Section of Microbiology
Universitetsparken 15, Build 1,
DK-2100, Copenhagen Ø

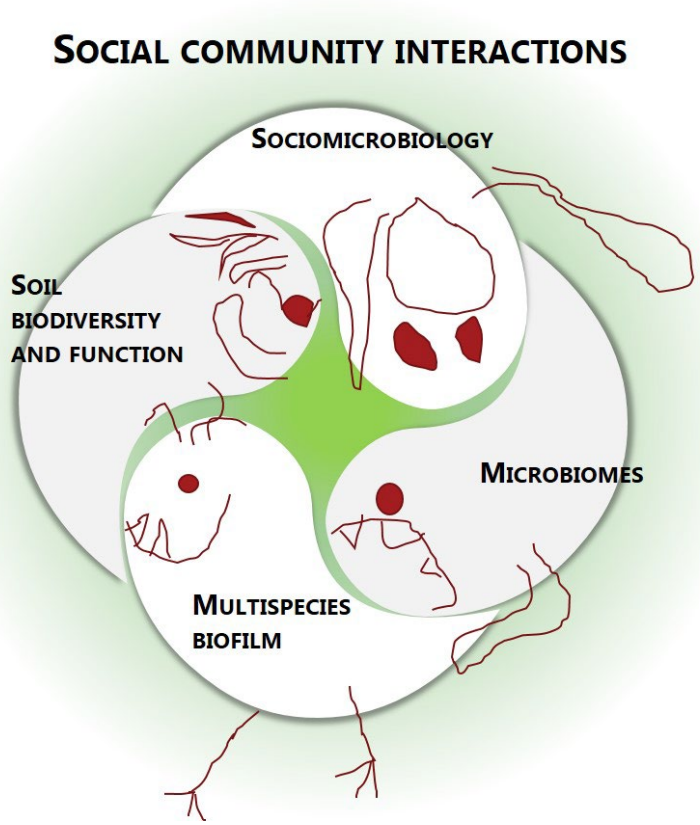
2022

Find more information on https://www1.bio.ku.dk/english/research/microbiology/studying-microbiology/

Student projects at the Section of Microbiology

Below is a list of suggested bachelor and master projects along with smaller student projects ("fagprojekter") in the Section of Microbiology. Students are in our perspective co-researchers, and we are always looking for new input and ideas, so feel free to contact us, if you have an idea to a project, that we have not yet thought about ourselves.

At the SECTION OF MICROBIOLOGY, we are working to understand and exploit the immense functional diversity and adaptive potential of natural microbial communities using cutting-edge molecular techniques. We do that under the 4 headlines you can see below.



Soil biodiversity and function

Write a project on Soil biodiversity and function

Project type: PUK, Bachelor, Master

Soils form the foundations for plant life, including crops. Soils also contain the majority of known and unknown microbial life. Nowhere else is life so complex – and so challenging to study.

Our research focusses on globally important soil systems, mainly Arctic permafrost soils, arable soils in temperate regions, and soils in deserts and other drylands. The bacteria and fungi in these soils have profound impact on not only plant productivity, but also the emission of carbon dioxide and other greenhouse gases to the atmosphere. We combine DNA- and RNA-based techniques with measurements of greenhouse production and consumption to understand the responses of microbial activity to climate change and its importance for future plant productivity. Our experimental approaches involve e.g. thawing of permafrost soil under controlled conditions in the laboratory, drying and/or wetting of drought-prone soils, and ecosystem manipulations in Greenland mimicking future climate change in the Arctic; the latter done under the banner of Center for Permafrost (www.CENPERM.ku.dk), a Center of Excellence financed by the Danish National Research Foundation.

Microbiology of thawing permafrost
Due to global warming permafrost is thawing. This increases microbial decomposition of the enormous stocks of organic material and increases emission of greenhouse gases. You may investigate how bacteria and fungi react to extremely low temperatures or to global change experiments in the field.

A project may include:
Assays for enzymes involved in production or consumption of greenhouse gases
PCR amplicons
Sequencing (only masters)
(Meta)transcriptomics (only masters)

Keywords: Biodiversity, climate change, bacterial activity

Supervisor: Anders Priemé, email: aprieme@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/soil-biodiversity-and-function/

Sociomicrobiology

Write a project on Sociomicrobiology

Project type: PUK, Bachelor, Master

Examples of proposed projects:

Exploiting evolution: Designing microbial interactions for industrial scenarios

This project will address the use of microbial communities to maintain increased food and energy production in an environmentally friendly and sustainable way.

We are planning to isolate and identify microbial communities (bacteria or fungi) to construct synthetic microbial consortia to help in bio-industrial processes and support Europe's developing bio-economy.

A project may include:
Microcosms enrichment
Fluorescent activated cell sorting
Classic culturing
Enzymes activities
PCR and qPCR analysis
Metagenome and metatranscriptome
sequencing and bioinformatic analysis

Keywords: Next generation sequencing, bioinformatics, bio-industry

Horizontal gene transfer - Spread of antibiotic resistance.

Increased antibiotic resistance in a wide range of human pathogens is a growing public health threat. This rapid spread of antibiotic resistance genes is mediated by mobile genetic elements like plasmids, which can be rapidly transferred between microorganisms.

We study plasmid transfer in various natural environments such as wastewater, soil and animal model systems.

A project may include:
Microcosms / Animal model systems
Genetically engineering
Fluorescent activated cell sorting
Metagenome sequencing
Bioinformatic analysis

Supervisor: Søren Sørensen, email: sjs@bio.ku.dk & Jonas Stenløkke Madsen, email: jsmadsen@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/sociomicrobiology/

Kortlægning af diversiteten af kloak-associerede bakteriearter

Normalt anser man CPE for at spredes via direkte patient-til-patient kontakt og det er ikke afklaret hvor stor en andel, der kan tilskrives smitte fra afløb. Dette ønsker vi med dette projekt at få klarhed over.

Projekttype: Master

Baggrund:
I den nationale overvågning af carbapenem-resistente enterobakterier (CPE) ser vi relativt ofte udbrud af visse typer bakterier, der normalt også kan findes i kloakker og afløb. Vi har i flere tilfælde kunne spore specifikke CPE udbrud tilbage til netop disse afløbs-reservoirs. Normalt anser man CPE for at spredes via direkte patient-til-patient kontakt og det er ikke afklaret hvor stor en andel der kan tilskrives smitte fra afløb. For at kunne uddybe dette spørgsmål nærmere, ønsker vi på sigt at lave en kortlægning af hhv. samfunds- og hospitalsreservoirs og efterfølgende bakteriel typning som beskrevet nedenfor. Men for at dette kan lade sig gøre skal der udvikles egnede metoder til prøvetagning og hurtig-screening af fundne isolater.

Formål:

1. At udvikle en metode til at isolere klinisk relevante bakterier (primært Citrobacter spp, Enterobacter spp og Klebsiella spp. Og evt også E. coli) fra kloakker
2. At afprøve en simpel PCR-typningsmetode til at opdele isolater fra kloakker/afløb i klonale grupper.
3. At sekventere og sammenligne udvalgte isolater fra kloakken og sammenligne disse med tilsvarende isolater fra vores nationale CPE overvågning.

Hypotese:

1. At afløb er tilholdssted for klinisk relevant bakterier som Citrobacter spp, Enterobacter spp og Klebsiella spp. (og måske E. coli også).
2. At der er bestemte typer (MLST-niveau), der er dominerende i kloakker/afløb.
3. At der er bestemte typer (MLST-niveau), der dominerer i kloakker/afløb uden for hospitalerne og at disse kan er forskellige fra dem man finder i infektioner hos indlagte patienter (CPE isolater og måske også isolater generelt).

Metoder:

1. Udvikle en metode til at tage biofilm-prøver i afløb og toiletter.
2. Udvikle/efterprøve metode til selektivt at opformere de relevante bakteriearter i laboratoriet.
3. Artsbestemmelse via Maldi-TOF analyse.
4. Evt. resistensbestemmelse af udvalgte isolater.
5. Eventuelt indsamling af de ovenfornævnte arter direkte fra en klinisk mikrobiologisk afdeling.
6. Udvikle/afprøve PCR metode, så som RAPD, til at se, om man kan gruppere bakterier efter klonalitet.
7. Helgenomsekventere udvalgte kloner og lave WGS analyser for at bestemme MLST typer og klonale typer. Sammenligning til kendte typer fra CPE overvågningen.
8. Evt. udføre biofilmassays på udvalgte succesfulde kloner på samme type af materiale, som de er isoleret fra (porcelæn eller rustfrit stål).

Forventet udbytte:
En kortlægning af diversiteten af kloak-associerede bakteriearter med fokus på dem, der oftest giver infektioner hos mennesker og som især relaterer sig til de typer, vi ser i vores CPE overvågning.

Kontaktinformation:
Såfremt du ønsker nærmere information omkring projektet, kan du kontakte: Henrik Hasman, Statens Serum Institut, tlf.: 40207660.

Intern vejleder: Søren Sørensen, e-mail: sjs@bio.ku.dk

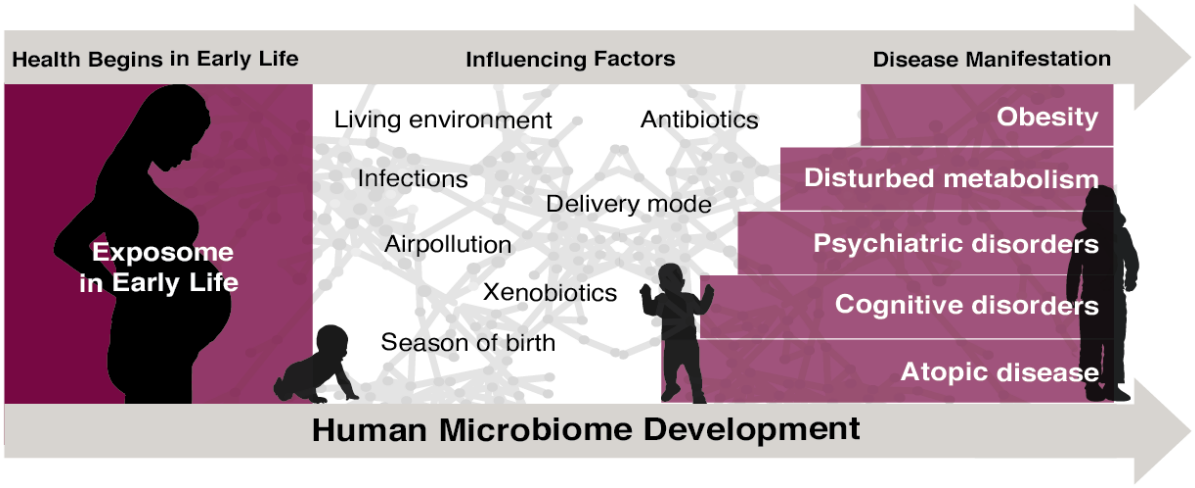
Microbiomes

Early life microbiome and later disease development

Project type: Masters

Background:
Asthma, eczema, and allergy (atopic diseases) are the first common chronic diseases to manifest during childhood. Approximately 20% of children develop asthma-like symptoms, and an estimated 300 million people suffer from asthma worldwide. A healthy embryo is considered essentially sterile and the first and very important colonization is established by its early contact with the environment. Therefore, the first years of our lives represent a critical period for susceptibility to environmental exposures – an open window – from which lasting effects can be imprinted on the developing immune system, which may in time lead to atopic disease. In collaboration with Copenhagen Prospective Studies on Asthma in Childhood (COPSAC), we study how the microbiome is an intermediary player in the interaction between the host and its environment, with a key focus in research into the extrinsic mechanisms that determine the transition from health to chronic disease.

$COPSAC_{2010}$ is an ongoing Danish cohort study of 738 unselected pregnant women and their 700 children followed from pregnancy week 24. The foundation of the project will be the vast amount of data from the COPSAC clinical birth cohort with extensive longitudinal microbial samples characterized by sequencing through the first year of life (1 week, 1 month, and 1 year), as well as later time points. The primary endpoints: asthma, eczema and allergy have been diagnosed prospectively by the COPSAC pediatricians.



Student projects at Section of Microbiology

Types of projects:
The applicant will join the Section of Microbiology and with the microbial expertise of Professor Søren J. Sørensen's lab, where the project will leverage a strong interdisciplinary research cooperation to pursue projects that:

- Investigate the early life exposome, which through gene-environment interactions cause immune deregulation, inflammation, and subsequent symptomatic disease.
- Examine the correlations between the early-life gut microbiome, antimicrobial resistome and later disease manifestation.
- Identify microbial interaction networks and other biological markers that are key for neurodevelopment and atopic disease.
- Develop synthetic microbial communities that can be used as part of future intervention strategies against later disease development.

Techniques involved:

- Bioinformatics (R and/or Python)
- Multivariate statistics
- Classical microbiology and molecular microbiology
- Animal experiments
- High resolution imaging (FACS and CLSM)
- DNA and RNA sequencing

For more information, please contact:
Urvish Trivedi (urvish.trivedi@bio.ku.dk)
Søren Sørensen (sjs@bio.ku.dk)

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/

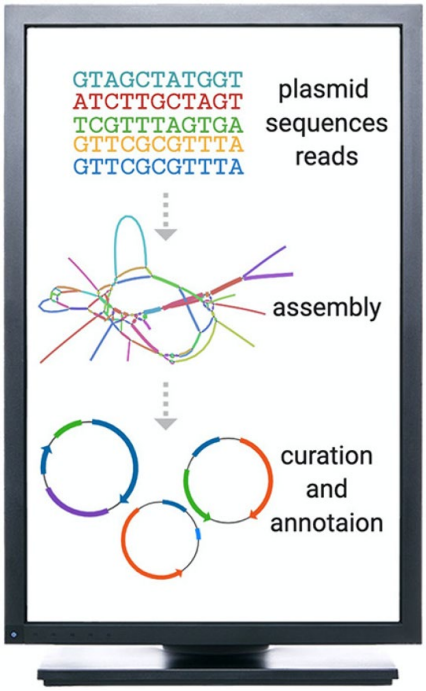
Plasmids – Gotta Catch 'Em All

Project type: Master & Bachelor

Background:
Plasmids are extra-chromosomal elements most often found in Bacteria and some Archaea. Their replication is independent of the chromosome, and some can readily transfer to new hosts. Conjugative plasmids notably encode all the genes necessary to establish cell-cell contact and initiate their transfer to a new host, while mobilizable plasmid require the help of conjugative plasmids to transfer. Besides the fundamental interest for plasmids as actors of bacterial genomes evolution by means of horizontal gene transfer, plasmids are also heavily involved in the spread of antimicrobial resistance: a very serious problem in healthcare systems. Yet, most of the knowledge acquired on plasmids focuses is quite limited owing first to the stark focus on a few pathogens hosts and AMR plasmids group, but also to their elusive nature in sequencing data prior to the long-read sequencing revolution. These missing pieces of information are necessary to understand more precisely how genes flow between populations of bacteria, notably between the reservoir of resistance genes in environmental bacteria and clinical pathogens where these are creating havoc.

Types of projects:
You will join Professor Søren Sørensen's research group, at the Section of Microbiology, where research benefits from strong interdisciplinary and international collaborations on projects that:

- Capture plasmids from the environment and sequence them, either directly (shotgun) or by recovery in a lab host (exogeneous isolation)
- Compare the genomic architecture and gene content of plasmids
- Investigate the genetic diversity within and between groups of plasmids
- Investigate the host range of genetically modified plasmids
- Develop innovative methods to capture plasmids without relying on cultivation of their hosts



Techniques covered:

- Classical microbiology & molecular biology
- Plasmid genetic manipulation
- Fluorescent activated cell sorting
- Long-read sequencing (PacBio, Oxford Nanopore)
- Bioinformatics

For more information, please contact:
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Søren Sørensen (sjs@bio.ku.dk)

READ MORE AT:
https://www1.bio.ku.dk/english/research/microbiology/

Searching for a mechanistic modulator of Tn7 transposition

Project Type: Master

Background:
The classical Tn7 transposon and recently discovered Tn7-CRISPR-Cas elements have been repurposed for development of a genomic DNA integration tool to engineer bacterial chromosomes in a specific manner: integration into the attTn7 site immediately downstream of the *glmS* gene for the former and into an RNA-guided site for the latter. In those applications, the Tn7 transposition follows a cut-and-paste mechanism, that allows a DNA fragment flanked by the Tn7 right and left ends to be excised from a donor plasmid and integrated into the target site. Nonetheless, the system can be modulated by the presence of a conjugative plasmid to switch from a cut-and-paste mechanism to a replicative manner, in which two copies of the DNA insert and/or a larger DNA fragment can be integrated into a target site, further expanding a potential use of the Tn7 transposon and Tn7-CRISPR-Cas elements. In this project, the candidate will identify the gene/protein encoded by the conjugative plasmid that is able to switch the mechanism of the Tn7 transposition and incorporate the discovered modulator into a new Tn7-mediated DNA integration tool.

Types of projects:
Development of experimental assays to screen a modulator of Tn7 transposition

Development of a replicative Tn7-mediated integration tool

Development of an Tn7-based integrative-conjugative biosensor

Techniques covered:
Molecular cloning
Functional genetics
PCR
TraDIS
DNA Sequencing (Sanger and/or Illumina short-read sequencing)
Conjugation assays

For more information contact:
Assistant professor Joseph Nesme (joseph.nesme@bio.ku.dk)
Professor Søren Sørensen (sjs@bio.ku.dk)

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/

Protein transfer during bacterial conjugations

Project type: Master

Background:
Conjugations are a bacterial sexual process in which a donor cell makes physical contact with a recipient cell, form a mating pair, and transfer a copy of the conjugative/mobilizable plasmid to the recipient cell. The genetic transfer from one cell to another enables the recipient cell to acquire additional inheritable phenotypes, such as antibiotic resistance, toxin production and adaptation to new niches. However, it remains debatable if transferred-DNA-independent proteins can move from the donor cell to the recipient cell through the mating machinery during conjugation. Such protein transfers may allow a rapid transient acquisition of non-inheritable phenotypes, leading to a quick response to sudden environmental stresses, that may play an important role in bacterial ecology and evolution. Furthermore, understanding what types of proteins can be transferred during conjugation can be employed to design a conjugation-based protein delivery system for antimicrobial therapies.
In this project, the candidate will design an assay to study the movement of protein probes during bacterial conjugation, determine the rules of transferable proteins (cell locations: cytoplasmic, membrane-bound, or periplasmic; protein size; DNA bound *vs.* unbound) and may use the generated knowledge to develop an antimicrobial biological agent.

Types of projects:
Development of experimental assays to monitor cell-to-cell protein movement during conjugation

Bacterial genomic engineering to integrate protein probes with different sizes, cell locations and DNA binding ability.

Techniques covered:
Fluorescence microscopy
Fluorescence-activated cell sorting
Molecular cloning and genomic manipulation
Antibiotic susceptibility assays
Conjugation assays

For more information contact:
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Professor Søren Sørensen (sjs@bio.ku.dk)

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/

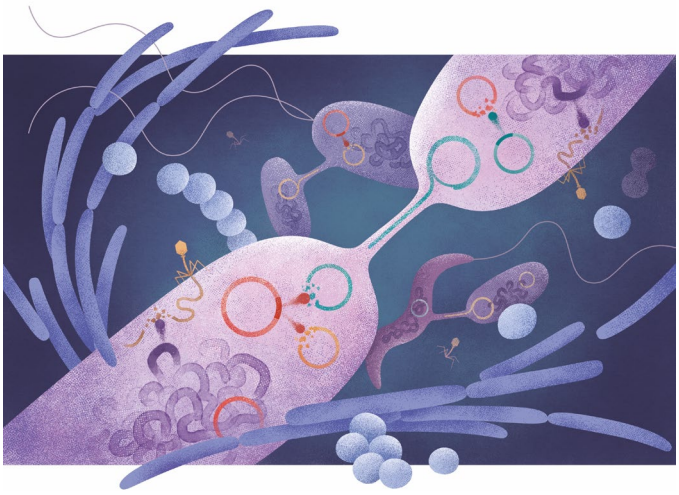
Discovery of bacterial defense systems

Project type: Master

Background:
Mobile genetic elements (MGEs), such as plasmids and phages, shape bacterial evolution by facilitating genetic exchange among community members, eg. antimicrobial resistance. However, MGEs often act as genetic parasites and bacteria have evolved immune systems to defend themselves against these invaders, including CRISPR-Cas, Restriction-Modification, Retrons, etc. The identification and functional characterization of new defense systems is crucial to understand gene flow across microbiomes and, thus, bacterial ecology and evolution. Moreover, defense systems comprise powerful machineries that are particularly well suited for the development of biotechnological tools (eg., in genome engineering, therapeutics, and diagnostics).

Types of projects:
- Develop computational approaches for mining novel bacterial defense systems.
- Develop experimental approaches for mining novel bacterial defense systems.
- Functional screening of candidate defense systems against plasmids and phages.
- Bioinformatic investigation of defense system prevalence, diversity, and taxonomic distribution.
- Genetic and biochemical characterisation of novel defense systems.
- Investigation of biotechnological applications of novel defense systems.

Techniques covered:
- Bioinformatics
- Comparative genomics
- Bacterial handling
- CRISPR-Cas
- Molecular cloning
- Phage & Plasmid manipulation



For more information, please contact:
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Rafael Pinilla, rafael.pinilla@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/

Plant-microbiome interactions for a sustainable future

Project type: Master

Background:
Modern agricultural practices, in a period facing profound climate changes and a growing population, are neither sustainable nor sufficient. The extensive use of chemical pesticides, herbicides, and fertilizers creates serious risks to biodiversity, soil health, water quality and human health. The transition to sustainable and climate-neutral cropping systems demands biological alternatives to agro-chemicals. Modern agriculture, due to its dependence on chemical input, has largely ignored the presence of- and interactions between- the plant and its microbiome. Plants form complex associations with diverse microorganisms, including bacteria, fungi, nematodes, and viruses (the plant microbiome) to meet their needs, such as, nutrient uptake, stress tolerance and disease resilience. In our research, we study the assembly of- and interactions between- microorganisms harboured in one of the most diverse microbial environments, the plant-soil nexus. We also investigate the role of the host microbiome in plant growth promotion and plant protection.

Types of projects:
The applicant will join Professor Søren Sørensen's research group, at the Section of Microbiology, where research benefits from strong interdisciplinary and international collaborations on projects that:

- Study the acquisition and selection of the plant microbiome from the environment
- Compare the microbiome assembly between domesticated and native plants
- Explore the temporal and spatial heterogeneity in the root microbiome development
- Identify networks of collaborating microbes that synergistically prevent plant pathogens
- Develop synthetic microbiomes targeted for specific community functions

Techniques covered:

- Classical microbiology
- *In-vitro* and *in-vivo* assays
- Microcosms experiments
- Fluorescent activated cell sorting
- PCR and qPCR
- Bioinformatics
- Metagenomics

For more information, please contact:
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Søren Sørensen (sjs@bio.ku.dk)

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/

Interpretation of Parabasalid DNA reads in pig facael samples as detected by metabarcoding

Write a project in collaboration with Statens Serum Institute (SSI)

Project type: Master

We used metabarcoding to detect and differentiate parasites in pig faecal samples.
Data on some of the parasites were already published here https://pubmed.ncbi.nlm.nih.gov/34073014/

However, data on Parabasalid organisms have not been collated and analyzed yet, and these data could potentially feed into a publication.

If you're interested, you could get access to this data, collate them, and analyse them as relevant.

The suitable candidate would be interested and fairly skilled in most of the following:

1. Alignment of DNA sequence data
2. Knowledge on genetic markers used for taxonomic annotation (e.g. SSU rRNA genes)
3. Phylogenetic analysis
4. Some basic knowledge on Parabasalids
5. Some basic interest in mapping the eukaryome (the eukaryotic component of the gut microbiome)

There would be a possibility to study relationships between these parabasalids (and other parasites) and accompanying bacterial microbiome.

No morphological data are available for this project.

Please contact Rune Stensvold run@ssi.dk for more information

Multispecies biofilm

In the laboratory bacteria are rarely grown as biofilms, although this is the way many bacterial species live in nature. A biofilm protects the cells from predation, antibiotics and physical stress among other things and the close proximity of the cells help facilitate social interactions including a high rate of horizontal gene transfer. The majority of genes necessary for biofilm formation are found on plasmids, again giving a direct link between biofilms and horizontal gene transfer. Biofilms are a large problem in both medical and industrial environments because biofilm forming bacteria are very hard to remove. Research in bacterial biofilms and especially multispecies biofilms is a large field within microbiology and is of great interest in the medical industry. Besides, multispecies biofilms are suitable models for studying essential aspects of social evolution of bacteria (sociomicrobiology).

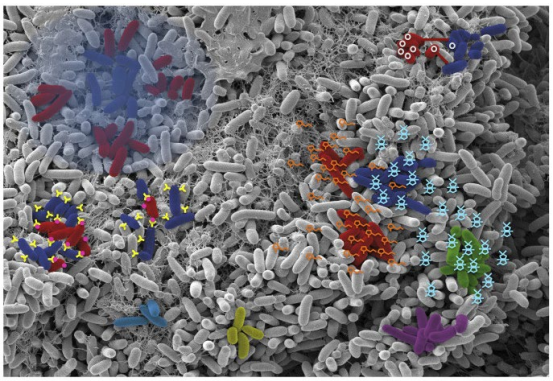
Investigate the properties of bacterial communities – Biofilms

If you want to study mechanistic and evolutionary aspects of how bacteria cooperate to form robust biofilms, then do not hesitate to contact us. We have a diverse range of ongoing projects.

Project type: PUK, Bachelor, Master

Living in an organized society is very advantageous. It enables individuals to specialize and become experts in specific tasks, thus benefitting the whole community. This concept applies not only to humans, but also microbes. Most bacteria live in so-called biofilm communities. In these communities, they unite forces and produce an extracellular matrix which encases them and acts as a shield from predators. The generation of local niches and detention of enzymes and metabolites benefits all the members of the community. As the community grows and becomes more heterogeneous, the emergent properties support a large degree of specialization. Traditionally, bacteria have been studied in planktonic cultures; in recent years, the focus has shifted to biofilms. Studying biofilms has shown that the spatial rigidity and community structure is of great evolutionary, ecological, biotechnological, and clinical relevance.

At Section of Microbiology, we work with various aspects of bacterial interactions and hence, are greatly interested in biofilms. We study the differences between planktonic and sessile biofilm-associated bacteria, how gene expression is altered, and multi-species communities. We also address why biofilms are more difficult to eradicate than their planktonic counterparts. This research is especially clinically relevant, as biofilm-formers tend to exhibit high tolerance towards antimicrobials and cause recalcitrant infections. Thus, biofilm research could enable novel treatment strategies.



If you want to study mechanistic and evolutionary aspects of how bacteria cooperate to form robust biofilms, then do not hesitate to contact us. We have a diverse range of ongoing projects, from analyzing how a biofilm environment can help generate new probiotics, to the exploitation of beneficial biofilms or even the eradication of unwanted biofilms. In addition, new projects are regularly initiated. If you have an interesting idea, we have the facility to support it.

The lab applies a range of techniques, which commonly include growing biofilms in different model systems, genetic manipulation, studying gene expression, advanced epifluorescence and confocal microscopy and image analysis. We also collaborate with Rigshospitalet, the Faculty of Health (KU-SUND) and other clinical and biotech partners to address more specific questions.

Please contact us for more information and feel free to come by and have a chat about developing a project to match your interests.

Contact information:
Supervisor Associate professor Mette Burmølle, LINK TO PROFILE
E-mail: burmolle@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/multispecies-biofilms/

Social evolution in microbial communities. Are we competing or working together?

Project type: Master

Diversity in societies enables a lot of opportunities. Individuals can specialize and perform tasks that benefit the entire community. Some are plumbers, while others are experts in hotel management. Adding other individuals to communities can have either positive or negative implications, depending on the properties of the newcomers and their relations to the native inhabitants. Often, it is unknown whether a new addition will be helpful or detrimental to a community. The same goes for microorganisms. Most bacteria live within a self-produced matrix of secreted biopolymers called a biofilm, where they perform different tasks at varying times and locations. In many cases, biofilms consist of multiple different species with different expertise that either compete for the same resources or benefit from each other's presence. In this project, we aim to investigate whether bacteria *cooperate* or *compete* when mixed and identify the underpinning traits.

We will use a catalogue of bacterial isolates. By mixing bacteria and quantifying their growth and biofilm formation capabilities, we can address whether they compete or cooperate and help clarifying to which extent diversity benefits communities.

The communities that serve either strong promotion or obstruction of biofilm formation will be further investigated to identify parameters determining cooperative and competitive behavior. Whole genome sequencing and subsequent bioinformatic analyses will allow for the identification of biofilm and metabolic genes. Metabolism will then be verified with the use of specific media, single carbon source growth assays and enzyme activity measurements. This information will allow us to delve deeper into the mechanistic processes occurring during biofilm development, rather than just looking at overall effects.

The project will be conducted at Section for Microbiology at Nørre Campus in Copenhagen. We have a diverse lab environment with researchers focusing on various aspects of microbiology, a high level of interproject interactions. You will have a day-to-day supervisor in the lab that will assist you with practical and scientific tasks and ensure your smooth transition into the group.

The project is flexible and will be well-suited for a microbiology or biochemistry student with an interest in evolution. Do not hesitate to contact us for more information and feel free to come by and have a chat about how to shape the project to match your interests.

Contact information:
Supervisor Associate professor Mette Burmølle, LINK TO PROFILE
E-mail: burmolle@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/multispecies-biofilms/

Extraction of biofilm matrix for proteomic analyses - A proof-of-concept study

Project type: Master

In nature, the predominant lifestyle of bacteria is living in polymicrobial communities. Most bacteria live in so-called biofilm communities in which cells are embedded in a self-produced extracellular matrix. The main components of the biofilm matrix are extracellular polymeric substances (EPS), including amyloid-like fibers. Biofilms provide many advantages for the members, such as protection from antibacterial compounds or generation of local niches, which facilitates cell specification. **We hypothesize that many of these advantages are linked to the structure and composition of the biofilm matrix, which is explored in the present project.**

In the Section of Microbiology, we use a four-species bacterial model community displaying synergistic features. We aim to understand the inter-species dynamics between the four members with various approaches, such as genetic manipulation, bioinformatic analyses, phenotypic assays, and microscopy. A specific research focus is the identification and quantification of proteins present in the biofilm matrix of different community compositions.
In this project, we will separate biofilm cells and matrix and perform proteomic analyses of the matrix fraction based on mass spectrometry analysis. To validate the matrix extraction, you will apply molecular techniques to follow and optimize the extraction protocol. Once the MS data is acquired, you will apply bioinformatic pipelines for proteomic comparisons of the matrix proteomes of wild-type strains and specific biofilm mutants.

The project will be conducted at the Section of Microbiology at Nørre Campus in Copenhagen. We have a diverse lab environment with researchers focusing on various aspects of microbiology and a high level of interproject interactions. You will have a day-to-day supervisor in the lab that will assist you with practical and scientific tasks and ensure your smooth transition into the group. The project is flexible and will be well-suited for a microbiology or biochemistry student interested in microbiology and bioinformatics. Do not hesitate to contact us for more information, and feel free to come by and have a chat about how to shape the project to match your interests.

Contact information:
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Postdoc Heiko T. Kiesewalter LINK TO PROFILE, E-mail: heiko.kiesewalter@bio.ku.dk

READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/multispecies-biofilms/

Embedment of probiotic bacteria in urinary catheter material to prevent infection

Project type: Master

Catheter associated urinary tract infections (CAUTI) are common, and they are hard to treat due to the formation of bacterial biofilms on the catheter material, as biofilms are highly tolerant to antibiotics. Despite various strategies aiming to reduce bacterial attachment to the catheter surface or inhibit/kill bacteria by antibacterial catheter coatings, yet no efficient strategy for preventing CAUTI has been developed. **This project aims to develop a proof-of-concept methodology for embedding live probiotic bacteria into catheter silicone material, and subsequently test their viability and ability to reduce the attachment of pathogenic bacteria.**

Probiotic bacteria inhibit the growth of pathogens and, in contrast to antibiotic treatment, do not select for antibiotic resistance development. The applied approach thus resembles that used by living organisms for protection against pathogens, e.g. in the digestive system. Here, the aim is not sterility, but the establishment of a robust community that prevents pathogen colonisation.

The project will be conducted in collaboration with the Danish Biotech company, Biomodics ApS, specialized in medical devices and material modification, and part of the work will be conducted here. Additionally, you will be working at Section of Microbiology at Nørre Campus in Copenhagen. We have a diverse lab environment with researchers focusing on various aspects of microbiology and a high level of interproject interactions.

The project tasks will include development of methods for probiotic embedment in catheter material. Embedded organisms will include members of lactic acid bacteria (*Lactobacillus* spp.) and the spore forming *Bacillus subtilis*. Activity measures will include pH and metabolic indicators. Model strains commonly identified in CAUTI will be used to assess the ability of the embedded bacteria to reduce pathogen attachment and biofilm formation.

Location
Nørre Campus, Copenhagen & Biomodics ApS, Rødovre

Contact information:
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READ MORE AT: https://www1.bio.ku.dk/english/research/microbiology/multispecies-biofilms/

Investigating anti-predator properties of bacterial multispecies biofilm communities

Project Type: Master

In nature, microorganisms such as bacteria, archaea, fungi, or single-celled eukaryotes live and interact in various microenvironments. These inter-microbial interactions impact fitness and survival and are highly diverse. They include competition for the same nutrient source or predation between two organisms, antagonism, such as the production and secretion of bioactive compounds, and synergism, like sharing public goods or using metabolic waste products from other species. **This project aims to explore inter-kingdom interactions between bacteria and protozoa.**

Most bacteria live in biofilms, whereby they gain plenty of advantages. In biofilms, bacterial cells are embedded in a self-produced matrix. Such biofilms are generally assembled by multiple members, provide local niches, allow cell specializations, and promote inter-species interactions. Furthermore, the individual members of a biofilm community are more protected against bioactive compounds or predators than planktonic cells would be since the biofilm functions as a shield. We hypothesize that bacteria present in a multispecies biofilm are better protected against phage predation due to the properties of the biofilm matrix.

In the Section of Microbiology, we use a four-species bacterial model community displaying synergistic features. We aim to understand the inter-species dynamics between the four members with various approaches, such as genetic manipulation, bioinformatic analyses, phenotypic assays, microscopy, and proteomic analyses. Additionally, we would like to extend our focus and investigate predatory interactions between our bacterial model community and bacteria-grazing protozoa.
In this project, we will expose the wild-type bacterial model community and different community variations, including specific biofilm mutants, to bacteria-grazing protozoa. The aims will be to explore the protection abilities of biofilms against protozoa and to examine the impact of specific biofilm matrix components.

The project will be conducted at the Section of Microbiology at Nørre Campus in Copenhagen. We have a diverse lab environment with researchers focusing on various aspects of microbiology and a high level of interproject interactions. You will have a day-to-day supervisor in the lab that will assist you with practical and scientific tasks and ensure your smooth transition into the group. The project is flexible and will be well-suited for a microbiology or biochemistry student interested in microbiology and microbial ecology. Do not hesitate to contact us for more information, and feel free to come by and have a chat about how to shape the project to match your interests.

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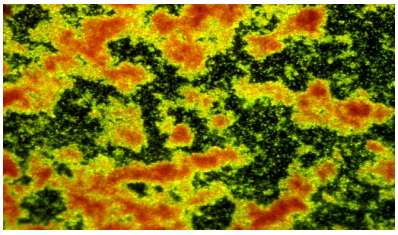
The functional role of the biofilm matrix in the productivity and protection of bacterial communities

Project type: Master



Bacteria are ubiquitous and essential for all life on earth. Bacterial communities affect everything from nutrient uptake in the bowels to the degradation of leaves in the fall. Traditionally, researchers studied bacteria as homogenous and uncoordinated populations of cells. Only recently has the view shifted to analyze bacteria as complex and heterogenous communities. Such communities are called biofilms. Researching how these community-based bacteria orchestrate their behavior has revolutionized the field of microbiology. Biofilms are embedded in an extracellular matrix which facilitates stable, close contact between cells, retention of enzymes and protection from predators.

When biofilms consist of multiple interacting species, community-intrinsic properties emerge. These properties would not occur if each species was living individually. At the Section of Microbiology, we use a four-species bacterial model community, which exhibits a large degree of synergy, to study this intriguing evolutionary phenomenon. We are especially interested in understanding how the community benefits from specific matrix components and which bacterial members produce them. To understand the dynamics between community members, the lab applies bioinformatic analyses, proteomics, genetic manipulation, various phenotypic assays, and advanced microscopy.

If you find this topic interesting, we can offer a flexible project where you will study the functional role of the matrix in single versus multi-species biofilms. The project can be tailored, so you focus on genetic manipulation or generation and analysis of omics data, depending on your interests. You will be part of a project team consisting of PhD students and post docs that will assist you when needed.

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Understanding the dynamics of viral infections in multispecies biofilms

Project type: Master

Have you ever gotten sick from a virus? Or even experienced getting infected by the causative agent of COVID-19, SARS-CoV-2? During a viral infection, we rely on our immune response to detect and eliminate the virus. The same applies for bacteria. Viruses that specifically infect bacteria are called bacteriophages. If a bacteriophage successfully infects a host, the outcome is often lethal for the bacterium. Interestingly, phages are the most abundant biological entity on earth. By infecting bacteria, they have an immense impact on ecology and evolution. Moreover, due to their lytic capabilities, phages also have clinical relevance as agents for treatment of bacterial infections. With an increasing number of pathogens developing antibiotic resistance, it is critical to research potential new ways to treat infections; studying phages could pave the way for the development of alternative treatments.

To fully understand the biology and application of phages, we need to examine the eco-evolutionary dynamics of bacteria-virus encounters. Most bacteria live in so-called biofilms, which are communities embedded in an extracellular matrix that facilitate several emergent properties. In this project, we will investigate what happens when bacterial biofilms are exposed to different phages, and whether those dynamics differ when a biofilm consists of more than one bacterial species. Specifically, you will be working with a three-species community of fluorescently tagged bacteria and an associated catalogue of phages. To elucidate the interactions between bacteria and phages, you will apply a range of techniques such as whole-genome-sequencing, bioinformatic analyses, metabolic profiling, confocal laser scanning microscopy (CLSM), and advanced image analysis. You will learn to construct plasmids, manipulate the chromosome of bacteria, grow biofilms, work with different bacteria and phages, and operate the CLSM.

The project will be conducted at Section for Microbiology at Nørre Campus in Copenhagen. We have a diverse lab environment with researchers focusing on various aspects of microbiology, a high level of interproject interactions and a penchant for being social after a period with too few gatherings. You will have a day-to-day supervisor in the lab that will assist you with practical and scientific tasks and ensure your smooth transition into the group.

The project is flexible and will be well-suited for a microbiology or biochemistry student with an interest in molecular microbiology. Do not hesitate to contact us for more information and feel free to come by and have a chat about how to shape the project to match your interests.

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