GMI 14 – SEPT 4th to 6th, Barcelona

- **"Setting the scene"** presentation Cost-benefit issues of WGS

Moderator: M. Allard (FDA)

- **Bradley Brown (FDA)**

Dr. J. Bradley Brown is the Senior Science Advisor for Economics and Policy within the Center for Food Safety and Applied Nutrition (CFSAN) at the U.S. Food and Drug Administration (FDA). He coordinates data and modeling efforts for economic and policy analysis, most recently monitoring the infant formula supply chain in the US during and after a major recall in 2022, and performing a return-on-investment study of the WGS program in the US.

Dr. Brown joined FDA in 2002. He was and Economics Team Lead at CFSAN during the development of the major FSMA regulations. He has performed analysis in support of The Egg Safety Rules, the HHS Task Force on Drug Reimportation, and the Bioterrorism Regulations. Dr. Brown earned his Ph.D. in Economics from The University of Texas, in Austin, with a concentration in the fields of Environmental and Natural Resource Economics, Computational Economics, and Econometrics.

Discussion Abstract:
As an introduction to GMI14, we dive into our study of the benefits and costs of the US Whole Genome Sequencing (WGS) program, discuss its applicability outside of the observed time frame and in other regions, and set the table for model updates and further discussion on alternative metrics to provide evidence of WGS program success. The FDA created the GenomeTrakr WGS Network in 2013. In 2021 we measured the impact of WGS implementation on food contamination and illnesses using a social welfare model. In the study, we conduct empirical tests using data from FDA regulated food commodity outbreaks and examine the effect of WGS program isolates on illnesses. Benefits and costs of the program are estimated based on the empirical results. Each additional 1,000 WGS isolates added to the National Center for Biotechnology Information (NCBI) database leads to a reduction of approximately 6 illnesses per WGS pathogen, per year. The analysis shows the effect holds, though we identify slightly more outbreaks for WGS pathogens each year relative to other pathogens, because WGS pathogen outbreaks are smaller on average. By 2019, the annual health benefits are nearly $500 million, compared to roughly $22 million invested by public health agencies. While this type of analysis may not be feasible in areas that have not adopted or only recently adopted WGS,

we discuss ways the results may be transferable as well as other metrics which may be of use in a prospective analysis of the benefits of WGS.

- *Global perspectives **FAO/WHO***

- **Josefina Campos (WHO)**

Josefina Campos served as the Director of the National Genomics and Bioinformatics Center at ANLIS Malbrán, Ministry of Health in Argentina. In this capacity, she worked on a national level to integrate genomics into the surveillance system for both infectious and non-communicable diseases, utilizing a One Health approach. She also took on the responsibility of coordinating national and international projects focused on integrated surveillance to better understand the dynamics and evolution of diseases with significant public health implications. She played a key role in establishing the National Genomics Network in Argentina. On a regional scale, Josefina provided guidance and expertise in genomics through her involvement with networks such as PulseNet LAC, Genome Trakr, and Relavra. At the global level, she contributed her insights to the PH4GE initiative within the Data Structure working group, the Global Biodata Consortium and the Global Typhoid Genomics Consortium. Additionally, she has taken the lead in organizing numerous genomics courses in Argentina and the Latin American region. She has an extensive publication record, with numerous articles in highly respected scientific journals that highlight the utility of genomics in public health. She was a Senior technical Advisor for IPSN until she joined the WHO Pandemic Hub as Unit Head of Genomics and Analytics in June.

- **Masami Takeuchi (FAO)**

Dr Masami Takeuchi is a Food Safety Officer at the Food and Agriculture Organization of the United Nations (FAO), with a main responsibility to provide various food safety scientific advice to countries and to the Codex Alimentarius Commission, an international food standard setting body. Her recent work is around risk assessment of food derived from emerging technologies, such as biotechnology, cell-based food production, gene editing, precision fermentation and vertical farming. She also works on emerging and cross-cutting food safety issues including the use of whole genome sequencing for food safety management. She has a field experience working at the regional office for Asia and

the Pacific in Bangkok, Thailand for 4 years, thus while she takes up various normative global initiatives on food safety, she also assists countries and regions for their food safety capacity development.

- **Session: AI, WGS and data sharing**

Moderator: Ruth Timme (FDA)

Dr. Ruth Timme leads the FDA's genomic epidemiology program, GenomeTrakr. She obtained her Ph.D. in 2006 from The University of Texas at Austin, specializing in plant phylogeny. At the FDA, her research focuses on validating genomic methods for public health and creating standards for genomic pathogen surveillance.

AI and WGS – overview WGS and ML
- **Dr Abani Pradhan (U. Maryland)**

Dr. Abani Pradhan is a Professor in the Department of Nutrition and Food Science (NFSC) & the Center for Food Safety and Security Systems, and the Director of NFSC Graduate Program at the University of Maryland, College Park (UMD). His research interests include food safety, quantitative microbial risk assessment, predictive microbiology, advanced data analytics (artificial intelligence and machine learning), supply chain and system modeling, food safety engineering, and molecular epidemiology. Dr. Pradhan has served on numerous committees at UMD and outside including the program committees of Society for Risk Analysis (SRA) and International Association for Food Protection (IAFP). He has received several honors, awards, and fellowships including the Chauncey Starr Distinguished Young Risk Analyst award from the SRA in 2015 and the Harry Haverland Citation award from the IAFP in 2023. In 2023, he was appointed to the US National Advisory Committee on Microbiological Criteria for Foods (NACMCF).

AI and WGS – Overview WGS and ML

Integrating whole genome sequencing and machine learning for improved food safety

Abani K. Pradhan1,2

¹Department of Nutrition and Food Science, ²Center for Food Safety and Security Systems, University of Maryland, College Park, MD 20742, USA

Whole genome sequencing (WGS) has seen widespread application in the fields of epidemiological investigations and surveillance of bacterial foodborne pathogens, resulting in a wealth of genome sequencing information being made available. Although this method is increasingly being used in pathogen source attribution and outbreak traceback, its incorporation in quantitative microbial risk assessment and predictive modeling remains in its infancy, due to the lack of defined bioinformatic and computational pipelines to incorporate these data into the mathematical models used in risk assessment. Recently, we have been exploring and working on integrating machine learning (ML), bioinformatics analysis, and statistical modeling for Salmonella enterica. In this presentation, a few studies in which we utilized ML techniques and WGS data to predict microbial behavior for improved food safety will be discussed. In one study, we attempted to transcend the issue of incorporating several predictor variables introduced by a WGS dataset into a statistical modeling framework using ML. In another study employing ML modeling, we attempted to identify gene signatures associated with Salmonella stress response during poultry processing using WGS data. Furthermore, we developed a genome-based ML model to predict antimicrobial resistance in Salmonella isolated from chicken meat.

The importance of data sharing for AI applications

- **Guillermo Torres (UAB)**

Dr. Guillermo Torres is a Lecturer and Senior Researcher at the Computer Vision Center (CVC) and the Computer Science Department at the Universitat Autònoma de Barcelona (UAB). He holds a Ph.D. in Informatics from UAB, where his research focuses on applying deep learning techniques in medical imaging, particularly for the early diagnosis of lung cancer. Dr. Torres has been involved in research projects aimed at developing

advanced diagnostic systems that integrate artificial intelligence with radiological imaging to enhance the accuracy and efficiency of lung cancer detection. His work has been published in high-impact journals, and he has presented at leading conferences in the field of medical imaging. In addition to his research, Dr. Torres is actively involved in mentoring graduate students and played a key role in developing a comprehensive early lung cancer database, which is set to become a valuable resource for the global research community.

Abstract

A key point for the development of reliable AI-based support systems is the collection of a large enough set of annotated data. This talk focuses on the process of data gathering and the way this has an impact on the training of machine learning methods: issues that can introduce a bias in AI systems, how to evaluate the trustworthiness of such systems, their reproducibility on unseen cases. I will also give you the basic rules to ensure that a federated data base is useful for training reliable, reproducible and trustworthy AI decision support systems for DNA sequencing of pathogens.

Marc Lorenzen (BfR)

Marc Lorenzen is a Senior Scientific Officer at the German Federal Institute for Risk Assessment (BfR) in the Department Safety in the Food Chain, Unit: Product Identity, Supply Chains and Traceability. Marc Lorenzen joined BfR in 2018 for his PhD (which he is currently finishing), working on agri-food chains and especially traceability data related to the Rapid Alert System for Food and Feed (RASFF). He developed the Rapid Alert Supply Network EXtractor (RASNEX), a software tool, implemented in the Konstanz Information Miner (KNIME), that allows for automated data extraction and visualization of agri-food chains from RASFF-notifications. Since 2021, he leads consecutive EFSA projects on the development of RASNEX, with a team further developing the application in Python, providing a user-friendly dashboard and applying AI. As a proof of principle, NLP is used to extract data, in particular operators and their locations, from follow-up notifications and attached documents in various formats.

The importance of data sharing for AI applications from a traceability perspective: Mining supply chain information from food and feed contamination notifications with the Rapid Alert Supply Network EXtractor (RASNEX)

Marc C. Lorenzen

German Federal Institute for Risk Assessment

Max-Dohrn-Str. 8-10, 10589 Berlin, Germany

Within Europe, National competent authorities of member countries use the Rapid Alert System for Food and Feed (RASFF) to report information on any (i) human health risks arising from food or feed, (ii) serious feed-related risks to animal health or the environment. It is of utmost importance to rapidly identify the operators affected and withdraw causative products, as the impact on human and/or animal health and the environmental and economic damage increase over time.

During an ongoing incident, relevant information collected in the RASFF system about affected product flows is distributed in PDF documents along with supporting attachments such as delivery lists, invoices, etc. While the notifications are mostly structured, sections of free text contain valuable information. Attached documents come in various formats, with semi-structured text, tabular data and varying quality (digital format, scans or photographs). As Member States continuously provide and update relevant information, rapid extraction and analysis of critical information is essential but challenging for risk managers and risk assessors.

To facilitate data sharing and the investigation of incidents, the German Federal Institute for Risk Assessment (BfR), is developing solutions such as RASNEX, the harmonized data format UTX or FoodChain-Lab.

- **Adriano di Pasquale (IZS)**

Adriano Di Pasquale has a PhD in Computer Science. In the past, he worked as IT expert in several national and international projects related to the Italian Ministry of Health. In 2016 he worked in EFSA as Data manager.

Currently, he is the head of the Bioinformatics Unit at IZSAM. He coordinates the development of the bioinformatic platform COHESIVE (https://cohesive.izs.it) and its extension: the official platform of the Italian National Reference Centre for WGS of microbial pathogens - GENPAT (https://genpat.izs.it).

Abstract

Today, artificial intelligence (AI) applications are of particular importance to public health. The usefulness of data sharing for AI applications will be presented focusing on developing machine learning algorithms for **source attribution** of the foodborne bacteria *Listeria monocytogenes* (*Lm*).

A first study (Castelli 2023) has been dedicated to the harmonization of ML practices for efficient source attribution of *Lm* given the most recent articles performing ML-based source attribution of foodborne bacteria from genomic data (Mughini-Gras 2022, Tanui 2020, Guillier 2020, Arning 2021, Im 2021).

A second study has been focused on the implementation into the Italian national platform called GENPAT (https://genpat.izs.it) of a ML-based workflow able to return the food source of any given *Lm* sequence entry.

The first study, based on a curated NCBI dataset of ~1100 samples (Tanui 2020), revealed good results on returning the correct food label, among around 10 food labels, for *Lm* sequences. However, the quality of the results decreased rapidly once datasets of samples from Italian routine surveillance were added.

Our hypothesis of this behaviour is the wrong food label assignment to samples of Italian routine surveillance. Indeed, the sampling source is provided as metadata together with NGS sequences. It's important to underline how difficult is to conduct ML studies based on this kind of metadata as it is impossible to test and verify the information's correctness and it is inherently based on trusting the data providers' declarations.

In the implementation of an ML-based workflow into the GENPAT platform, we concentrated on how to get good results using real samples from the Italian National Reference Laboratory (NRL). Besides the above limitation and "noise" introduced by wrong label assignment, the meat origin can be predicted with high accuracy in Italian samples.

Together, these two studies emphasize that the training and testing datasets are as important as the used ML algorithm for genomic data-based source attribution of *Lm*, and that the high quality metadata sharing is fundamental for efficient AI applications.

- **Aitana Neves (SIB)**

Aitana Neves is Associate Director Clinical Bioinformatics at the SIB Swiss Institute of Bioinformatics. She co-leads the Swiss Pathogen Surveillance Platform (SPSP), being notably responsible for overseeing its maintenance and development. SPSP is the 3rd largest world-wide provider of open SARS-CoV-2 raw genomic data. She also co-leads the European ELIXIR Focus Group on Pathogen Data and is the PI of a NIH BRC project aiming to establish a global network of locally-hosted pathogen data hubs and portals.

Abstract
Maturity models are a useful tool to support data platform management when assessing current gaps in their maturity and development lifecycle. The Pathogen Data Platform maturity model specifically targets data platforms which host on pathogens, and associated, contextual sensitive, personal metadata. It was developed within ELIXIR-CONVERGE and tested in a pilot run within BY-COVID project. In this talk, the Maturity Model and results from the pilot run will be presented, prior to discussing an outlook on how to best disseminate it and empower the community with such a tool.

- **Session: WGS, One Health and Global Perspectives**

Moderator: Masami Takeuchi (FAO)

WGS in within the One Health framework

- **Patricia Mejias Moreno (FAO)** *Pending to receive information.*

- **Gregorio Torres (WOAH)**

Gregorio Torres is the head of the Science Department of the World Organisation for Animal Health based in Paris. He oversees the WOAH's systems for identifying, implementing science arising from development and review of international standards. Dr Torres is actively involved in the implementation of global disease control programmes, including avian influenza, African swine fever, rabies and zoonotic tuberculosis, working in close coordination with FAO and WHO.

Gregorio is a veterinarian graduated from Cordoba University (Spain). He obtained his MSc in Veterinary epidemiology at London University and a MVM at Glasgow University.

- **Dr Celeste Donato (U. Melbourne)**

Dr Celeste Donato is a postdoctoral researcher at the Peter Doherty Institute for Infection and Immunity, Australia. She is also an Affiliate of the Centre for Pathogen Genomics, University of Melbourne and the Enteric Diseases Group, Murdoch Children's Research Institute. Celeste has led national and international pathogen surveillance programs and has extensive experience in WGS for enteric and respiratory pathogens of relevance to human and animal health. Celeste leads the One Health and Candida auris projects within the Australian Pathogen Genomics program at the Doherty Institute.

The design and implementation of a One Health genomic surveillance program in Australia

The Australian Pathogen Genomics Program aims to optimise pathogen genomic surveillance approaches in the Australian public health system, utilising the AusTrakka platform to enable real-time sharing, analysis and reporting of pathogen genomic data.

One Health principles are important in pandemic preparedness and public health. E. coli represented an ideal pathogen in the development of One Health surveillance. Stakeholders were engaged across human health, veterinary health, agriculture and livestock, food safety and the environment to inform sampling strategies and provide key insights into the unique participatory requirements of each sector. Nine months into a 12-month pilot study, >1200 samples have been collected, generating >9000 E. coli isolates. This project represents an opportunity to extend the scope of AusTrakka. However, WGS in a One Health context generates unique considerations for data sharing given the complex, extensive metadata associated with the samples. Unique governance and data sharing issues arise when working with diverse sectors, and extensive stakeholder engagement is required to ensure data is communicated in a meaningful way relevant to each sector and address the concerns industry may have around potentially sensitive data. Further, clustering thresholds applied in a clinical outbreak context are not appropriate for One Health, requiring new approaches.

WGS in– country case studies

- **Syafinaz Binti Amin Nordin (U. Putra Malaysia)**

Syafinaz Amin-Nordin is a Professor in Medical Microbiology and Consultant Clinical Microbiologist at Universiti Putra Malaysia (UPM), Malaysia. Dr Amin-Nordin has an interest in modern and innovative concept of diagnostics, including molecular diagnostics. She is currently leading the next generation sequencing facility at UPM's teaching hospital, with activities include SARS-CoV-2 genomic surveillance and multi-resistant organism genomic characterization from various sources such as animals, food and the environment. She was also an expert contributor to a document for Food and Agriculture Organization of the United Nations, on Group B Streptococcus in freshwater fish. She had initiated the interest group on zoonosis in the Malaysian Society of Infectious Diseases and Chemotherapy.

- **Mayrén Cristina Zamora Nava (Senasica Mexico)**

Degree in Food Chemistry from the National Autonomous University of Mexico (UNAM). She has 23 years of experience in public administration in the field of food safety in the promotion, regulation, certification, surveillance and systems for food contamination risk reduction, as well as in the development and operation of the National Strategy for Food Safety derived from fisheries and aquaculture and analytical control of food.

She is currently in the National Service of Health, Quality and Agri-Food Safety (SENASICA) as Director of the National Reference Center for Food Safety and Biosecurity, official laboratory that defines and carries out analytical tests for the detection of pesticide residues and biological contaminants, including whole genome sequencing of bacteria of agri-food interest and GMO identification, within the framework of the Integral Quality System, with the aim of protecting the health of consumers and promoting the national and international marketing of national agri-food products.

Presentation abstract

The globalization of markets has accelerated the commercial exchange of food; a situation that has led governments to implement strategies that contribute to ensuring food safety. In Mexico, since the National Service of Health, Quality and Agri-Food Safety (SENASICA) and specifically from the National Reference Center for Food Safety and Biosecurity (CNRIBA) of the General Directorate for Agro-alimentary, Aquaculture and Fisheries Safety it has been implemented the Whole Genome Sequence as an essential technique for the identification of agri-food bacteria of interest. Here we present the journey, the alliances, the results and the goals that CNRIBA has achieved over the years, in order to protect the national agriculture, contributing to the food security and the well-being of producers and consumers.

- **Dr. Henda Triki (Institut Pasteur Tunis)**

Biography

After medical studies in the Faculty of Medicine of Sfax and obtention of the National Diploma of Speciality in Microbiology in 1990, Henda Triki joined the Pasteur institute of Tunis in 1991 and was assigned at the head of the Laboratory of Clinical Virology. This laboratory basically conducts diagnostic activities in human virology and also acts as a WHO Regional Reference Laboratory in the Eastern Mediterranean Region (EMR) for poliomyelitis, since 1992, and for Measles since 2002. Henda Triki became Assistant Professor in Virology in 1993, Associate Professor in 1998 and Professor in Virology in 2006. She worked as Director of Public Health & Medical Affairs in the Pasteur Institute of Tunis from 2002 to 2006 and was member of several national and international committees on vaccine preventable diseases. Beside her diagnostic and Public health activities, Henda Triki is also involved in Research with a special interest in viral hepatitis, enteric viruses and emerging viral diseases. She was Director of a Research Unit

on Hepatitis and epidemic viral diseases in the Pasteur Institute of Tunis from 2002-2004 which was enlarged to a Research Laboratory on Genetic Diversity of Hepatic and Enteric viruses from 2005 to 2016. Presently, she is a member of the Research Laboratory: "Viruses, Vectors & Hosts: One Health approach & technologic innovation for a better health". Up to August 2024, she was the authors of 133 research articles published in indexed international revues.

Report on collaborative activities between IZS-Teramo and Institute Pasteur-Tunis in the frame of the MED-NET project
Henda Triki
Laboratory of Clinical Virology
Institut Pasteur de Tunis – Tunisia

A collaboration between the Istituto Zooprofilattico Sperimentale Teramo and Institut Pasteur Tunis started in 2020 during the COVID-19 pandemic, in the frame of the MED-NET project entitled "Operational and strategic partnership for the Mediterranean area in the context of "One Health" on emerging public health issues". With a financial support from WHO, bilateral visits, acquisition of an NGS plateform and training of scientists from Tunisia in IZS were conducted. The project was drafted and was recently accepted for financial support from the Italian goverment. SARS-CoV2 sequences from Tunisia were generated and special studies were conducted, some already published and others in process. Most of them were on SARS-CoV2 infection in the general population, in immunocompetant and immunocompromised children and used NGS technologies and metagenomics. During the next phases of the project collaborations will expand to other centers/sectors in Tunisia. The activities will target several pathogens/diseases i.e, SARS-CoV2 and other respiratory viruses, West Nile & other Arboviruses, Monkeypox, multidrug resistant bacteria and any other emerging viral or bacterial pathogen.

- **Session: Global interoperability of the laboratory networks and industry partners.**
Moderator: Mirko Rossi

Data management

- **Katja Alt (BMEL)/representative TBC**

Dr. Katja Alt is Senior scientific advisor at the Federal Ministry of Food and Agriculture (BMEL) in Germany. Born in Guatemala, Dr. Alt studied veterinary medicine and earned her doctorate in microbiology in Berlin. In 2009, she began her scientific career at the Federal Institute for Risk Assessment (BfR) in Berlin, focusing on the epidemiology of

zoonoses. Her work included leading the federal-state zoonosis-monitoring program along the food chain, addressing antibiotic resistance, and developing software to make data publicly accessible.

Between 2012 and 2014, Dr. Alt pursued epidemiology studies at the Robert Koch Institute (RKI), concentrating on foodborne outbreaks. Since 2022, she has been with the BMEL, where her primary role is to establish a cross-sectoral system for comparing whole genome sequencing (WGS) data from food surveillance and public health sectors. This system aims to enhance the monitoring and control of foodborne pathogens, significantly contributing to improved public health outcomes.

Short Abstract

Dr. Katja Alt, on behalf of the federal-state working group on WGS-datamanagement

In 2022, an initiative was launched by the Federal Ministry of Food and Agriculture (BMEL) in response to a prompt from the states. The BMEL approached the Federal Ministry of Health (BMG), resulting in the development of a working document that outlined the current status of whole genome sequencing (WGS) technology and its application in the surveillance of foodborne outbreaks. This document also included proposals for the federal and state governments on establishing a WGS data management system.

In 2023, collaborative efforts began with approximately 60 participants from both federal and state sectors. These participants engaged in numerous meetings focusing on bioinformatics and cross-sectoral communication. To date, a comprehensive concept for data flows within and between sectors has been established, alongside a metadata exchange framework.

Next steps involve initiating a test phase with a basic system to refine these concepts through practical application. Ultimately, the developed concepts will require approval from the states following a thorough data protection review. This initiative aims to enhance the monitoring and control of foodborne pathogens through improved data management and cross-sectoral collaboration, significantly contributing to public health.

- **Valentina Rizzi (EFSA)**

Valentina Rizzi is a senior scientific officer in EFSA, in the Biological Hazards, Animal Health and Welfare (BIOHAW) Unit, with more than 20 years of work experience in food microbiology and food safety. She joined EFSA in 2008, and since 2016 she has been leading the Team in charge to produce the annual European Union Summary Reports on zoonoses, foodborne outbreaks and antimicrobial resistance, prepared jointly with the European Centre for Disease Prevention and Control (ECDC). She helped develop the new EFSA system for

the collection of Whole Genome Sequencing (WGS) data on isolates of foodborne pathogens from food and animal samples. This tool interoperates with the ECDC molecular typing system and is used on a weekly basis to support the detection of cross-sectorial cluster and investigation of multi-country foodborne outbreaks. She also supervises the production of joint ECDC-EFSA Rapid Outbreak Assessments (ROAs) in the context of multi-country foodborne events.

Abstract

In 2019, the European Commission (EC) sent a mandate to ECDC and EFSA to implement and manage two interoperable systems for the collection and analysis of Whole Genome Sequencing (WGS) data of Salmonella enterica, Listeria monocytogenes and Escherichia coli isolates from human and non-human origins, respectively. The EFSA One Health WGS System represents the single collection point in EFSA of WGS data of isolates of non-human origin (animal, food and environmental samples) and aims: to build a database of genome profiles that can be queried in case of foodborne outbreaks (preparedness), to support the real-time investigation of multi-country foodborne outbreaks (response), and to support cross-sectorial collaboration and partnership among Member States in the food safety sector (engagement). Data provision, access, and visualisation are done through a user-friendly interface. The food and veterinary users from EU/EEA countries can submit their data on a voluntary basis; few countries started to submit data proactively, but most of data submissions were triggered by the data calls launched by EFSA in conjunction with the production of joint EFSA-ECDC multi-country outbreak assessments. Basic statistics of the use of the system are presented as well as the interaction with the ECDC OH WGS system during cluster detection.

- **Tuyet Hoang (U. Melbourne)**

Ms Hoang is Strategy and Governance Manager for the Centre for Pathogen Genomics and Business Manager for the Microbiological Diagnostic Unit Public Health Laboratory, University of Melbourne at the Peter Doherty Institute. She holds a Bachelor's Degree in Biomedical Science, Masters in Public Health and is currently completing her Juris Doctor at Monash University Law School. Her expertise sits within policy and governance, with experience across government, public health implementation and academia. She currently leads a local and international portfolio of pathogen genomics programs across country capacity building, governance systems, and implementation of genomics into public health systems.

- **Eric Stevens (FDA)**

Eric L. Stevens PhD is an International Policy Analyst in the Office of International Engagement at the Center for Food Safety and Applied Nutrition. He received his Ph.D. in Human Genetics and Molecular Biology from The Johns Hopkins School of Medicine with an emphasis on human population genetics and estimating genetic relatedness. From 2013 – 2014 he completed a Postdoctoral Fellowship analyzing RNA sequencing data to find differentially expressed genes and isoforms related to schizophrenia.

In 2014 he became an FDA Commissioner's Fellow at the Center for Food Safety and Applied Nutrition (CFSAN), applying the use of whole-genome sequence data in linking foodborne outbreaks. Dr Stevens worked in engaging other federal and international stakeholders in applying WGS methodologies to track foodborne outbreaks through CFSAN's GenomeTrakr. In his current position as an International Policy Analyst, Dr. Stevens continue to work closely with FDA's international sequencing partners in addition to monitoring other international science interests for CFSAN, including work with Codex Alimentarius, WHO, FAO, and EFSA. Finally, Dr. Stevens is the Co-Alternate Delegate to the Codex Committee on Food Hygiene.

- Experience at the regional and Spanish national levels

Moderator: Sara Bover (IRTA)

- **Cristina Ocerin (AESAN)**

Cristina Ocerín is a veterinarian by training and currently head of the data collection unit at the Spanish Agency for Food Safety and Nutrition (AESAN). She joined AESAN in 2010, where she has performed tasks related to biological risk management. Her current unit collects all the results of the monitoring of zoonoses and other foodborne microbiological agents in food samples. She participates in the Scientific Network for Zoonoses Monitoring Data, as well as in the antimicrobial resistance and whole genome

sequencing subgroups. She is a user of the EFSA One Health WGS System with country officer profile, ensuring coordination at country level.

- **Alberto Chaves (Junta de Andalucia)**

Jesús Alberto Chaves Sánchez holds a degree in Veterinary Medicine from the University of Córdoba (1999) and completed a master's in food safety at the University of Seville. He obtained the Intermediate Certificate in Applied HACCP Principles from the Royal Institute of Health, UK.

A career civil servant, he has worked in the Department of Agriculture and Environment and later as Head of Food Safety at the Extremadura Health Service. Since 2017 to date, he serves as Head of the Food Safety Service in Seville, under the Department of Health and Consumer Affairs of the Junta de Andalucía.

Throughout his career, he has been involved in managing food safety alerts as a contact point for the SCIRI Network and has participated in the design and implementation of the integrated genomic epidemiology system of Andalucía (SIEGA), among other initiatives.

Abstract

This presentation outlines the public health framework and initiatives in Andalusia related to WGS applied to food safety field. The region, with a population of 8.5 million, and The region is a significant hub for food and agri-food production, importing and exporting globally, and facing challenges such as migration and climate change impacts.

The presentation discusses Andalusia's innovative health surveillance strategies and the implementation of a "One Health" system, enhancing sensitivity and interoperability with international standards. Key components include an own sequencing circuit, an integrated bioinformatics application, and autonomous control over sequence sharing. The project emphasizes precision, integration, anticipation, and research promotion, aiming to improve pathogen source attribution and overall public health responses.

To date the system hosts over own 2200 sequences of pathogens such as Salmonella, Listeria, E. Coli, Legionella, Yersinia, and Campylobacter, and will soon incorporate sequences of Klebsiella and viruses such as HIV

Current challenges and future perspectives focus on breaking barriers to sequence integration, routine use of whole genome sequencing (WGS), and ensuring intercomparability of bioinformatics analyses. The ultimate goal is to develop a reliable system for strain association with high confidence and transparency, addressing public health threats effectively.

- **Carlos Sanchez (Junta de Andalucia)**

Dr. Carlos S. Casimiro-Soriguer is a postdoctoral researcher under the Juan de la Cierva grant at the Andalusian Public Foundation for Progress and Health (FPS), working within Dr. Joaquín Dopazo's "Computational Medical Platform." His current research is centered on the Integrated System of Genomic Epidemiology of Andalusia (SIEGA), focusing on the integration of genomic data for the monitoring and control of infectious diseases, including the analysis of SARS-COV-2 variants.

Previously, Dr. Carlos S. Casimiro-Soriguer served as a researcher at FPS, where he conducted quality control analysis of human exome reads for disease diagnosis and contributed to the genomic analysis for personalized medicine projects. At the Andalusian Public Foundation for the Management of Health Research (FISEVI), he specialized in bacterial and viral sequencing using Oxford Nanopore technology within the Microbiology Service's COVID Section. His academic background includes a Ph.D. and a role as a senior bioinformatics technician at the Andalusian Center for Developmental Biology (CABD).

Abstract
Whole Genome Sequencing (WGS) has revolutionized the field of epidemiological surveillance by providing unparalleled resolution in differentiating genetically related strains and enabling detailed phylogenomic analyses. In Andalusia, the SIEGA genomic surveillance system has been established to host bacterial genomes from various sources, including food and clinical samples, offering a crucial tool for monitoring and managing health threats.

SIEGA currently includes data from eigth key pathogens: Listeria monocytogenes, Yersinia enterocolitica, Salmonella enterica, Legionella pneumophila, Escherichia coli, Campylobacter jejuni/coli, Mycobacterium tuberculosis and Klebsiella Pneumoniae. More than 2800 samples have been analyzed, providing valuable insights that have assisted the Ministry of Health and Consumption of the Andalusian Regional Government in resolving complex epidemiological cases, especially those complicated by geographical and temporal factors.

The implementation of genomic surveillance systems like SIEGA demonstrates the power of WGS in enhancing the detection and monitoring of infectious diseases. These systems enable public health authorities to respond more rapidly and effectively to outbreaks, support the identification of transmission patterns, and facilitate the development of targeted preventive strategies, ultimately improving public health outcomes.

- **Laura Alcalde (ACSA)**

Dr. Laura Alcalde Sanz is a Public Health Officer in the Planning, Auditing, Risk Assessment and Communication Service at the Public Health Agency of Catalonia at the Department of Health of the Government of Catalonia.

Dr. Laura Alcalde Sanz specializes in microbiological and chemical risk assessment in water and food evaluating the risk for consumer's health of different food categories and water use for agricultural irrigation. She contributes to support the scientific opinions of the Scientific Advisory Committee on Food Safety of the Catalan Food Safety Agency and to develop scientific studies commissioned to universities and research centers for the assessment of consumers' dietary exposure to different hazards.

- **Belen Martin (IRTA) (Catalunya)**

Dr. Belén Martín is a researcher in IRTA's Food Safety and Functionality Program. Since joining IRTA in 2005, she has worked on developing and implementing rapid molecular techniques for identifying, characterizing, and typing microorganisms, with the ultimate goal of improving food safety and quality.
In recent years, her work has focused on applying omic approaches, including whole genome sequencing, for the characterization and typing of food-borne pathogens, mainly Salmonella and Listeria monocytogenes. Additionally, she has been studying microbial communities in various food matrices through 16S metabarcoding. She has been involved in optimizing laboratory methods and analyzing data to gain a comprehensive understanding of the microbial landscape in food, contributing to the enhancement of food safety and quality.

Abstract L. Alcalde-Sanz and Belén Martín

Experience at the regional level on Whole Genome Sequencing (WGS), specifically at the Catalan Autonomic Community, presenting the structure and organization of Public Health Services and the surveillance and control of foodborne diseases where WGS has been applied in order to improve foodborne disease response, and enhance outbreaks investigation. In this framework, the genomic diversity of 152 Salmonella spp. collected in Catalonia during Salmonella surveillance (from 2018 to 2022) were analysed through WGS to investigate their phylogenetic relationships and possible transmission paths. Genome analyses revealed that close related clones of the monophasic variant of S. Typhimurium 4,[5],12:i are circulating through pig and pork sectors in Catalonia.

- **Antonio Español Pueyo (Aragon)**

Veterinary Medicine graduate from the University of Zaragoza in 1990. Since June 1994, he has served as a Veterinary Officer in the Public Health Administration, working in the Food and Environmental Safety Service of the Directorate General of Public Health of the Government of Aragón. He held the position of Provincial Deputy Director of Public Health in Huesca from July 2014 to the end of 2018, coordinating the Food Hygiene, Epidemiological Surveillance, Health Promotion, and Environmental Health Sections. In 2019, he was in charge of the Aragón Public Health Laboratory at its Huesca location, where he had previously worked as a technician for several years. Since 2020, he has served as the Head of the Food and Environmental Safety Service.

He holds a PhD from the University of Zaragoza in Animal Production and Food Science, with his doctoral thesis titled "Effectiveness of the Application of Control Measures for *Listeria monocytogenes* in Ready-to-Eat Meat Product Industries (RTE)."

Abstract

The "Integrated Epidemiological Sequencing of Pathogens in Aragón" (SEIPA) plan. I will explain the reasons behind it, the established tasks, and the objectives we aim to achieve. Next, I will discuss the systematic collaboration between the strain providers and the Aragón Biomedical Research Center (CIBA), which is our sequencing laboratory. I will then review what has been accomplished so far and conclude with our immediate challenges.

- *USA and EU challenges and opportunities of WGS*

- **Don Prater -FDA** (Pending)

- **Martial Plantady EU Commission**

Martial Plantady is a legislative officer working for the Directorate-General for Health and Food Safety of the European Commission. Graduated as a doctor in veterinary medicine with an additional Master degree in veterinary public health, he held different positions at the French Ministry of Agriculture from 1997 to 2006, dealing mainly with animal health issues, before joining the European Commission in 2007 where he is currently responsible for the development and the management of various policies related to the control of food-borne zoonosis.

Martial PLANTADY — ABSTRACT GMI 14 – 5 SEPTEMBER 2024

WGS has the potential to facilitate faster detection and more targeted investigations and control of foodborne outbreaks since it enables to establish links between different isolates recovered from humans, food, animals, feed and the related environment.

With the support of its scientific agencies (EFSA and ECDC), the EU has therefore developed a platform allowing the sharing and joint analysis of WGS data of isolates of several pathogens recovered from different compartments with a 'One Health' perspective. This platform has the ambition to support real-time detection and help assessing multi-country foodborne outbreaks occurring within the EU. WGS data is submitted by EU Member States to the platform on a voluntary basis for now, but the European Commission has recently proposed to the EU Member States to make mandatory the submission of WGS data to the system within the frame of epidemiological investigations of multi-country foodborne outbreaks.

Besides technical challenges, public sharing of WGS data is also challenging due to legal, political and commercial issues. The EU has high standards regarding data protection and any public sharing should be duly justified and limited to what is essential for the success of investigations. EU Member States remain the ultimate owners of the data and have full discretion over sharing it.

- GMI13 - Canada - Outcomes and Action Items-

- **Emma Griffiths**

Dr. Emma Griffiths is a university research associate at the Centre for Infectious Disease Genomics and One Health (CIDGOH) in the Faculty of Health Sciences at Simon Fraser University in Vancouver, Canada, which hosted GMI in 2023.

Her work focuses on developing and implementing ontologies and data standards for public health, One Health, and food safety pathogen genomics with the aim of improving data harmonization and integration in many different Canadian and international surveillance initiatives. She is also a member of the Standards Council of Canada as well as the WHO's International Pathogen Surveillance Network's Data Community of Practice, and leads the Public Health Alliance for Genomic Epidemiology (PHA4GE) Data Structures Working Group - which is a global coalition that works to improve the interoperability, reproducibility and portability of public health bioinformatics.

Abstract

GMI13 explored the technical and social/ethical/legal aspects of microbial genomics data sharing which included mechanisms, initiatives and solutions for: building interoperability of systems and datasets, developing data governance principles and practices, building equitable partnerships, sustaining sequencing efforts and tools, and coordinating different efforts around the globe. In this talk, GMI13 outcomes and action items resulting from the strategic planning session, themed breakout sessions, and meeting discussions will be presented. It is anticipated that the action items can provide talking points for GMI14.

- Overview: Raise awareness of opportunities Discussion
  Moderator: Emma Griffiths

- **Dr. Sofonias Kifle Tessema (African CDC)** (Pending)

- **Noah Hull –(APHL)** (Pending)

- **Heather Carleton (PNI)**

Dr. Heather Carleton, MPH, PhD currently serves as the chief of the Enteric Diseases Laboratory Branch (EDLB) in the Division of Foodborne, Waterborne and Environmental Diseases at the US Centers for Disease Control and Prevention (CDC). Her expertise lies in the field of enteric diseases, molecular epidemiology, bioinformatics, and next generation sequencing. As Chair of the PulseNet USA and PulseNet International networks, she and her branch play a crucial role in connecting foodborne, waterborne, and One Health-related illness cases using genomics.

Under Dr. Carleton's leadership, EDLB focuses on various aspects related to enteric diseases including prevention strategies, antimicrobial resistance studies, bioinformatics

analysis, metagenomics methods development, and next-generation sequencing technologies. Her branch conducts cutting-edge research to better understand these diseases and develop effective interventions.

Overview: Raise awareness of opportunities discussion

Heather Carleton – Overview of PulseNet International and discussion of data sharing approaches

PulseNet international (PNI) is a network of over 90 countries in 8 regional networks. During this session, I will provide an overview of data sharing in some of our regional networks including approaches to Memorandum's of Understanding and Terms of Reference, approaches to sharing data between regional networks, and highlight how WGS data related to outbreaks is communicated in the larger PNI network. We will also introduce PNI WGS feasibility study work, and the insights gained as WGS is implemented in PNI regional networks.

- **Torsten Seemann (U. Melbourne)**

A/Prof Torsten Seemann is a Research Fellow at the Doherty Institute and Head of Bioinformatics at the Centre for Pathogen Genomics, both based at The University of Melbourne in Australia. He is a global leader in bioinformatics for the analysis of microbial genome sequencing data, and has developed many key software tools such as Prokka, Snippy and Mlst. He founded and implemented AusTrakka, Australia's nationally endorsed pathogen genomics surveillance system. He is a strong advocate of open source software, open science, and data sharing, and has made Australia the third largest contributor to GenomeTrakr. Through his roles in the Centre for Pathogen Genomics and PulseNet International, he is contributing to capacity building and global health equity in the Asia-Pacific region.

- Industry presentations
  Moderator: Armand Sanchez

- **Celina To (Oxford-Nanopore)**

Celina To is the global segment marketing manager for food at Oxford Nanopore Technologies. She works closely with the commercial and marketing team in supporting the food industry in the implementation of genomic and metagenomic solutions for food safety and quality. She graduated from Purdue University with a master's degree in food microbiology and from California Polytechnical State University with a bachelor's degree in food science. To has held a variety of positions throughout her career, including research assistant at NASA Johnson Space Center and Hilmar Cheese Company, quality assurance supervisor at Safeway-Albertsons, and technical support/sales manager at Hygiena. She continues to be an active member of multiple food industry associations, including planning and microbiology committees, to support the exchange of new knowledge and best practices in emerging issues in food safety.

Short abstract:

The mission of Global Microbial Identifier (GMI) emphasizes the importance of real-time, comprehensive genomic characterization to address global health challenges. In alignment with GMI's goals, our presentation will showcase how Oxford Nanopore Technologies is advancing One Health genomics through innovative sequencing solutions. Biological contamination monitoring and infectious disease outbreaks necessitate rapid, accurate detection and tracking of pathogens and antimicrobial resistance. Our scalable platforms enable laboratories to perform on-site, real-time sequencing, providing immediate insights crucial for risk assessment and outbreak management. We will present end to end workflow updates like the Nanopore-only, microbial isolate sequencing solution (NO-MISS) and recent case studies demonstrating the application of nanopore sequencing in identifying and monitoring contamination and outbreaks. These studies illustrate the effectiveness of our technology in generating complete microbial genomes, profiling antimicrobial resistance, and resolving plasmids and mobile genetic elements that has made an impact in food safety, animal and plant safety, and public health.

- **Salvatore Conti (Thermofisher)**

He studied biology university in University La Sapienza di Roma and then the 4 years of speciality in human genetics at Cattolica University of Rome.
I joint to life tech in June 2012.

After several years working in research in several institutions (Plant genetics in public agronomy Institute (2003-2008), Human genetics in Gemelli Hospital (2004-2007), Oncology sequencing in Istituto Regina Elena Institute (2008-2009), Sequencing Service project manager in Genechron Lab (2009-2012)) he joined to Life Technologies as a field application member in our support team.

In 2017 becames a NGS business developer and from 2021 he is part of our NGS sales network in Italy.

Ion Torrent technology in Infectious disease: how to monitor epidemic from complex genotypes and targeted identification.

NGS Metagenomics, whole-genome sequencing (WGS) and targeted deep-sequencing are the best tools for genetic identification and characterization of viral/microbial agents, for studying their variability, and identifying genetic markers associated with virulence in order to control any pandemic. Really often the inadequate quality of samples and the low copies of genomes of interest reduce the results in terms of uniformity and variant calling. We show how the targeted deep-sequencing tool AmpliseqTM can overcome the issue of poor-quality sample and mitigate the data analysis overwork compared to the metagenomics approach. The new AmpliseqTM bioinformatic pipeline, to create a complex amplicon panel containing different genotypes, is able to provide accurate consensus sequences from unknow low titer genotypes in a single end-to-end workflow. Further, this technology can be used for a rapid identification of specific regions providing bacterial lineage and drug resistance in clinical samples of several bacteria like Mycobacterium tuberculosis. We show how AmpliseqTM provides higher sensitivity and specificity than usual metagenomics methods trough faster flexible solutions as fast as 24 hours from sample to data results in combination with GenexusTM System.

- **Jane Pouzou (Epix analytics)**

Dr. Jane Pouzou is a Senior Consultant for EpiX Analytics. Since joining the EpiX team after her doctoral program at the University of Washington, she has specialized in risk assessment on public health topics with a focus on environmental health. Jane works on projects in the areas of microbial food safety, antimicrobial resistance, chemical residues in food and the environment, and nutrition.

Title: Yes, Genomics and Risk Analytics Can Be Used Today to Create Safer Food Systems
Authors: Jane Pouzou, Dan Taylor, Regis Pouillot, Solenne Costard, and Francisco Zagmutt.

Abstract: Despite significant investments in surveillance and control, non-Typhoidal Salmonella (NTS) illnesses have leveled off and remain consistent in many places like the European Union and the United States. Regulators and producers are thus seeking new strategies. We have developed a framework using genomic data and machine-learning processes to rapidly classify NTS isolates detected through in US animal proteins into higher and lower virulence categories. Epidemiological data from US illnesses show that there are significant differences in the illnesses caused by serotypes which compose

each cluster. This approach has been used to inform a recently released proposed change to Salmonella regulation for poultry processing in the US. We also developed a QMRA model to evaluate the impact of strategies based on targeting higher virulence serotypes and the impact of concentration-based diversion of products. Diverting product above 1 CFU/g and above 10 CFU/g yielded similar results across various levels of proportion of product testing. Targeting higher virulence serotypes alone also prevented significant numbers of illnesses and resulted in less product lost compared with targeting all Salmonella species.

- **Session "Looking to the future: New challenges and opportunities"**
  Moderator: Mirko Rossi (EFSA)/ Christophe Cordevant (ANSES)

- **Annette Fagerlund (NOFIMA)**

Annette Fagerlund is a Senior Scientist in the Department of Food Safety and Quality at the Norwegian food research institute Nofima. Dr. Fagerlund joined Nofima in 2014 and applies molecular biological methods and DNA sequencing for the study of microbes in food and the food chain, with a current focus on the use of Whole Genome Sequencing (WGS) to study persistence and spread of Listeria monocytogenes. Dr. Fagerlund recently led a transdisciplinary research project, PathoSeq, which aimed to identify opportunities and barriers related to the use of WGS technology for preventative contamination control in the food industry. This project included partners from the meat and salmon food industries and a work package dedicated to legal research. The outcomes included practical analysis strategies and clarification of legislative and other regulatory aspects relevant for implementation of WGS for regulation and control of food safety.

Abstract

"Legal perspectives and challenges for use of WGS for Listeria control in the food industry.

WGS holds significant potential for ensuring safer food products on the market through use in the food industry for risk-based food safety management and problem solving. However, WGS is still rarely used by food business operators (FBOs). The presentation will include results from a study designed to elucidate some of the legal and regulatory barriers that may affect implementation of WGS of bacterial pathogens in the food industry, using L. monocytogenes as a case study. The work combined analysis of existing law with empirical mapping of stakeholder attitudes, and a brief normative analysis of ideal law. Existing legal provisions were examined for interpretational flexibility and compared against stakeholders' expressed needs and attitudes. The focus was on the Norwegian

context, although account was also taken of the experiences and practices of certain other European states, particularly Austria. Three issues were in focus: (i) the role of WGS data in assessing the safety of food; (ii) access by food safety authorities to WGS data, or isolates on which to perform WGS, from the food industry; and (iii) FBOs' ability to receive isolates and sequences held by the authorities."

- **Patricia Mejias (FAO)** (Pending)

- **Marion Gottschald (BfR)**

Marion Gottschald is a scientific officer at the German Federal Institute for Risk Assessment (BfR). Her main responsibilities are to coordinate national and European research projects around supply chain traceability and the tracing software FoodChain-Lab (FCL, https://foodrisklabs.bfr.bund.de/foodchain-lab/) e.g. in the framework of the EFSA-BfR cooperation, the FDA-BfR cooperation, the FoodSafeR project and the One Health EJP "COHESIVE" project. Her tasks include managing the development of FCL to fit stakeholder needs, applying FCL in foodborne incidents and conducting user trainings. Together with the FCL team and EFSA, she works on a universal traceability data format for foodborne incident investigation to foster interoperability of and data exchange between tracing software solutions in Europe.

Interoperable tracing software, harmonized supply chain data and the link to genomic information

Marion Gottschald, German Federal Institute for Risk Assessment
As global food supply chains become increasingly complex, and concerns about food safety grow, advanced traceability approaches are crucial to enhance the efficiency and accuracy of tracing investigations during foodborne incidents. This presentation delves into recent advancements in digital food traceability, with a particular focus on the development of interoperable software frameworks designed to facilitate seamless information exchange. Central to these frameworks is the harmonization of data elements, which enables enhanced collaboration among stakeholders in the food sector. The integration of genomic and supply chain traceability represents another significant advancement in the field of food safety. This approach combines genetic analysis of pathogens with detailed tracing the movements of food products throughout the supply chain to manage foodborne incidents. All in all, the establishment of interoperable or integrated systems improves the efficiency of foodborne incident investigations enabling more precise risk assessments and targeted interventions and preparedness for future crises.

-        **Baldissera Giovani (Euphresco)**

Dr. Giovani holds a PhD in biochemistry and molecular biophysics and worked for a number of years as a researcher in world leading universities, governmental agencies and private companies. Since 2008 he has been interested in research funding, international research cooperation and transnational public-public partnership. Currently, he is the coordinator of Euphresco, a network of research funders, policy makers and research organization that operate in the field of statutory plant health.

WGS from the plant health perspective

B. Giovani
Euphresco, 21 Bd Richard Lenoir, 75011 Paris, France

Euphresco is a network of organizations that collaborate together on plant health research matters. Started in 2006 as a European initiative, Euphresco has now evolved into an international network of more than 70 organizations from more than 50 countries worldwide.

Every year, Euphresco members identify common research priorities on which transnational collaborations are set. Diagnostics is an important activity and every year several research projects with a diagnostic component are initiated.

The presentation will provide an overview of the Euphresco network, its activities, and the views of network members on whole genome sequencing.

- Which should the working groups be?
  Moderators: (Ruth Timme-Emma Griffiths)

- Which should be the topics of the working groups and frequency
  Moderators: (Ruth Timme-Emma Griffiths)

Suggestions for future actions (according the past and current GMI steering committee)

- **Eric Stevens (FDA)**

Eric L. Stevens PhD is an International Policy Analyst in the Office of International Engagement at the Center for Food Safety and Applied Nutrition. He received his Ph.D. in Human Genetics and Molecular Biology from The Johns Hopkins School of Medicine with an emphasis on human population genetics and estimating genetic relatedness. From 2013 – 2014 he completed a Postdoctoral Fellowship analyzing RNA sequencing data to find differentially expressed genes and isoforms related to schizophrenia.

In 2014 he became an FDA Commissioner's Fellow at the Center for Food Safety and Applied Nutrition (CFSAN), applying the use of whole-genome sequence data in linking foodborne outbreaks. Dr Stevens worked in engaging other federal and international stakeholders in applying WGS methodologies to track foodborne outbreaks through CFSAN's GenomeTrakr. In his current position as an International Policy Analyst, Dr. Stevens continue to work closely with FDA's international sequencing partners in addition to monitoring other international science interests for CFSAN, including work with Codex Alimentarius, WHO, FAO, and EFSA. Finally, Dr. Stevens is the Co-Alternate Delegate to the Codex Committee on Food Hygiene.

- **Marc Allard (FDA)**

Marc W. Allard is a Senior Biomedical Research and Biomedical Product Assessment Services Officer in the Division of Microbiology in FDA's Office of Regulatory Science. Dr. Allard joined The US FDA in 2008 where he uses Whole Genome Sequencing (WGS) of foodborne pathogens to identify and characterize outbreaks of bacterial strains, particularly *Salmonella, E. coli,* and *Listeria*. Dr. Allard specializes in both phylogenetic analyses, as well as the biochemical laboratory methods which generate the WGS information. Dr. Allard helped develop the first distributed network of laboratories that utilize whole genome sequencing for pathogen identification and traceback called the GenomeTrakr database, which is part of the NCBI Pathogen Detection web site. These

tools are used daily for outbreak investigations and compliance. Dr. Allard acts as senior scientist to advise the US FDA on both WGS and phylogenetic methods as they apply to public health.

Economic Benefit of using WGS for Food Safety Management

M. Allard and E Stevens

U.S. Food and Drug Administration, College Park MD USA. Marc.allard@fda.hhs.gov

A network of federal, state, academic, and international laboratories has been using WGS data to rapidly characterize pathogens since 2012. Sequences from this GenomeTrakr network are available through the NCBI Pathogen Detection web portal. Public health agencies (FDA, CDC, and USDA-FSIS) collect and share data as soon as possible. This rapidly growing database is regularly used in outbreak investigations. The GenomeTrakr database has demonstrated how a distributed network of desktop WGS sequencers can be used in concert with traditional epidemiology for source tracking of foodborne pathogens. Our results demonstrate economic global benefits of having an open data model. Understanding root causes of foodborne contamination and assisting our academic, public health and industry partners to develop preventative controls to make food safer globally. The averted illnesses support over a billion US dollars in annual benefits, and we are seeing expansion with our international partners.