK Food Standards Agency, London, United Kingdom

DONALD PRATER, U.S. Food and Drug Administration, Silver Spring, MD, USA

HELEN TAYLOR, ZERO2FIVE Food Industry Centre, Cardiff Metropolitan University, Cardiff, Wales, United Kingdom

PURNENDU VASAVADA, University of Wisconsin-River Falls, River Falls, WI, USA

10.00 – 10.30 Networking Coffee in the Exhibit Hall

T4 Technical Session 4 – Molecular Analytics, Genomics and Microbiome

Suite 4

Convenors: Kalmia Kniel, Celina To

T4-01 8.30 Metataxonomic Surveillance of Contamination Pathways in Food Processing Environments: From Observational Studies to Practical Applications
CRISTIAN BOTTA, Dimitra Tsoureki, Elisabetta Chiarini, Davide Buzzanca, Ilario Ferrocino, Valentina Alessandria, Selene Rubiola, Francesco Chiesa, Kurt Houf, Luca Cocolin, Kalliopi Rantsiou, Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy

T4-02 8.45 First Enterotoxigenic Confirmation of *Staphylococcus argenteus* as a Foodborne Pathogen
MARINA CAVAIUOLO, Donatien Lefebvre, Isabelle Mutel, Noémie Vingadassalon, Déborah Merda, Jacques-Antoine Hennekinne, Yacine Nia, Laboratory for Food Safety, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), France, Paris, France

T4-03 9.00 Colonisation Dynamics of *Listeria monocytogenes* in Food Processing Environments, and Genetic Features of Strains Showing Persistent Contamination
EDWARD FOX, Jessica Gray, Lydia Fox, Séamus Fanning, Northumbria University, Newcastle Upon Tyne, United Kingdom

T4-04 9.15 Design of a Biofilm Model Based on Metagenomic Characterization of Drains in Seafood and Dairy Processing Facilities
MARTIN LAAGE KRAGH, Nanna Hulbaek Scheel, Pimlapas Leekitcharoenphon, Paw Dalgaard, Lisbeth Truelstrup Hansen, Research Group for Food Microbiology and Hygiene, National Food Institute, Technical University of Denmark, Kgs. Lyngby, Denmark

T4-05 9.30 Understanding *Listeria monocytogenes* Behavior That Triggers Survival Under Severe Acidity
DIMITRA TSOUREKI, Cristian Botta, Sara Bover-Cid, Heidy den Besten, Luca Cocolin, Kalliopi Rantsiou, Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy

T4-06 9.45 Bettercallsal: Analysis Tool for Precise Detection of Multiple *Salmonella* Serovars from Culture Enrichments Using Shotgun Metagenomic Profiling and Its Application in an Outbreak Setting
PADMINI RAMACHANDRAN, Elizabeth Reed, Mark Mammel, Rebecca Bell, Karen Jarvis, Christina M. Ferreira, Rachel Binet, Andrea Ottesen, Amanda Windsor, Christopher Grim, Kranti Konganti, U.S. Food and Drug Administration – CFSAN, College Park, MD, USA

10.00 – 10.30 Networking Coffee in the Exhibit Hall

■ – Symposia ■ – Roundtables ■ – Technicals *Student Award Competitor

S7 Microbiological Contaminants in Plant Protein Ingredients – Assessing Potential Risks

Suite 2B

Organizer: Marjon Wells-Bennik
Convenor: Karin Beekmann

10.30 Predominance of Bacterial Spore Formers in Plant Protein-Based Ingredients
MARJON WELLS-BENNIK, NIZO Food Research, Ede, The Netherlands

11.00 What Do We Know about *Bacillus licheniformis* in Plant-Based Dairy Alternatives?
MARIEM ELLOUZE, Nestle, Lausanne, Switzerland

11.30 Microbiological Risk Assessment of *Bacillus cereus* Considering Diverse Phenotypic Traits
YVAN LE MARC, ADRIA Food Technology Institute – UMT ACTIA 19.03 ALTER'iX, France, Quimper, France

12.00 Lunch Available in the Exhibit Hall

RT3 Creating Capacity of the Next-Generation Food Safety Researchers and Implementers through International Collaboration: Experience of Low- and Middle-Income Countries (LMICs)

Suite 3

Organizers: Kebede Amenu, Delia Grace
Convenor: Kebede Amenu

DELIA GRACE, NATURAL Resource Institute, University of Greenwich, Kent, United Kingdom

MESERET BEKELE, Uppsala University in Sweden, Uppsala, Uppsala, Sweden

WIGDAN OMER, University of Khartoum, Khartoum, Sudan

HIMADRI PAL, Natural Resources Institute, Chatham, United Kingdom

SHWE PHUE SAN, University of Greenwich, Yangon, Yangon, Myanmar

STACEY DUVENAGE, Natural Resource Institute, University of Greenwich, Kent, United Kingdom

15.00 – 15.30 Networking Coffee in the Exhibit Hall

T5 Technical Session 5 – Antimicrobials, Dairy and Microbial Food Spoilage

Suite 4

Convenor: Francois Bourdichon

T5-01 10.30 Heat Inactivation of *Bacillus licheniformis* Spores in Plant-Based, Bovine Milk and Broth
CHRYSANTHI CHAMPIDOU, Mariem Ellouze, Nabila Haddad, Jeanne-Marie Membré, Oniris INRAE Secalim & Nestlé Research, Lausanne, Switzerland

T5-02 10.45 Cold Shock Proteins Promote Nisin Tolerance in *Listeria monocytogenes* through Modulation of Cell Envelope Modification Responses
FRANCIS MUCHAAMBA, Joseph Wambui, Roger Stephan, Taurai Tasara, Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland

T5-03 11.00 Genome Mining within the Psychrophilic *Clostridium estertheticum* Complex Uncovers Estercin A, A Novel and Potent Bacteriocin with Bio-Preservative Potential Against Major Foodborne Pathogens
JOSEPH WAMBUI, Marc J.A. Stevens, Roger Stephan, Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland

T5-04 11.15 Comparison between MIC and WGS-Predicted Antimicrobial Resistance of *Staphylococcus aureus* from Bovine Mastitis Milk from Italy
GIULIA MAGAGNA, Lorenzo Gambi, Paolo Daminelli, Michela Tilola, Virginia Filipello, Franco Paterlini, Food Safety Department, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Brescia, Italy

T5-05 11.30 Dairy Powder Industry: Risk Area Associated with Thermophilic Sporeforming Bacteria Using Their Growth Limits
Louis Delaunay, Florence Postollec, Anne-Gabrielle Mathot, IVAN LEGUERINEL, LUBEM UBO University – UMT ACTIA 19.03 ALTER'iX, Quimper, France

T5-06 11.45 Monitoring of Antimicrobial Resistance Indicator Genes in a Benthic Food Web in the English Channel and the North Sea
ERWAN BOURDONNAIS, Cédric Le Bris, Thomas Brauge, Graziella Midelet, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Laboratory for Food Safety, Boulogne-sur-Mer, France

12.00 Lunch Available in the Exhibit Hall

Thursday, 4 May

S8 *Bacillus cereus* and Related Organisms: Differentiating Friend from Foe

Suite 2B

Organizers: Mariem Ellouze, Laura Carroll, Maria Teresa Da Silva Felicio
Convenor: Claudia Guldimann

13.30 Keeping up with the *Bacillus cereus* Group in the Whole-Genome Sequencing Era
LAURA CARROLL, Umeå University, Umeå, Sweden

14.00 Same but Different: Modeling *Bacillus cereus* Behavior in Plant-Based Milk Alternatives and Bovine Milk
MARIEM ELLOUZE, Nestle, Lausanne, Switzerland

14.30 Risk Assessment of *Bacillus cereus* Group in Food
MARIA TERESA DA SILVA FELICIO, European Food Safety Authority (EFSA), Parma, Italy

15.00 – 15.30 Networking Coffee in the Exhibit Hall

S9 Food Safety of Infant Foods: Care for Our Most Precious

Suite 3

Organizer and Convenor: Marcel Zwietering

10.30 Hazard Identification and Risk Ranking for Microbial Risks in Infant Foods
KAH YEN CLAIRE YEAK, Wageningen University, Wageningen, Gelderland, The Netherlands

11.00 Hazard Control in Infant Foods Using Emerging Processes Technologies
SARA BOVER-CID, IRTA (Institute of Agrifood Research and Technology), Food Safety and Functionality Program, Monells, Girona, Spain

11.30 Traditional and DNA-Based Analytics for Microbial Hazard Detection and Behaviour in Infant Foods
KALLIOPI RANTSIOU, Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy

12.00 Lunch Available in the Exhibit Hall

T6 Technical Session 6 – Food Safety Systems

Suite 4

Convenors: Neela Badrie, Lisa O'Connor

T6-01 13.30 The Effect of Dry Salting on the Survival of *Escherichia coli*, *Vibrio* spp., *Listeria monocytogenes*, and *Salmonella* on Inoculated Sugar Kelp during Storage
JENNIFER PERRY, Richa Arya, Denise Skonberg, University of Maine, Orono, ME, USA

T6-02 13.45 Practical Experiences in Setting up *Listeria monocytogenes* Environmental Sampling in the Food Industry
KOEN DE REU, Geertrui Rasschaert, Liesbeth Jacxsens, Ellen Lambrecht, Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Melle, Belgium

T6-03 14.00 Development and Evaluation of Low-Cost, Easily Deployable Molecularly Imprinted Polymer for Norovirus Detection
Sarbjeet Kaur, Jake McClements, Pankaj Singla, Amy Dann, Mark V. Sullivan, Nicholas W. Turner, Minji Kim, SLOANE STOUFER, Matthew D. Moore, Inderpreet Kaur, Marloes Peeters, University of Massachusetts Amherst, Amherst, MA, USA

T6-04 14.15 Whole-Genome Sequence Analysis of *Listeria monocytogenes* CC7 Associated with Clinical Infections and Persistence in the Food Industry
TROND MØRETRØ, Eva Wagner, Even Heir, Solveig Langsrud, Annette Fagerlund, Nofima, *Ås*, Norway

T6-05 14.30 Maturing Food Safety Culture with Nudging in Food Manufacturing Environments in the UK
CAROL WALLACE, Lone Jespersen, Sophie Tongyu Wu, University of Central Lancashire, Preston, United Kingdom

T6-06 14.45 Impact of Mlst Genetic Diversity on *Listeria monocytogenes Growth*
NATHALIE GNANOU BESSE, Carolina Rosa Rodrigues de Souza, Patricia NG, Laurent Guillier, Benjamin Félix, Alexandre Leclercq, Helene Bergis, ANSES Laboratory for Food Safety, Maisons Alfort, France

15.00 – 15.30 Networking Coffee in the Exhibit Hall

■ – Symposia ■ – Roundtables ■ – Technicals *Student Award Competitor

S10 Testing and Improving HACCP Team Proficiency to Strengthen Food Safety Culture

Suite 2B

Organizers: Lone Jespersen, Shingai Nyarugwe
Convenor: Veronika Bulochova

15.30 Using HACCP Proficiency Testing to Upskill HACCP Teams and Build the Foundations for Culture Improvement
CAROL WALLACE, University of Central Lancashire, Preston, Lancashire, United Kingdom

16.00 Connecting HACCP and Food Safety Data to Mindset and Cultures, How Data Is Gathered and Utilized to Generate Behavioural Insights and Drive Change
LONE JESPERSEN, Cultivate Food Safety, Hauterive, Switzerland

16.30 Hazard and Risk Awareness: Foundational Food Safety Knowledge, Risk Awareness and Culture
SHINGAI NYARUGWE, University of Central Lancashire, Preston, United Kingdom

S11 Raw Milk Safety and Climate Dynamics: Integrating Geographical and Seasonal Variation from Farms of Southern Europe and the Middle East

Suite 3

Organizers and Convenors: Jan F. M. Van Impe, Jeanne-Marie Membré, Vasilis Valdramidis

15.30 Predictive Modelling of Maltese Raw Milk Production Traits Under Climate Dynamics
LYDIA KATSINI, KU Leuven, Ghent, East Flanders, Belgium

16.00 Dairy Farming in the Middle East: Insights from Raw Milk Microbiology and Quality
RODNEY FELICIANO, INRAE, Nantes, France

16.30 Raw Milk Safety Under the Climatic Influence in North Spain
STYLIANI ROUFOU, University of Malta, Msida, Malta

T7 Technical Session 7 – Modeling and Risk Assessment and Viruses and Parasites

Suite 4

Convenors: Ákos Jóźwiak, Aricia Possas

T7-01 15.30 Trends and Early Signals of Emerging Risks Identified in the Food Chain
Zsuzsa Farkas, Erika Országh, Szilveszter Csorba, Tekla Engelhardt, Andrea Zentai, ÁKOS JÓŹWIAK, University of Veterinary Medicine, Digital Food Institute, Budapest, Hungary

T7-02 15.45 Sym'Previus MAP: A Web Application for the Design of Food Packaging to Improve the Preservation of Food Products
Jonathan Thévenot, YVAN LE MARC, Catherine Denis, Janushan Christy, Valérie Michel, Didier Majou, Valérie Stahl, Emilie Gauvry, Emmanuel Jamet, Fanny Tenenhaus, Jean-Christophe Augustin, Narjes Mtimet, Sabin Jeuge, Jeanne-Marie Membré, Anna Jofre, Alizée Guérin, Aline Rault, Stella Planchon, Véronique Huchet, Olivier Couvert, Louis Coroller, ADRIA Food Technology Institute - UMT ACTIA 19.03 ALTER'iX, France, Quimper, France

T7-03 16.00 Implementation and Application of Quality and Predictive Microbiology Models of Strawberries and Tomatoes in Microhibro for a Holistic Approach for Shelf-Life Assessment
ARICIA POSSAS, Francisco Jiménez-Jiménez, Laura Rabasco-Vílchez, Cristina Díaz-Martínez, Zeynep Turgay, Matthias Brunner, Fernando Perez-Rodriguez, University of Córdoba, Córdoba, Spain

T7-04 16.15 Comparing the Performance of Two Predictive Models When Fitting Noisy Data
MAHA ROCKAYA, Mariem Ellouze, Jozsef Baranyi, University of Debrecen, Debrecen, Hungary

T7-05 16.30 Method for Tick-Borne Encephalitis Virus Detection in Raw Milk Products
CATHERINE HENNECHART-COLLETTE, Gaëlle Gonzalez, Lisa Fourniol, Audrey Fraisse, Cécile Beck, Sara Moutailler, Laure Bournez, Nolwenn Dheilly, Sandrine Lacour, Sylvie Lecollinet, Sandra Martin-Latil, Sylvie Perelle, ANSES, Laboratory for Food Safety, University of Paris-Est, Maisons-Alfort, France

T7-06 16.45 Zebrafish Embryo: A Simple and Robust Tool for the Cultivation of Human Noroviruses
MALCOLM TAN, National University of Singapore, Singapore

T4-01 Metataxonomic Surveillance of Contamination Pathways in Food Processing Environments: From Observational Studies to Practical Applications

Cristian Botta[1], Dimitra Tsoureki[1], Elisabetta Chiarini[1], Davide Buzzanca[1], Ilario Ferrocino[2], Valentina Alessandria[1], Selene Rubiola[3], Francesco Chiesa[3], Kurt Houf[4], Luca Cocolin[1] and Kalliopi Rantsiou[1]
[1]Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy, [2]Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy, Italy, [3]Department of Veterinary Sciences, University of Turin, Turin, Italy, [4]Ghent University, Merelbeke, Belgium

Introduction: Metataxonomics represents a user-friendly omics technique for culture-independent characterisation of microbiota composition. Although it is a well-established approach applied for a decade in medical and environmental microbiology, most of the studies in food science are only observational and its practical implementation in the food industry seems still far away.

Purpose: Therefore, we aimed to assay the pros and cons of using metataxonomic surveillance (MS) to characterise contamination pathways in food processing establishments and discover MS-based biomarkers of pathogen and spoilage bacteria presence.

Methods: Over 700 environmental and food samples were collected from cattle slaughterhouses, a poultry abattoir, and a baby food facility. The 16S rRNA amplicon-based sequencing outputs were compared to the targeted detection of microbes by counts, enrichment, and quantitative PCR (RT-qPCR).

Results: Cattle slaughterhouses' microbial biogeography showed that resident bacteria varied between premises as a function of temperatures and longitudinally along temporal phases of cleaning/sanitising. Moreover, selective bacterial inactivation by the cleaning/sanitising was only detected through MS. Contamination patterns plotted in the poultry abattoir showed that resident microbiota mainly originated from broilers' skin, in which *Arcobacter butzleri* was largely present. Targeted detection confirmed the high environmental persistence of this pathogen and flocks› cross-contaminations conveyed by carcass transport lines. In the baby food processing plant, the fluctuation of biodiversity and the succession of resident communities along a one year period were strongly influenced by the type and the microbiota composition of incoming raw materials. The parallel detection of alive spore-forming pathogens by RT-qPCR significantly correlated with low biodiversity and the presence of specific taxa.

Significance: Our studies have shown that MS is a valid approach to defining contamination patterns in the processing plant, from the environment to the food products and back. As demonstrated by the benchmark with targeted cultural methods, the time for MS integration in microbiology quality control of food industries has now come.

T4-02 First Enterotoxigenic Confirmation of *Staphylococcus argenteus* as a Foodborne Pathogen

Marina Cavaiuolo[1], Donatien Lefebvre[2], Isabelle Mutel[3], Noémie Vingadassalon[3], Déborah Merda[3], Jacques-Antoine Hennekinne[4] and Yacine Nia[4]
[1]Laboratory for Food Safety, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), France, Paris, France, [2]Laboratory for Food Safety, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Maisons-Alfort, France, [3]Université Paris-Est, ANSES, Maisons-Alfort, France, [4]Laboratory for Food Safety, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Université Paris-Est, Maisons-Alfort, France

Introduction: When present in food, some coagulase-positive staphylococci can produce staphylococcal enterotoxins, whose ingestion has been reported as the cause of staphylococcal food poisoning outbreaks (SFPOs). SFPO investigations revealed that *S. aureus* is the most prevalent species responsible for foodborne diseases. For this reason, current detection and typing methods have been developed for *S. aureus* and its enterotoxins. In the last ten years, however, few studies have highlighted the potential involvement of *S. argenteus*, another coagulase-positive *Staphylococcus*, in foodborne outbreaks. Nonetheless, its ability to produce enterotoxins remains questionable.

Purpose: The objective of this work was to determine if *S. argenteus* is a causative agent of food poisoning. We also addressed the limitations of the various methods available to study SFPOs and for monitoring staphylococci in food.

Methods: In this study, we characterized in-depth two staphylococci strains isolated from two independent outbreaks that occurred in France. We used a combination of methods currently used for SFPO investigations including PCR, whole genome sequencing (WGS), liquid chromatography-mass spectrometry (LC-MS), and ELISA.

Results: While both PCR and phenotypic analyses did not allow identification of staphylococci isolates to the species level, WGS allowed classification of them as *S. argenteus* and to determine the full content of virulence genes. Some enterotoxins were produced in artificially *S. argenteus*-contaminated milk and detected with LC-MS and ELISA methods. The toxin concentration measured in milk was comparable to concentrations reported from SFPO. From a collection of 250 publicly available genomes, the complete enterotoxin gene set of *S. argenteus*, including variants and pseudogenes was determined. The most prevalent genes were *sex*, followed by *sel26*, *sel27* and *sey*. The *egc* cluster was less frequent and most of the time carried a dysfunctional *seg* gene.

Significance: Our results highlighted the enterotoxigenic properties of *S. argenteus* and will help to improve the characterisation of SFPO and to monitor *S. argenteus* as an emerging foodborne pathogen.

T4-03 Colonisation Dynamics of *Listeria monocytogenes* in Food Processing Environments, and Genetic Features of Strains Showing Persistent Contamination

Edward Fox[1], Jessica Gray[2], Lydia Fox[3] and Séamus Fanning[4]
[1]Northumbria University, Newcastle Upon Tyne, United Kingdom, [2]CSIRO, Coopers Plains, QLD, Australia, [3]Northumbria University, Newcastle upon Tyne, United Kingdom, [4]UCD Centre for Food Safety, University College Dublin, Dublin, Ireland

Introduction: The foodborne pathogen *Listeria monocytogenes* presents a significant contamination challenge for food processing environments (FPEs). Once strains of the bacterium enter these environments, they can colonise niches present, and persist for months or even years in the environment. This presents an increased risk for ongoing contamination of food products produced. Strains possess a range of genetic features influencing biofilm production, stress tolerance, and cell-to-cell communication, which can impact these colonisation dynamics.

Purpose: This study examined the colonisation mechanisms of *L. monocytogenes* in simulated FPE conditions, as well as the genetic markers associated with persistent contamination.

Methods: In this study, 52 food system-associated isolates of *Listeria monocytogenes* were characterised for their ability to colonise stainless steel surfaces, using phenotypic and genotypic approaches. In addition, persistent strains from a single FPE were subjected to whole genome sequencing to characterise their genetic landscape and compare with that of presumed non-persistent strains also isolated from the same FPE.

Results: Results suggested differences in colonisation dynamics were not due to *agr*-dependant cell signaling, and that strain-specific transcriptional responses were observed, largely characterised by upregulation of diverse metabolic pathways associated with nutrient acquisition/scavenging. Interestingly, persistent strains showed greater heterogeneity in their virulence gene markers, with mutations suggesting a loss of virulence relative to other strains.

Significance: Taken together, these results provide new insights into how *L. monocytogenes* adapts to, and colonises, the FPE, and describes the genetic features of persistent strains.

T4-04 Design of a Biofilm Model Based on Metagenomic Characterization of Drains in Seafood and Dairy Processing Facilities

Martin Laage Kragh[1], Nanna Hulbæk Scheel[1], Pimlapas Leekitcharoenphon[2], Paw Dalgaard[3] and Lisbeth Truelstrup Hansen[1]
[1]Research Group for Food Microbiology and Hygiene, National Food Institute, Technical University of Denmark, Kgs. Lyngby, Denmark, [2]Research Group for Genomic Epidemiology, National Food Institute, Technical University of Denmark, Kgs. Lyngby, Denmark, [3]Research Group for Food Microbiology and Hygiene, National Food Institute (DTU Food), Technical University of Denmark, Kgs. Lyngby, Denmark

Introduction: Mock biofilm drain models that reflect the microbiota in floor drains in industrial food processing environments are needed to understand and optimize sanitation schemes.

Purpose: The purpose of this study was to develop a mock drain biofilm model suitable for studies investigating the efficacy of biocides.

Methods: Eleven stainless steel floor drains in different food industries (shrimp, n=4; fish, n=4; dairy, n=3) were sampled. Dairy drains were sampled twice, nine months apart. For culture-dependent

analysis, 20 aerobic culturable bacteria were isolated from each drain (n=220) and identified using MALDI-TOF and 16s rRNA sequencing. DNA extracted from each drain were whole genome amplified before shotgun metagenomic sequencing (Illumina). Taxonomic classification, alpha- and beta diversity and statistical analyses were assessed using CLC Genomics Workbench.

Results: Forty-two unique genera were found among the aerobic cultivable drain isolates with *Pseudomonas* spp., *Chryseobacterium* spp., *Microbacterium* spp., and *Acinetobacter* spp. dominating (37%). Fourteen genera were found in both seafood and dairy drains. No differences in alpha diversity were observed among the drain types. The microbiota of cheese and shrimp drains were significantly (P_{ajd}<0.05) different, however, there were no significant (P_{ajd}>0.05) differences among other drain types (cheese vs. fish, shrimp vs. fish, $cheese_{2021}$ vs. $chesse_{2022}$). Across all samples (n=14) Pseudomonadaceae constituted 22% of the drain microbiome. Individual taxonomic profiling showed considerable microbiome variance between drains within the same production environment. Highly abundant genera in the metagenomic analysis and frequently isolated drain bacteria were selected for the final multispecies biofilm model (n=31, 24 genera) to be tested for tolerance to different biocides at industrial concentrations.

Significance: The present study developed a biofilm model that reflects the microbiota in industrial floor drains and can be used to test the efficacy of biocides under simulated industrial conditions. Results from this research will contribute to the design and optimization of current and new sanitation schemes.

T4-05* Understanding *Listeria monocytogenes* Behaviour That Triggers Survival Under Severe Acidity

Dimitra Tsoureki[1], Cristian Botta[1], Sara Bover-Cid[2], Heidy den Besten[3], Luca Cocolin[1] and Kalliopi Rantsiou[1]
[1]Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco (TO), Italy, [2]Institute of Agrifood Research and Technology (IRTA), Monells, Catalunya, Spain, [3]Wageningen University and Research, Wageningen, Netherlands

Introduction: Foodborne diseases are a constant threat to public health and an important onus for the socioeconomic status worldwide. *Listeria monocytogenes* is the causative agent of listeriosis, the fifth most commonly reported zoonosis in humans in European Union nowadays, with a progressive rise of outbreaks and an elevated number of deaths. This foodborne pathogen is ubiquitous and survives in a wide range of strong stresses, like refrigeration temperatures and harsh food processing conditions, with the ability to create reservoirs and persist for years.

Purpose: This study aimed to investigate the mechanisms that allow *Listeria monocytogenes* to persist in acidic conditions, obtain acid resistance, and thus sustain viability upon severe acidic treatment.

Methods: The growth of one *L. monocytogenes* strain, isolated from a human skin lesion, was monitored through conventional culturing methods, measuring of optical density, and pH values. Three were the *in vitro* cultures, two submitted to citric acid to reach pH values of 5.5 and 5.2, as well as a control culture without any pH adjustment. The differences in robustness at various phases of growth were quantified by exposure the cultures in different growth phases to an acidic shock at pH 2 for 30 min.

Results: Low pH-adapted cultures showed an increasing resistance in comparison with the control culture and the robustness was physiologically expressed at the stationary phase. The strain showed during the adaptation at pH 5.2 a biphasic growth curve, where more resistance was reported at the two stationary phases, contrariwise to the two exponential phases. The same behaviour was exhibited in cultures grown at both 10°C and 37°C under anaerobic conditions.

Significance: Coupled to the physiological observations described above, RNAseq was performed to delineate the transcriptomic response of the strain. This information should shed light to molecular mechanisms involved.

T4-06 Bettercallsal: Analysis Tool for Precise Detection of Multiple *Salmonella* Serovars from Culture Enrichments Using Shotgun Metagenomic Profiling and its Application in an Outbreak Setting

Padmini Ramachandran[1], Elizabeth Reed[2], Mark Mammel[3], Rebecca Bell[4], Karen Jarvis[5], Christina M. Ferreira[2], Rachel Binet[2], Andrea Ottesen[2], Amanda Windsor[6], Christopher Grim[6] and Kranti Konganti[6]
[1]U.S. Food and Drug Administration – CFSAN, College Park, MD, [2]U.S. Food and Drug Administration, Center for Food Safety & Applied Nutrition, College Park, MD, [3]Office of Applied Research and Safety Assessment, Center for Food Safety and Applied Nutrition, U.S. Food and Drug Administration, Laurel, MD, [4]Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, MD, [5]US Food and Drug Administration, Office of Regulatory Science, College Park, MD, [6]U.S. Food and Drug Administration – Center for Food Safety and Applied Nutrition, College Park, MD, USA

Introduction*:* Current surveillance for *Salmonella* is limited to only detecting the most abundant serovars from culture-based approaches. Here we introduce a tailored, publicly available workflow, "bettercallsal," for *Salmonella* serovar identification using shotgun metagenomics or quasi-metagenomics datasets.

Purpose: To develop a comprehensive analysis tool for precise identification of multiple serovars of *Salmonella* in metagenomic datasets and test its utility in a complex outbreak scenario.

Methods: An *in-silico* benchmark dataset, comprising 29 unique *Salmonella*, 46 non-*Salmonella* bacterial and 10 viral genomes, was generated using InSilicoSeq with read depths from 0.5 million to 5 million read pairs. Metagenomic data of *Salmonella* culture positive nonselective 24 h (H24), and selective 48 h (H48) papaya outbreak sample enrichments were analyzed. Analyses were performed using a custom-built k-mer tool, SeqSero2 and bettercallsal. A detailed method and workflow is publicly available at https://github.com/CFSAN-Biostatistics/bettercallsal.

Results: The *in-silico* dataset analyzed with bettercallsal revealed that precision and recall increased as read depth increased for single-end and concatenated reads, to 96% and 90% respectively. In the papaya outbreak, proportional abundance of *Salmonella* ranged from undetectable to 2.5% in H24 enrichments. On average, 10-25% proportional abundances of *Salmonella* were identified through k-mer analysis in H48 enrichments (n=9), with multiple serovars, Newport and Infantis being detected in some samples (n=3). SeqSero2 identified partial antigen profiles in (n=2) H48 selective enrichments and 3 enrichments harbored Kiambu, Senftenberg and Gaminara. In contrast, bettercallsal identified multiple serovars in concordance with previous Bioplex assay results from papaya enrichments (n=9), and the genome hits assigned to the samples clustered with *Salmonella* isolates from the papaya outbreak clearly evident by the SNP cluster information seen through this pipeline.

Significance: Precise identification of multiple *Salmonella* serovars from complex food and environmental matrices is essential for successful outbreak investigations pertaining to public health.

T5-01* Heat Inactivation of *Bacillus licheniformis* Spores in Plant-Based, Bovine Milk and Broth

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Introduction: The consumer demand for plant-based milk alternatives has been increasing in the last years. The potential food spoilage induced by spore-forming bacteria from plant-based ingredients is an emerging research topic.

Purpose: The objective of the present study was to characterize the thermal inactivation of spores of spoilage organisms in plant-based and bovine milk and assess the potential protective matrix effect.

Methods: *Bacillus licheniformis* was chosen as a model microorganism due to its common involvement in spoilage incidents in milk and vegetables. To investigate the impact of food matrix on the inactivation profile of spores, experiments were carried out in several plant-based milk alternatives, half-skimmed bovine milk and BHI broth, used as a reference. *B. licheniformis* CTCPA 3107001 spores were inoculated to the selected matrices with an initial concentration of 9 log CFU/mL. Samples were subjected to heating at five different temperature levels, 97.5, 100, 102.5, 105 and 110°C, following the methodology of thermal treatment with capillary tubes in an oil bath. All matrix/temperature combinations were analyzed in biological triplicates.

Results: In BHI broth, inactivation followed a linear trend, however, the kinetics obtained in food products included shoulders and tails. Thus, the linear regression model fitted to the data showed non-satisfactory goodness of fit; therefore, non-linear models were fitted. In addition, the inactivation parameter estimates revealed differences between the various plant-based milk alternatives, indicating the need for more precise inactivation assessments to fully characterize spore inactivation in these products.

Significance: This study is of a great importance since, to the best of our knowledge, it is the first attempt to describe inactivation kinetics

P1-31* Antibiotic Resistance and Virulence of *Arcobacter butzleri* in the Large-Scale Poultry Slaughtering Chain

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***Introduction*:** *Arcobacter butzleri* is a Gram-negative bacterium identified worldwide as a zoonotic pathogen. The ingestion of contaminated food is considered the main route of transmission to humans. *Arcobacter butzleri* has been isolated from several meat supply chains, including the poultry industry. Therefore, poultry products and their production chain represent the main transmission routes of this microorganism.

***Purpose*:** The present study aimed to assess the antibiotic resistance and to characterize the virulence capacity of *A. butzleri* isolated from broiler carcasses during slaughtering and from the slaughterhouse surfaces.

***Methods*:** One-hundred seventeen isolates were examined for their antimicrobial resistance to different antibiotic concentrations. After selection of the most resistant and susceptible isolates, infectivity on mucus-secreting human cells (HT29-MTX-E12) was tested, as well as their capability on forming biofilm.

***Results*:** All isolates showed resistance to at least one antibiotic, highlighting a multi-resistance phenomenon. The greatest resistance was found to ampicillin (98/117 isolates). 73% of the isolates were resistant to more classes of antibiotics. The results showed that *A. butzleri* from slaughterhouse surfaces were more resistant to antibiotics than those from broilers. All the isolates were able to infect the HT29-MTX-E12 cells and displayed moderate biofilm production. The colonization and the biofilm production abilities were not correlated to the isolation sources.

***Significance*:** The antibiotic resistance detected is of remarkable relevance considering the possible transmission of resistance factors to humans. Subsequent whole-genome sequencing analyses will be conducted to understand the genomic traits correlated to the high antibiotic resistance of strains and to their persistence. The results obtained highlight the importance of increasing optimization actions in slaughter processes to reduce the incidence *A. butzleri* considering the risk to which the population is subjected.

P1-32 Temperature Level of Domestic Refrigerators: The Italian Experience

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***Introduction*:** Temperature is considered one of the most important factors capable of determining and influencing the multiplication and survival capacity of microorganisms in food, in particular in those ready-to-eat (RTE). Compliance with temperatures during all stages of food production, transport, and marketing is a responsibility of the Food Business Operator (FBO), as indicated by the EC Reg. 852/2004 and 853/2004; on the contrary, compliance with the domestic storage temperature is due exclusively to the diligence and microbial risk awareness of the final consumer.

***Purpose*:** The project aimed to define the average temperature level of domestic refrigerators related to the geographical, seasonal, and demographic characteristics of Italy; at the same time the project provided useful information to the competent Health Authorities, FBOs, and citizens.

***Methods*:** On the basis of the number of households in Italy (approximately 16 million) we consider a list of 800 families (target population). For measuring the temperature inside the domestic refrigerators and outside we used specific dataloggers capable of continuously detecting and recording the temperature value.

***Results*:** Between January 2019 and February 2020 1,516,325 surveys were carried out inside 761 refrigerators, and 505,440 surveys outside them. The average temperature was 7.4°C (sd 1.8°C). The results broken down by probe position showed that the temperatures recorded at the top and bottom of the refrigerator were very similar, averaging 7.0 and 6.8°C respectively, while the temperatures recorded in the refrigerator door were higher (average 8.3°C).

***Significance*:** To determine the shelf life of RTE foods in a scientifically sustainable way, the storage conditions must reflect the reasonably foreseeable conditions in which the food will be stored also at home and up to consumption. The *Listeria monocytogenes* risk assessment in RTE foods indicates the inadequate storage temperature of food as a determining factor for the increase of listeriosis at the human level.

P1-33 Evaluation of HACCP Implementation in Food Manufacturing Companies in the Middle Eastern Region

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***Introduction*:** The way that food is produced and distributed has undergone fundamental changes in recent decades particularly in Dubai and the Middle Eastern region. The food safety area has become more complex, driven by widespread changes in methods of food production and processing, coupled with rapid increases in global food trade and increased tourism. Consumers today are demanding more meaningful information about food safety and quality. To meet this demand, some companies are engaging third-party audit bodies to provide greater assurance that their products meet quality and safety requirements.

***Purpose*:** The purpose of the study was to evaluate the level of implementation and operation of hazard analysis critical control points (HACCP) and Prerequisite Programme (PRPs) as per the Codex Alimentarious commission protocol of 12 logical steps and Codex Good Hygiene Practices (GHP)

***Methods*:** Both qualitative and quantitative analysis techniques of in-depth interviews, observations and review of documents were used in this study to complement each other. The triangulation method used in this research was to look at the problems from different angles. Five cluster random samples were collected from the sampling frame of 112 food manufacturing companies of Dubai Municipality Food Control Department (DM FCD) list.

***Results*:** Research identified lower compliance rates of Good Hygiene practices (PRPs) which compromise 37.4% for the sampled factories and 31.8% compliance rate for HACCP protocol logical steps. A number of barriers exist to the successful implementation and operation of HACCP and also perceived benefits. Barriers included various aspects like difficulties in identifying hazards and inadequacy of knowledge.

***Significance*:** Findings from this study provide insights into a fairly new but evolving research area of HACCP implementation in the food manufacturing sector in the Emirates. The outcomes of this study are expected to have national implications for the enhancement of food safety management system implementation through effective training and enforcement.

P1-34 How European Food Processors are Responding to Regulatory and Environmental Changes

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***Introduction*:** Many changes have occurred in the scientific and regulatory environment for food processors in the past decade. Processors have had to significantly change many of their daily procedures, including processing, testing, training, and reporting. This situation has created a new set of challenges and responses from food processors. Much has been written about what processors may be or should be doing, but it is important to find out what they have actually been doing.

***Purpose*:** The purpose of this survey study was to better understand these changes and responses implemented by food processors and the areas in which they plan to focus their resources over the next few years.