

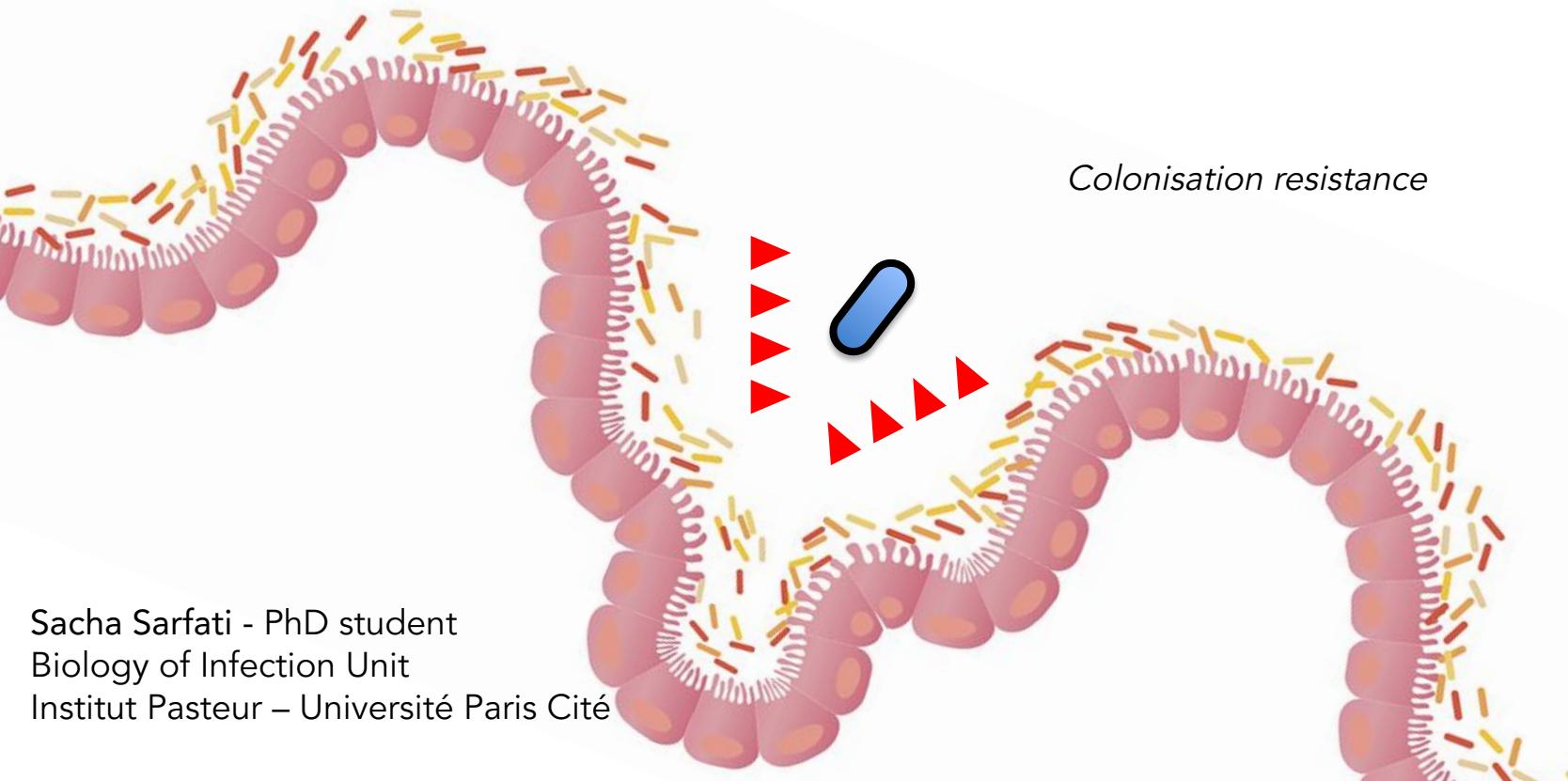


Lightning Presentations

Tuesday July 4

Please add 1-2 slides about your research, your goals for the workshop, or yourself!

Impact of the gut microbiota on *Listeria monocytogenes* intestinal carriage



Sacha Sarfati - PhD student
Biology of Infection Unit
Institut Pasteur – Université Paris Cité



Cystic fibrosis



cysticfibrosisnewtoday.com

Preterm infants



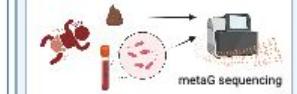
lungdiseasenews.com

WP 1: Data acquisition & processing

PRIMAL cohort



Sepsis subcohort



Fullterm breastfed cohort



Public pre- & fullterm
microbiome & clinical data



WP 2: Microbiome characterization

- shaping factors
- principles guiding colonization
- key species, functions, biomarkers
- define "healthy" microbiome

WP 3: Risk factors for neonatal sepsis

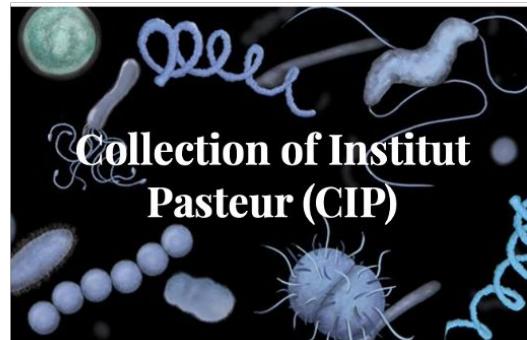
- microbiome susceptibility to pathogens
- clinical risk factors
- putative health consequences

WP 4: Actionable insights and translation

- develop late onset sepsis risk score
- advance microbiome modulation in preterms
- derive new clinical recommendations and interventions

Translation of microbiome research to the bed-side.

Hello all! I am Mennat El Ghalid



- Bacteria
- Viruses
- Fungi
- Other projects

Microbiome → Develop a method of culturomics to study
the human microbiota

Culturomics

Metagenomics

→ We are at the beginning of the project; that's why
the environmental and clinical workshop is spot
on!

Natalie Kokroko (Ghana)





Analysis of phage diversity in drinking network system of Paris

Presented by Mathilde Duvivier

Supervisors :

Pr Yann Héchard

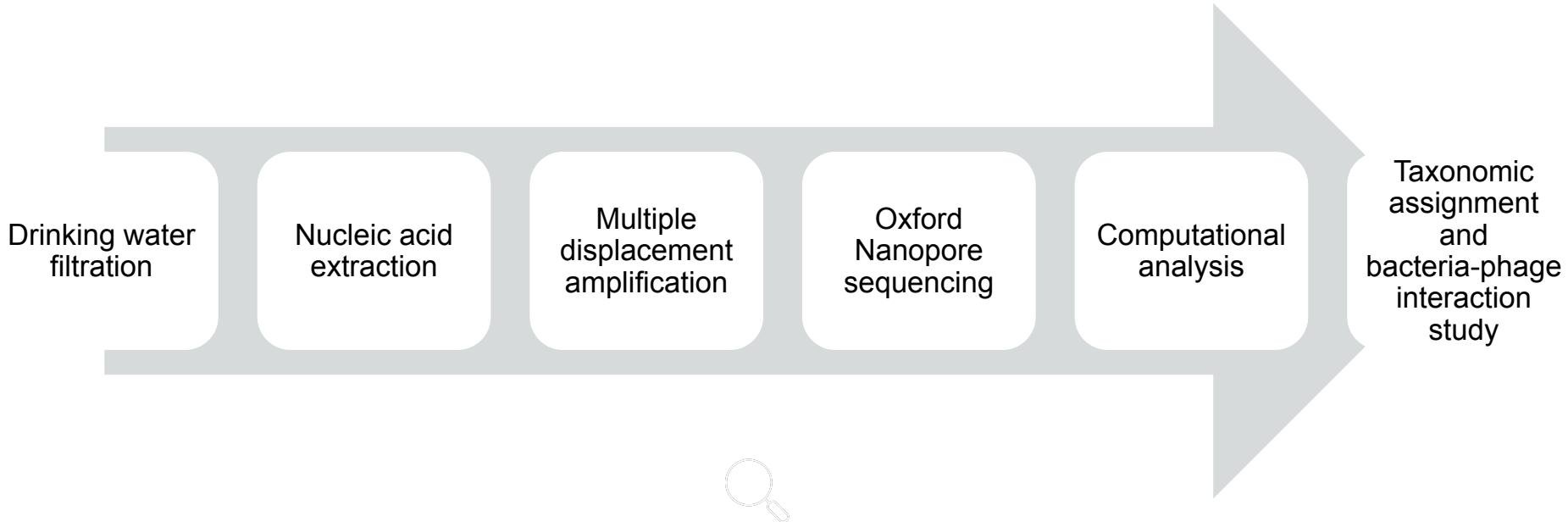
Dr Vincent Delafont

Dr Sébastien Wurtzer

Dr Laurent Moulin

Dr Moumen Bouziane

Experimental pipeline to study phage diversity



Bioinformatic workflow

Assembly

- Flye – comparaison et choix de paramètres d'assemblage

Polishing – mapping

- Abundance

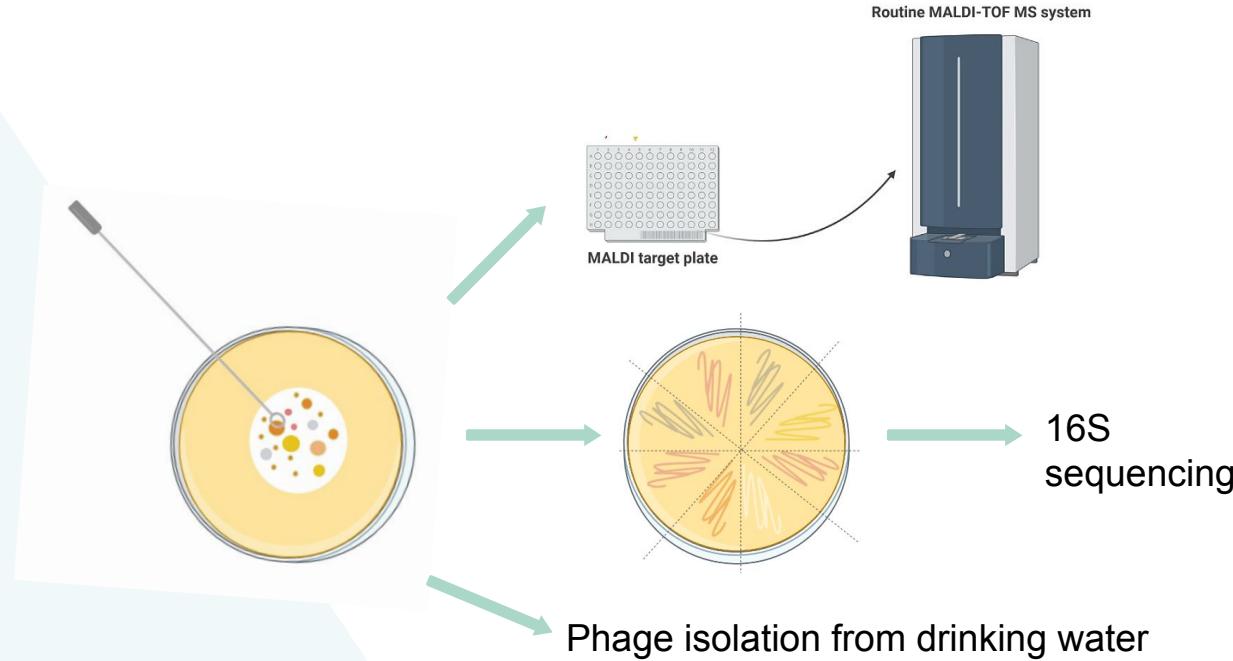
Distinction between viral contigs and non viral contigs

- VIBRANT - VirSorter2 – DeepVirFinder - ...

Taxonomic assignment

- Megablast – Diamond - ...

Bacteria and phage isolation from drinking water system





eau
seine
NORMANDIE
Agence de l'eau
ÉTABLISSEMENT PUBLIC DE L'ETAT



USE OF WASTEWATER-BASED EPIDEMIOLOGY TO ESTIMATE THE DYNAMICS OF URBAN SURFACE WATER CONTAMINATION

Morgane LEVERT

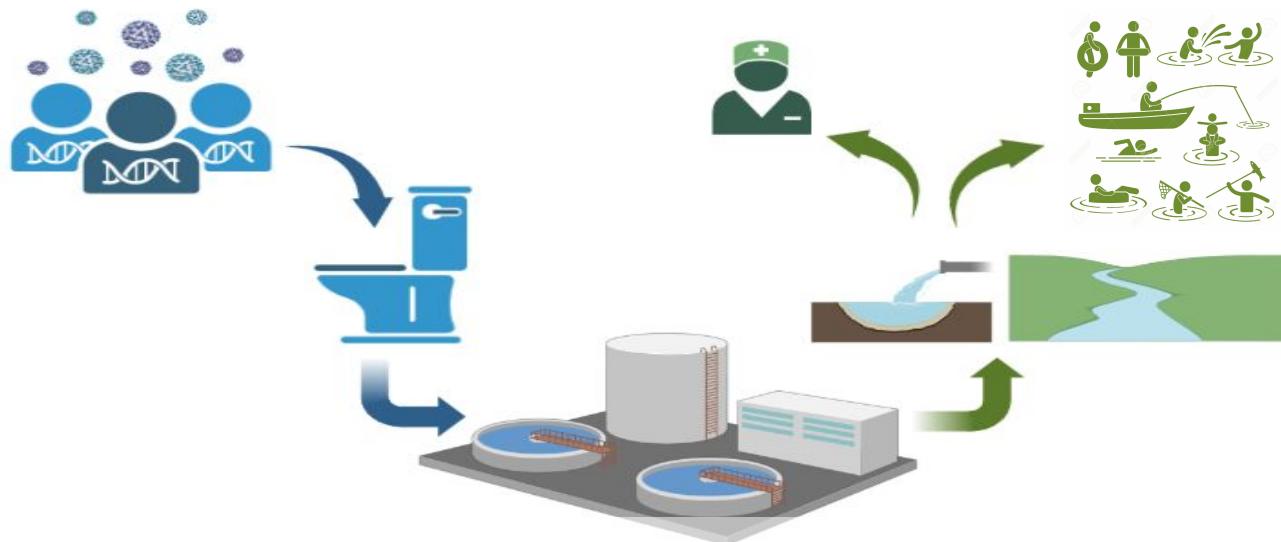
Thesis director: Jean-Marie MOUCHEL (Sorbonne University)

Supervisors : Laurent MOULIN & Sébastien WURTZER

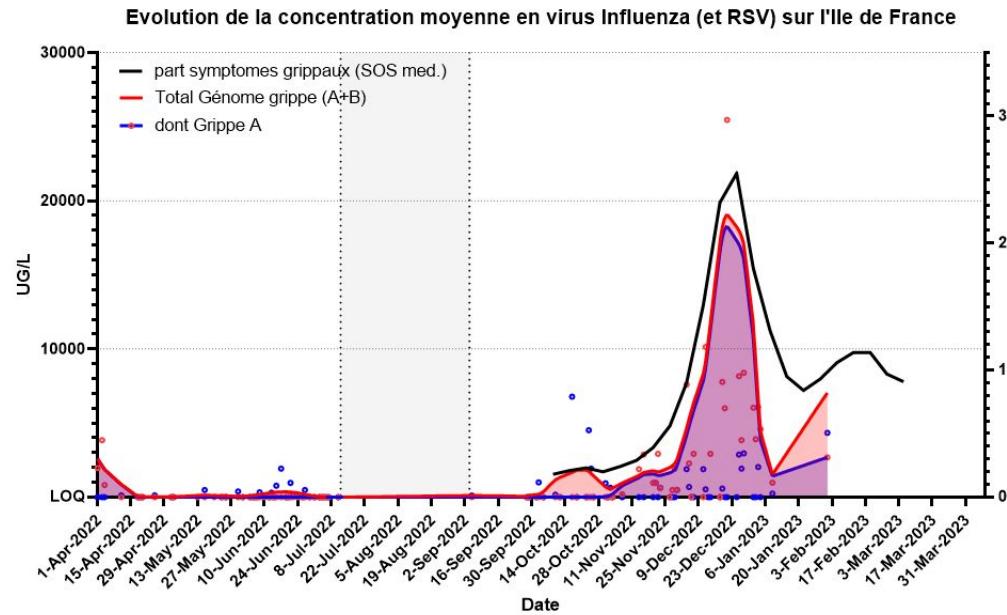
CINEMA WORKSHOP 04th of july 2023

Questions of thesis

- Can the approach used to detect SARS-CoV-2 in wastewater be deployed on other pathogenic microorganisms of interest? (Upstream of wastewater treatment plant/sewer)
- Can we use wastewater epidemiology to understand the risk associated with bathing for users ? Will this tool be useful for epidemiologists or clinicians? (Downstream of the sewer system)



Preliminary results



- Goal: Compare WW data with epidemiological data and see if there is a correlation/anticipation
- Sewage benefits: Allows a particular pathogen to be associated with a specific time in the epidemic wave that cause non-specific symptoms
- Sequencing benefits: Genotyping of certain species, identification of emergent variants

Whooping cough



- ✓ Respiratory disease due to *B. pertussis* (or *B. parapertussis*)
- ✓ Highly contagious through aerosols, severe in fragile individuals (infants <6 months old not yet fully protected by vaccination), pregnant women and elderly or immunocompromised individuals
- ✓ epidemic cycles every 3 to 5 years
- ✓ Protection through vaccination, treatment based on macrolides

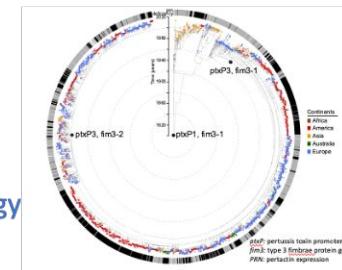


Biological diagnosis of Whooping cough

- ✓ Real-time PCR targeting a transposase *IS481* for *B.pertussis* is possible only if <21 days of cough
- ✓ Culture is possible when bacterial load is high in the sample (Ct-*IS481*<25) and if < 15 days of cough



- Microbiological characterization of strains
- Production of virulence factors
- Systematic whole genome sequencing=> genomic epidemiology



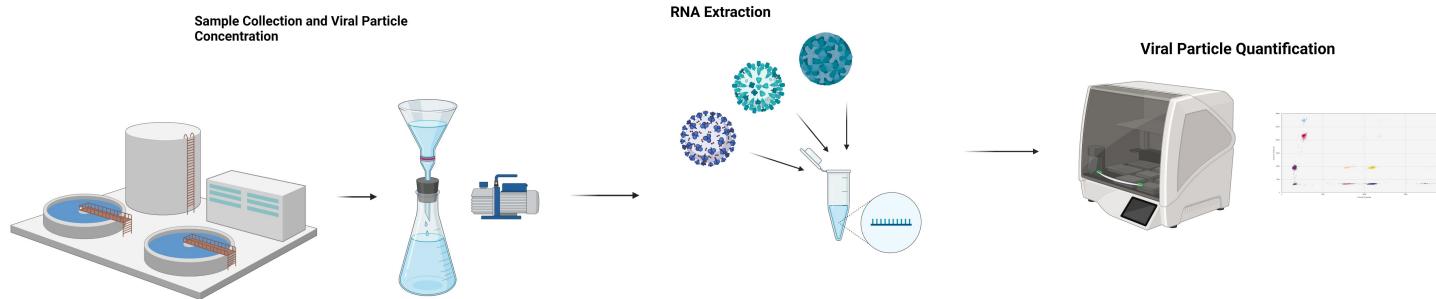
- ✓ Less and less labs are performing culture
- ✓ We need to be able to sequence *B. pertussis* genome directly from respiratory samples without the need of a culture step

How can we capture *Bordetella* DNA within human DNA in respiratory samples??

Wastewater-Based Epidemiology



- Real-time wastewater monitoring of SARS-CoV-2, Influenza A, and Norovirus



- Future Interests: WW Genomic Surveillance and Host-Range of ARGs

Microbial ecology of drinking water distribution systems

Marco Gabrielli
Eawag

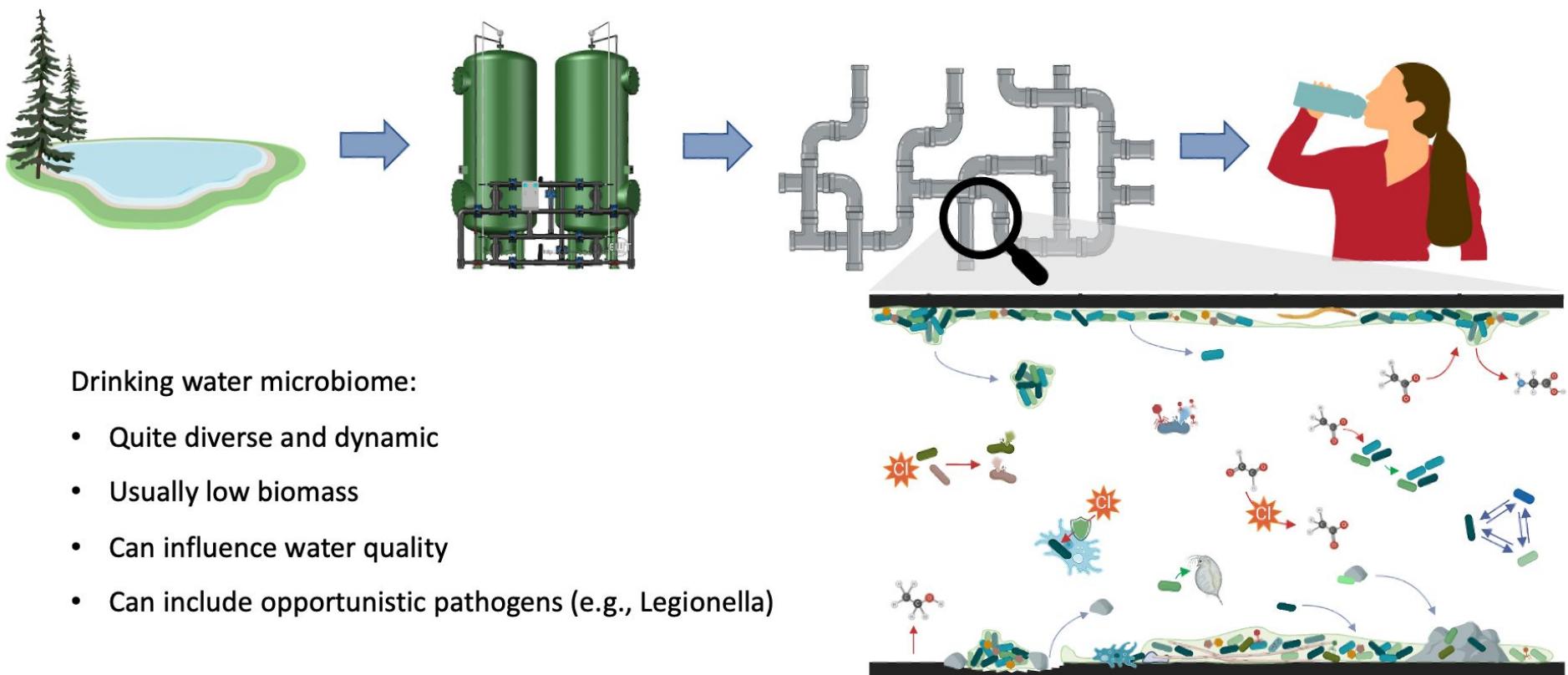
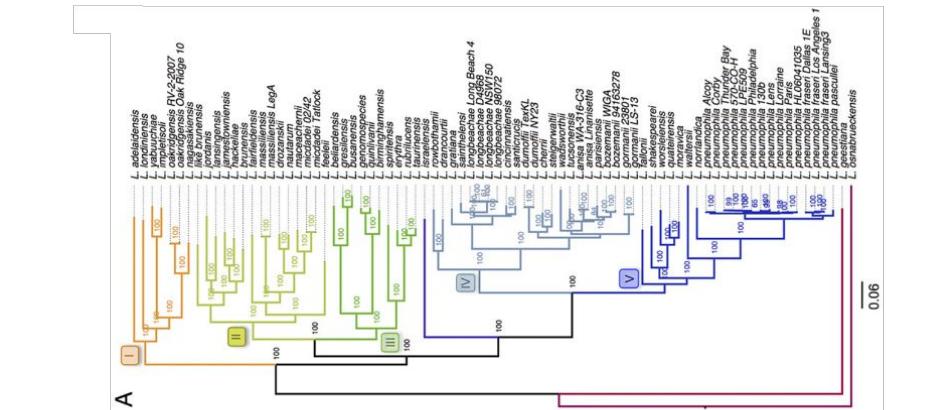


Figure created using BioRender

My research interests:

- Ecological differences among *Legionella* species
- Diversity and ecological roles of eukaryotes within drinking water systems
 - Effect of protistan grazing on biofilms
 - Interactions between *Legionella* and free-living amoebas



Gomez-Valero et al. (2019), PNAS



Figure created using BioRender

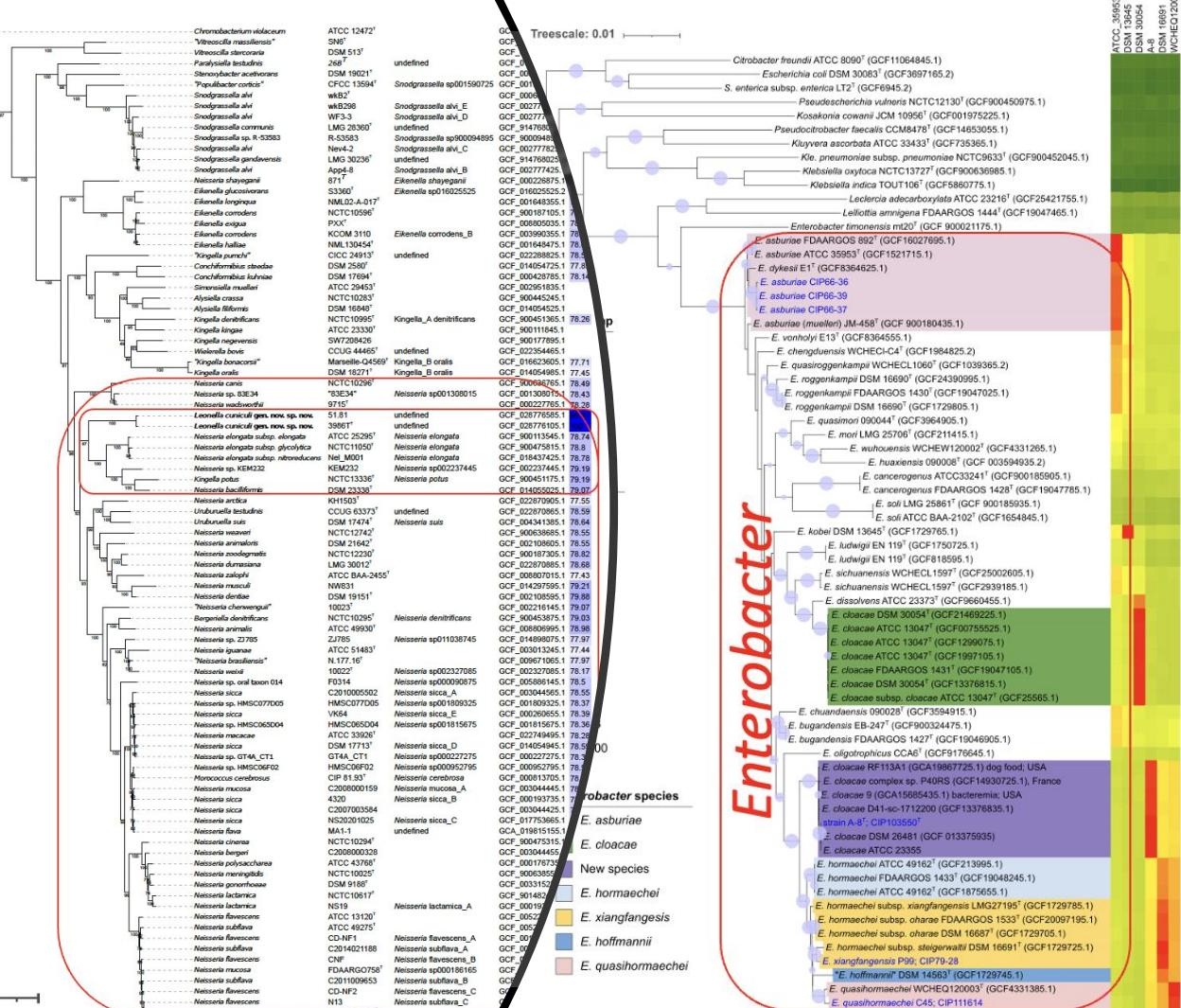
Praveen RAHI

Institut Pasteur, Université Paris
Cité, Collection of Institut Pasteur
(CIP), F-75015 Paris, France

Some species are still not monophyletic in the GTDB tree

Core-gene phylogeny and ANI values allowed the correct identification of species within ECC

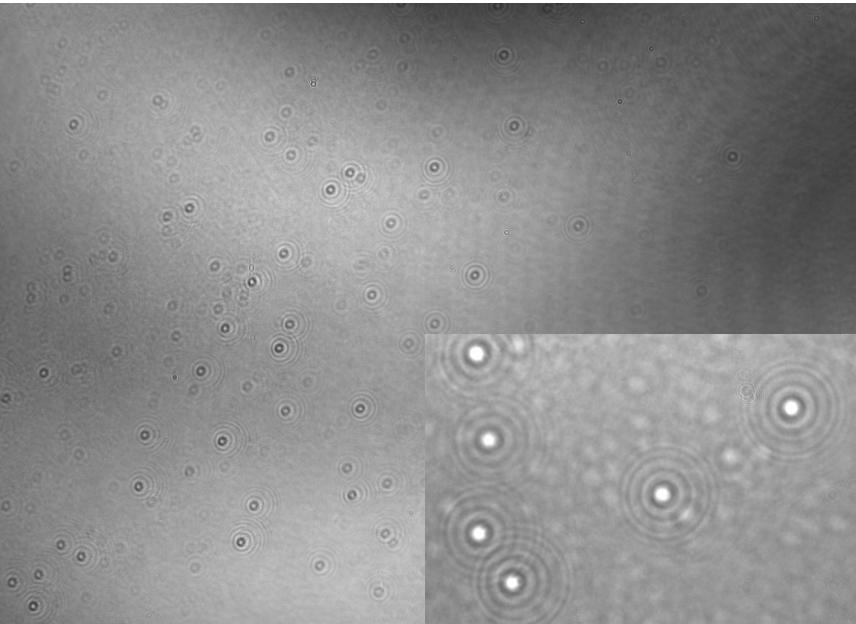
Genome sequence data: the key driver in shaping prokaryotic systematics



Some species are still not monophyletic in the GTDB tree

Core-gene phylogeny and ANI values allowed the correct identification of species within ECC

Digital Holographic Microscopy at IP



Strain: *E. coli* CIP 54.8

Motivation to attend CINEMA

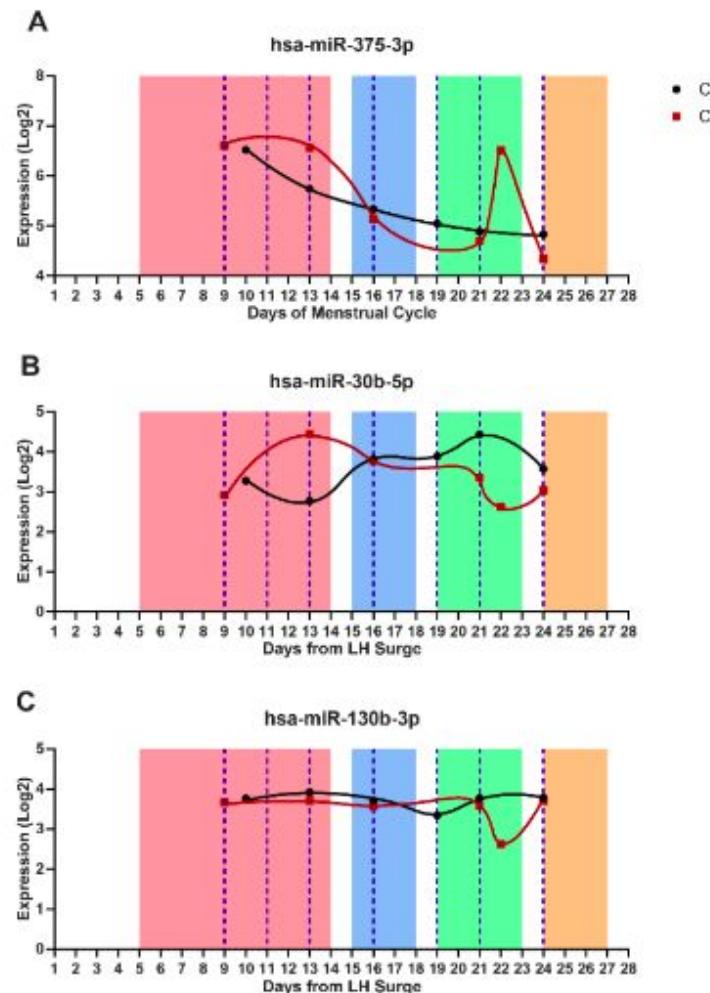
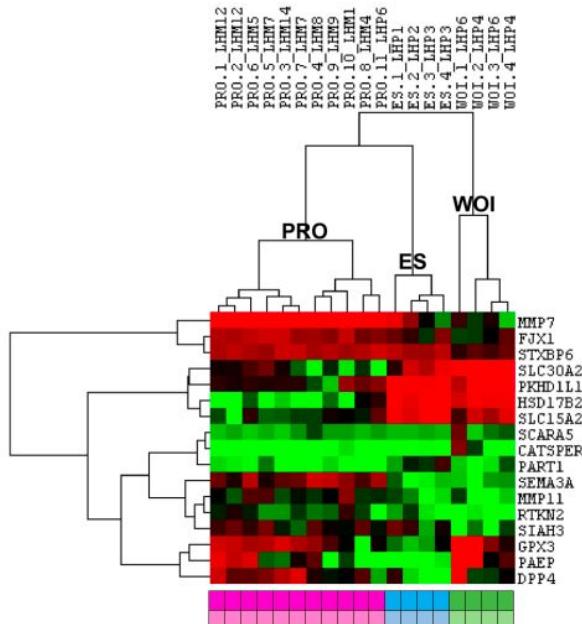
- Look into metagenomic databases for the sequences identical to the potential new taxa.
- Exploit the metagenome sequencing to validate.

Hello everyone!

My name is Ege Dedeoglu

Academic Work (Bilkent and Acıbadem University):

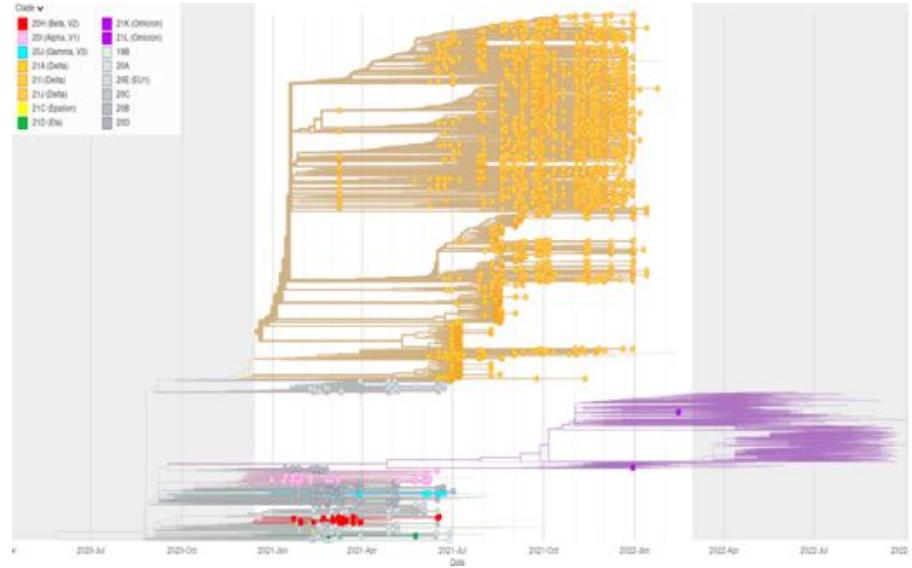
Predicting the Window of Implantation using RNA-based biomarkers:



Current Work (WHO CO TR):

Trainings of Introductory Bioinformatics to Public Health Institute Turkey

Scientific writer and technical support to the MoH - TR



More experience in Metagenomic Analysis for further support to the MOH.

Wastewater surveillance activities increasing limited bioinformatics capacity in TR.

Andele Conradie, Robert Koch Institute, Berlin

- Building international genomic surveillance capacities
- Global Outbreak Alert and Response Network (WHO Hub, Berlin)
- Improving current pathogen surveillance workflows
 - NGS and Third Generation Sequencing and analysis

Examples:

- Southern African – respiratory pathogens (SARS-CoV-2, Influenza, RSV...)
- West Balkans – AMR surveillance in health care settings



Workshop expectations

Learn about metagenomics and data analysis

- Computational approaches to analyze data and put into practice
- Discover tools and resources for metagenomic data
- Metagenomics-enabled microbial surveillance
- Integration in my work (focus on public health sector)

Thank you!

"The interplay of microbiome with mucus in internal and environmental alterations of the host"

PhD Candidate

Jennifer Nazat
Martínez Medina

04.07.2023

AG Forslund

AG Forslund
AG Fulde
AG Siegmund

AG Forslund
AG Fulde
AG Siegmund
AG +

Mucus
sample
types and
microbiota

Mucus-
associated
microbiota
interplay with
mucus and
factors

Mucus-
associated
microbiota in
hypertensive
kidney
damage

AG Forslund
AG Wilck



Masters Student
Carlotta



Meta-
analysis
Mucus-
associated
microbiota in
health and
disease

PhD

Mucus-
associated
microbiota
in pigs

AG Forslund
AG Fulde
AG +

Side projects

AG Forslund
Collaborators

Covid2,
microbiota,
metabolites

Hypoxic brain
damage in
the perinatal
period and
microbiota

AG Forslund
Collaborators



General objective:

To identify the **mucus-associated microbiota** in different **sample types** from two host models.

Biopsy -> Colonoscopy > forceps

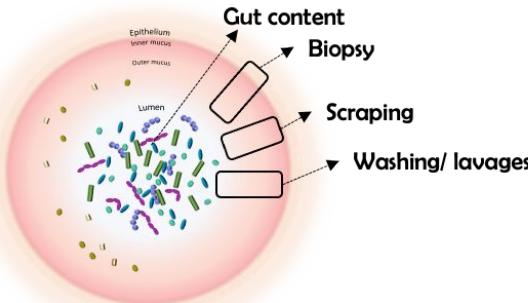
Washing -> Syringe + Cateter > NaCl



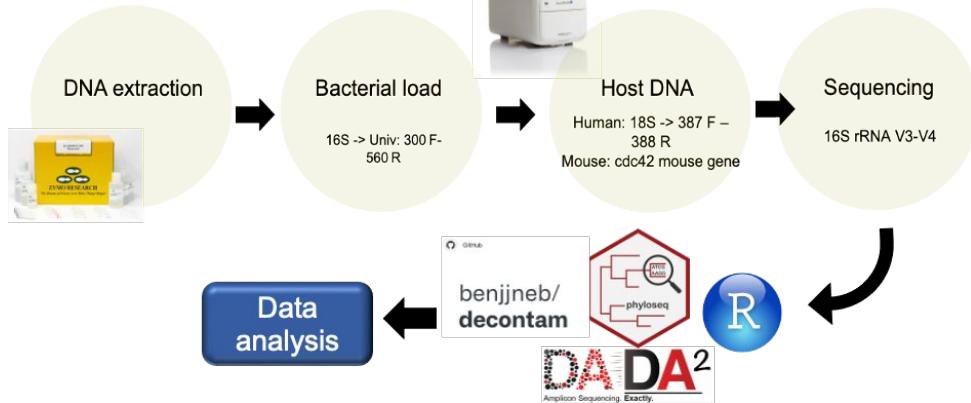
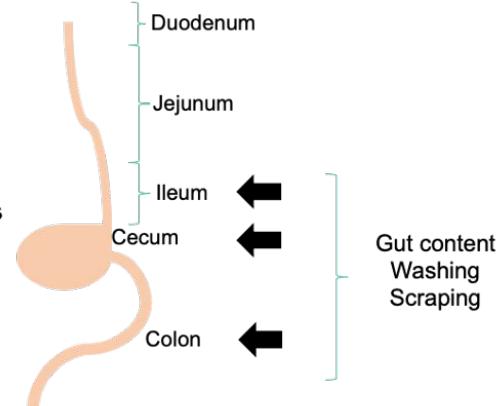
Gut content / Washing



Scraping



Jennifer NMM

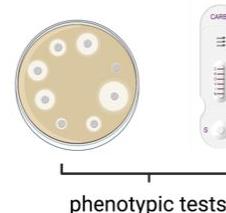


Wastewater surveillance of carbapenem-resistant bacteria and carbapenemase genes

clinical surveillance



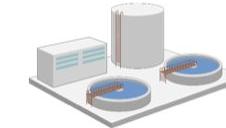
CRE is currently primarily associated with inpatient healthcare settings



wastewater surveillance



Community-associated CRE infection, ranging from 0.04% to 29.5%.



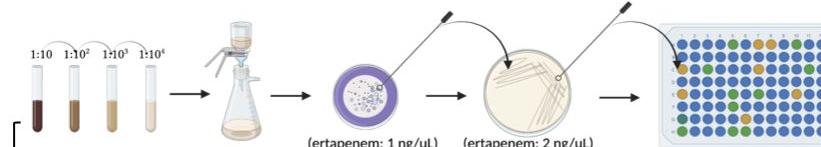
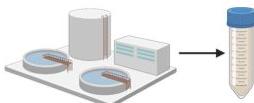
phenotypic method



molecular-based method

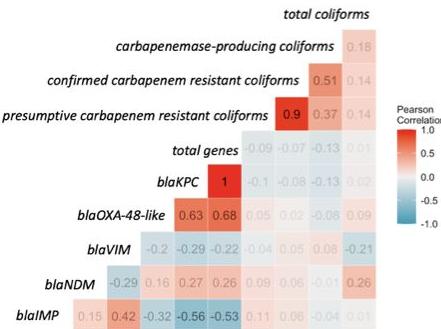
presumptive carbapenem resistant coliforms → confirmed carbapenem resistant coliforms → carbapenemase-producing coliforms

(Culture-based method)

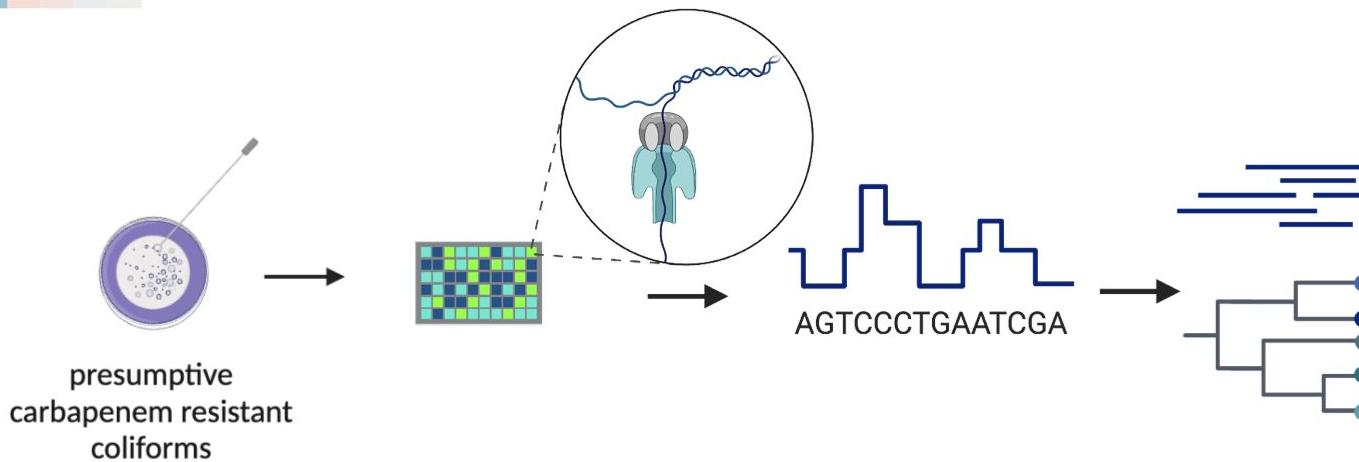


(ddPCR-based method)

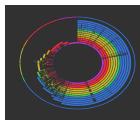
5-plex ddPCR (carbapenemase genes: blaKPC, blaNDM, blaVIM, blaIMP, blaOXA-48-like)



We observed weak or no correlation between the carbapenemase gene abundances and carbapenem resistant colonies



Using long-read sequencing to screen for various mechanisms that may be responsible for the resistant phenotype



Microbial Evolutionary
Genomics Unit

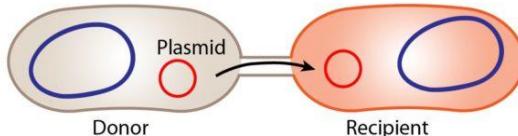


Supervisor:
Eduardo Rocha

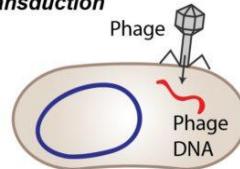
2nd year PhD student

B. Horizontal evolution

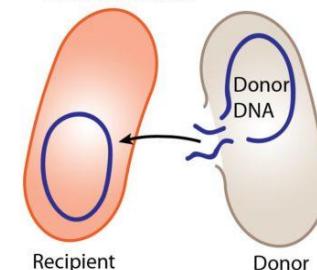
Conjugation



Transduction

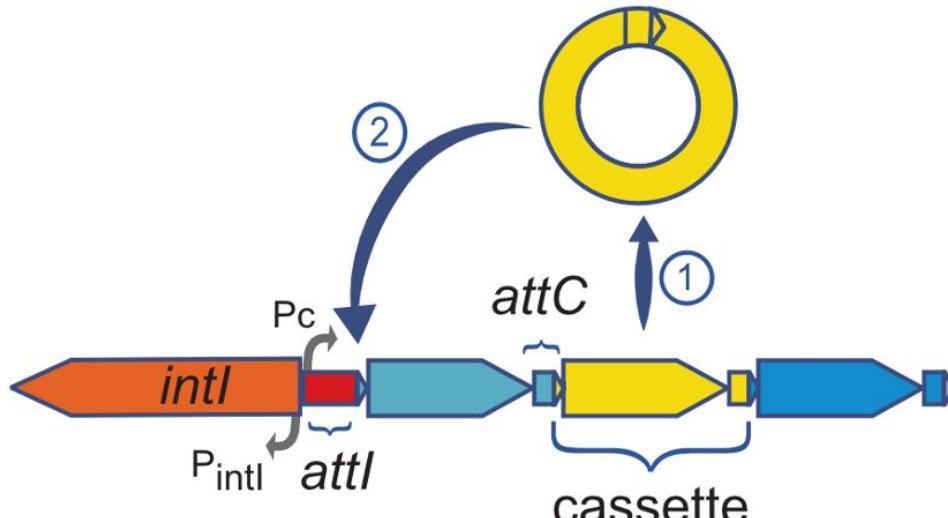


Transformation



*Wellcome Genome Campus Advanced
Courses and Scientific Conferences*

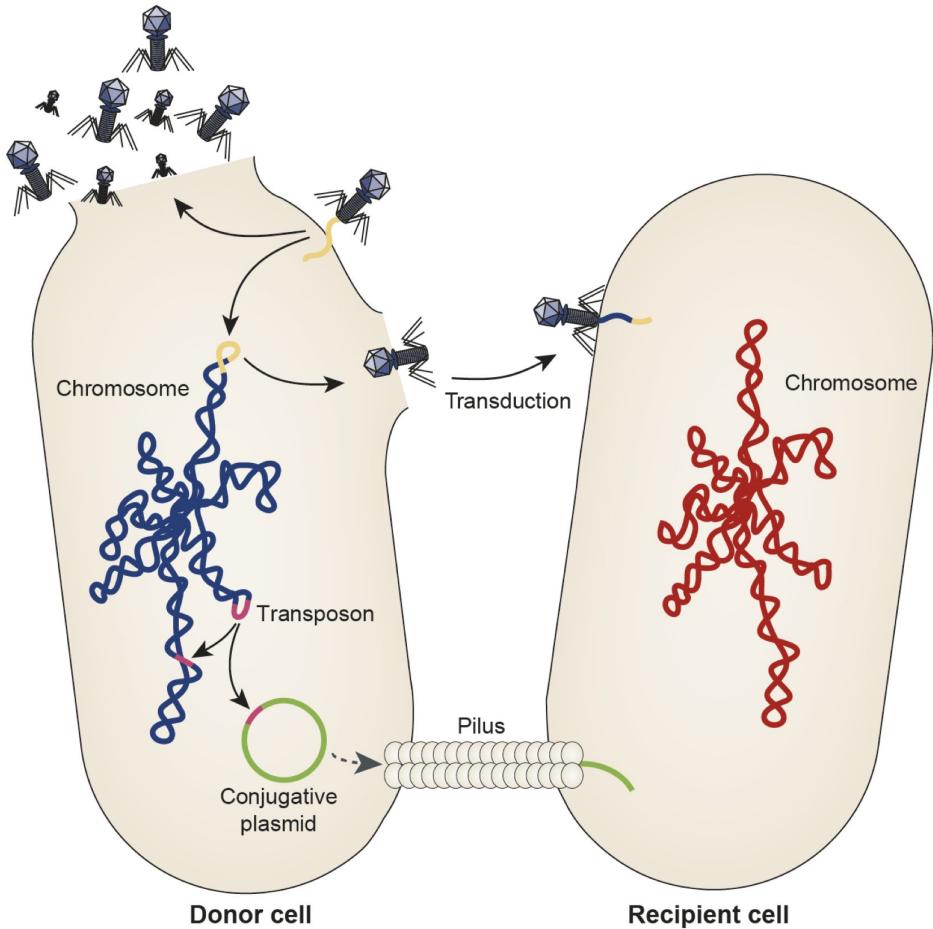
Integrons: adaptive gene-exchanging platforms



- Identified in 1989
- Dissemination of ARGs
- Essentially Gram- bacteria

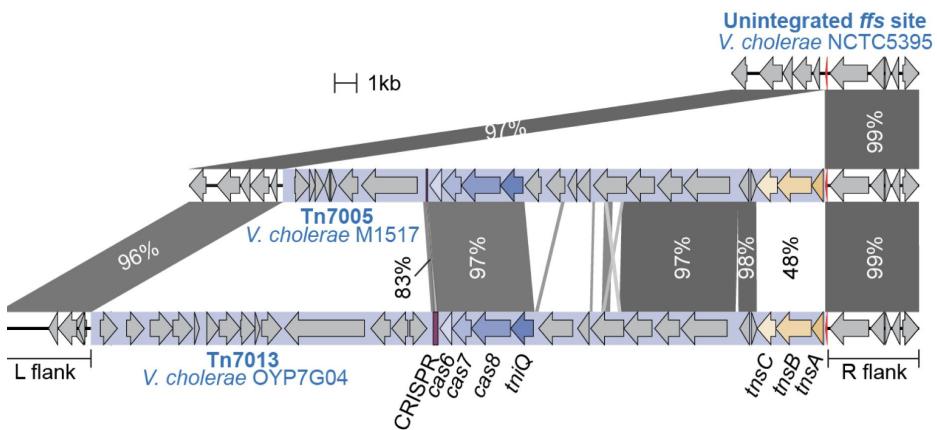


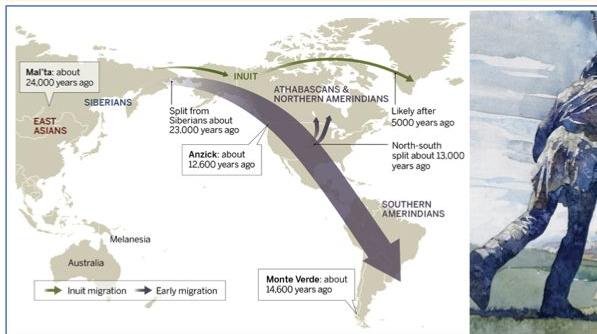
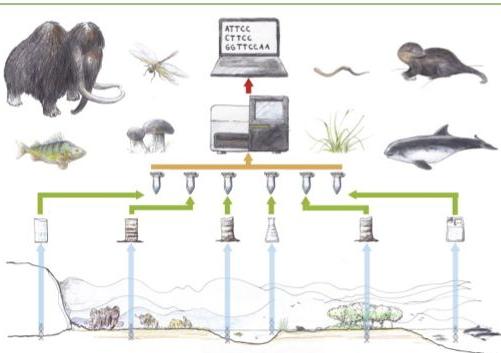
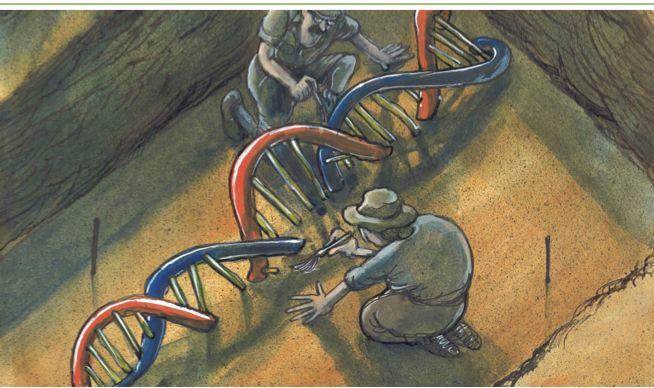
Néron*, Littner* et al., 2022



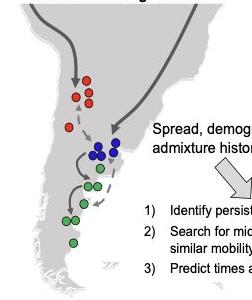
Sanne Klokme
(Postdoc @ Pasteur)

- Transposons
- Anti-phage defense
- Modified phage genomes

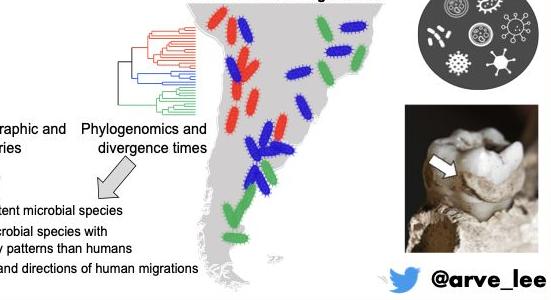




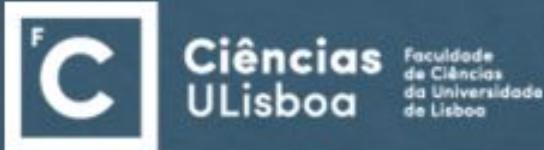
Ancient Human genomes



Ancient microbial genomes



@arve_lee



João Rebelo

PhD student in Evolutionary Ecology of Microorganisms group (Faculty of Sciences of the University of Lisbon)

Biologist



Bioinformatics and
Computational Biology
Master

Predict treatment outcomes during *Salmonella* gut infections using experiments and a computer model -> Plasmid transfer, Indirect Resistance, Persistence

Interest in metagenomics

- ❖ Master's degree in bioinformatics where the topic piqued my interest
- ❖ Looking for antibiotic resistance profiles in genomes namely the correlation between antibiotic resistance and virulence and between different antibiotic resistance classes
- ❖ That maybe could be extended to metagenomic data



Ciências
ULisboa

Faculdade
de Ciências
da Universidade
de Lisboa



Biodiv
Post-Graduation



Célia Domingues

FACULTY OF SCIENCES OF THE
UNIVERSITY OF LISBON

My Path

- Degree in Biology (Genetics and Molecular Biology)
- Masters in Bioinformatics and Computational Biology

Study involving the comparative metagenomic analysis of sediments from oyster and gilthead sea bream aquacultures to study the antibiotic resistance present in these sediments [1]



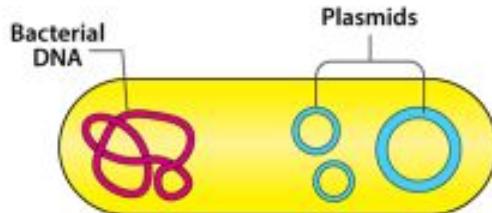
Try to find and identify the plasmids present in the samples

[1] Silva, D. G., Domingues, C. P., Figueiredo, J. F., Dionisio, F., Botelho, A., & Nogueira, T. (2022).

Estuarine Aquacultures at the Crossroads of Animal Production and Antibacterial Resistance: A Metagenomic Approach to the Resistome. *Biology*, 11(11), 1681.

PhD

I intend to confirm the existence and characterize cryptic plasmids both in **metagenomes** and genomes.



Teresa Nogueira
cE3c, INIAV



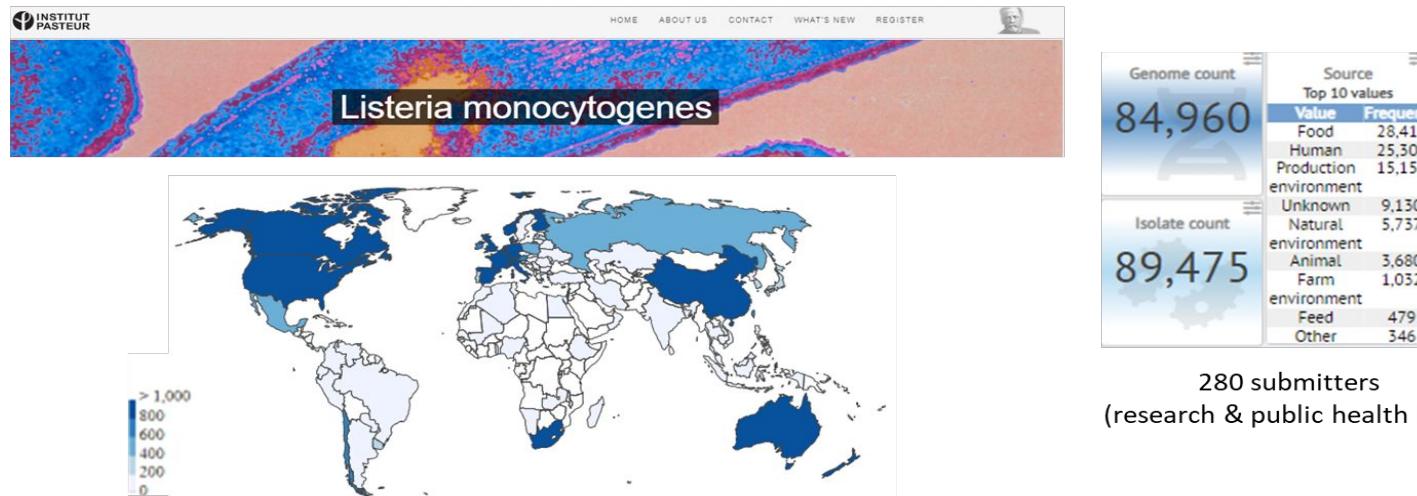
Francisco Dionísio
cE3c

A cryptic plasmid is defined as a plasmid not coding for any trait phenotypically, other than its transfer and replication machineries.

Listeria population genomics: ecology, phylogeography and evolution of pathogenesis



Listeria international database (~85K genomes)



Listeria population genomics: ecology, phylogeography and evolution of pathogenesis

Genomic surveillance of *Listeria* (FR ≥ 2015; clinical and food isolates):

- improved outbreak detection
- reduced nr of cases per cluster
- still ~80% of human clusters w/**unknown source** of contamination



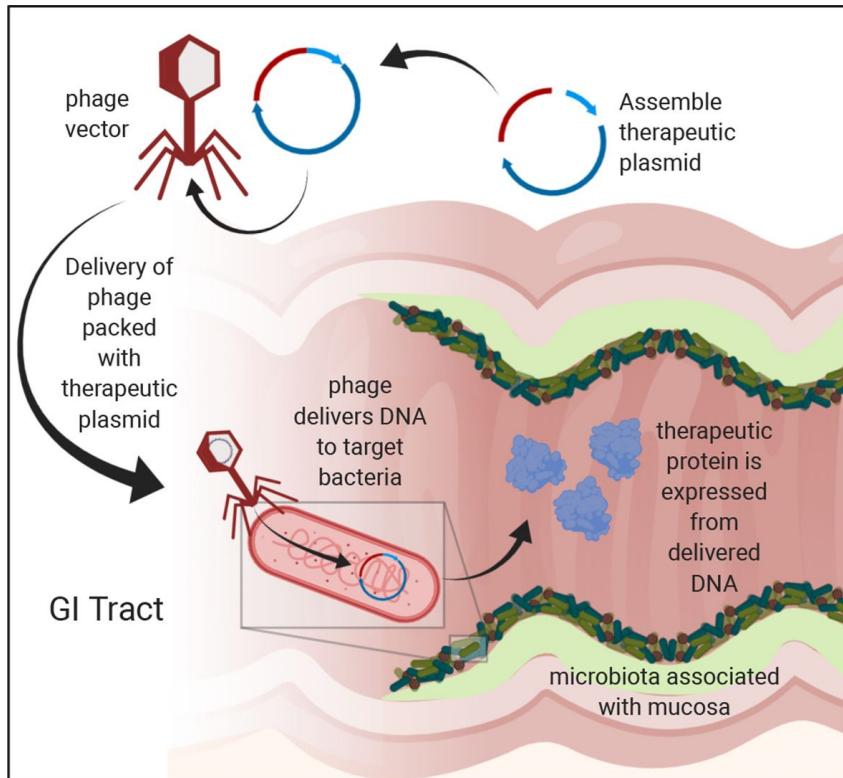
So far:

- Strain typing from assemblies/short-reads (Illumina)
- PacBio & Nanopore (R9) to resolve closed chromosomes and plasmids
- **No *Listeria* signal in 2K public metagenomes** (only in 16S datasets)

Setting up:

- Strain typing from **metagenomes** (CSF, stools) w/Nanopore R10
- Mining **public metagenomic datasets (~34K)**
- Recover *Listeria* from ancient DNA (calibrate phylogenetic trees, date emergence/spread)

- Full picture of the **reservoirs of specific pathogenic *Listeria* clades and species**
- Clarify **microbiota patterns** of associated w/ *Listeria* carriage
- **Enhance surveillance** (faster response; strain typing directly from human samples)



Voorhees et al., 2020

Using phages for *in situ* gut microbiome engineering

Beatriz Beamud



Synthetic Biology Group, David Bikard



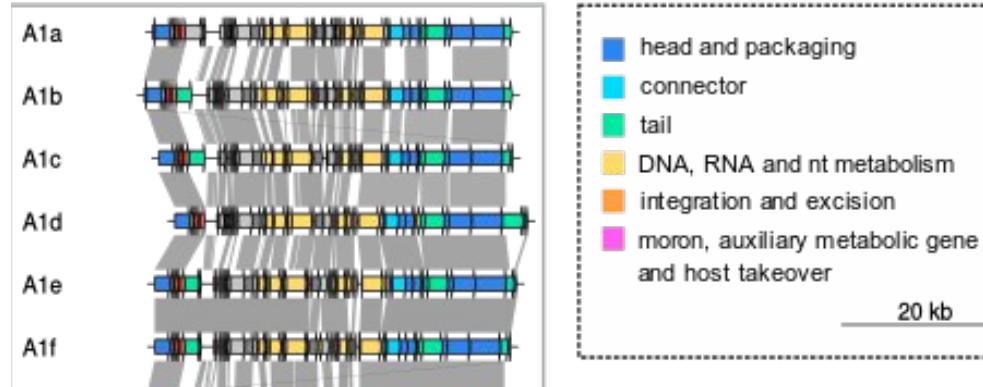
bbeamuda@pasteur.fr



@BeatrixBeamud

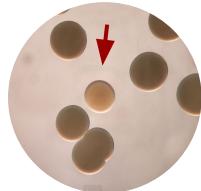
1. Can we obtain the accessory genome of phages from metaviromes?

1. Autographiviridae, Slopekvirinae, Drulsvirus

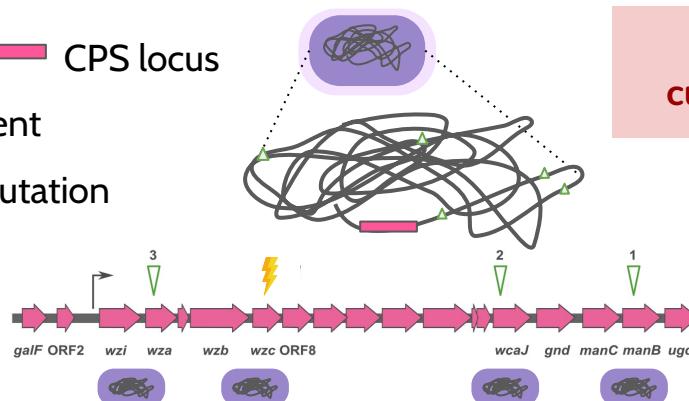


Identification of phage receptor binding proteins

2. Can we quantify *cps* truncation from metagenomes?



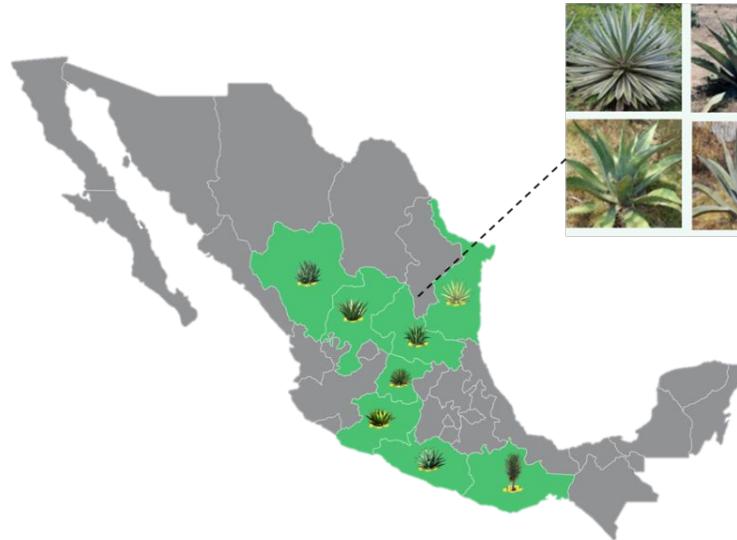
CPS CPS locus
IS-element Point mutation



No bias due to culture conditions



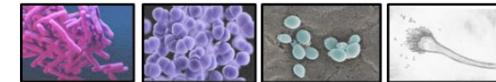
Description of the microbial composition during agave fermentation process using Meta-HiC



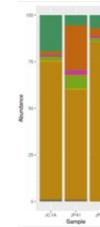
Identify the microbial communities
during the fermentation process
using Meta-HiC.



I. Describe the microorganism diversity in each fermentation phase.



II. Determine the relative abundance of each specie and the metabolic capacity.



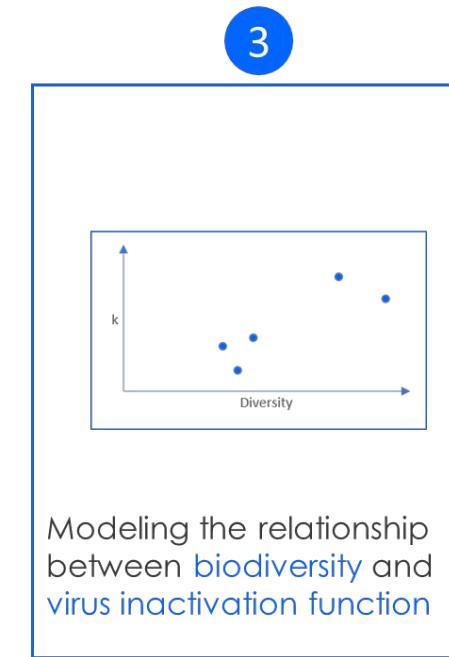
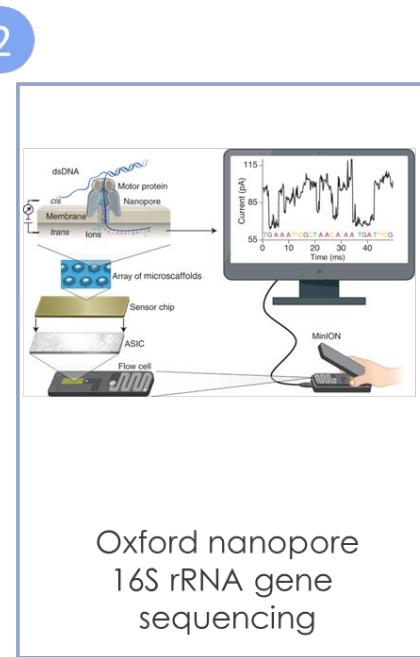
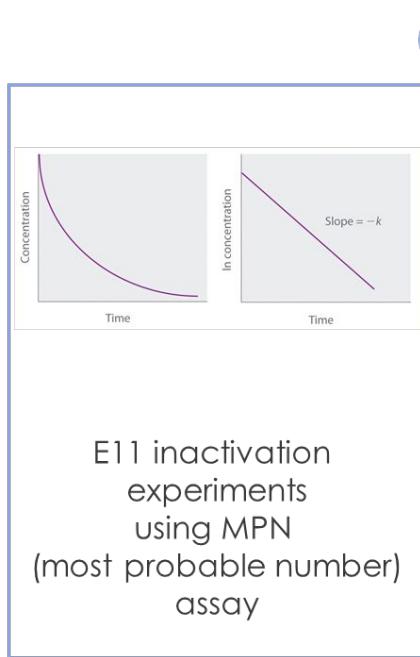
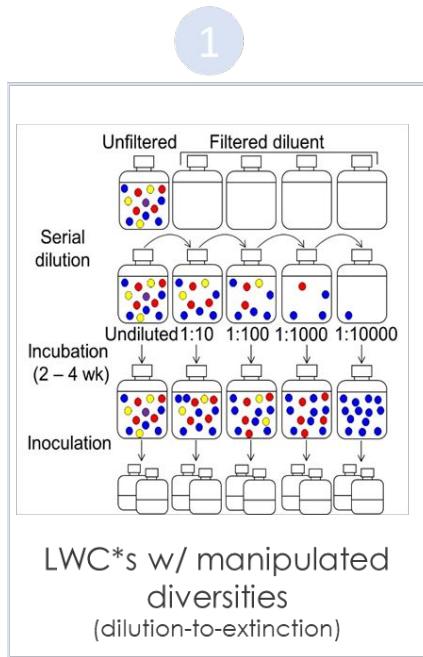
III. Identify if there are *Saccharomyces* hybrids



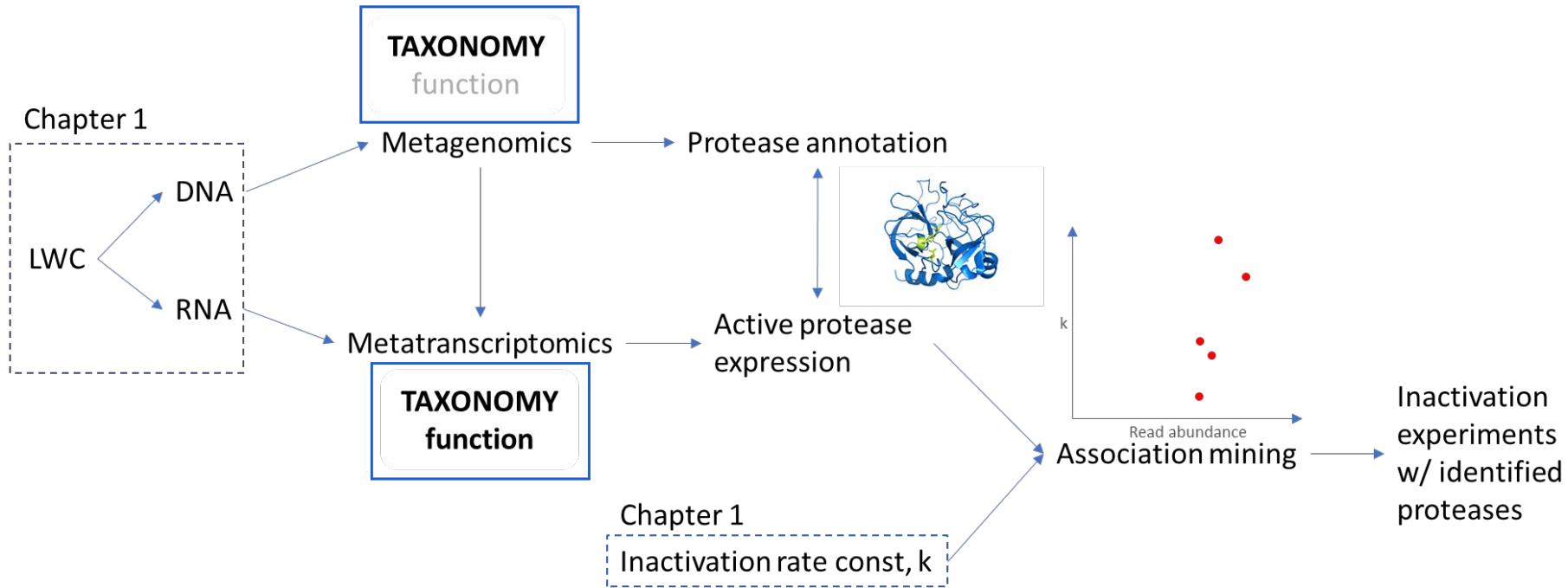
Biotechnological application??

Andrii Romanenko

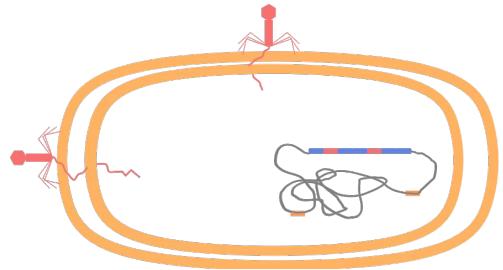
Hypothesis: The rate of virus inactivation is faster in lake communities with higher diversity



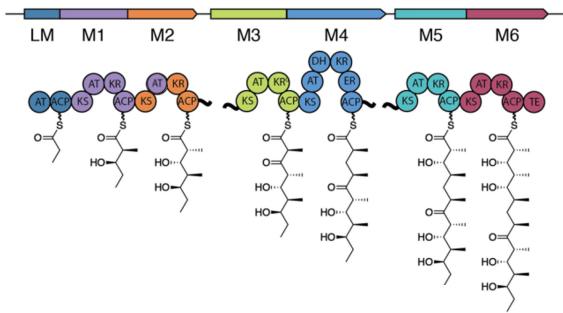
Hypothesis: Actively expressed proteases statistically correlate with virus inactivation rate constants



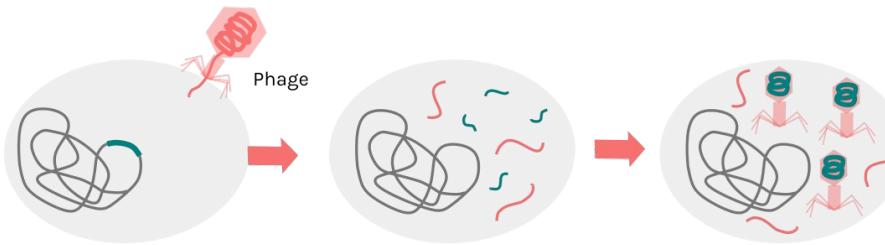
Paula THIEL PIZARRO



From molecular biology to genetics to evolution



Phage satellites are parasites of parasites.
They **parasite phages**, which are parasites of bacteria.

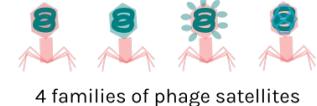


Study the evolution of **polyketide synthases** (PKSs).



Universität
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4 families of phage satellites



Unknown phage satellites

