

Microbiology Day 2024



Program of the day:

8:30-9:00 Morning coffee / breakfast

9:00-9:10 Welcome words

9:10-9:50 Keynote 1: Biotechnology, Yvonne Nygård VTT

9:50-10:10 Annika Lintala

10:10-10:30 Liinu Nummela

10:30-10:50 Veera Partanen

10:50-11:10 Peter Petros

11:10-12:10 Lunch

12:10-12:50 Keynote 2: Human & clinical microbiology, Tommi Vatanen, University of Helsinki

12:50-13:10 Mert Erdin

13:10-13:30 Marianne Lalli

13:30-13:50 Meeri Piispa

13:50-14:10 Shah Rucksana Akhter Urme

14:10-14:35 Afternoon coffee

14:35-15:15 Keynote 3: Environmental microbiology, Eeva Eronen-Rasimus, SYKE

15:15-15:35 Laura Häkkinen

15:35-15:55 Renata Majamäki

15:55-16:15 Rashmi Shrestha

16:15-16:35 Svetlana Sofieva-Rios

16:35-16:50 Break

16:50-19:00 Cocktails, poster pitches and posters

Event date: Thursday 16th of May

Location: Info center, Viikki campus

Best talk and poster will be awarded a 1000€ travel grant!

Microbiology Day 2024 Organizers:

Mia Vehkaoja PhD, Specialist, Research Services

Matilda Kattilakoski, Doctoral researcher in the MBDP programme

Renata Majamäki, Doctoral researcher in the MBDP programme

Rasmus Malmgren, Doctoral researcher in the MBDP programme

Ada Pajari, Doctoral researcher in the MBDP programme

Aigerim Tuganbay, Doctoral researcher in the MBDP programme

Sirja Viitamäki, Doctoral researcher in the MBDP programme

Abstracts for talks

Session 1. Molecular microbiology

Presenter: Annika Lintala

Title: Reptarenaviruses Compete in Persistent- and Superinfections with Closely Related

Abstract:

Reptarenaviruses cause boid inclusion body disease (BIBD) destroying snakes' life quality leading to death. A snake with BIBD often carries more than a single pair of genetically distinct reptarenavirus small (S) and large (L) segments, and the segment swarm can vary between tissues and organs. The role of reptarenavirus coinfection in development of BIBD remains unknown, and it is unclear how the infection affects the susceptibility to superinfection by homologous viruses. We hypothesized that coinfection would only occur if the infecting viruses were genetically distant. We saw this when superinfecting persistently infected cells but not in fresh co-inoculations with a selection of reptarenavirus isolates. We then studied whether passaging of the co-inoculated cells would reveal competition between the virus isolates. We monitored released segments with qRT-PCR into the supernatant. The results suggested that co- and superinfection have a very subtle effect on the replication of the tested isolates, but during passaging, we saw some competition between genetically similar segments. To study hypothesis that the presence of viral matrix/Z protein (ZP) affects replication, we generated ZP expressing cell lines, and compared virus replication in ZP expressing cells to naïve cells. The ZP production did not have a negative impact on the replication. Our findings suggest that reptarenavirus infection does not prevent superinfection with a homologous virus, thus the coinfections commonly seen in snake collection are likely a result of consecutive superinfections during captivity.

Presenter: Liinu Nummela

Title: Characterization of *Aspergillus niger* sugar transporters

Abstract:

Filamentous fungi, like *Aspergillus niger*, play a crucial role in the degradation and modification of plant biomass, contributing significantly to terrestrial carbon cycling. Their abilities are also widely exploited in biotechnological applications. One of the key aspects of the fungal plant biomass conversion process is the uptake of the biomass-derived small sugar compounds into the fungal cells where they are metabolized as carbon and energy sources. Surprisingly, the knowledge of filamentous fungal sugar transporters (STs) is limited, despite of their significant biological role and biotechnological potential as targets of genetic engineering to improve fungal biomass conversion. In this study, we systematically investigate the overall sugar transport ability of *Aspergillus niger* by characterizing 90 identified candidate STs both physiologically and biochemically. Determination of the *in vivo* roles of the transporters is facilitated by *A. niger* ST deletion strains, whereas their *in vitro* functions are studied in *Saccharomyces cerevisiae*. Our comprehensive data aims not only to provide information of the role of individual STs in plant biomass conversion by *A. niger*, but also identify novel candidate genes for engineering of industrial fungi at the level of sugar transport. Highlights of these studies will be presented.

Presenter: Veera Partanen

Title: New barcode system allows tracking the spread of multiple genes simultaneously

Abstract:

Mobile genetic elements, such as conjugative plasmids, are tricky in terms of antimicrobial resistance problem. They can carry multiple resistance genes (ARGs) and make new strains multi-resistant in a single transfer event. However, we know very little about the factors affecting the horizontal gene transfer (HGT). We created a sequence barcode based system to track HGT of ARGs in a microbial community. Combined with Emulsion, Paired-Isolation and Concatenation PCR (epicPCR) we could see on a single cell level where the gene copies had ended up in from their original genetic environment. Based on our sequencing results, we could detect the barcodes from both epicPCR amplicons and metagenomes. We saw significant effect of our temperature and antibiotic treatments as well as the original genetic environment to the final host species count, but the effects were small. However, this system shows promise in researching different factors affecting HGT, the mobilization to different genetic context and also some promise in the ways of transfer as the introduced genes can always be recognized based on their barcode.

Presenter: Peter Petros

Title: Evaluating fermentation of paludiculture biomass fractions with basidiomycota

Abstract:

Paludiculture is a vital practice that can improve industrial agriculture towards a healthier and more regenerative direction for greenhouse gas emissions mitigation, soil restoration, carbon sequestration, water pollution reduction and promotion of biodiversity particularly in areas where peatland drainage has been prevalent. Typha and Salix are two major paludiculture crops that grow well in wet soils, offer rapid regenerative growth and harvest as a short-rotation coppice (SRC), but lack industry application and market demand stalls widespread paludiculture adoption. By applying fungi in the downstream processing stages of SRC willow and cattail biomass fractions, myceliated biomass and mycelium composites can be produced, offering further use cases for the crop feedstocks in various industries. To date, little-to-no research studies have analysed the potential of SRC Typha and Salix biomass fractions as feedstocks for basidiomycete fermentation. In this study, extracted and unextracted Typha and Salix biomass fractions are compared and evaluated for their performance as substrates for mycelial growth using key wood-decayer fungal species. Hyphal extension, observable fungal morphology, lignocellulose and ergosterol content are measured. Subsequent analyses will be conducted to assess the biochemical and fermentation characteristics of each fungi-substrate combination, with the longer-term project goal to work towards thermoacoustic mycelium-composite materials.

Session 2. Human / clinical microbiology

Presenter: Mert Erdin

Title: Hantaviridae trends differential evolutionary patterns across its species

Abstract:

Orthohantaviruses are tri-segmented, single-stranded RNA viruses and members of Hantaviridae family. These viruses are globally distributed and were reported from small-mammals until today. Rodent-borne orthohantaviruses are divided into three major groups: Murid-borne, non-arvicolinae cricetidae-borne, and arvicolinae-borne. Murid-borne orthohantaviruses are majorly spread across Eurasia, such as Orthohantavirus dobravaense (DOBV), and some of them associated with hemorrhagic fever with renal syndrome in humans. Arvicoline-borne orthohantaviruses recently suggested as evolutionary bridge between old world and new world orthohantaviruses. The members of this group are either non-pathogenic or they cause mild infections. Traditionally, orthohantaviruses thought to be strict to their reservoir host species, which means 'one orthohantavirus, one reservoir host species'. However, recent studies slowly reveal the high viral divergence with wide host range for some members. We initially analyzed dispersal history and phylogenetic characteristics of DOBV. Our analyses suggested that host-dependent lineage separation followed by strong geographic clustering for DOBV. Furthermore, DOBV root location in phylogeographic reconstruction in discrete space was estimated in eastern Europe. In addition, we characterized evolutionary dynamics, phylogeography, and host jumps of *O. tulaense* (TULV, Arvicoline-borne orthohantavirus). TULV phylogeny followed the pattern of geographical lineage separation and host-dependent clustering. We also observed wide host range with preliminary host jump routes across rodent species. We observed that even the phylogenetic pattern for two members of Hantaviridae were different from one another. Our studies show that there is so much to reveal to draw general evolutionary conclusion for Hantaviridae due to evolutionary divergencies across different groups of rodent-borne orthohantaviruses.

Presenter: Marianne Lalli

Title: Dietary fibers shape the infant gut microbiome composition and metabolism

Abstract:

Background: The infant gut microbiome undergoes temporal changes supporting normal development and health. While diet shapes this process, the role of fibers in complementary diets on gut microbiome development is not well-understood. **Objectives:** This study examined how the transition from breast milk and its fiber to fibers in complementary foods affects the taxonomic and functional maturation of the gut microbiome within the first year. **Methods:** We assessed the longitudinal and cross-sectional development of gut microbiomes (N=68) and metabolomes (N=33) using linear mixed models, focusing on the impact of dietary fibers and their sources. Fiber intakes were evaluated using 3-day food records. Bacterial species identification and metabolomic profiling were conducted using MetaPhlAn2 and LC-MS, respectively. **Results** The study places the infant gut microbiome maturation in a fiber-dependent context. We discovered 176 complementary food derived fiber-bacterial species associations. Most of these associations (147, 84%) were direct, whereas breastfeeding and its fiber tended to be inversely associated with the same species, showing the strongest inverse correlations to later trajectory species indicative of slower maturation.

Both bacterial species and metabolomic profiles displayed pronounced longitudinal shifts in response to fibers from complementary foods. Introduction of new fiber sources was linked to microbiome diversification, underlining fiber-species specific temporal patterns. Conclusions: Adequate dietary fiber intake from various sources during weaning appears crucial for developing a stable and diverse gut microbiome, underscoring the importance of dietary fibers in early-life gut microbiome maturation.

Presenter: Meeri Piispa

Title: Developing Phage Therapeutics to Target Cystic Fibrosis Lung Pathobiome

Abstract:

Cystic fibrosis (CF) is a genetic disorder that results in the malfunction of the cystic fibrosis transmembrane conductance regulator (CFTR) ion channel. This leads to a wide range of different symptoms with lungs being the most severely affected. Impaired ciliary function and increased mucus viscosity in the lungs facilitate the colonization of airways by pathogens followed by infections and decline in lung function. CF lung infections are typically polymicrobial and antibiotics are the primary treatment method. However, antibiotic-resistant strains are increasingly reducing their effectiveness and as a result, alternative treatments are needed. Bacteriophages (phages) have emerged as a promising alternative or supplement to antibiotics. However, phage efficacy in polymicrobial CF microbiomes is yet relatively unclear. Especially, the role of existing viruses and their interactions with the CF pathobiome for the efficacy of phage therapies has received little attention. The aim of my PhD is to find out what is the role of phages in the CF lungs as a part of natural microbiota and how can we use this information to optimize phage treatment to target the whole CF pathobiome. To achieve this, we will analyze metagenomics, metatranscriptomics and direct cultures of CF lung sputum samples. We will also evaluate the efficacy of phages in vitro, polymicrobial model bacterial communities. Findings will increase understanding how lung virome is linked with CF progression and to develop novel phage therapeutics that evade pre-existing resistance and can target polymicrobial CF pathobiome in clinically realistic lung organoid model.

Presenter: Shah Rucksana Akhter Urme

Title: Evaluation the Antimicrobial Activity of Phytochemicals from Tea and Agarwood

Abstract:

Antibiotic-resistant bacteria are becoming increasingly common, leading to a global health crisis. The effects of abusing antibiotics not only increase pathogenic resistance but cause various diseases and syndromes as well. Gut microbiota contains many beneficial roles for health, while antibiotics kill both pathogens and gut microbiota which is considered one of the major side effects of antibiotic. In fact, new antibiotic compounds are needed in this urgent scenario; phytoremediation is the oldest but most effective method, and research on the antibacterial properties of several types of medicinal plants has already been done. Tea and agarwood plants are well known for their economic contribution in both beverage and cosmetic production, as well as their medicinal value. In this study, tea and agarwood leaf extracts were analyzed for their antimicrobial activity against both pathogenic and beneficial bacteria. Fresh tea (*Camellia sinensis*) leaves were collected in three varieties, namely BT-6 from Sylhet, BT-7 from Moulvibazar, BT-8 from Habiganj, also Green tea (non-fermented tea), black tea (fully fermented tea), and agarwood (*Aquilaria malaccensis*) were collected from Sylhet region of Bangladesh. Unlike commercial antibiotics, which have side effects on probiotics (beneficiary bacteria), leaves extracts activities were analyzed to check if they had positive effects on probiotics that can be found in gastrointestinal tract as well as dairy products. A potential beneficiary bacteria, *Lysinibacillus macroides* strain SRU-001 (NCBI accession no. MW665108) and a pathogenic bacteria, *Aeromonas caviae* strain YPLS-62 (NCBI accession no. MW666783), were isolated from the small intestines of poultry and curd, respectively. Tea and agarwood leaves (5g powder /80 mL methanol) with solvents were kept for seven days at room temperature, and extracts were applied for antimicrobial assays by disc diffusion assay against the isolated bacteria. Both 50 μ L of each leaves extracts were examined against 50 μ L each bacterial culture, where Gentamicin was a control. After 24 hours of incubation, tea and agarwood leaves extracts showed an 11 to 15 mm zone of inhibition against pathogenic *A. caviae* while only BT-8 showed 7 mm (disc diameter 6mm) against probiotic *L. macrolides*. However, compared to leaves extracts Gentamicin showed a 27mm zone of inhibition against both *L. macrolides* strain SRU-001 and *A. caviae* strain YPLS-62 bacteria. This research clearly indicates that Gentamicin kills both pathogenic and beneficiary bacteria, while leaves extracts from tea and agarwood plants contain antimicrobial activity against only pathogenic *A. caviae* but no effects on probiotic *L. macrolides*. This outcome indicates not only the potential therapeutic values of tea and agarwood leaves as antibiotics over commercial antibiotics but also the chance of having pathogens in curd and potential beneficial bacteria from poultry small intestine.

Session 3: Environmental microbiology

Presenter: Laura Häkkinen

Title: Cover crop root fungal communities under contrasting soil phosphorus levels

Abstract:

Cover-cropping is a widely used regenerative farming practice with many benefits to soil health and fertility. Cover crop (CC) species have been shown to influence soil fungal communities and potential functions. For instance, some Brassicaceae CC species can lower the abundance of potential plant pathogens, whereas species of the Fabaceae family can increase nutrient uptake benefitting arbuscular mycorrhizal fungi (AMF). Yet, the contribution of many cover crop species to fungal communities is not well understood. In this study, a greenhouse experiment with 12 common Finnish CCs and two CC mixes in P-fertilized and non-P-fertilized soil was set up to investigate differences in CC root fungal communities with ITS2 sequencing. Fungal communities in the CC roots differed significantly. We found highest proportion of AMF in Fabaceae roots, but tall fescue from the Poaceae family had similar proportion of AMF. The AMF communities could be separated according to CC family except for rye, which habited distinct AMF community compared to other Poaceae CC. Although, soil P-fertilization did not influence fungal communities overall, specific fungal functional groups, such as potential plant pathogens and symbiotrophs, including the AMF, were affected by P-fertilization in some CC species. Typically, under P-fertilization potential plant pathogens were higher and symbiotrophs lower, but in some CCs the effect was opposite indicating that the P-fertilization effect is CC specific. These results can benefit crop planning: the correct choose of CC can diversify the fields' AM communities and potentially increase crop resilience and nutrient uptake.

Presenter: Renata Majamäki

Title: Baltic Sea ferromanganese concretion growth rates and conditions

Abstract:

More than 10% of Finland's sea area is covered by a layer of ferromanganese (Fe-Mn) concretions, centimeter-scale accumulations of iron and manganese oxides. Concretions contain hi-tech metals, such as cobalt. Due to increasing demand for hi-tech metals near future, companies will likely start mining concretions from the Baltic Sea. The concretions host diverse microbial communities that can regulate metal and nutrient cycling in the concretions. The seafloor ecosystem must not be damaged while concretions are extracted. This study provides information on Baltic Sea Fe-Mn concretion growth rates and conditions in laboratory experiments. The Fe-Mn concretions were collected from the Baltic Sea for 12-week laboratory experiments. We assessed the concretion growth with X-ray computed tomography and freshly formed concretion material with a scanning electron microscope. We analysed the headspace methane concentrations and pH of the incubation solution. We measured phosphorus and metal concentrations of the incubation solution with triple quadrupole ICP-MS. Concretions grew in laboratory conditions, and new growth was 5-10 μm in 12 weeks. Headspace methane concentrations decreased in all samples during incubation but least in abiotic controls, where the microbial activity was eliminated, indicating that concretions have methanotrophic communities.

Incubation solutions' metal analysis showed that metal concentrations increased more in the abiotic controls than in biotic triplicates after a 12-week incubation. Metals thus dissolved from concretions into the incubation solution faster without the activity of microbial communities. We suggest that microbes in the concretions affect the concretions' growth and accumulation and release processes of metals.

Presenter: Rashmi Shrestha

Title: Impacts of diverse undersown cover crops on root associated fungi in Finnish agriculture

Abstract:

Root-associated fungal (RAF) species can live on the rhizoplane or endosphere and are a subset of all fungi present in the bulk soil. Plants can influence the composition of RAF communities via root exudates and litter production. RAF communities in turn can influence the plant performance as mutualists, endophytes, saprotrophs and pathogens. For instance, arbuscular mycorrhizal fungi are dominant mutualists that improve plant performance by increasing plant nutrient uptake in exchange for plant-derived carbon. It has been shown in grasslands that increasing plant species richness had either positive or no effect on RAF richness. Studies have also shown the effects of plant functional group identity on RAF communities, for e.g., grasses have higher root endophyte abundance and diversity than forbs. However, the effect of plant diversity on RAF communities in agricultural soil remains largely unexplored as agriculture diversification is still not so common. My PhD project aims to investigate the impacts of plant diversity on RAF in Finnish agricultural soil. Here, we used a newly established agricultural experimental field where barley is undersown with 1, 2, 4 and 8 cover crop species varying in their functional traits (shallow or deep rooted, ability of N₂-fixation or not). The root samples were collected from barley and cover crops in 2019 and 2020 to determine the root fungal colonization level by staining and microscopy and community by sequencing. The preliminary results will be presented and discussed.

Presenter: Svetlana Sofieva-Rios

Title: Antarctic viruses and ice nucleation

Abstract:

Biological micro-organisms are known to be among the most efficient ice nucleating particles, being able to initiate freezing at temperatures up to -2 C. In atmosphere, this activity has an important role in cloud formation and dynamics. For the microbes in the air this activity was suggested to be a survival mechanism to tolerate cold atmospheric conditions. The best known ice nuclei are bacteria whereas very few reports exist about viruses as ice nuclei. Recently, different types of model viruses were shown to be able to nucleate ice at temperatures up to -12 C. However, specific component responsible for the observed activity has not been determined. One hypothesis was that the overall organization of the virion surface architecture could result in ice nucleation activity. This observation was supported by the variation in ice nucleation activity of viruses with different architectures.

The viruses ice nucleation activity of most active tested viruses has been shown to have potential significance in cloud glaciation over the marine area. To further explore the ice nucleation potential for viruses, two environmental viruses extracted from Antarctic sea ice were tested for their activity. In warming climate due to melting ice caps, the emerging species and their potential functions may have a significant role in the environment. The ice nucleation results for the tested two viruses coincide with previous findings for the model viruses and highlight the potential importance of viruses in cloud glaciation over polar marine regions.

Abstracts for posters

Presenter: Fang Chi (*also pitching*)

Title: Alpha-synuclein aggregation and reduced lifespan elicited by *Desulfovibrio* bacterial metabolite in a *C. elegans* Parkinson's model

Abstract:

Parkinson's disease (PD) is typically characterized by the aggregation of alpha-synuclein (α -syn) in the human brain, a process that has been demonstrated to occur in gut cells as well. Our previous research has shown that pathogenic gut microbes *Desulfovibrio* bacteria from PD patients, induce significantly greater and larger α -syn aggregation in a *Caenorhabditis elegans* model of PD. In this study, we investigate the effects of *Desulfovibrio* bacteria metabolites on the acceleration of alpha-synuclein aggregation and reduction in longevity of *C. elegans*. Our findings demonstrate that *Desulfovibriobacteria* from PD patients induce more alpha-synuclein aggregation and higher mortality rates compared to those from healthy individuals. Future research will focus on identifying specific metabolites that influence alpha-synuclein aggregation and lifespan.

Presenter: Ada Pajari (*also pitching*)

Title: Elucidating the molecular dynamics of *E. coli*'s heat/cold shock proteins

Abstract:

In their natural environment, bacteria encounter temperature fluctuations outside of their optimal growth temperatures. As a physical variable, temperature profoundly affects the cellular biochemistry including enzymatic reaction rates, protein folding and lipid membrane fluidity. The bulk of our current understanding of these temperature-dependent processes come from in vitro studies, in which enzymes, lipids and other macromolecules have been studied in isolation without the complexity of the living cell. In bacteria, the biochemical properties of the cytoplasm, such as molecular crowding and viscosity, are emerging as important regulators of molecular dynamics. The physicochemical properties are highly temperature-dependent; however, how temperature-induced changes in these properties affect molecular dynamics, is largely unknown. Consequently, the aim of my project is to use super-resolution microscopy and single-molecule tracking to elucidate the interplay between temperature, cytoplasmic properties and molecular dynamics both above and below the optimal growth temperatures in the model organism *Escherichia coli*.

Presenter: Dongming Zhang

Title: Enhancing Bread Nutritional Quality and Postbiotic activity with Spent Yeast

Abstract:

In my study, the specific Spent Brewer's Yeast (SBY) from probiotic *Saccharomyces boulardii* brewery is innovatively utilized as the substrate to enhance human health nutrients through bioprocessing with various functional bacteria. The SBY ferments containing enriched human-nervous nutrients, Gamma-aminobutyric acid (GABA), and B12 vitamin (B12), are applied as ingredients together with *S. boulardii* in bread making to obtain the postbiotic bread with bioactivities. The dynamic changes of these nutrients will be monitored during the fermentation process and in the final bread. Furthermore, the microbiological and chemical properties of nutrients-enriched probiotic bread are determined. It aims to comprehensively understand the postbiotic activity of the novel human neural beneficial bread and improve the valorization of beer by-products.

Presenter: Nina Zhang (also pitching)

Title: A Lactose and Protease Positive Probiotic *Lactobacillus rhamnosus* GG

Abstract:

Lactobacillus rhamnosus GG (LGG), a probiotic that has been extensively investigated for over three decades¹, enhances growth, reduces the incidence of gastrointestinal infections and immune-related diseases in infants. In the administration of non-probiotic drugs, dairy and infant formula are the most common matrices used for delivering LGG. There are already marketed infant formula with LGG proved its effectiveness in improving children's tolerance to cow's milk. Nevertheless, despite the numerous beneficial attributes of LGG on health, challenges persist in achieving effective colonization especially in preterm infants. The constrained ability of LGG to break down casein and lactose possibly may be one of the reasons that impede its colonization process within the intestine. This becomes especially significant given that human milk and infant formula, the exclusive sources of nutrition during the first six months of life, are rich in lactose and casein⁹. Therefore, we implemented a non-GMO approach and created a LGG derivative strain (LAB53) with the capability to metabolize both lactose and casein. The aim of this study is to validate the strain and evaluate its stability and functional attributes.

Presenter: Kim Kreuze (also pitching)

Title: Role of temperate phages on the developing infant gut microbiome

Abstract:

The gut microbiome is crucial for the human infant development, impacting the immune system, metabolism, and disease. However, the role of the infant gut phageome (bacteriophages of the microbiome) in this interplay remains unclear. Infant phageome development begins with a post-birth spike of induced phage particle concentrations in the stool. This is followed by a gradual increase in phage particle concentrations while the proportion of induced phages decreases. The infant gut also contains mobile genetic elements (MGEs) like plasmids and phage satellites which compete with prophages for bacterial hosts and have evolved to inhibit one another.

These elements interact in complex ways that affects bacterial fitness and thus likely influence ecological and evolutionary dynamics of the microbiome. In my PhD I aim at understanding the MGE dynamics in the context of the mass induction spike during early infancy. My hypotheses are: 1) phage induction expands phage host range, enhancing horizontal gene transfer, and 2) bacterial mortality from the mass induction event increases MGE prevalence, potentially transferring fitness enhancing genes to bacteria. To complete this study, I will analyze bulk and VLP enriched gut metagenomes from both in-house and publicly available infant cohort studies. From the metagenomes I will assemble MAGs (Metagenome Assembled Genomes) of bacteria and phages and annotate them with state-of-the-art software. The results from my PhD will bring us closer to a full understanding how natural, host-associated phage communities can impact human health.

Presenter: Aditya Thiruvaiyaru

Title: Host factors required for efficient replication of alphaviruses

Abstract:

Alphaviruses are a group of arboviruses with +ssRNA genomes. The family includes chikungunya, which has been prevalent around the globe and Sindbis virus which causes recurring epidemics during late summer in Finland. Alphavirus non-structural proteins (nsP1-4) recruit several host factors to form membrane invaginations (spherules) which act as their replication factories. The host factors involved in this process are poorly characterised, suggesting a need for better insight of the alphavirus replication biology. To further our knowledge of the micro-environment of these replication factories, we generated a mutant Semliki Forest virus (SFV) wherein nsP3 was fused with a biotin ligase capable of biotinylating during replication. The biotinylated proteins were purified and analysed with mass spectrometry. Among the top hits our dataset, we found known interactors including stress granule associated G3BPs, adapter proteins like CD2AP and SH3KBP1, and membrane remodelling proteins like BIN1 (Amphiphysin-2). However, most of the identified proteins were novel in context of alphavirus infections. We have performed a siRNA-based screen against the novel hits from our dataset and found host proteins that have a pro-viral role which included chaperones and translation factors. Currently, we are performing functional assays to establish the role of the identified pro-viral proteins in the replication of alphaviruses. Identifying the key components in the life cycle of alphaviruses will play an important role in the development of host-targeted antivirals.

Presenter: Vinaya Venkat

Title: Suitability of saliva for NGS-based diagnostic surveillance

Abstract:

Monitoring the prevalence of respiratory viruses within a population serves a crucial tool for tracking ongoing infections and informing measures to curb their spread. This project aims to develop an innovative sequencing-based approach to detect respiratory viruses in saliva samples. Leveraging the non-invasive nature of saliva, I seek to establish it as a convenient medium for surveillance. Specifically targeting respiratory viruses, the project seeks to enrich the virome of saliva samples, with a focus on prevalent pandemic-causing viruses like SARS-CoV-2 and Influenza. The objective is to not only monitor the presence of these viruses but also assess other circulating viruses, determining their endemicity and potential pandemic threat. The study involves the analysis of over 150 saliva samples from a biobank. If the work is successful, the proposed method could be implemented for routine diagnostic surveillance, contributing to healthcare monitoring at both the national and regional levels.

Presenter: Jiahui Zhu

Title: Molecular epidemiology of the SARS-CoV-2 omicron variant in Finland

Abstract:

Background: The omicron variant of SARS-CoV-2 has been proven as a diversified variant with lower risk for public health than the previous variants. Public health policy has been adjusted toward endemic COVID-19. Understanding the molecular evolution and epidemiological characteristics of omicron variant is vital to evaluate the current public health policy and project future epidemic. **Method:** In this study, we collected sequencing data of omicron variant based on Finnish dataset to identify the dominant circulating lineages responsible for epidemic wave and high frequency mutations (HFM) driving the evolution of the omicron variant. We planned to combine sequencing data of omicron variant with surveillance data of daily number of COVID-19 cases to qualify the transmission dynamics of SARS-CoV-2 omicron variant. A multivariable regression model will be fitted to identify HFM significantly associated with transmissibility of the omicron variant. **Preliminary progress:** A total of 22,828 SARS-CoV-2 omicron whole-genome sequences with high coverage from Finland (November 2021 to June 2023), were included in the analysis. During Nov.21-Jun.23, six clades of omicron variant were detected (BA.1, BA.2, BA.4, BA.5, BQ.1, XBB,). The BA.1 lineage of the SARS-CoV-2 omicron variant was first identified in Finland in November 2021, and had been spread rapidly around the country. The BA.2 lineage outcompeted BA.1 lineage and became predominant in 2 months from first identified in January 2022. The BA.5 (first identified in May 2022) lineage showed considerably steeper growth, becoming predominant lineage in around 1 month. The XBB lineage was first identified in October 2022 and took over the BQ.1 lineage in February 2023. The study is ongoing. **Significance:** The research is expected to yield insights into the genetic and epidemiological characteristics of the omicron variant in transition from pandemic into potential endemic, project the future epidemiology of COVID-19, and inform public health policy.

Presenter: Anne Tyvijärvi

Title: How is soil C stabilized in the subarctic tundra?

Abstract:

Arctic tundra ecosystems store a significant proportion of the global soil organic carbon (C). However, warming-induced shrub encroachment and reindeer (*Rangifer tarandus* L.) grazing regimes promoting graminoid vegetation may strongly influence tundra soil C stability. We studied how reindeer grazing intensity and experimental warming affect soil C stabilization in a subarctic tundra ecosystem. We hypothesized that under light grazing, persistent complexes formed by fungal necromass (FNM) and condensed tannins (CT) from shrub roots stabilize the soil C, whereas, under heavy grazing, the soil C stabilization is affected by glomalin-related soil proteins (GRSP) produced by arbuscular mycorrhizal fungi of graminoids. In addition, we expect warming to mediate grazing effects, diminishing the potential for C stabilization. Our results show no effect of grazing on stable C concentration, however, under light grazing the labile C concentration was higher. We found higher concentrations of chitin and tannins under light grazing, indicative of soil C stabilization potential through FNM-CT complexes. By contrast, we found more root ergosterol under heavy grazing, suggesting a high abundance of endophytes, usually melanized, and a slightly higher GRSP concentration. Warming did not cause changes in stable C concentration but was associated with changes in the soil chemical quality. We conclude that different soil C stabilization mechanisms operate under light and heavy grazing pressures and that these mechanisms are closely linked to changes in the vegetation and the fungi typically associated with them.

Presenter: Yue Yin (also pitching)

Title: Enhanced Pathogen Suppression by Two Interacting Competitive Microbes

Abstract:

This study demonstrates that the competitive interaction between *Ralstonia pickettii* and *Acinetobacter calcoaceticus* significantly enhances the inhibition of *Ralstonia solanacearum* beyond the effects observed with either species alone. Through transcriptome and metabolome analysis, we identified key mechanisms that underlie this enhanced pathogen suppression, including the upregulation of competition-related genes and metabolic pathway in *R. pickettii*, as well as the release of toxins by lysis of *A. calcoaceticus*. These strategies not only mediate mutual inhibition between *R. pickettii* and *A. calcoaceticus* but also significantly bolster pathogen suppression. These insights offer promising strategies for enhancing microbial-based pathogen control in diverse environments, warranting further exploration into their applicability across natural and engineered microbial communities.