Programme & Abstracts

The Danish Microbiological Society

Annual Congress 2019

11 NOVEMBER 2019

EIGTVEDS PAKHUS

COPENHAGEN · DENMARK

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Index

Programme

09.00	**Registration, poster mounting and coffee**		
	ROOM II *Second floor*	**ROOM III** *Second floor*	
10.00	**Welcome and opening address by DMS President** Carsten Suhr Jacobsen	**Welcome and opening address by DMS Vice-president** Trine Rolighed Thomsen	
10.15	**[O01] Citizen science in systematic and applied microbiology** Speaker: Preben Nielsen, Novozymes	**[O02] Vaccine hesitancy – a major threat for global health** Speaker: Kåre Mølbak, Statens Serum Institut	
10.45	**Coffee and exhibition** *First & second floor*		
	PARALLEL SESSIONS		
	ROOM II *Second floor*	**ROOM III** *Second floor*	**ROOM IV** *Second floor*
	Biodiversity and biogeography Chair: Per Halkjær Nielsen, Aalborg University DMS co-chair: Trine Thomsen, Teknologisk Institut	**Vaccines** Chair: Anders Miki Bojesen, University of Copenhagen DMS co-chair: Mette Burmølle, University of Copenhagen	**Microbial food web in soil** Chair: Tim Urich, Universität Greifswald DMS co-chair: Carsten Suhr Jacobsen, Aarhus University
11.00	Chair introduction	Chair introduction	Chair introduction
11.05	**[O03] Microflora Danica meets Earth Microbiome Project** Per Halkjær Nielsen, Aalborg University & Daniel McDonald, University of California, San Diego, USA	**[O06] Preventing disease and antimicrobial use in animals by vaccination** Anders Miki Bojesen, University of Copenhagen	**[O09] Predatory bacteria in soil: key-stone taxa of microbial foodwebs?** Tim Urich, Universität Greifswald, Germany
11.30	**[O04] Project SoilTracker - solving crimes with soil-microbiodiversity** Tobias Guldberg Frøslev, Centre for GeoGenetics, University of Copenhagen	**[O07] Using viruses to fight viruses – perspectives for future vaccines** Allan Randrup Thomsen, University of Copenhagen	**[O10] Significance of micro-predator diversity in the rhizosphere** Flemming Ekelund, University of Copenhagen
11.45	**[O05] Atmospheric microorganisms in the Arctic** Tina Santl-Temkiv, Aarhus University	**[O08] Adjuvants: From immunologist's dirty little secret to vaccinologist's requisite for success** Dennis Christensen, Statens Serum Institut	**[O11] Patterns of microbiome predator communities at a global scale** Stefan Geisen, Department of Terrestrial Ecology, Netherlands Institute of Ecology, NIOO-KNAW
12.00	**Flash poster presentations (see page 7)**	**Flash poster presentations (see page 7)**	**Flash poster presentations (see page 7)**
12.15	**Lunch** *Salon C, ground floor*		
12.15	**Exhibition** *First & second floor*		
12.35	**GENERAL ASSEMBLY Det Danske Pasteur Selskab** ROOM IV, second floor		
12.45	**POSTER SESSION (EVEN NUMBERS)** *SALON B, ground floor & first floor*		

12:35-13:00	**Bruker Symposium:** **ISO 16140-6 validation of Maldi Biotyper (see p. 31)** *ROOM II, second floor*		
13:10-13:35	**Nordic Biosite Symposium:** **Standardizing microbiomics - removing bias in collection, purification and analyses (see p. 31)** *ROOM II, second floor*		
	PARALLEL SESSIONS		
	ROOM II Second floor	**ROOM III** *Second floor*	**ROOM IV** Second floor
	Big data and deep learning meets microbiology Chair: Mads Albertsen, Aalborg University DMS co-chair: Trine Thomsen, Teknologisk Institut	**Novel antimicrobial therapies** Chair: Ole Højberg, Aarhus University DMS co-chair: Rikke Louise Meyer, Aarhus University	**The challenge of slow growing bacteria** Chair: Peter Stougaard, Aarhus University DMS co-chair: Kasper Nørskov Kragh, University of Copenhagen
13.45	Chair introduction	Chair introduction	Chair introduction
13.50	**[O12] Microbes inside and out** Daniel Mc Donald, University of California San Diego, USA	**[O15] ICARS - The International Center for Antimicrobial Resistance Solutions** Robert Skov, Statens Serum Institut	**[O18] Microbiological and pathogenesis features distinguishing Lyme disease and relapsing fever spirochetes** Sven Bergström, Umeå University
14.15	**[O13] Binning microbial genomes using deep learning** Simon Rasmussen, University of Copenhagen	**[O16] Fecal transplants – the ultimative probiotic for pigs?** Nuria Canibe, Aarhus University	**[O19] Tuberculosis – diagnosis from a laboratory point of view** Dorte Bek Folkvardsen, Statens Serum Institut
14.30	**[O14] Trash to treasure: exploring the wastewater system with high quality MAGs from large-scale Nanopore data** Caitlin Singleton, Aalborg University	**[O17] Local drug delivery to target biofilm infections** Rikke Meyer, Aarhus University	**[O20] Slow-growth and no-growth in natural environment** Hans Røy, Aarhus University
14.45	**Flash poster presentations (see page 7)**	**Flash poster presentations (see page 7)**	**Flash poster presentations (see page 7)**
15.00	**Coffee and exhibition** *First & second floor*		
15.15	**POSTER SESSION (UNEVEN NUMBERS)** *SALON B, ground floor & first floor*		
15:15-15:40	**Leymus Genomics Symposum:** **Long-read single molecule on Illumina instruments for a ground-breaking new level of bacteria identification (see p. 33)** *ROOM II, second floor*		
15:50-16:15	**Clinical Microbiomics Symposium:** **Nothing in biology makes sense except in the light of evolution (see p. 33)** *ROOM II, Second floor*		
16.15	**Pasteur travel grant ceremony** *ROOM III, Second floor*		
16.30	**[O21] Keynote by Kevin Foster** *ROOM III, Second floor* Cooperation and competition in bacteria: from model systems to the microbiome		
17.30	**Reception with fermented beverage** *SALON C, ground floor*		
19.00	**Optional congress dinner** *Spiseloppen, Christiania*		

Flash poster presentations

PARALLEL SESSIONS, MORNING			
	ROOM II *Second floor*	**ROOM III** *Second floor*	**ROOM IV** *Second floor*
	Biodiversity & biogeography	Vaccines	Microbial food web in soil
12.00	[P021] Metagenomics profiling uncovers diversity, ecological success and habitat preference of comammox nitrospira *Barth Smets, Technical University of Denmark*	[P077] Campylobacter phages mimic the host defense strategy by using phase variation to create new phenotypes with modified receptor binding proteins *Martine Sørensen, University of Copenhagen*	[P049] Two novel bacteriophage genera discovered in a groundwater reservoir indicate large predator-prey diversity in subsurface environments *Ole Hylling, Aarhus University*
12.05	[P013] Smoke on the water: Drafting the genome of the pigmented algea mesotaenium berggrenii that darkens the greenland ice sheet *Athanasios Zervas, Aarhus University*	[P101] One size does not fit all; the gap between standardized in vitro biofilm-infected wound models and in vivo clinical settings *Ida Clement Thaarup, University of Copenhagen*	[P050] Biological drivers of bacterial communities in the arctic water inflow region revealed through manipulations of microbial food web interactions *Oliver Müller, University of Bergen*
12.10	[P075] MIDAS 4: A comprehensive reference database of microbes in wastewater treatment systems across the globe *Morten Simonsen Dueholm, Aalborg University*	[P097] Effect of A-hemolysin producing e. coli in two different mice strains/ breads in a dss model to study ibd *Hengameh Chloe Mirsepasi-Lauridsen, Statens Serum Institut*	[P071] Multi-kingdom microbial communities in earthworms *Rumakanta Sapkota, Aarhus University*

PARALLEL SESSIONS, AFTERNOON			
	Big data and deep learning meets microbiology	Novel antimicrobial therapies	The challenge of slow growing bacteria
14.45	[P036] Increasing the phylogenetic resolution of pseudomonas in soil microbiomes by rpod-specific primers *Jonas Greve Lauritsen, DTU Bioengineering*	[P004] Antibacterial cue from ecological neighbor increases holomycin production in photobacterium galatheae *Yannick Buijs, Technical University of Denmark*	[P089] Domain analysis of the cell wall proteinase, lactocepin, of lactococcus lactis *Ida Nynne Laforce, National Food Institute*
14.50	[P037] Big production without the use of antibiotics - impact on the pig resistome and microbiome *Katrine Wegener Tams, DTU Bioengenerring*	[P008] Combination of cannabidiol and bacitracin against resistant bacteria *Claes S. Wassmann, University of Southern Denmark*	[P084] Deep purple: The biological darkening of the greenland ice sheet *Laura Halbach, Aarhus University*
14.55	[P043] Uncovering the hidden diversity of asgard archaea *Jakob Brandt, Aalborg University*	[P002] Potential of a bacteriophage cocktail to treat rainbow trout fry syndrome (RTFS): Comparison of delivery methods *Valentina Laura Donati, Technical University of Denmark*	[P083] The oxygen consumption rate of cable bacteria *Stefano Scilipoti, Aarhus University*

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.

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Speakers' abstracts

[O01] CITIZEN SCIENCE IN SYSTEMATIC AND APPLIED MICROBIOLOGY

Preben Nielsen[1]

[1]*Novozymes, Microbe Technology, Lyngby, Denmark*

"Masseeksperimentet 2018" was an extensive Citizen science project conducted by school children from all over Denmark. We wanted to nurse the interest in biology and biotechnology, show that "good" microbes are surrounding us, and that by relatively simple tools we can show the presence of Lactic Acid Bacteria.

In 3 weeks, 25,000 pupils collected samples and tested for presence of lactic acid bacteria by a simple fermentation experiment. More than 11,000 positive samples were found and submitted to the project. From a subset of 5,000 samples, 12,000 bacterial strains were identified to species level, of which 4000 unique isolates were cultivated, preserved in a strain collection and characterized by shut gun WGS. Based on comparative WGS a subset of the strains could be affiliated to at least 10 novel species. The data were presented to the pupils in a FAST-ANI tree linking up to a map of Denmark showing sample locations and metadata (see bacteriadanica.dk).

[O02] VACCINE HESITANCY - A MAJOR THREAT FOR GLOBAL HEALTH

Kåre Mølbak[1]

[1]*Statens Serum Institute, Department of Infectious Disease Epidemiology, Department of Infectious Disease Epidemiology, Copenhagen, Denmark*

In 2019, WHO identified vaccine hesitancy as one of the ten threats to global health. Thus, vaccine hesitancy ranks among major health threats including ebola and other high-threat pathogens, pandemic influenza, dengue and antimicrobial drug resistance.

Vaccine hesitancy is the reluctance or refusal to vaccinate despite the availability of vaccines, and threatens to reverse progress made in tackling vaccine-preventable diseases. Vaccination is one of the most cost-effective ways of avoiding disease – it currently prevents 2-3 million deaths a year, and a further 1.5 million could be avoided if global coverage of vaccinations improved.

Measles, for example, has seen a 30% increase in cases globally. The reasons for this rise are complex, and not all of these cases are due to vaccine hesitancy. However, some countries that were close to eliminating the disease have seen a resurgence. Weak health care and consequences of conflicts may play an important role - but in many settings, vaccine hesitancy is part of the challenge.

The reasons why people choose not to vaccinate are complex. Lack of awareness of vaccine-preventable diseases, inconvenience in accessing vaccines, belief in advantages of natural infections, and lack of confidence to experts and authorities are key reasons underlying hesitancy. In spite of research that confirm the safety of the MMR vaccine, myths about association between MMR vaccine and autism continues to play a role in the public discourse. In Denmark, concerns about the safety of HPV vaccines caused a temporary set-back for the HPV vaccination programme. This concern was based on case stories that were disseminated by sensationalist media coverage and social media platforms.

Research has not been able to confirm the association between HPV vaccine and adverse events including autonomic dysfunctions. Nonetheless, the concerns seems to linger on as vaccination uptake is not yet back to the level we saw before the crisis.

Suboptimal vaccine coverage should not automatically be framed as vaccine hesitancy. Research shows that vaccine hesitancy is not the major cause for being non-vaccinated in Denmark. While nearly all infants receive the first vaccine at 3 months of age, some parents (in the busy every-day life) simply forget about vaccines when children grow older. We envisage that a new national and "smart" reminder service will serve as a tool to further increase vaccination coverage in Denmark.

[O03] MICROFLORA DANICA MEETS EARTH MICROBIOME PROJECT

Per Halkjær Nielsen[1], Mads Albertsen[2], Daniel A. McDonald[3]

[1]*Aalborg University, Aalborg University, Dep. of Chemistry and Bioscience, Aalborg, Denmark*
[2]*Aalborg University, Center for Microbial Communities, Dept. Chemistry and Bioscience, Aalborg, Denmark*
[3]*University of California, San Diego, United States*

How many microbial species exist on the planet, and how do environments shape their communities? How are they distributed across natural and cultivated habitats on a local and global scale? These are some of the questions the two projects, "Microflora Danica" and "Earth Microbiome Project" are trying to answer. Novel DNA-based sequencing technologies now allow a robust and high-throughput identification of microorganisms in any habitat. Here, we present the plans and first results for Microflora Danica, or "the Microbiome of Denmark", where over the next 3 years we will establish a reference database over "all" microbes in Denmark cross various habitats. In conjunction with the Earth Microbiome Project and The Microsetta Initiative, we applied the same DNA-based sequencing technique to a collection of over 500 samples from a diverse set of geographically distributed environments. These samples include host and non-host associated collections, including multiple distinct human populations, and provide a glimpse of deep bacterial RNA operon diversity at a global scale. We show a recapitulation short read based observations of the 16S gene for the same samples, provide substantial increase in taxon specificity, and describe the distribution operon elements with respect to environmental variables. These data provide a critical expansion to these open-access resources pairing with other rich data generation presently underway for the same Earth Microbiome Project sample set.

[O04] PROJECT SOILTRACKER - SOLVING CRIMES WITH SOIL MICRO-BIODIVERSITY

Tobias Guldberg Frøslev[1]

[1]*Terrestrial Ecology, University of Copenhagen, Denmark*

DNA extracted from environmental samples (eDNA) – especially soil – is beginning to find use in forensic case work. It has been established that using eDNA metabarcoding to derive "biologigal fingerprints" of soils can be used for matching of soil samples. the same kind of data is beginning to be used in provenance prediction of unknown samples. As part of the SoilTracker project we evaluated the performance of different molecular marker for provenancing soil traces of unknown origin. We tested the performance of eDNA metabarcoding of different genetic markers to predict the origin of unknown soil samples, and also to predict habitat characteristics (forest, meadow, agriculture, etc..) of the sample origin. Overall, we achieved good predictions of environmental gradients and habitat classes to derive a relatively accurate description of the "crime scene". Thus, we conclude, that there is a large potential for the use of metabarcoding provenancing of soil trace samples.

[O05] ATMOSPHERIC MICROORGANISMS IN THE ARCTIC

Tina Šantl-Temkiv[1], IPG Marshall[2], C Mignani[3], M Alsved[4], D Beddows[5], M Lever[2], P Starnawski[2], J Löndahl[4], U Gosewinkel[6], R Lange[6], A Massling[6], H Wex[7], K Finster[8]

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[6]*Aarhus University, Department of Environmental Science, Roskilde, Denmark*
[7]*Leibniz Institute for Tropospheric Research, Leipzig, Germany*
[8]*Aarhus University, Department of Bioscience, Microbiology Section, Aarhus University, Stellar Astrophysics Centre, Department of Physics and Astronomy, Aarhus, Denmark*

Arctic is affected by several climatic feedback processes, caused by changes in albedo, sea-ice extent, ice-sheet melt, and glacial retreats, which have an impact on the Arctic radiation budget. Microorganisms dispersing through the atmosphere can affect some of these processes, either by their role in cloud formation or by changing the albedo, and consequently the melt processes of icy surfaces. In addition, melting of terrestrial ice opens up new environments for microbial colonization and succession. For all these reasons, the Arctic is of special interest for aeromicrobiology[1]. We performed several field campaigns at different locations in the Arctic, i.e. Nuuk Basic Research Station, Villum Research Station and during a cruise in Baffin Bay to investigate bacterial diversity, sources and environmental impacts of airborne microbial communities. We collected air samples with high-volume impingers[2] and on filters, precipitation samples and potential local terrestrial and marine source samples[3,4]. Samples were investigated for (i) bacterial concentrations using cell counts and qPCR targeting 16S rRNA genes, (ii) concentration of total and proteinaceous ice-nucleation particles, (iii) community composition of total and active bacterial communities using next generation sequencing of 16S rRNA molecules and genes. Selected results of these studies will be presented that reveal latitudinal and seasonal trends in the concentrations of airborne bacteria, their predominant terrestrial and marine sources and their airborne activity, in particular in relation to their climatic relevance.

Key words: airborne bacteria – atmospheric dispersal – Arctic atmosphere – bacterial activity –biogenic ice nucleating particles

References

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[O06] PREVENTING DISEASE AND ANTIMICROBIAL USE IN ANIMALS BY VACCINATION

Anders Miki Bojesen[1]

[1]*University of Copenhagen, Department of Veterinary Disease Biology, Frederiksberg C, Denmark*

Bacteria are common causes of disease in animals kept for food production. For more than a 100 years prevention of disease by vaccination has been an option employed to increase animal welfare and production yield. With the advent of antimicrobials prevention of bacterial infections by vaccination was significantly less popular yet with the rise of antimicrobial resistance renewed interest has been placed in research and development of vaccines targeting bacteria.

Two major challenges to veterinary vaccine development include a considerable antigenic variation within individual bacterial species and a requirement of a very low production cost in order to allow an economically viable product. Regarding antigenic variation many animal pathogens contain from a few to several hundred serotypes, each of which in principle would require an individual vaccine to ensure protection against disease. For this reason the practical implementation of vaccination at farm level has been focused on the most prevalent serotypes knowing that other types could represent a risk. Current vaccine research is therefore highly aware of the need for broad scope vaccines that cover broader than just one or a few serotypes. As profit margins in the animal production generally are very small any intervention like vaccination need to be cheap to be justified economically. This not only applies to the cost of the actual vaccines but also the cost of administering the vaccine. Having to inject a vaccine into each and every animal is not an option *e.g.* in a poultry flock of 50.000 individuals. Technological advances allowing mass administration of vaccines while securing proper stimulation of a protective immune response is thus a very important requirement.

Finally, the trend of moving production animals back to their natural habitat as happens in free-range or organic production systems re-introduce a much broader spectrum of disease causing microorganism including bacteria, demands a considerably more elaborate prevention effort.

[O07] USING VIRUSES TO FIGHT VIRUSES – PERSPECTIVES FOR FUTURE VACCINES

Allan Randrup Thomsen[1]

[1]*University of Copenhagen, Department of Immunology and Microbiology, Copenhagen, Denmark*

Most current vaccines work through the induction of humoral immune responses resulting in the production of protective antibodies. However, protection against a number of important human infections like HIV and hepatitis C also require the generation of cell-mediated immunity; even in the case a viral infection like flu, a cell-mediated immune response is likely to improve protection. We therefore need vaccines, which are capable of inducing potent and long-standing T-cell mediated immunity. While live attenuated vaccines will do that, newer split vaccines are generally not efficient in raising efficient cell-mediated immunity. Returning to our original roots, the next generation of vaccines are therefor likely to involve various vector based, but replication impaired vaccines that mimic the antigen presentation associated with live bacteria or viruses. Examples of this line of thinking will be presented.

[O08] ADJUVANTS: FROM IMMUNOLOGIST'S DIRTY LITTLE SECRET TO VACCINOLOGIST'S REQUISITE FOR SUCCESS

Dennis Christensen[1]

[1]*Statens Serum Institute, Copenhagen S, Denmark*

Novel vaccine strategies include the so-called subunit vaccines, which encompass only the part of the pathogen to which immune recognition results in protection. The high purity of these vaccines make adverse events less likely, but it also makes the vaccines less immunogenic and therefore potentially less effective. Vaccine adjuvants that increase and modulate the immunogenicity of the vaccine are therefore added to solve this problem. Besides aluminum salts, which have been used in vaccines for 90 years, a number of novel vaccine adjuvants include delivery systems like liposomes and emulsions have been included in licensed vaccines over the last 30 years. However trial-and-error has been the explorative approach of choice, for the design of novel vaccine adjuvants due to major gaps in the knowledge about immunological activation processes. Increasing insight into immunological mechanisms and how to manipulate them has replaced empirical with rational design of adjuvants, leading to vaccine adjuvants with increased and customized immunogenicity profiles without compromising vaccine safety. I will present an overview of where vaccine adjuvant research is today.

[O09] PREDATORY BACTERIA IN SOIL: KEY-STONE TAXA OF MICROBIAL FOODWEBS?

Tim Urich[1]

[O10] SIGNIFICANCE OF MICROPREDATOR DIVERSITY IN THE RHIZOSPHERE

Flemming Ekelund[1]

[1]*University of Copenhagen, Denmark*

While food web models of aboveground ecosystems normally operate with well-defined species with well-defined characteristics; and include terms such as generalists and specialists, belowground models assemble organisms in broad trophic groups; e.g. bacteria, protozoa, nematodes. The vast taxon richness belowground is most likely a major reason for this difference. Still, we would probably achieve a much better understanding of the dynamics and functioning of the belowground network if we acknowledged that bacteria, protozoa, nematodes etc. cannot satisfactorily be described in this simplistic way and that, for example, the generalist vs. specialist concept also is relevant when describing underground systems. I will present a few examples that support this point of view and argue that future research that follow this road will be fruitful. In particular, I suggest to search for bacterial specialist and generalist predators from soil, using largely inedible and largely edible bacteria as bait, and to test whether presence of certain specialist predators may provide more diverse and functionally superior bacterial communities.

[O11] PATTERNS OF MICROBIOME PREDATOR COMMUNITIES AT A GLOBAL SCALE

Stefan Geisen[1]

[1]*Netherlands Institute of Ecology (Nioo-Knaw), Wageningen, Netherlands*

The microbiome has a key role in host performance and in environmental functioning. We are increasingly understanding the processes that structure microbiomes with profound efforts in the last years being conducted in soils. Most studies focused on bacteria and fungi, the primary drivers of many processes in soils. Yet, we lack an understanding of larger microbiome components, while often ignoring (trophic) interactions that likely contribute in structuring soil microbiomes. Here I will show the recent advances that help in filling these knowledge gaps. I will highlight work on protists and nematodes, both representing the key predators of bacteria and fungi and as such likely are important in structuring the microbiome. After giving an overview on these groups of organisms, I will show their functional importance and global efforts that aim at deciphering their community structures in soils. Together I will show that this work will help in furthering our knowledge on the global distribution and functioning of soil biodiversity.

[O12] MICROBES INSIDE AND OUT

Daniel McDonald[1], Justin Shaffer[2], Gail Ackermann[2], Yan He[3], Hongwei Zhou[3], Junjun Wang[4], Gabriela Sheets[5], Jordan Bisanz[6], Alexandra Obregon-Tito[7], Gregor Reid[8], Maria Gloria Dominguez-Bello[9], Emily Vogtmann[10], Rashmi Sinha[10], Global Microbiome Conservancy consortium[11], Mathilde Poyet[12], Mathieu Groussin[12], Eric Alm[12], Edgar Diaz[13], Rob Knight[14]

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Populations differ in host genetics, diet, lifestyle and environment. Within that background, unattributed factors drive variation in the gut microbiome. Here, we bring together data from The Microsetta Initiative and the Global Microbiome Conservancy, projects which spans multiple populations, and integrate these data in a meta-analysis with other population datasets that used the Earth Microbiome Project protocols. The combined analysis spans over 30,000 human samples. Specifically, 16S rRNA V4 amplicon data from The Microsetta Initiative and other studies using common molecular protocols were integrated using Qiita. These data recapitulate and extend Yatsunenko et al. (2012, Nature), showing that European, Australian, and North American populations are more similar to one other than each is to South American or sub-Saharan African populations. Unexpectedly, individuals from Bangladesh, the Philippines and Iran exhibit an intermediate relationship between Western and non-Western groupings. These data were then integrated with the Earth Microbiome Project, highlighting the microbial connection between humans and the environment. Defining how populations relate is a critical step in translating microbiome results. This backdrop carries medical implications, as it is presently unknown whether such massive differences in microbial community composition among populations have the potential to modulate microbiome therapies.

[O13] BINNING MICROBIAL GENOMES USING DEEP LEARNING

Jakob Nybo Nissen[1], Joachim Johansen[2], Rosa Lundbye Allesøe[2], Casper Kaae Sønderby[3],
Jose Juan Almagro Armenteros[4], Christopher Heje Grønbech[3], Henrik Bjørn Nielsen[5], Thomas Nordahl Petersen[6], Ole Winther[7], Simon Rasmussen[8]

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[8]*Nnf Center for Protein Research, University of Copenhagen, København N, Denmark*

Despite recent advances in metagenomic binning, reconstruction of microbial species from metagenomics data remains a challenging task. Here we use recent advances in deep learning to develop an algorithm that uses deep variational autoencoders to encode sequence co-abundance and *k*-mer distribution information prior to clustering. We show that our variational autoencoder is able to integrate these two distinct data types without any prior knowledge of the datasets. Our method outperforms existing state-of-the-art binners on contig datasets, reconstructing 127-167% as many precise and complete genomes. Additionally, we developed a multi-sample and splitting strategy, that enables assembly of 23-89% more strains compared to commonly used single binning strategies. Furthermore, our method enables direct high-resolution taxonomic profiling across samples.

Finally, to demonstrate the scalability of our method, we bin a human gut microbiome dataset from 1,000 samples. By employing GPU acceleration for training and clustering we reconstruct 30% more near-complete bins compared to state-of-the-art and even ensemble strategies. Our method Variational Autoencoders for Metagenomic Binning (VAMB) can be run on standard hardware and is freely available at https://github.com/RasmussenLab/vamb.

[O14] TRASH TO TREASURE: EXPLORING THE WASTEWATER SYSTEM WITH HIGH QUALITY MAGS FROM LARGE-SCALE NANOPORE DATA

Caitlin Singleton[1], Martin Andersen[2], Rasmus Kirkegaard[2], Thomas Michaelsen[2], Søren Karst[2], Morten Dueholm[2], Per Nielsen[2], Mads Albertsen[2]

[1]Aalborg University, Centre for Microbial Communities, Department of Chemistry and Bioscience, Aalborg University, Aalborg, Denmark
[2]Aalborg University

Improvements to wastewater resource recovery and treatment efficiency are essential for fulfilling the UN sustainable development goals for both sustainable cities (goal 11) and responsible production and consumption (goal 12). Microbes are central to the processes underpinning wastewater treatment, however knowledge of this complex community is limited to isolates, marker genes or incomplete genomes. To improve our capacity to characterise this community at the genome level, we conducted large-scale long-read sequencing of 23 Danish full-scale wastewater treatment plant (WWTP) metagenomes using the Nanopore PromethION platform, producing >1 Tbp (or 17 TB raw) of long-read data. These data enabled the recovery of 987 metagenome-assembled genomes (MAGs), including 36 circular genomes, after short-read data polishing (>0.9 Tbp Illumina). The recovered MAGs met stringent high-quality draft requirements of >90% completeness, <5% contamination and full-length rRNA genes. The MAGs included known and uncharacterised, abundant and rare lineages, and accounted for 25% of the populations present in the metagenomes. With these MAGs we present a HQ reference database for WWTP systems that will facilitate the connection of genomic potential to historical and future amplicon studies.

[O15] ICARS-THE INTERNATIONAL CENTER FOR ANTIMICROBIAL RESISTANCE SOLUTIONS

Robert Leo Skov[1]

[1]SSI, Microbiology, Denmark

Despite recent global efforts to mitigate the impact of antimicrobial resistance (AMR), information and evidence on the effects of AMR on health and the economy have so far failed to be translated into actions in many parts of the world, especially in low and middle income countries (LMICs). The International Centre for Antimicrobial Resistance Solutions – ICARS – is a new partnership that aims to conduct policy relevant applied research at international, national and local level to identify knowledge and evidence-based solutions in close collaboration with countries and key stakeholders. ICARS will support LMICs to conduct applied research relevant to their local challenges and therefore implementing aspects of their AMR National Action Plans (NAPs). It will aim to bridge the gap between science and policy translating national action plans into evidence based practices on the ground. Projects and activities will aim to build local capacity and capability to sustain and scale up the evidence-based solutions identified. Output will be made accessible and where appropriate in open repositories. ICARS will work internationally as a solution development partnership with projects and activities in various locations around the world. Through its work, ICARS will aim to partner with governmental bodies, policymaker and civil society foundations to support the delivery of the United Nations (UN) General Assembly AMR Resolution agreed in September 2016 and fill some of the gaps in the global response highlighted by the recent recommendations of the UN Inter Agency Co-ordination Group (IACG) on AMR in April 2019. ICARS - will operate as partnership, co-ordinated through, and anchored by, hubs in Denmark, the International Livestock Research Institute (ILRI) based in Kenya, and elsewhere as ICARS expands over time. The partnerships will include research, policy, and technical participation from collaborating countries, academic institutions, and national and international organisations.

[O16] FECAL TRANSPLANTS – THE ULTIMATIVE PROBIOTIC FOR PIGS?

Nuria Canibe[1]

[1]Aarhus University, Tjele, Denmark

It is becoming increasingly evident that the gastrointestinal microbiota has a significant impact on the overall health and performance of the pig. This has led to intensified studies on the composition of the gastrointestinal microbiota, factors affecting it, and the impact of the microbiota on health, growth performance, and more recently, behavior of the host. Pig production research has been heavily focused on assessing the effects of feed additives and dietary modifications to alter or take advantage of select characteristics of gastrointestinal microbes to improve health and feed conversion efficiency. Research on faecal microbiota transplantation (FMT) as a possible tool to improve outcomes in pigs through manipulation of the gastrointestinal microbiome is very recent and limited data is available. Results on FMT in humans demonstrating the transfer of phenotypic traits from donors to recipients and the high efficacy of FMT to treat *Clostridium difficile* infections in humans, together with data from pigs relating gut microbiota composition with growth performance has likely played an important role in the interest towards this strategy in pig production.

There are obvious inherent biosecurity and regulatory issues in this strategy, since the donor's microbiome can never be completely screened for all possible non-desirable microorganisms. However, considering the success observed in humans, it seems worth investigating this strategy for certain applications in pig production.

Further, FMT research may lead to the identification of specific bacteria or bacterial group/s providing improved health, i.e., probiotics, rather than the broader approach applied in FMT. This, besides eventually improving and standardizing the output, would also overcome the biosecurity issues.

[O17] LOCAL DRUG DELIVERY TO TARGET BIOFILM INFECTIONS

Rikke Louise Meyer[1], Raoul Walter[2], Signe Maria Nielsen[2], Pernille Ommen[2], Line Hansen[2],
Hieu Quang[3], Jørgen Kjems[2], Alexander Zelikin[4], Rikke Christiansen[5]

[1]Interdiciplinary Nanoscience Centre (Inano), Faculty of Science and Technology, Aarhus University, Aarhus, Denmark
[2]Interdisciplinary Nanoscience Center (Inano), Aarhus University, Aarhus, Denmark
[3]Aarhus University, Denmark
[4]Department of Chemistry, Aarhus University, Aarhus C
[5]Interdisciplinary Nanoscience Center (Inano), Aarhus University, Denmark

Antibiotic treatment of biofilm infections often fail because the dose that can be administered safely is insufficient to eradicate the biofilm. We hypothesize that treatment will be more effective if drugs are delivered or synthesized at the site of infection, leading to a high local concentration with minimal side effects. We aimed at delivering a high local dose of antibiotics through two different approaches: i) targeted delivery of encapsulated antibiotics, and ii) local drug synthesis through prodrug therapy.

Targeted drug delivery uses drug encapsulation, accumulation in the biofilm, and a triggered burst release. We encapsulated vancomycin and rifampicin in temperature-sensitive liposomes decorated with aptamers that bind *Staphylococcus aureus*. Accumulation, drug release, and kill efficiency was quantified on *S. aureus* biofilms.

Prodrug therapy uses immobilized enzymes to convert non-toxic prodrugs to the active drug. We developed a novel method for synthesizing glucuronide prodrugs, opening the door for antimicrobial prodrug therapy. We immobilized the catalyst (β-glucuronidase) in a layer-by-layer coating on titanium implants. Glucuronide prodrugs of moxifloxacin was administered in solution, and the effect on *S. aureus* viability and biofilm formation was quantified.

Aptamer-targeted liposomes accumulated in *S. aureus* biofilms, resulting in eradication of biofilms in vitro, while non-targeted liposomes were less effective. Although this result is promising, the burst release offers little control over dosage and exposure time. We therefore proceeded with prodrug therapy. The embedded enzyme continuously converted the prodrug to moxifloxacin at the implant surface, which prevented biofilm formation, even under flow.

Targeted drug delivery and pro-drug therapy enable local antibiotic therapy. Drug the exposure time and concentration is better controlled in prodrug therapy, and we believe that our encouraging results will pave the way for implementing more potent drugs that target persister cells in treatment of biofilm infections.

[O18] MICROBIOLOGICAL AND PATHOGENESIS FEATURES DISTINGUISHING LYME DISEASE AND RELAPSING FEVER SPIROCHETES

Sven Bergstrom[1]

[1]Molecular Biology, Umeå University, Umeå, Sweden

The recent proposal of splitting the genus *Borrelia* into two genera in the newly formed family of Borreliaceae, i.e. *Borrelia* and *Borreliella* has motivated us to reflect upon how these organisms has been characterized and differentiated. Herein we therefore aim to take a closer look on the biology and virulence attributes of the two suggested genera, i.e. those causing Lyme borreliosis and relapsing fever borreliosis, respectively.

In fact, both these genera has a lot in common with similar infection biology features . They are both characterised as bacterial zoonoses, transmitted by hematophagous arthropods with almost identical microbiological appearance. Nevertheless, a closer look at their genotypic and phenotypic characteristics clearly reveals several differences that might motivate the suggested split. On the other hand, a change of this well-established classification within the genus *Borrelia* might impose an economical burden as well as a great confusion in the society, including medical and scientific societies as well as the general population.

[O19] TUBERCULOSIS–DIAGNOSIS FROM A LABORATORY POINT OF VIEW

Dorte B. Folkvardsen[1]

[1]Statens Serum Institut, International Reference Laboratory of Mycobacteriology, Copenhagen S, Denmark

Mycobacteria are a diverse group of actinobacteria, comprising more than 100 species. The most well-known and well characterized, *Mycobacterium tuberculosis* (Mtb), is the causative agent of tuberculosis (TB). Other species are *Mycobacterium leprae*, causing leprosy and non-tuberculous mycobacteria (NTM) that are common in the environment and some of them are opportunistic pathogens.

It is not an easy group of bacteria to culture, ranging from a few days to positive culture for the NTM fast growers, to 56 days until a negative culture for the majority, to the almost-impossible-to-grow *Mycobacterium leprea.*
Tuberculosis is the number one cause of death related to an infectious disease, recently it has surpassed HIV/AIDS.

The quest for the fastest way to diagnose TB in the lab is still ongoing, and a number of molecular tests to rapid detection in primary specimens have been developed. However, the sensitivity is still lower than for culture, which besides taking several weeks, requires expensive equipment, specialized media, and skilled personnel. A big portion of the analyzes applied to TB specimens, are still delayed until sufficient growth of an isolated culture is obtained.

Mtb is an enigma -a slow growing, not very contagious, hard to culture bug, with huge success worldwide.

Speakers' abstracts

[O20] SLOW-GROWTH AND NO-GROWTH IN NATURAL ENVIRONMENT

Hans Røy[1]

[1]*Institute for Bioscience, Aarhus University, Aarhus C, Denmark*

Research within the ocean drilling projects have demonstrated large populations of prokaryotes that live deep below the seafloor under extreme energy limitation. These organisms are not merely the dying remains of the once thriving surface community, but cells that live in a delicate balance with the flux of energy that can be harvested from slow degradation of ancient organic material. The community composition is distinctively different from that of the energy rich and dynamic sediment surface, but the transition between the two occur only 10 cm below the seafloor. Close examination of the ratio between community size and community respiration confirms that the energy available for the individual organisms this close to the seafloor is just as meager as for those that have been buried for millions of years without resupply of organic substrates. This demonstrate a life strategy linked to cellular metabolism far below what we know from laboratory cultures, which is still distinct from dormancy. This this type of organisms are not restricted to exotic niches buried deeply below the seafloor. They can be studied with relative ease in sedimentary environments where they constitute a dominating fraction of the community. In environments where they co-exist with fast growing types, however, their activity may easily escape detection.

Keynote abstract

[O21] COOPERATION AND COMPETITION IN BACTERIA: FROM MODEL SYSTEMS TO THE MICROBIOME

Kevin Foster[1]

[1]*University of Oxford, Oxford, United Kingdom*

Microbes display a dizzying array of social traits, from enzymes released to break down nutrients and antibiotics, through slimey secretions that protect and disperse, to draconian molecular machines that stab, rupture and poison their competitors. But what determines whether microbes cooperate or compete with each other, and how does this affect their hosts? To answer these questions, we combine theory and experiments with pathogenic bacteria and the mammalian microbiome. This has revealed that clonemate patches naturally emerge in microbial communities, which favours strong cooperation by kin selection. But interactions between strains and species are often competitive. We find that bacteria are often at war and are even capable of reciprocation, detecting incoming attacks and responding collectively in devastating counterattacks. Microbial interactions follow the same evolutionary principles that were first understood through the study of animal behavior. However, one fascinating property of microbes is that their entire ecosystem can lie within another evolving organism – a host - that is trying to control them and their interactions. The result appears to be a complex coevolutionary dance with the host and its immune system on one side, and the whole microbiota on the other.

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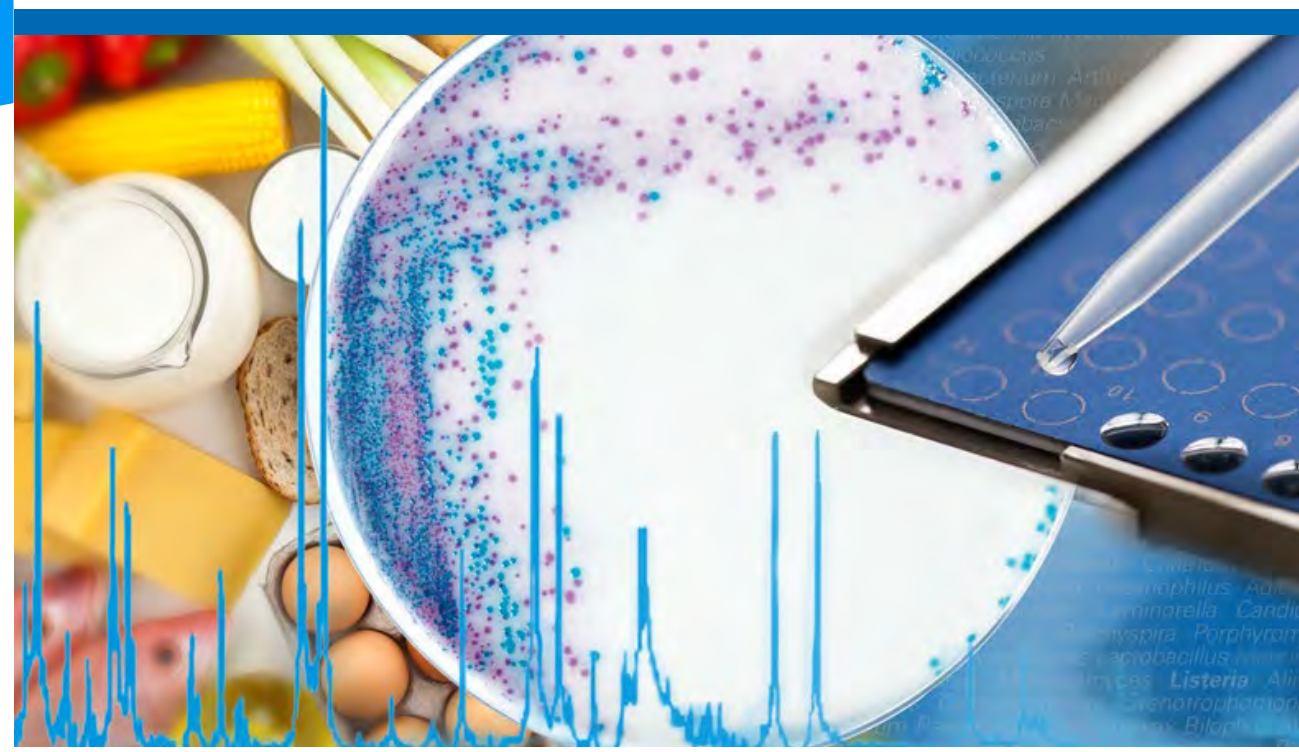

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Industry symposia

Bruker symposium

ISO 16140-6 validation of MALDI Biotyper

Time: 12.35-13.00
Room: Room II, second floor
Speaker: Erik Dahm, Fødevarestyrelsen

ISO 16140-6 validation of MALDI Biotyper

- Microbiology of the food chain — Method validation — Part 6: Protocol for the validation of alternative (proprietary) methods for microbiological confirmation and typing procedures
- Microval – An international certification organisation
- The validation protocol
- The validation of MALDI Biotyper

Nordic Biosite Symposium

Standardizing Microbiomics – Removing Bias in Collection, Purification and Analyses

Time: 13.10-13.35
Room: Room II, second floor
Speaker: Julia Kappel, Zymo Research

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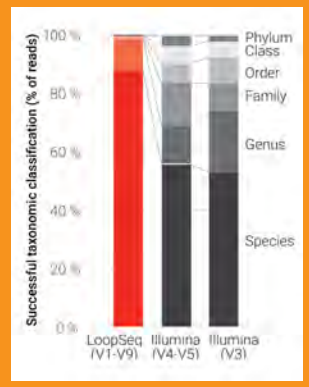

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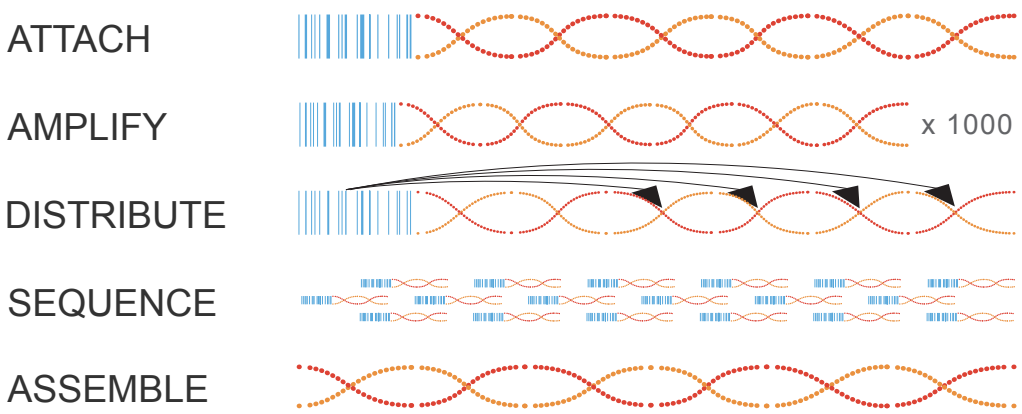

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Industry symposia

Leymus Genomics Symposium

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Time: 15.15-15.40
Room: Room II, second floor
Speaker: Rasmus Brøndum, Founding CEO of Leymus Genomics

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Clinical Microbiomics Symposium

Nothing in Biology Makes Sense Except in the Light of Evolution

Time: 15.50-16.15
Room: Room II, second floor
Speaker: Henrik Bjørn Nielsen, PhD, Chief Scientific Officer at Clinical Microbiomics

clinical microbiomics

Clinical-Microbiomics offers custom-tailored microbiome research as a service, including data-generation and bioinformatics analysis. Here we present our framework for ultra-high resolution (UHR) microbiomics. UHR microbiomics allows us to accurately profile the microbial composition of samples and to build phylogenetic trees that relate sub-species populations across samples and subjects. Phylogenetic trees elegantly condense vast amounts of details into simple data-structures that can be used for statistical analysis and for deriving functional insights. Moreover, it allows us to track therapeutic strains, to monitor microbial population dynamics, and even to gain insight to microbial inherence of accessory genes.

Poster sessions and Poster Index

The posters will be presented at two different breaks – please see the schedule. If you have a poster at DMS 2019, please be present during the assigned time according to your poster number.

Time	Numbers
12:45 - 13:45	Even numbers
15:15 - 16:15	Uneven numbers

Poster no.	Title	Presenter
Antimicrobial compounds and therapies		
P001	ISOLATION AND CHARACTERIZATION OF NOVEL CLOSTRIDIUM PERFRINGENS BACTERIOPHAGE SUSFORTUNA	Julie Stenberg Pedersen
P002	POTENTIAL OF A BACTERIOPHAGE COCKTAIL TO TREAT RAINBOW TROUT FRY SYNDROME (RTFS): COMPARISON OF DELIVERY METHODS	Valentina Laura Donati
P003	ANTIMICROBIAL ACTIVITY ANALYSIS OF SILVER NANOPARTICLES FROM GINKO BILOBA	Arvind Kumar Yadav
P004	ANTIBACTERIAL CUE FROM ECOLOGICAL NEIGHBOR INCREASES HOLOMYCIN PRODUCTION IN PHOTOBACTERIUM GALATHEAE	Yannick Buijs
P005	THE ROLE OF ELLAGIC TANNINS TO REDUCE ANTIBIOTICS TREATMENTS IN PIG HERDS FROM 300% TO 10%	Klaus Sall
P006	A MODIFIED ISOLATION CHIP FOR IN SITU CULTIVATION AND ISOLATION OF ANTIMICROBIAL DRUG-PRODUCING BACTERIA FROM SOCIAL SPIDER NESTS	Seven Nazipi
P007	ISOLATION AND CHARACTERIZATION OF BACTERIOPHAGES TARGETING ESBL-PRODUCING E. COLI IN DANISH PRIMARY PRODUCTION	Amira Vitt
P008	COMBINATION OF CANNABIDIOL AND BACITRACIN AGAINST RESISTANT BACTERIA	Claes S. Wassmann
P009	GENETIC POTENTIAL FOR SECONDARY METABOLITE BIOSYNTHESIS IN THE NEST MICROBIOME OF SOCIAL SPIDERS	Lasse Jensen
P010	REMOVAL OF ANTIBIOTICS AND ANTIBIOTIC RESISTANCE-PROMOTING PHARMACEUTICALS IN A COLUMN STUDY SIMULATING MANAGED AQUIFER RECHARGE (MAR)	Jakub Modrzynski
P011	ISOLATION OF NOVEL PHAGES TARGETING PSEUDOMONAS SYRINGAE	Jacob Bruun Jørgensen
P012	EXTENDED MIC VALUES: DETERMINING TENTATIVE EPIDEMIOLOGICAL CUT-OFF VALUES FOR ANTIBIOTICS IN BACTERIAL MINK PATHOGENS	Nanett Kvist Nikolaisen
Microbial – omics		
P013	SMOKE ON THE WATER: DRAFTING THE GENOME OF THE PIGMENTED ALGEA MESOTAENIUM BERGGRENII THAT DARKENS THE GREENLAND ICE SHEET	Athanasios Zervas
P014	UNIVERSAL DERMAL MICROBIOME IN HUMAN SKIN	Lene Bay
P015	POST TRANSCRIPTONAL CLEAVAGE OF CELL-CYCLE RGEGULATOR CTRA BY TOXIN-ANTITOXIN SYSTEM HIGBA IN CAULOBACTER CRECENTUS	Koyel Ghosh
P016	INVESTIGATING FUNGAL ADAPTATIONS TO EXTREME ENVIRONMENTS USING HERBARIUM SPECIMENS	Benjamin Conlon
P017	PRENATAL DIETARY SUPPLEMENTS INFLUENCE THE INFANT AIRWAY MICROBIOTA IN A RANDOMIZED FACTORIAL CLINICAL TRIAL	Mathis Hjelmsø
P018	ASSESSING VERTICAL TRANSMISSION AND CONFLICT AMONGST GUT BACTERIAL SYMBIONTS IN TERMITES	Justinn Hamilton Renalias
P019	FACETS OF DIAZOTROPHY IN THE OMZ OFF PERU REVISITED: WHAT WE COULD NOT SEE FROM A SINGLE MARKER GENE APPROACH	Christian Christiansen

Poster index

Poster no.	Title	Presenter
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P021	METAGENOMICS PROFILING UNCOVERS DIVERSITY, ECOLOGICAL SUCCESS AND HABITAT PREFERENCE OF COMAMMOX NITROSPIRA	Barth Smets
P022	THE INFLUENCE OF THE ENVIRONMENT ON THE POTENTIAL FOR NATURAL PRODUCT BIOSYNTHESIS	Aileen Geers
P023	A NOVEL AND DIRECT MOBILOME APPROACH IMPROVES THE DETECTION OF LARGER-SIZED CIRCULAR ELEMENTS ACROSS KINGDOMS	Katrine Skov Alanin
P024	SPECIES DETERMINATION OF NONTUBERCULOUS MYCOBACTERIA (NTM) BASED ON CORE SEQUENCES OF THREE GENES IN A MULTIPLEX PCR	Erik Michael Rasmussen
P025	THE GUT, ORAL, AND NASAL MICROBIOTA IN PEDIATRIC ALLOGENEIC HSCT AND PREDICTION OF ACUTE GVHD	Anna Ingham
P026	PHYLOGENY AND SECONDARY METABOLITE GENE CLUSTERS FROM THE TERMITE FUNGAL CROP TERMITOMYCES.	Suzanne Schmidt
P027	ACTINOBACTERIA: GENOME SEQUENCING AND ASSEMBLY	Tue Jørgensen
P028	INVESTIGATION OF SMALL, CIRCULAR DNA ELEMENTS REVEAL TRANSPOSITION FREQUENCY AND MECHANISMS OF MOBILE GENETIC ELEMENTS AND THEIR POTENTIAL INVOLVEMENT IN RESISTANCE DEVELOPMENT	Tue Nielsen
P029	GLOBAL GENOME-CENTRIC METATRANSCRIPTOMICS UNRAVELS FOOD WEBS IN COMPLEX MICROBIAL COMMUNITIES	Thomas Yssing Michaelsen
Microbial ecology		
P030	MICROBIAL DIVERSITY IN SUBTROPICAL BEACHROCK	Aidas Marijus Vysniauskas
P031	WHAT MAKES A "CULT-WINE"? PRODUCTION-CHAIN MICROBIAL DIVERGENCES IN VINEYARDS AND WINES FROM RIBERA DEL DUERO	Alex Gobbi
P032	RESCUING ROLE OF STAPHYLOXANTHIN IN MIXED MICROBIAL COMMUNITIES	Rune Overlund Stannius
P033	THE POTENTIAL OF SOIL-BORNE BIOCONTROL AGENTS: ELUCIDATING THE FUNCTION, VARIATION AND BIOCONTROL POTENTIAL OF SECONDARY METABOLITES BY BACILLUS SUBTILIS ISOLATES	Heiko Thomas Kiesewalter
P034	BACILLUS SUBTILIS BIOFILM FORMATION AND EVOLUTION ON PLANT ROOTS	Mathilde Nordgaard
P035	STUDYING B. SUBTILIS IN ROOT COLONIZATION OF DIFFERENT PLANT SPECIES	Christopher Blake
P036	INCREASING THE PHYLOGENETIC RESOLUTION OF PSEUDOMONAS IN SOIL MICROBIOMES BY RPOD-SPECIFIC PRIMERS.	Jonas Greve Lauritsen
P037	PIG PRODUCTION WITHOUT THE USE OF ANTIBIOTICS - IMPACT ON THE PIG RESISTOME AND MICROBIOME	Katrine Wegener Tams
P038	A BROAD-HOST RANGE, READILY PROGRAMMABLE CAS9 NUCLEASE DELIVERY VECTOR FOR RAPID AND PREDICTABLE PLASMID-CURING OF NATURAL ISOLATES	Sarah Camara Wilpert
P039	THE ROLE OF MOBILE GENETIC ELEMENTS AND BACTERIOPHAGES IN PORCINE ENTEROTOXIGENIC ESCHERICHIA COLI (ETEC) VIRULENCE AND ECOLOGY.	Michela Gambino

Poster no.	Title	Presenter
P040	WASTEWATER BIOFILMS: HOW SOCIAL INTERACTIONS INFLUENCE BIOFILM FORMATION BY WASTEWATER BACTERIA	Ana Silva
P041	OPTIMIZING HOST SURVIVAL STRATEGY THROUGH RAPID PROPHAGE EVOLUTION	Anna Dragos
P042	DIVERSITY, LOCALIZATION, AND MICROENVIRONMENTS OF THE SPECIFIC BACTERIAL SYMBIONTS OF SOCIAL SPIDERS (STEGODYPHUS DUMICOLA) DIVERSITY, LOCALIZATION, AND MICROENVIRONMENTS OF THE SPECIFIC BACTERIAL SYMBIONTS OF SOCIAL SPIDERS (STEGODYPHUS DUMICOLA)	Tobias Sandfeld
P043	UNCOVERING THE HIDDEN DIVERSITY OF ASGARD ARCHAEA	Jakob Brandt
P044	CLOACAL SWABS AND ALCOHOL BIRD SPECIMEN ARE GOOD PROXIES FOR COMPOSITIONAL ANALYSES OF GUT MICROBIAL COMMUNITIES OF WILD BIRDS	Kasun Bodawatta
P045	EXPERIMENTAL EVOLUTION ON PLANT ROOT SHAPES GENO- AND PHENOTYPIC ADAPTION OF BACILLUS THURINGIENSIS	Yicen Lin
P046	IMAGING NEAR-INFRARED RADIATION DRIVEN PHOTOSYNTHESIS OF CHLOROPHYLL F-CONTAINING CYANOBACTERIA IN BEACHROCK BIOFILMS	Maria Mosshammer
P047	ROLE OF THE SOLONAMIDES IN PHOTOBACTERIUM GALATHEAE S2753	Laura Louise Lindqvist
P048	MUTATION ACCUMULATION EXPERIMENT SHOWS HIGH EVOLVABILITY IN P. AERUGINOSA.	Igor Grekov
P049	TWO NOVEL BACTERIOPHAGE GENERA DISCOVERED IN A GROUNDWATER RESERVOIR INDICATE LARGE PREDATOR-PREY DIVERSITY IN SUBSURFACE ENVIRONMENTS	Ole Hylling
P050	BIOLOGICAL DRIVERS OF BACTERIAL COMMUNITIES IN THE ARCTIC WATER INFLOW REGION REVEALED THROUGH MANIPULATIONS OF MICROBIAL FOOD WEB INTERACTIONS	Oliver Müller
P051	DICKEYA DADANTII PHAGE AMAETHON DEMONSTRATES A WIDESPREAD OCCURRENCE OF 5-METHYLCYTOSINE MODIFICATIONS IN PHAGE GENOMES	Amaru Djurhuus
P052	DISCOVERY OF NOVEL CLASS 1 AND CLASS 2 CRISPR-CAS INHIBITORS THAT CROSS SUB-TYPE BARRIERS	Rafael Pinilla
P053	PLASMIDS PERSIST IN A MICROBIAL COMMUNITY BY PROVIDING FITNESS BENEFIT TO MULTIPLE PHYLOTYPES	Liguan Li
P054	THE IMPACT OF PLASMID HOST RANGE ON THE DISSEMINATION OF ANTIBIOTIC RESISTANCE GENES TO THE URBAN WASTEWATER MICROBIOME	Asmus Olesen
P055	GASTRIC CORE MICROBIOME OF THE CORAL GALAXEA FASCICULARIS	Cecilie Ravn Gøtze
P056	AN EASILY MODIFIABLE CONJUGATIVE PLASMID FOR STUDYING HORIZONTAL GENE TRANSFER	Qinqin Wang
P057	PREVALENCE OF HAEMOSPORIDIAN PARASITES IN BIRDS ALONG ABIOTIC GRADIENTS.	Celia Vinagre-Izquierdo
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