Programme & Abstracts

The Danish Microbiological Society

Annual Congress 2021

15 NOVEMBER 2021
COPENHAGEN · DENMARK

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Content

Programme

09:00	**Registration & Coffee**		Marmorhallen
09:00	**Poster mounting**		CPSC forhallen
	Auditorium A81.01	Auditorium A70.03	
10:00	**Welcome and opening address by DMS President** Thomas Bjarnsholt	**Welcome and opening address by DMS Vice-president** Trine Rolighed Thomsen	
10:15	**SARS-coronavirus-2 origin tracing** Speaker: Thea Kølsen Fisher, Denmark	**Microbial Ecology in the Green Transition** Speaker: Mette Haubjerg Nicolaisen, Denmark	
10:45	**Coffee and exhibition**		Marmorhallen
	PARALLEL SESSIONS		
	Auditorium A81.01	Auditorium A70.03	Auditorium A70.04
	Session: Multi-dimensional approaches towards diagnosing and treating persistent infections Chair: Helle Krogh DMS co-chair: Mette Burmølle	Session: Molecular mechanisms in microbes Chair: Ditlev Brodersen DMS co-chair: Rikke Meyer	Session: Microbial Food Safety Chair: Lisbeth Tuelstrup Hansen DMS co-chair: Katrine Uhrbrand
11:00	Chair introduction	Chair introduction	Chair introduction
11:05	**Multi-dimensional investigations of persistent P. aeruginosa airway infections** Helle Krogh, Denmark	**Bacterial kinases involved in survival and pathogenesis** Ditlev Brodersen, Denmark	**Listeria monocytogenes survival in the food processing environment – how does it do it?** Lisbeth Tuelstrup Hansen, Denmark
11:30	**Antibiotic resistance from a diagnostic and genomic perspective** Susanne Häußler, Denmark & Germany	**Molecular exploration of RelA-SpoT Homologues: (p)ppGpp and beyond** Vasili Hauryliuk, Sweden	**Controlling mold growth and toxin production in fermented meat products – is bioprotection the solution?** Gry Carl Terrell, Denmark
11:45	**Bacterial infections and phages/phage therapy** Ville Friman, United Kingdom	**Bacterial second messengers and antimicrobial resistance & tolerance (Bac-SMART)** Yong E. Zhang, Denmark	**The antimicrobial reuterin system – multiple functions not only in food products** Clarissa Schwab, Denmark
12:00	**Flash poster presentations (3x5min)**	**Flash poster presentations (3x5min)**	**Flash poster presentations (3x5min)**
12:15	**Lunch & Exhibition**		Marmorhallen
12:35	**GENERAL ASSEMBLY Det Danske Pasteur Selskab**		Auditorium A70.03
12:45	**Poster Session**		CPSC forhallen
12:35-13:00	**Industry symposium: Qiagen**		Auditorium A81.01

13:10-13:35	**Industry symposium: Nordic Biosite**		Auditorium A81.01
	PARALLEL SESSIONS		
	Auditorium A81.01	Auditorium A70.03	Auditorium A70.04
	Session: Necrotizing soft tissue infections (flesh-eating bacteria) Chair: Marco Bo Hansen DMS co-chair: Thomas Bjarnsholt	Session: Microbial remediation of water at trace pollutant concentrations Chairs: Jens Aamand, Lea Ellegaard DMS co-chair: Ole Højberg	Session: Novel research frontiers in marine science Chair: Ronnie Glud DMS co-chair: Michael Poulsen
13:45	Chair introduction	Chair introduction	Chair introduction
13:50	**Flesh-eating bacteria: What can we learn from the tragic patient stories?** Marco Bo Hansen, Denmark	**Stable Isotope Fractionation to Explore Pollutant Transformation Pathways and Mass Transfer Limitation in Biodegradation** Martin Elsner, Germany	**Life and element cycling in the deepest trenches on Earth** Ronnie Glud, Denmark
14:15	**Special conditions for antibiotic efficacy during necrotizing fasciitis** Claus Moser, Denmark	**Increased performance and persistence of bioaugmentation strain by altering water composition and flow of sand filters** Lea Ellegaard-Jensen, Denmark	**Non-phototrophic oxygen production by ammonia-oxidizing archaea** Beate Kraft, Denmark
14:30	**Title: Current research and application of hyperbaric oxygen therapy (HBO2) in necrotizing soft tissue infections** Ole Hyldegaard, Denmark	**Title: Broad dissemination of plasmids across groundwater-fed rapid sand filter microbial communities** Asmus Kalckar Olesen, Denmark	**Title: Electric mud - how cable bacteria influence sediment processe** Lars Peter Nielsen, Denmark
14:45	**Discussion**	**Flash poster presentations (3x5min)**	**Flash poster presentations (3x5min)**
15:00	**Coffee and exhibition**		Marmorhallen
15:15	**Poster Session**		CPSC forhallen
15:15-15:40	**Industry symposium: Triolab and Molzym**		Auditorium A81.01
15:50-16:15	**Industry symposium: Ares Genetics**		Auditorium A81.01
16:15	**Prize ceremony & Exhibition Draw**		Auditorium A81.01
16:30	**Keynote: The two-edged sword of antibiotics: climate change in miniature** Martin Blaser, United States		Auditorium A81.01
17:30	**Reception with fermented beverages**		CPSC forhallen
20:15	**Optional congress dinner** (tickets must be purchased)		Madklubben, Frederiksberg

Flash poster presentations

PARALLEL SESSIONS, MORNING			
	Auditorium A81.01	Auditorium A70.03	Auditorium A70.04
	Multi-dimensional approaches towards diagnosing and treating persistent infections	Molecular mechanisms in microbes	Microbial Food Safety
12.00	**[PA41] Human milk oligosaccharides induce compositional changes in the gut microbiota of conventional mice and specifically induce an acute yet reversible increase in the abundance of the genus phocaeicola,** Andrea Holst Technical Unity of Denmark	**[PA27] CRISPR-CAS systems are widespread accessory elements across plasmids,** Rafael Pinilla University of Copenhagen	**[PA03] Adaptation of bacillus thuringiensis to plant colonization affects differentiation and toxicity,** Yicen Lin Technical University of Denmark
12.05	**[PA43] Adaptive laboratory evolution and independent component analysis disentangle complex vancomycin adaptation trajectories,** Anaëlle Fait University of Copenhagen	**[PA38] Quorum sensing autoinducer-3 in salmonella typhimurium: from its biosynthesis to its impact on cell physiology,** Claire Lallement Roskilde University	**[PA02] CRISP – circumventing recurrent incidences of soft-rot pectobacteriaceae,** Julie Pedersen University of Copenhagen
12.10	**[PA39] Transcriptomic fingerprint of bacterial infection in lower extremity ulcers,** Blaine Fritz University of Copenhagen	**[PA33] Potential genes involved in bacterial persistence,** Nanna Boll Greve University of Copenhagen	

PARALLEL SESSIONS, AFTERNOON			
	Auditorium A81.01	Auditorium A70.03	Auditorium A70.04
		Microbial remediation of water at trace pollutant concentrations	Novel research frontiers in marine science
14.45		**[PB58] Experimental evolution of bacillus subtilis on arabidopsis thaliana roots reveals fast adaptation and improved root colonization in the presence of soil microbes,** Mathilde Nordgaard Technical University of Denmark	**[PB25] Bioturbation is a key driver of microbial community assembly in marine sediments,** Casper Thorup Aarhus University
14.50		**[PB59] Candidatus accumulibacter: a refined phylogeny reveals the existence of novel species, their potential function, and their global distribution,** Francesca Patriglieri Aalborg University	**[PB21] Chemotaxis may assist marine heterotrophic bacterial diazotrophs find microzones suitable for n2 fixation in the pelagic ocean,** Søren Hallstrøn University of Copenhagen
14.55		**[PB64] Biomining synergy: can indigenous bacteria work together to decalcify magnesite ores?** Lorrie Maccario University of Copenhagen	**[PB30] Influence of microbial secondary metabolites on the interaction between two marine bacteria, pseudoalteromonas piscicida and phaeobacter sp.,** Peter Svendsen Technical University of Denmark

About DMS

The Danish Microbiological Society (DMS) is a professional association in the fields of human and veterinary medical microbiology, general microbiology, food microbiology, environmental microbiology and biotechnology. DMS has existed since 1958, and is dedicated to the advancement of microbiology, both applied and basic, and promotes microbiological information to the public. These aims are achieved by organizing annual congresses, workshops and symposia - and by taking part in the current microbiological debate.

Furthermore, DMS collaborates with the Danish Pasteur Society on the award of travel grants to students and researchers in microbiology, immunology and related science.

Being a member of DMS, you are part of the advancement of microbiology in Denmark. Additionally, as a member of DMS, you are entitled to discounts at FEMS meetings (Federation of European Microbiological Societies) and for FEMS journals.

Contact

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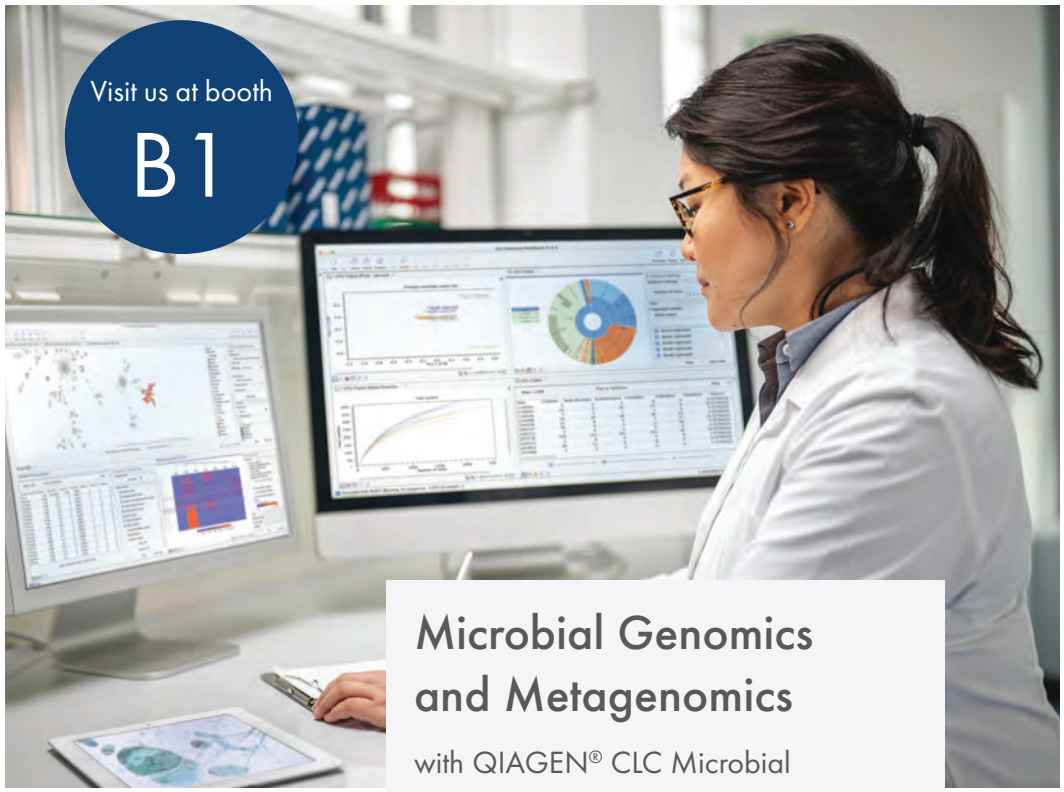

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Sample to Insight

Speakers' abstracts

[O01] Microbial Ecology in the Green Transition

Mette Haubjerg Nicolaisen[1]

[1]*University of Copenhagen, Denmark*

Microbes play a pivotal role in the green transition, e.g. by providing community services through plant-microbe interactions. While the impact of microbes on plant nutrient uptake, stress resilience and pathogen combat is well established and acknowledged, the understanding of drivers for microbial expression of beneficial traits under natural conditions where the soil complexity is at play, is understudied. Whether we aim to use the microbes as inoculants for improved nutrient uptake, or as biological control agents, we need to understand their ecology in the soil system in more detail, as it has been shown repeatedly that the translational power of findings from lab studies to field performance is low. Only by providing a knowledge base for these interactions in under more complex scenarios will we be able to feed into novel breeding and management practices which is a central part of the green transition.
We approach this by developing novel isolation strategies as the basis for inoculant development, by using synthetic communities to study the impact of specific metabolites on microbiome assembly on the root, as well as by studying the impact of root morphology as drivers for microbial assembly and bacterial functional profiles.

[O02] MULTI-DIMENSIONAL INVESTIGATIONS OF PERSISTENT P. AERUGINOSA AIRWAY INFECTIONS

Helle Krogh Johansen[1], Søren Molin[2]

[1]*Rigshospitalet, Department of Clinical Microbiology, afsnit 9301, Copenhagen, Denmark*
[2]*Technical University of Denmark, The Novo Nordisk Foundation Center for Biosustainability, Kgs. Lyngby, Denmark*

I will discuss some of the mechanisms by which bacteria infecting humans may survive and establish persistent infections, despite being fully susceptible to antibiotics. We have characterized almost 500 *Pseudomonas aeruginosa* isolates obtained from the lungs of cystic fibrosis patients who were infected by environmental bacteria for different periods of time, from few months to more than 40 years. Through whole genome sequencing, phenotyping and metabolic analysis we have mapped a number of evolutionary trajectories representing different adaptation strategies when bacteria invade new environmental niches. Surprisingly, we found that the genome sequences were the least informative concerning adaptive trajectories, whereas phenotypic traits such as antibiotic tolerance, growth rates and metabolism offered a much better framework for understanding bacterial persistence. Antibiotic susceptibility may be impacted by external factors, e.g., composition of nutrients, bacterial growth rate, stress factors, and interactions with the host. These complicating factors explain why persistent infections display various levels of antibiotic tolerance, and why treatment of apparently antibiotic sensitive bacterial populations fail to eradicate the bacteria. Continuous unsuccessful antibiotic treatment will eventually result in genetically determined resistance, not only of the targeted infecting bacteria, but also of commensal bacterial populations residing in the patients.

[O03] ANTIBIOTIC RESISTANCE FROM A DIAGNOSTIC AND GENOMIC PERSPECTIVE

Susanne Häussler[1]

[1]2Twincore, Zentrum für Experimentelle und Klinische Infektionsforschung GmbH , Molecular Bacteriology, Hannover, Germany

Against the background of increasing numbers of infections caused by multi-drug resistant bacterial pathogens, we are working on a project for the complete genome sequencing of bacterial isolates of selected problematic pathogens (*Pseudomonas aeruginosa, Escherichia coli, Klebsiella pneumoniae*). The sequence data obtained will be aligned with antibiotic resistance data using conventional culture-based methods in medical microbiology. Our vision is that Whole Genome Sequencing (WGS) of bacterial pathogens will provide detailed information not only on the bacterial resistance profile, but also on the phylogenetic relatedness of nosocomial pathogens and thus promise to be the basis for a more targeted antibiotic treatment and the implementation of effective infection control measures. In this respect the WGS data will be used to: 1. build a pan-genomic database covering all possible sequence variations of a bacterial species, as a pre-requisite for the robust and automated read out of sequence information; 2. Match phenotypically determined resistance with molecular resistance markers, with the ultimate goal of genotypically predicting resistance; and 3. develop a tool to present the results of genotyping.

[O04] USING ECOLOGY AND EVOLUTION TO DESIGN EFFECTIVE PHAGE THERAPEUTICS

Ville-Petri Friman[1]

[1]University of York, Biology, York, United Kingdom

Bacterial viruses - phages - shape the structure of natural bacterial communities and can be effective antimicrobial agents to treat bacterial infections. In the clinical setting, phage efficacy is however often limited by the rapid evolution of phage resistance, which could reduce the lifespan of phage therapeutics. In this talk, I will revise our recent work on designing phage combinations that limit *Pseudomonas aeruginosa* pathogen resistance evolution. This can be achieved already using simple phage combinations that target different surface receptors, and hence, reduce the likelihood of cross-resistance evolution. Furthermore, phage species can be chosen based on the trade-offs they impose on the pathogen. For example, some resistance mutations are highly costly and can reduce pathogen virulence, while other resistance mutations increase pathogen sensitivity to antibiotics. Finally, I will discuss the challenges of using simple lab models for studying the ecology and evolution of phage-bacteria interactions in the light of a recent *in vivo* experiment.

[O05] BACTERIAL KINASES INVOLVED IN SURVIVAL AND PATHOGENESIS

Ditlev E. Brodersen[1]

[1]*Department of Molecular Biology and Genetics, Aarhus University, Denmark*

The importance of protein kinases in bacterial cell biology has been underappreciated for many years, but from whole genome sequencing we now know that many microorganisms do contain a wide range of such enzymes. We have recently characterised a set of novel bacterial kinases involved in survival some of which are configured as so-called toxin-antitoxin systems. Structural and functional analysis of these protein complexes have revealed a hitherto unrecognised level of complexity in regulation that we are only just starting to understand suggesting that kinases could be central to bacterial survival against antibiotics, phages, and other challenges.

[O06] MOLECULAR EXPLORATION OF RELA-SPOT HOMOLOGUES: (P)PPGPP AND BEYOND

Vasili Hauryliuk[1]

[1]*Lund University, Experimental Medical Science, Lund, Sweden*

When bacteria encounter stressful situations, they produce the alarmone (p)ppGpp, a nucleotide messenger that inhibits the process of protein production and bacterial growth to save and redirect resources until conditions improve. Intracellular levels of (p)ppGpp are controlled by members of RelA-SpoT Homolog (RSH) protein family. Guided by the evolutionary analyses of RSH enzymes, we employed an array of microbiological, biochemical and structural methods to investigate diverse RSHs from bacteria and bacteriophages. These studies have uncovered novel biological functions of RSHs (such as toxic effectors of toxin-antitoxin pairs (1)), novel chemical reactions catalysed by RSHs (such as synthesis of (p)ppGpp analogue (p)ppApp (1) and pyrophosphorylation of the tRNA 3' CCA (2)), as well as novel regulatory mechanisms mediated by (p)ppGpp (such as the molecular mechanism of Rel/RelA control by the alarmone (3)).

References:

1. Jimmy S *et al.* (2020) A widespread toxin-antitoxin system exploiting growth control via alarmone signaling. PNAS, 117(19) 10500-10510
2. Roghanian *et al.* (2021) (p)ppGpp controls stringent factors by exploiting antagonistic allosteric coupling between catalytic domains. Molecular Cell, 81(16), 3310-3322.e6

Kurata T *et al.* (2021) RelA-SpoT Homologue toxins modify the CCA end of tRNA to inhibit protein synthesis. Molecular Cell, 81(15): 3160-3170.e9

[O07] BACTERIAL SECOND MESSENGERS AND ANTIMICROBIAL RESISTANCE & TOLERANCE (BAC-SMART)

Yong Zhang[1]

[1]*University of Copenhagen, Department of Biology, København N, Denmark*

Bacteria use various nucleotide-derived second messengers (NSMs) to convey environmental (stress) signals into physiological changes for better ecological survival. NSMs, due to their intrinsic small sizes and thus fast diffusion rate, likely reach their target proteins more rapidly to elicit prompt host cell responses. My lab focuses on studying the dynamic homeostasis and the target proteins of NSMs during bacterial survival of chemical and biological assaults. I will present several stories concerning the NSMs cyclic AMP and ppGpp in different bacterial organisms.

[O08] *LISTERIA MONOCYTOGENES* SURVIVAL IN THE FOOD PROCESSING ENVIRONMENT – HOW DOES IT DO IT?

Lisbeth Truelstrup Hansen[1], Martin Laage Kragh[1]

[1]*National Food Institute, Technical University of Denmark*

Listeria monocytogenes is a Gram-positive foodborne bacterium, which continues to cause outbreaks and serious illness in especially young, older or immunocompromised affected individuals. The psychrotrophic *L. monocytogenes* is found widespread in the environment, meaning that it can contaminate raw materials in the field or on the farm. Several studies have shown that the same sequence type of the bacterium can be repeatedly isolated from food production facilities, indicating it clearly knows how to survive in this environment. Contamination of equipment leads to cross-contamination events which is particularly detrimental to the safety of ready-to-eat food products, which are consumed without further treatment to control the bacterium.
This presentation will present results from our on-going research which looks at factors that enables *L. monocytogenes* to survive in the production environment, including its ability to produce biofilms, survive being dried and resistance to commonly used disinfectants.

[O09] CONTROLLING MOLD GROWTH AND TOXIN PRODUCTION IN FERMENTED MEAT PRODUCTS – IS BIOPROTECTION THE SOLUTION?

Anette Granly Koch[1], Tomas Jacobsen[1], Gry Terrell[2]

[1]*Dmri at Danish Technological Institute*
[2]*Danish Technological Institute, Danish Meat Research Institute, Food Safety, Taastrup, Denmark*

Bioprotection, the use of harmless bacteria to avoid growth of unwanted microorganisms, is a discipline going far back in history. Good bacteria have been used in fermented food and in ready-to-eat products to inhibit *Listeria* or spoilage bacteria. Twenty years ago, some scientific papers described how different lactic acid bacteria (LAB) could be used to inhibit growth of fungi. In recent years new reports on this topic have emerged in the literature. At DMRI we have been investigating specifically the use of LAB to inhibit growth of *Penicillium* spp in processed meat.

LAB from the DMRI culture collection and cultures from commercial suppliers were screened for inhibitory properties. A total of 56 different cultures were tested and 15 strains were able to inhibit one or more of the fungi *P. nordicum, P. salami* and *P. brevicompactum* in an agar spot assay. The nine strains exhibiting the best anti-fungal activity were used for fermenting miniature sausages. The sausage surfaces were inoculated with fungal spores. Fungal growth was analyzed intermittently during fermentation, maturation, and drying. Toxin production was analyzed at the end of the manufacturing process. Four strains were able to both reduce pH and markedly reduce growth of the three *Penicillium* strains. These four strains are currently being evaluated for their sensory profile in fermented sausage both in combination with commercial starter cultures for fermented sausages, but also as single cultures.

[O10] THE ANTIMICROBIAL REUTERIN SYSTEM – MULTIPLE FUNCTIONS NOT ONLY IN FOOD PRODUCTS

Clarissa Schwab[1]

[1]*Aarhus University, Biological and Chemical Engineering, Aarhus, Denmark*

Traditionally, reuterin has been considered a natural broad range antimicrobial active against bacteria, yeast and fungi. Reuterin was successfully used to inhibit spoilers and pathogens in dairy. Reuterin also detoxifies dietary heterocyclic amines, a bioactivity that is much less known. Reuterin is produced from glycerol by food microbes harbouring the enzyme glycerol/diol dehydratase (GDH), and forms a multicomponent system composed of 3-hydroxypropanal, its hydrate, dimer and the toxic aldehyde acrolein. We recently suggested that acrolein is responsible for both bioactivities, antimicrobial activity and heterocyclic amine detoxification, attributed to reuterin.

Based on metagenomic data, we predicted that, in addition to food microbes, gut microbes are able to produce reuterin. Reuterin formation was experimentally confirmed for the common gut microbes *Anaerobutyricum hallii, Blautia obeum,* and *Flavonfractor plautii,* and for complex intestinal microbiota with *A. hallii* being a key species in acrolein formation. Reuterin formation could be enhanced by addition of *A. hallii* and glycerol to intestinal microbiota.
Taken together, these studies show that one enzymatic activity can play various roles in different ecosystems. Whether acrolein formed by the intestinal microbiota *in vivo* confers beneficial or adverse effects, and should be enhanced through microbial modulation, will be investigated in future research.

[O11] FLESH-EATING BACTERIA: WHAT CAN WE LEARN FROM THE TRAGIC PATIENT STORIES?

Marco Bo Hansen[1]

[1]*sani nudge, Denmark*

DR, the official broadcasting company of Denmark, has provided a series of documentaries, podcasts, and articles on necrotizing soft tissue infections (NSTIs), otherwise known as flesh-eating bacteria. This has increased the focus on the disease, and now national guidelines are currently being established.

The science and data presented in the documentaries are based on the EU-funded INFECT-project, conducted between 2013-208 and supported by the FP7 Health framework. The project included 14 multidisciplinary partners from across Europe, Israel and the US. The overall goal of the project was to advance our understanding of NSTIs.

With the INFECT project, the world's largest NSTI patient cohort was established with an extended clinical registry and associated biobank providing a unique resource for the proposed studies. The project has provided important insight into the clinical aspects of NSTIs providing the basis for evidence-based guidelines for patient management and care. Furthermore, the project has advanced our understanding of these life-threatening infections.

During this session, you will learn what the tragic patient cases presented in the documentaries can teach us as healthcare professionals, and you will learn about the disease based on the results from the INFECT project.

[O12] SPECIAL CONDITIONS FOR ANTIBIOTIC EFFICACY DURING NECROTIZING FASCIITIS

Claus Moser[1]

[1]*University of Copenhagen, Denmark*

Serious and acute bacterial infections such as necrotizing fasciitis needs optimized antibiotic therapy for best possible outcome, as well as a number of non-antibiotic treatment strategies. For choosing an appropriate antibiotic therapy, knowledge of expected and possible microbial etiology as well as susceptibility patterns in the primary focus and the relevant geographical region are mandatory. However, in addition to the necessary spectrum of the administered antibiotics a number of additional parameters and conditions influences the antibiotic effect and can be involved in personalizing the treatment strategies of necrotizing fasciitis. Such factors will be discussed during this presentation.

[O13] CURRENT RESEARCH AND APPLICATION OF HYPERBARIC OXYGEN THERAPY (HBO2) IN NECROTIZING SOFT TISSUE INFECTIONS

Ole Hyldegaard[1]

[1]*Rigshospitalet, Denmark*

In Denmark a multidisciplinary management algorithm for patients with necrotizing soft tissue infections is applied in high-volume treatment centers and treatment in high-volume hospitals, i.e. centers receiving a case load of >8 patients per year, have been shown to be associated with lower mortality. Rarity of the disease and heterogenous patient characteristics makes future research and therapy improvements more depended on centralized treatment efforts. Surgical exploration is required for diagnosis, but as for other treatment modalities evidence based on randomized trials is scares in NSTI patients in general. Several biomarkers have been identified as being associated to prognosis, either individually or as part of patterns of biomarkers, but none have been validated as definitive diagnostic in the early phases of NSTI. Tools for beside-decision algorithms based on early prognosis is under development but validation is required. The use of immunoglobulin for GAS NSTI and HBO2 is considered adjuvant therapies. HBO2-treatment serves as an adjunct in more than one-third of all NSTI cases in Denmark and is associated with improved survival compared to centers not providing the therapy. Likewise, A recent meta-analysis using observational data found that patients treated with HBO2 treatment had a reduced risk of dying. HBO2 treatment has also been associated with an increase in plasma level of inter cellular adhesion molecules (sICAM-1) and a reduction in proinflammatory cytokines and modulation of reactive oxygen species (ROS), thereby potentially lowering the risk of collateral damage, increasing bacteriostatic and bacteriocidic effects of antibiotics and improving clinical outcome. Accordingly, current research are indicative of several important HBO2-mediated immunomodulatory effects in patients with NSTI associated to an improved overall outcome. However, HBO2 administration is dependent on local logistics, in-hospital equipment used for its proper application and staffing. Careful attention to these conditions is mandatory requirements when evaluating the use of HBO2 in NSTI patients or when designing a possible future large multicenter, multinational randomized controlled trial in effort to provide final causal support for the continued use of HBO2 in the treatment of NSTI.

[O14] STABLE ISOTOPE FRACTIONATION TO EXPLORE POLLUTANT TRANSFORMATION PATHWAYS AND MASS TRANSFER LIMITATION IN BIODEGRADATION

Martin Elsner[1], Benno Ehrl[2], Fengchao Sun[3], Sviatlana Marozava[2], Mehdi Gharasoo[4], Kundu Kankana[5]

[1]*Technische Universität München, Institute of Hydrochemistry, Garching, Germany*
[2]*Helmholtz Zentrum München - Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH), Institute of Groundwater Ecology, München, Germany*
[3]*University of Waterloo, Department of Earth and Environmental Sciences, Waterloo, Canada*
[4]*CMET - Center for Microbial Ecology and Technology, Faculty of Bioscience Engineering, University of Ghent, Gent, Belgium*

A powerful feature of compound-specific isotope fractionation analysis (CSIA) is its ability to detect *in situ* biodegradation and pollutant transformation pathways in the environment. Gas chromatography – isotope ratio mass spectrometry (GC-IRMS) can analyze natural stable isotope ratios (e.g., $^{13}C/^{12}C$, $^{15}N/^{14}N$) of individual organic contaminants in environmental samples. Since kinetic isotope effects depend on underlying (bio)chemical reactions, changes in these isotope ratios can reflect associated transformation mechanisms. (10.1039/C0EM00277A; 10.1016/j.copbio.2016.04.014). Recently we discovered that CSIA can also reveal bottlenecks of biodegradation by detecting mass transfer limitations (10.1021/acs.est.7b06599). As long as changes in isotope values are observable, this implies that pollutant mass transfer into and out of bacterial cells is not limiting. If isotope fractionation is pronounced at high concentrations, but disappears at trace levels, however, this reveals that mass transfer becomes limiting specifically at low concentrations (10.1021/acs.est.8b02498). Our results (i) pinpointed cell-membrane permeation as bottleneck of degradation when atrazine (10.1021/acs.est.8b05175) and 2,6-dichlorobenzamide (10.1021/acs.est.0c08566) concentrations reached low microgram/L values, while (ii) complementary proteomics suggested that this mass transfer limitation triggered subsequent regulation of activity (10.1038/s41396-019-0430-z). This intrinsic limitation expected for any bacterial cell provides a new perspective on why biodegradation is commonly observed to be slow at trace pollutant levels.

[O15] INCREASED PERFORMANCE AND PERSISTENCE OF BIOAUGMENTATION STRAIN BY ALTERING WATER COMPOSITION AND FLOW OF SAND FILTERS

Lea Ellegaard-Jensen[1], Morten Dencker Schostag[2], Ole Hylling[3], Mahdi Nikbakht Fini[4], Nora Badawi[5], Alex Gobbi[6], Christian N. Albers[7], Jens Muff[8], Jens Aamand[9], Lars H. Hansen[10]

[1]Aarhus University , Department of Environmental Sciences, Roskilde, Denmark
[2]DTU, DTU BIOENGINEERING, Kgs. Lyngby, Denmark
[3]TNO, Energy Transition Unit, LE Petten, Netherlands
[4]Geological Survey of Denmark and Greenland, Department of Geochemistry, København, Denmark
[5]University of Copenhagen, Department of Plant and Environmental Sciences, Denmark
[6]Aalborg University, Esbjerg, Denmark

Drinking water resources, such as groundwater, are threatened by pollution. One concern is the pesticide metabolite 2,6-dichlorobenzamide (BAM) frequently found in groundwater in concentrations exceeding the EU legal limit of 0.1 µg/L. In this context, bioaugmentation of sand filters with specific degrader organisms is proposed as a green technology for removal of such recalcitrant pesticide residues from abstracted groundwater. However, previous studies applying the degrader *Aminobacter niigataensis* MSH1 in sand filters in order to remove BAM, found that its population size decreased – along with degradation efficiency – shortly after inoculation.
We therefore developed a new system to prolong the performance and persistence of the inoculated bacteria. Our approach was threefold: 1) development of a novel inoculation strategy, 2) lowering the flowrate, and 3) increasing the concentration of nutrients in feed water. The two latter were achieved via modifications of the inlet water by applying membrane treatment which, besides producing an ultra-pure water fraction, produced a residual water stream with all nutrients including BAM concentrated in a 2-10x reduced volume. This was done to alleviate starvation of degrader bacteria in the otherwise oligotrophic biofilters and to reduce washout of cells.

We showed in experiments of increasing complexity - from batch to pilot field scale experiments - that removal of BAM by *A. niigataensis* MSH1 can be stimulated (batch) and prolonged in bioaugmented sand filters (pilot scale) receiving membrane residual water. Molecular targeting of the degrader strain and community analysis by high throughput sequencing showed that the population of degrader bacteria persisted for at least 40 days.

[O16] BROAD DISSEMINATION OF PLASMIDS ACROSS GROUNDWATER-FED RAPID SAND FILTER MICROBIAL COMMUNITIES

Rafael Pinilla-Redondo[1], Asmus Olesen[2], Jakob Russel[3], Lisbeth Elvira de Vries[4], Lisbeth Damkjær Christensen[5], Sanin Musovic[6], Joseph Nesme[7], Søren Johannes Sørensen[8]

[1]University of Copenhagen, Section of Microbiology, Copenhagen, Denmark
[2]University College Copenhagen, Department of Technology, Copenhagen, Denmark
[3]The Danish Technological Institute, Taastrup, Denmark

Biological rapid sand filtration is a commonly employed method for the removal of organic and inorganic impurities in water, which relies on the degradative properties of microorganisms for the removal of diverse contaminants, but their bioremediation capabilities vary greatly across waterworks. Bioaugmentation efforts with degradation-proficient bacteria have proven difficult due to the inability of the exogenous microbes to stably colonize the sand filters. Plasmids are extrachromosomal DNA elements that can often transfer between bacteria and facilitate the flow of genetic information across microbiomes, yet their ability to spread within rapid sand filters have remained unknown. Here, we examined the permissiveness of rapid sand filter communities towards four environmental transmissible plasmids; RP4, RSF1010, pKJK5 and TOL (pWWO), using a dual-fluorescent bioreporter platform combined with FACS and 16S rRNA gene amplicon sequencing. Our results reveal that plasmids can transfer at high frequencies and across distantly related taxa from rapid sand filter communities, emphasizing their potential suitability for introducing bioremediation determinants in the microbiomes of underperforming water purification plants.

[O17] LIFE AND ELEMENT CYCLING IN THE DEEPEST TRENCHES ON EARTH

Ronnie Glud[12]

[1]*University of Southern Denmark, Dept. of Biology, Odense, Denmark*
[2]*Tokyo University of Marine Science and Technology, Tokyo, Japan*

Hadal trenches stretch from 6 to 11km of water depth and represent the deepest, most remote, and scantly explored habitats on Earth. However, recent findings document that trenches act as depocenters for organic material and are far more dynamic and diverse than previously recognized. Surprisingly, trench sediments have been proven to host intensified biological activity that is dominated by microbes and meiofauna flourishing at extreme hydrostatic pressure. The use of autonomous in situ equipment and sophisticated pressure tank facility has given new insights on how life decomposes organic matter and cycles elements and nutrients at hadal depth. By comparing trenches from contrasting oceanic settings the talk will present a general analysis of hadal biogeochemistry and the role of deep trenches in the oceans, as well as fundamental new insights to the composition and functioning of microbial communities at extreme pressure.

[O18] NON-PHOTOTROPHIC OXYGEN PRODUCTION BY AMMONIA-OXIDIZING ARCHAEA

Beate Kraft[1], Alejandra Elisa Hernandez-Magaña[2], Laura Bristow[3], Martin Könneke[4], Bo Thamdrup[3], Donald Canfield[3]

[1]*University of Southern Denmark, Biology, Odense, Denmark*
[2]*University of Oldenburg, Institute for Chemistry and Biology of the Marine Environment (ICBM), Oldenburg, Germany*

Ammonia-oxidizing archaea are one of the most abundant groups of microbes in the world's oceans and key players in the nitrogen cycle. Their energy metabolism, the oxidation of ammonia to nitrite, requires oxygen. Nevertheless, ammonia-oxidizing archaea are abundant in environments where oxygen is undetectable. Their role in such environments has remained unknown and a metabolism by ammonia-oxidizing archaea that does not depend on the supply of external oxygen has so far remained undiscovered. Here, we present evidence for a metabolic pathway in the ammonia-oxidizing archaeon *Nitrosopumilus maritimus*, that operates in an oxygen depleted environment.

We show that after oxygen depletion, *N. maritimus* produces oxygen and dinitrogen with nitric oxide as an intermediate. The produced dinitrogen originates solely from nitrite (and not ammonia). Part of the produced oxygen is directly re-used for ammonia oxidation. This keeps oxygen levels in the nanomolar range, thus evading detection with oxygen sensing methods standardly used to study *N. maritimus* physiology.

Considering their vast abundance in the global oceans, an oxygen producing pathway that is widely distributed and active in ammonia-oxidizing archaea would have far reaching implications on the microbial ecology and biogeochemical cycles in oxygen depleted environments.

[O19] ELECTRIC MUD – HOW CABLE BACTERIA INFLUENCE SEDIMENT PROCESSES

Lars Peter Nielsen[1]

[1]*Center for Electromicrobiology, Aarhus University*

Cable bacteria are centimeter-long, multicellular bacteria with internal electric wires. Represented by many different species, they are widespread in marine and freshwater sediments where they place themselves across oxic-anoxic interfaces and gain energy from oxidizing sulfide at the anoxic side and pass the extracted electrons to oxygen reduction at the other side by means of the electrical wires. This unique spatial separation of metabolic oxidation and reduction halfreactions results in distinct gradients in the sediment of electric potential, pH, and chemical species with multiple implications for element cycles and aquatic life. The presentation will focus on impact of cable bacteria on carbon and sulfur fluxes and interactions with plants and animals.

[O20] THE TWO-EDGED SWORD OF ANTIBIOTICS: CLIMATE CHANGE IN MINIATURE

Martin J. Blaser[1]

[1]*Rutgers University, New Brunswick, New Jersey, USA*

Why have so many diseases erupted in the last 70 years?
These disorders include asthma, obesity, allergies, auto-immune diseases, autism spectrum diseases and other neurodevelopmental disorders, and more. If 10 diseases rise more or less synchronously, do they have 10 different causes, or is it more parsimonious to consider that there is a single cause underlying them all? I hypothesize that such a factor is a change in the human microbiome. Just as tectonics or global warming, each a single process, can have multiple disparate consequences, so could microbiome disruption play out on the stage of human health and disease. There is much evidence that this idea, which I call The Theory of the Disappearing Microbiota, is correct. Multiple changes in modern life in industrialized countries could play roles, but for now I focus on antibiotics, sufficient in the scale and timing of human exposure and their selective power to be major influences. Multiple studies associate early life antibiotic exposure with increased disease risk. Added to association are experimental studies in model systems that provide consistent evidence of causal roles, crossing host generations. This represents a serious and increasing problem that requires directed solutions. These include better clinical utilization of antibiotics, limiting the extent of their use, narrow spectrum approaches to anti-bacterial activities, and strategies for restoration of missing microbes and their host-signaling modalities and pathways.

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A Bioinformatics Pipeline For Routine Spoilage Detection In Dairy Production From Metagenomic Oxford Nanopore Reads

Time 12.35-13.00
Room Auditorium A81.01
Speaker Patrick Ettenhuber, Qiagen

Food and feed safety is a main concern for food authorities, centers of disease control, departments of agriculture and public health laboratories, specifically the surveillance of and acting on epidemiological outbreaks of food-borne pathogens such as Salmonella, Listeria, Vibrio, E. coli, Shigella, Campylobacter and Cronobacter reported by hospitals and doctors. Additionally, food spoilage is a major concern for large food producing companies as this can have a direct impact on revenue margins, the environment, food going to waste and last but not least brand reputation. Historically, the identification of food pathogens and spoilers involved culturing bacteria from suspected sources using specialized bacterial growth media to isolate the causal agent, followed by strain typing, a workflow that can take several days or weeks for some slow growing agents, if it is at all possible. At this stage, the damage has been done, and the impacts are wide. For this reason, there is a strong industry trend towards NGS-based approaches to sample characterization, namely whole-genome sequencing of isolates and taxonomic profiling of bacterial communities. Food quality laboratories are now routinely equipped with desktop sequencing machines from Illumina or IonTorrent and portable devices from Oxford Nanopore to provide the sequences. Here we demonstrate how a bioinformatic analysis of metagenomic sequencing reads from an Oxford Nanopore sequencer can be performed using the CLC Genomics Workbench premium, a workflow that has been developed in a collaboration between QIAGEN and Arla Foods for the detection of spoilers and pathogens in dairy production.

Nordic Biosite symposium

Improving the Accuracy and Reproducibility of Microbiome Measurements Across Labs

Time 13.10-13.45
Room Auditorium A81.01
Speaker Dr. Patrick Tripp
(Laboratory Director, Zymo Research Europe)

From sample collection to library preparation and analysis - Zymo Research's product portfolio offers a complete solution for your microbiome workflow.

- DNA/RNA Shield® Sample Collection Devices guarantee preservation of the sample's nucleic acid profile while inactivating infectious agents completely
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- The ZymoBIOMICS® Microbial Community standards are well-defined, accurately characterized microbial mock communities that allow to improve and maintain quality and reproducibility of your microbiome analysis
- The Quick-16S Plus NGS Library Prep Kit offers an automation-friendly, fast library preparation protocol involving only a single PCR-step and without the need for normalization

Triolab and Molzym symposium

Broad-Range Molecular Identification of Bacteria and Fungi Direct from Samples: from Research towards Clinical Diagnostics

Time 15.15-15.40
Room Auditorium A81.01
Speaker Malin Wollens, Product Manager Diagnostic Business Line

This symposium will focus on Molzym's solutions for the culture-independent detection and identification of bacteria and fungi from human and animal samples. The unique host DNA depletion technology, MolYsis™, as well as the ultra-pure reagents and PCR assays with various applications in research and clinical routine diagnostics will be highlighted. The diagnostic performance and clinical impact of Molzym's Molecular Diagnostic Solutions (MMDx™) will be illustrated by a summary of peer-reviewed articles for diverse applications with a focus on bloodstream infections, bone and joint infections, bacterial meningitis and infective endocarditis.

Ares Genetics symposium

Surveillance and AI-Powered Prediction of AMR to Inform Antibiotic Therapy

Time 15.50-16.15
Room Auditorium A81.01
Speaker Arne C. Materna
Authors Stephan Beisken, Johannes Weinberger, Peter Májek, Lukas Lüftinger, Ines Ferreira, Thomas Weinmeier, Arne C. Materna

The burden of antimicrobial resistance (AMR) has been acknowledged worldwide by leading health institutes. Besides the need for new antibiotics, efforts are required in the field of AMR surveillance and diagnostics for effective infection prevention and empirically informed selection of first line treatments. Next-generation sequencing (NGS), has emerged as an alternative to established molecular tests for the detection, identification, typing and functional characterization of AMR pathogens. The advantage of NGS over other tests resides in the technique's potential to integrate into a single assay i) the sensitive and comprehensive detection of pathogens with ii) the characterization of AMR based on genomic information. Yet, several limitations impair adoption of NGS for AMR testing, including a lack of validated NGS and bioinformatics workflows, as well as slow turnaround times associated with NGS. For complex samples types such as native patient or environmental specimen, common in culture-free testing, high concentrations of background DNA relative to pathogen DNA further diminishes the utility of the technology.

To overcome the aforementioned challenges, we have designed a set of isolate-based and culture-free assays for the identification and characterization of AMR pathogens. In this talk, we present our findings from the routine application of these assays in our lab and explore the results from their clinical validation.

Poster sessions and poster index

The posters will be presented at two different breaks – please see the schedule.
If you hav a poster at DMS2021, please be present during the assigned time according to your poster number.

12.45-13.45 A poster numbers
15.15-16.15 B poster numbers

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Multi-dimensional approaches towards diagnosing and treating persistent infections		
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PA40	MECHANISM BEHIND ANTIBIOTIC ENHANCED PLASMID TRANSFER AND IDENTIFICATION OF COMPOUNDS WHICH INHIBIT THIS MECHANISM.	Jennifer Moussa
PA41	HUMAN MILK OLIGOSACCHARIDES INDUCE COMPOSITIONAL CHANGES IN THE GUT MICROBIOTA OF CONVENTIONAL MICE AND SPECIFICALLY INDUCE AN ACUTE YET REVERSIBLE INCREASE IN THE ABUNDANCE OF THE GENUS PHOCAEICOLA.	Andrea Holst
PA42	MOBILIZATION OF ANTIBIOTIC RESISTANCE GENES DIFFER BY RESISTANCE MECHANISM	Tue Kjærgaard Nielsen
PA43	ADAPTIVE LABORATORY EVOLUTION AND INDEPENDENT COMPONENT ANALYSIS DISENTANGLE COMPLEX VANCOMYCIN ADAPTATION TRAJECTORIES	Anaëlle Fait
PA44	UNIQUE MICROBIOTA IN ATOPIC DERMATITIS SKIN	Lene Bay
PA45	A SYSTEMATIC SCREENING OF A LARGE COLLECTION OF CLINICAL PSEUDOMONAS AERUGINOSA ISOLATES REVEALS STRAIN- AND ANTIBIOTIC-SPECIFIC BIOFILM TOLERANCE PATTERNS	Janne Gesine Thöming
PA46	ISOLATION OF NOVEL EPISOMES INVOLVED IN ANTIGENIC VARIATION IN MYCOPLASMA GENITALIUM	Henrik Frederik Bekkevold Johansen
PA47	THE IMPORTANCE OF TAXONOMIC CLASSIFICATION SOFTWARE AND MACHINE LEARNING ALGORITHMS FOR THE PREDICTION OF COLORECTAL CANCER	Sebastian Mølvang Dall
PA48	FROM DAYS TO HOURS: DEVELOPMENT AND IMPLEMENTATION OF METAGENOMIC DNA-SEQUENCING IN CLINICAL MICROBIOLOGY DIAGNOSTICS	Morten Eneberg Nielsen
PA49	FOUR-SPECIES CLINICAL UROPATHOGEN BIOFILM MODEL TO STUDY CATHETER ASSOCIATED URINARY TRACT INFECTION	Jiapeng Hou
PA50	EXPLORING THE PHENOTYPIC AND GENOTYPIC DIVERSITY OF PSEUDOMONAS AERUGINOSA, CLINICAL ISOLATES	Kasandra Pedersen
PA51	BIOFILM FORMATION IN THE UDDERS OF DAIRY COWS WITH CHRONIC MASTITIS	Regitze Renee Pedersen
PA52	THE EARLY LIFE SKIN MICROBIOTA AND ATOPIC DERMATITIS - A BIRTH COHORT STUDY	Mathis Hjelmsø

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PA54	OVERCOMING CHALLENGES IN ANTIMICROBIAL RESISTANCE PREDICTION FROM GENOMIC DATA	Lukas Lüftinger
PA55	LIPOTEICHOIC ACID AND MEMBRANE INTEGRITY IS ESSENTIAL FOR STAPHYLOCOCCUS AUREUS TOLERANCE TO D-SERINE	Kasper Mikkelsen
PA56	POTENTIAL FOR ZOONOTIC SPREAD OF MULTI-RESISTANT CLOSTRIDIOIDES DIFFICILE	Semeh Bejaoui
PA57	QUANTIFYING ENTEROTOXIGENIC E. COLI INFECTING PHAGE FROM FAECES	Norbert Acs
PA58	ANTIVIRULENCE TROJAN HORSE (CRISPR-CAS IN PHAGE) APPLICATION AGAINST PSEUDOMONAS AERUGINOSA INFECTIONS	Rodrigo Ibarra Chavez
PA59	TINY EARTH DENMARK: STUDENT-SOURCING ANTIBIOTIC DISCOVERY	Thomas Tørring
PA60	THE GUT MICROBIOME AND GROWTH IN EARLY LIFE	Christina Poulsen
PA61	THE ROLE OF EARLY LIFE GUT VIROME IN HEALTH AND DISEASE	Cristina Leal Rodríguez
PA62	PHAGE INFECTION RESTORES PQS SIGNALING OF A PSEUDOMONAS AERUGINOSA LASI QUORUM-SENSING MUTANT	Nina Molin Høyland-Kroghsbo
PA63	INTESTINAL MICROBIOTA IN PATIENTS WITH ULCERATIVE COLITIS AND HEALTHY CONTROLS FROM GHANA AND DENMARK	Hengameh Chloe Mirsepasi-Lauridsen
PA64	TARGETED SCREENING OF PROBIOTICS WITH ANTI-VIRULENCE ACTIVITY AGAINST STAPHYLOCOCCUS AUREUS IN ATOPIC DERMATITIS	Stephanie Fulaz Silva
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PA22	MICROBIAL SINGLE-CELL RNA SEQUENCING TO DIG INTO PLASMID MANAGERIAL CAPABILITIES OF BACTERIAL POPULATIONS	Valentine Cyriaque
PA23	DO NITRIFICATION INHIBITORS AFFECT NON-TARGET SOIL MICROORGANISMS?	Zivile Buivydaite
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PA30	SYNTHETIC COMMUNITY INVASION DEPENDS ON SECONDARY METABOLITE PRODUCTION IN BACILLUS SUBTILIS	Carlos N. Lozano-Andrade
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PB31	AMMONIA-OXIDIZING ARCHAEA METABOLISM AT NANOMOLAR OXYGEN CONCENTRATIONS.	Elisa Hernandez-Magana
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PB32	BACTERIA SWARMING AROUND CABLE BACTERIA IS COMMON AND CONSISTENT BEHAVIOR IN OUR FRESHWATER SEDIMENT ENRICHMENTS	Jamie JM Lustermans
PB33	DO HIGH CO2 LEVELS HELP PROTECT TERMITOMYCES AGAINST ANTAGONISTS?	Suzanne Schmidt
PB34	ASCOM: AN ECOSYSTEM-SPECIFIC REFERENCE DATABASE FOR INCREASED TAXONOMIC RESOLUTION IN SOIL MICROBIAL PROFILING	Christina Overgaard
PB35	UNRAVELING BIOTIC AND ABIOTIC FACTORS DETERMINING BACILLUS SUBTILIS ABUNDANCE	Xinming Xu
PB36	MICROFLORA DANICA – THE MICROBIOME OF DENMARK	Thomas Bygh Nymann Jensen
PB37	MICROFLORA DANICA: SINGLE PRIMER ENRICHMENT OF BACTERIAL RRNA GENES	Emil Aarre Sørensen
PB38	SHAPING THE TRIPARTITE SYMBIOSIS: TERMITE MICROBIOME DIRECTED BY HORIZONTALLY ACQUIRED FUNGAL CULTIVAR	Veronica Sinotte
PB39	A DOMESTICATED FUNGAL CULTIVAR RECYCLES ITS CELLULAR CONTENTS AS NUTRITIONAL REWARDS FOR ITS LEAFCUTTER ANT FARMERS	Caio Leal-Dutra
PB40	THE KEY TO A GOOD RELATIONSHIP : INTER-KINGDOM COMMUNICATION IN A FUNGAL-ANT NUTRITIONAL SYMBIOSIS	Benjamin Conlon

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PB41	MICROFLORA DANICA - ESTABLISHING A PIPELINE FOR FUNCTIONAL CHARACTERISATION AND TAXONOMIC CLASSIFICATION OF 10 000 METAGENOMES	Frederik Platz
PB42	DISCOVERY OF MUTATIONAL LANDSCAPES IN EVOLVING BACTERIAL POPULATIONS	Guohai Hu
PB43	MYCOVIRUSES: A HITHERTO UNKNOWN MEMBER OF THE SOIL FOOD WEB	Cátia Carreira
PB44	TOTALRNA SOIL METATRANSCRIPTOMICS: SIMULTANEOUS ANALYSIS OF THE ENTIRE ACTIVE SOIL COMMUNITY AND ITS FUNCTIONS.	Athanasios Zervas
PB45	HOW WELL IS THE GLACIER ALGAE ADAPTED TO LIFE ON THE GREENLAND ICE SHEET?	Marie Bolander Jensen
PB46	DEVELOPING NEW BIOINFORMATIC METHODS TO SUPERCHARGE GENOME-CENTRIC METAGENOMICS USING MACHINE LEARNING	Søren Heidelbach
PB47	HUNDREDS OF VIRAL FAMILIES IN THE HEALTHY INFANT GUT	Shiraz Shah
PB48	ACTIVATION AND IDENTIFICATION OF A GRISEUSIN CLUSTER IN STREPTOMYCES SP. CA-256286 BY EMPLOYING TRANSCRIPTIONAL REGULATORS AND MULTI-OMICS METHODS	Charlotte Beck
PB49	VIRAL SIGNATURES ON THE GREENLAND ICE SHEET	Laura Perini
PB50	THE DIVERSITY AND ACTIVITY POTENTIAL OF THE AIR AND SNOW MICROBIOMES IN THE HIGH ARCTIC, AND HOW THEY ARE LINKED THROUGH BIOPRECIPITATION	Lasse Jensen
PB51	APPLICATION OF A NOVEL IN SITU CULTURING APPROACH ON THE GREENLAND ICE SHEET	Ate Jaarsma
PB52	FINDING A NEEDLE IN A WAXSTACK: TRACKING DOWN PAENIBACILLUS LARVAE IN MODERN AND ANCIENT BEESWAX SAMPLES	Guillermo Rangel-Pineros
PB53	VISUALIZATION OF THE INTERNAL PH IN BACTERIAL COLONIES USING A GENETICALLY ENCODED SENSOR PROTEIN AS NOVEL TOOL FOR HIGH-THROUGHPUT SCREENINGS	Gerd Seibold
PB54	LARGE-SCALE IDENTIFICATION OF PHAGE-INDUCIBLE CHROMOSOMAL ISLANDS	Asker Brejnrod
PB55	REWIRING METABOLIC FLUX FOR EFFICIENT PRODUCTION OF AROMATIC AMINO ACIDS AND DERIVATIVES FROM LIGNOCELLULOSIC BIOMASS.	Sheila I. Jensen
PB56	ISOLATION, CHARACTERIZATION AND GENOMES OF NOVEL YEASTS FROM THE INTESTINAL TRACT OF TERMITES	Guangshuo Li
PB57	TRANSPORT OF MICROORGANISMS VIA WORK CLOTHES - DO WE TAKE MICROORGANISMS WITH US?	Signe Møller

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