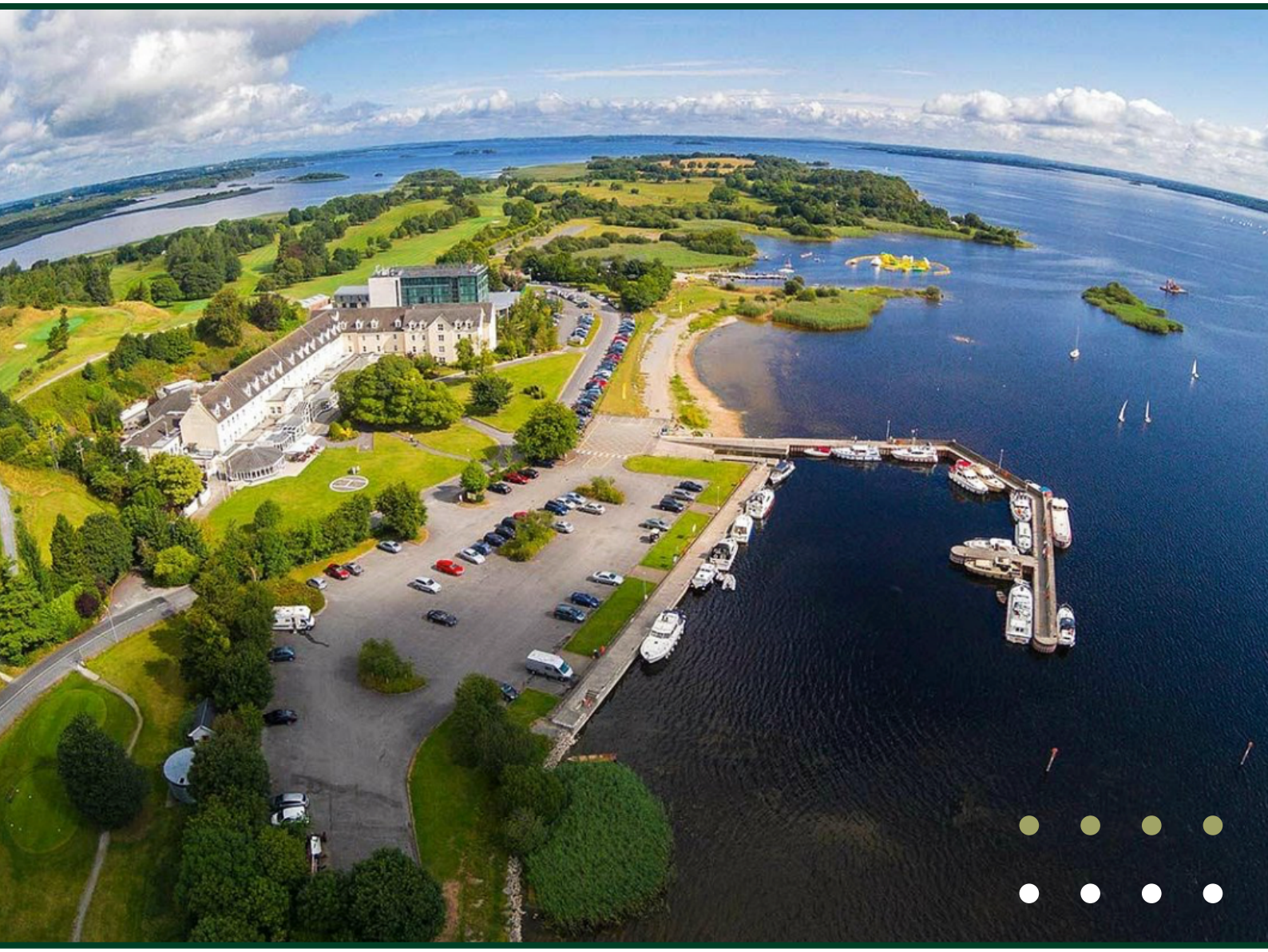
MICROBIOLOGY SOCIETY ANNUAL MEETING IN IRELAND

Hodson Bay Hotel, Ireland
5–6 November 2024

INVITED AND OFFERED TALKS



#MicrobioIrish24

MICROBIOLOGY SOCIETY

Invited talk : No guts no glory: a role of the gut microbiome athletic performance

Orla O'Sullivan

Teagasc, Carlow, Ireland

Abstract

The human intestinal tract is host to an extensive population of microorganisms working in concert to play a pivotal role in human health. Almost every aspect of modern lifestyles can impact the gut microbiota; recently diet and fitness have been established as important modulators. Previously, we observed that elite athletes have significantly increased gut microbial diversity compared to non-athlete controls. Functional metagenomic analysis revealed this elevated diversity translated into the athletes' microbiome being primed for energy harvest as well as muscle and tissue repair. However, a subsequent 8-week exercise intervention study failed to reproduce the same high microbial diversity. This lead us to hypothesize that it's physical fitness, not exercise, that is pivotal to increased microbial diversity. We propose to mine datasets to identify "fitness" associated microbes and metabolites and investigate their implications for human health.

Offered talk (10 minutes)

5

Spatiotemporal dynamics of Shiga toxin-producing *Escherichia coli* (STEC) serogroups O157 and O26 in the Corrib catchment (Ireland): implications for waterborne transmission.

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Abstract

Shiga toxin-producing *Escherichia coli* (STEC) is a zoonotic pathogen causing human infections, ranging in severity from asymptomatic infection to haemolytic uraemic syndrome. STEC infections are commonly associated with O157 and O26 serogroups, with waterborne transmission representing a key exposure route in Ireland. We sought to investigate STEC concentrations in surface waters and groundwater wells across the Corrib catchment over an 11 month period.

19 sites comprising river (n=5) and groundwater (n=14) sources were sampled fortnightly between May 2023 and April 2024 (417 samples). Colilert-18® and quantitative polymerase chain reaction (qPCR) were employed to detect and quantify total coliforms, *E. coli*, STEC O157 and O26.

E. coli was detected in 262/417 (63%) samples, including 115 (44%) river and 147 (56%) groundwater samples. At least one STEC serogroup appeared in 277/417 (66%) samples and in 177/262 (68%) of *E. coli* positive samples. Overall, 244/417 (59%) samples tested positive for STEC O157, comprising 49/115 (43%) river and 195/302 (65%) groundwater samples. STEC O26 was detected in 97/417 (23%) samples and was more prevalent in rivers (n=29, 25%) than groundwaters (n=68, 23%). Weak correlations were observed between *E. coli* concentrations and mean monthly rainfall ($r = 0.159$, $p = 0.001$), STEC O157 and mean monthly temperature ($r = 0.171$, $p < 0.001$), and STEC O26 and mean monthly rainfall ($r = -0.174$, $p < 0.001$).

This study highlights the dynamics of STEC in surface and groundwaters within an Irish catchment, providing insights for improved source protection and risk management of drinking water supplies.

9

Resistant and Biofilm Forming *Escherichia coli* from Flooded and Non-Flooded Agricultural Soils

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Maynooth University, Maynooth, Ireland

Abstract

Introduction: Little is known about the impact of climate change on antimicrobial resistance. It's predicted that Ireland will experience increased annual flooding due to heavy rainfall events, impacting agricultural lands, increasing the risk of infection due to *Escherichia coli* and other *Enterobacterales.*

Methods: Agricultural sites (n = 8) were identified and soil samples were taken from flooded and non-flooded areas. Through enrichment, *E. coli* were selected using EMB agar. 16S rRNA PCR and sequencing was used to determine *E.coli* identity. Disk diffusion and minimum inhibitory concentration methods were used to test antibiotic susceptibility. To test biofilm formation, 96-well plates and crystal violet staining have been utilised. *Escherichia coli* isolates with antibiotic resistance underwent whole genome sequencing (Novogene).

Results: More *E.coli* (n=47) were isolated from flooded than non-flooded soil (n=15). Almost all *E.coli* (n=14) from non-flooded soils were susceptible to all antibiotics investigated. In flooded soils, 11 isolates exhibited multi-drug resistance (ampicillin, tetracycline, ciprofloxacin, trimethoprim, sulphonamide, trimethoprim/sulfalomethoxazole), which has been determined to be plasmid mediated. In total 91% of *E.coli* isolated can form biofilm of varying degree.

Conclusion: A greater number of *E.coli* were isolated from flooded than non-flooded soils, 47 and 15 respectively, suggesting flooded soils are potential reservoirs for *E.coli*. *Escherichia coli* from flooded soils displayed greater antibiotic resistance, including plasmid mediated multi-drug resistance. *Escherichia coli* from both soil types have the ability to form biofilms.

16

“Cardboard Waste Utilisation: Exploring the Potential to Substitute Conventional Microbial Fermentation Feedstocks with Treated Landfill-Bound Cardboard for a Greener Future”

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Abstract

This research focuses on innovative approaches to repurpose landfill-bound lignocellulosic waste as a feedstock for the synthesis of Polylactic Acid (PLA). The aim of this research is to investigate the parameters influencing the fermentation of lactic acid by various species of Lactobacillus to provide a use for this otherwise discarded material.

Lactic acid itself is a versatile chemical, with uses across diverse industries, including the synthesis of sustainable PLA plastics. This adaptable biopolymer holds the potential for the manufacture of eco-friendly materials, with applications spanning from 3D printed medical grade implants to sustainable food packaging. The European Commission’s “Circular Economy Action Plan” aims to achieve a 60% recycle rate for paper and cardboard packaging and the research reported herein aligns with this imperative to enhance circular sustainability practices within the EU (Directive (EU) 2018/852).

This study investigates the influence of substrate concentration, temperature, pH, and aeration on the growth of lactic acid bacteria (LAB) and more importantly, the yield of lactic acid using waste paper as the carbon substrate. Pre-treatment conditions such as the use of enzymatic degradation required to prepare the cardboard-derived feedstock to optimise lactic acid yield were also studied. The optimal temperature for lactic acid yields was 30°C which conflicts with the current literature which focuses on growth rather than yields.

In conclusion, this research aims to explore the potential for sustainable waste degradation that aligns with and contributes to environmental conservation, circular economy principles and the development of eco-friendly PLA plastics for a greener future.

17

Oligopeptide-modified oligonucleotides as targeted therapeutics for the ESKAPE pathogens

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Abstract

Finding novel, innovative and sustainable ways to preserve the efficacy of currently-licensed antimicrobial drugs is a central part of efforts to address the antimicrobial resistance (AMR) crisis. Anti-sense oligonucleotides (ASOs) are short oligonucleotides that can provide a pathway for gene silencing by RNase H degradation. Recent improvements in the design and chemistry of ASOs have opened up a new outlet for this technology as tools for basic research and drug discovery.

The overarching objective of this project is to evaluate the hypothesis that ASOs have therapeutic potential as inhibitors of growth and resistance in ESKAPE pathogens. In order to test this, preliminary bioinformatic analysis, disk diffusions assays and MICs were carried out to characterise the resistance profiles of the ESKAPE pathogens used in this study.

To deliver ASOs into cells, cell-penetrating oligopeptides (CPPs) were synthesised using Fmoc solid-phase peptide synthesis with specific linkers. Confocal microscopy and flow cytometry is being used to evaluate the incorporation rate and percentage of fluorescently labelled CPPs into cells of Gram-negative and Gram-positive ESKAPE pathogens. pVec (a CPP) has been synthesised with different linkers to date.

Conjugation experiments are underway to establish optimal click-chemistry conditions for biological applications. Susceptibility tests carried out to date revealed some highly resistant strains, and the genes responsible for these resistances are being evaluated further, through bioinformatics analyses, as potential ASO targets. This multidisciplinary project aims to enable the re-purposing of antibiotics as part of efforts to overcome resistance in the ESKAPE pathogens.

18

Proteomic dissection of initial Aspergillus fumigatus development within the Ex-vivo pig lung model

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Abstract

Aspergillus fumigatus is an environmental saprophyte and an opportunistic pathogen of the human airway. *A. fumigatus* can cause chronic infections, typically in the context of preexisting lung damage or disease, colonising dead or dying tissue. Animal models of this condition are costly and often cannot reflect an accurate phenotype observed in patients. The ex-vivo pig lung model (EVPL) was developed for conducting bacterial infection studies as pigs share a 90% immunological homology to humans and in addition to share many anatomical similarities. EVPL retains resident immune cells and richer cell type complexity compared to organoid models, in addition to a microbiome. We have adapted this model to study chronic pulmonary aspergillosis. Proteomic analysis enabled tracking of molecular changes to the pathogen and the host during the initial establishment of fungal infection. Results revealed increased abundance of proteins identified associated with carbohydrate metabolism at 48 hours and protein metabolism at 72 and 96 hours. Importantly proteins associated with amino acid metabolic, and biosynthesis processes were detected prior to the detection of fungal toxin biosynthesis. This supports clinical findings that amino acid biosynthesis is an important process in fungal virulence as it may fuel the production of many toxic metabolites. This similarity in response validates the use of the model and contributes supporting evidence that this process is of clinical importance during early-stage fungal colonisation and establishment of infection.

20

Profiling phage-host interactions between *Skunavirus* receptor binding proteins and lactococcal cell wall polysaccharide structures

Kelsey White[1,2], Giovanni Eraclio[3], Brian McDonnell[1], Gabriele Andrea Lugli[4], Tadhg Crowley[5], Marco Ventura[4], Federica Volonté[3], Christian Cambillau[1,6], Fabio Dal Bello[3], Jennifer Mahony[1,2], Douwe van Sinderen[1,2]

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Abstract

Mesophilic starter cultures rely on the activity of lactic acid bacteria such as *Lactococcus lactis* and *Lactococcus cremoris* for the acidification of milk. This biotechnological process can be affected by bacteriophage infection of bacterial starter strains resulting in failed or delayed fermentations. The majority of studied lactococcal phages commence infection with the binding of a tail-associated receptor binding protein (RBP) to a host surface-exposed cell wall polysaccharide (CWPS). In the present study, phage prevalence and phage diversity in whey samples originating from fermentations performed in various European countries and employing mesophilic undefined, complex starter cultures were investigated using phageome analysis. The diversity and prevalence of *Skunavirus* RBP genotypes of phageome-identified *Skunavirus* contigs was evaluated. Through sequence and structural analysis of available *Skunavirus* RBP sequences, the previous *Skunavirus* RBP grouping system (group I-V) was refined and expanded to now encompass eleven groups and several subgroups. Through the generation of His-tagged GFP-RBP fusion proteins, attempts were made to link specific RBP (sub)groups to the CWPS type of the corresponding host(s) of phages encoding a given RBP. These findings vastly improve our knowledge on lactococcal *Skunavirus* RBP diversity and their specificity towards CWPS receptor structures, thereby improving the predictability of fermentation outcomes and robustness of starter culture rotations or blends. In addition, this study demonstrates the increasing genetic and structural diversity exhibited by both host surface-exposed receptors and phage-encoded RBP through the co-evolution of bacteria and their infecting phages.

25

Introducing the Predictive RISk Mapping of AMR in Ireland (PRISMA) project

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Abstract

Antimicrobial resistance (AMR) poses a significant threat to human, animal, and environmental health. Antimicrobial misuse is often thought to be the main cause of AMR, but a variety of biological and non-biological factors can increase AMR risk in the environment. Bacteria and antimicrobials released into the environment by wastewater discharges, livestock excreta, and other sources are key drivers of AMR. In addition, heavy metals and geographic factors, including livestock populations, can affect the spread and persistence of AMR bacteria in the environment, thereby increasing the risk of AMR. For the effective development of AMR control measures, it is key to determine how AMR risk varies in the environment at local, regional and national scales.

PRISMA's overarching aim is to develop AMR risk maps that can subsequently be used to predict how this risk changes over time. Our first task is to identify relevant monitoring programmes, and research groups, public and private, that hold data on AMR drivers in Ireland. Subsequently, we will gather relevant data from research groups, public databases, and research articles and build a database containing AMR driver data linked to spatial coordinates and stratified based on the risk posed to AMR spread. These data will be used to develop "on demand" AMR risk maps for Ireland. A central component of the project is engagement with stakeholders in the agricultural, public health, AMR surveillance sectors and the research community, to identify knowledge gaps and ensure that PRISMA's AMR risk maps provide tangible benefits to environmental AMR mitigation.

40

Computational development of a new class of antibiotic targeting the purine metabolism of *Helicobacter pylori*

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Abstract

Introduction: Resistance to many of the antibiotics used to treat *Helicobacter pylori* (HP) infection is on the rise. Indeed, the WHO has included *H.pylori* on their priority list of antibiotic-resistant bacteria to guide research and development into novel antimicrobials. To this end, protein-ligand docking of 550k+ compounds was carried out against the purine nucleoside phosphorylase enzyme (PNP), a key survival enzyme of HP.

Aims: (i) perform i*n silico* docking to identify compounds with potential activity against HP via PNP enzyme inhibition, (ii) and to test the in vitro antimicrobial and cytotoxicity activity of the compounds.

Methods: The binding site of the PNP enzyme was computational analysed and a library of compounds was virtually screened via protein ligand docking to identify several lead-hits to carry forward to in vitro screening. Lead-hits were tested for antimicrobial efficacy against reference strains (J99 and ATCC60190) and clinical isolates of HP using a broth microdilution approach. Selectivity was established using a viability assay with a stomach epithelial cell line AGS.

Results: Lead-hits were selected from protein-ligand docking results and tested in vitro. All compounds showed antimicrobial activity against the reference strains and both clarithromycin-sensitive and clarithromycin-resistant clinical isolates of HP (MIC 4.34-73 pg/mL). 2 compounds showed significant selectivity against human cells, having no activity on the viability of human gastric cells.

Conclusion: Protein-ligand docking provided a cost-efficient method to identify selective antimicrobial agents for *H. pylori* resulting in the identification of several lead targets that may be further developed to increase selectivity and potency.

44

Screening and characterisation of various fermented Plant-Based Milk Alternatives to evaluate their gut microbiome modulating capacities.

Jane Lavin[1,2], Tom Beresford[1], Linda Giblin[1], Paul Cotter[1,3,4], Torres Sweeney[2], Harsh Mathur[1]

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Abstract

Plant-based diets are gaining popularity due to perceived advantages in terms of health, ethics and environmental impact. Microbial fermentation of plant-based milk alternatives (PBMAs) has the potential to enhance their nutritional properties by increasing bioavailability of nutrients, antioxidant activity and release of polyphenols. Six PBMAs (almond, soy, oat, coconut, hazelnut and cashew) were fermented using Lactic Acid Bacteria (LAB), with five strains originating from plant sources and six from dairy sources. PBMAs were inoculated with each strain at 2%. Viable cell counts and pH analyses were conducted immediately after inoculation and again after 24hr of fermentation at 37 ºC, to determine if the LAB strains could proliferate in the PBMA matrix. The glycolytic and proteolytic activities present in PBMA fermentates were assessed against non-fermented negative controls. Ten of the eleven strains demonstrated a minimum of 1-log increase in each variety of PBMA after 24hrs of fermentation. Fermentates selected for screening in the micro-Matrix bioreactor platform (Applikon®), an *ex-vivo* model of the distal colon included strains from plant and dairy sources. Selected fermented PBMAs (1ml) and non-fermented controls were added of the micro-Matrix reactions every 24hrs for a total duration of 96hrs of fermentation at which time aliquots were collected for analysis. LAB fermentation data and gut microbiota modulation capacities of twenty fermentates will be presented.

49

Use of a small cationic chlorin for antimicrobial Photodynamic Therapy in clinical isolates from patients with diabetic foot infections

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Abstract

Diabetic foot ulcers (DFUs) are one of the major complications of diabetes mellitus and the principal cause of lower limb amputations. Antimicrobial photodynamic therapy (aPDT) is a promising alternative therapeutic strategy because it is not limited by drug resistance.

A new photosensitizer – a low molecular weight dicationic imidazolyl chlorin – was developed for aPDT to improve permeation in biofilms and absorption in the phototherapeutic window. The efficacy of aPDT with IC-H-Me^{2+} was tested in biofilms from clinical isolates from patients with DFUs both alone and when potentiated by potassium iodide (KI). aPDT was performed using 1μM IC-H-Me^{2+} and 50 mM KI with one-hour incubation period, followed by exposure to a light dose of 5 J/cm^2 using a 660 nm LED.

The fifteen different clinical isolates of MRSA, MSSA, *S. epidermidis* and *Pseudomonas aeruginosa* produced different levels of biofilm when growing for the same period of time (9 logs CFU to 20 logs CFU). The susceptibility of biofilms to respond to aPDT depends on the amount of biofilm and the more mature biofilms tend to have a poorer response to treatment. Nevertheless, all biofilms showed more than 3 logs CFU inactivation when aPDT was performed with 1μM IC-H-Me^{2+} and light, and most of them where eradicated when aPDT was potentiated by the addition of 50 mM KI.

IC-H-Me^{2+} has excellent physical and photochemical properties as a photosensitizer for aPDT. Our results offer the basis for the development of formulations that can selectively eradicate biofilms established in infected wounds using aPDT.

55

Lessons from the COST Action ML4Microbiome: "Optimising machine learning for human microbiome research"

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Abstract

The rapid growth of ML in microbiome analysis presents challenges in interpretability and optimization. Our experience through the ML4Microbiome Cost Action emphasizes the importance of creating user-friendly tools with transparent standards to foster continued innovation. Contributions to open training material helped to utilize synergies between the COST action members and is creating long-lasting impact in disseminating methods that were evaluated and benchmarked as part of the ML4microbiome COST action.

The DREAM challenge highlighted, for the first time, the relative performance of alternative modelling strategies in predicting future disease risk based on microbiome signatures. The independent benchmarking of the competing methods will support the development of novel prospective signatures not only for heart failure but potentially for other diseases. In addition, the analysis of the predictive microbiome features provides insights into the possible underlying mechanisms in microbiome-mediated disease associations.

Data analysis poses various challenges, primarily stemming from the multitude of steps and methods involved, even for experts. We were able to produce an analyst-friendly summary of this process along with guidelines for it optimization, which we have published in several papers in a Special Issue in Frontiers Microbiology. In addition to having created a large and dynamic inter-disciplinary network of ML-microbiome scientists, we believe that these guidelines will contribute significantly to the establishment of microbiome analysis as a standard clinical practice to the benefit of human health.

57

Microbiome-related biomarkers for relapse prediction in treatment-naïve paediatric ulcerative colitis patients

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Abstract

This study aims to enhance treatment protocols for pediatric ulcerative colitis (UC), an inflammatory bowel disease, by identifying microbial biomarkers associated with relapse in treatment-naive. Current first-line treatments, such as 5-ASA drugs and corticosteroids, are effective in only half of the patients. Identifying those at risk of relapse could enable early introduction of more aggressive treatments, like immunosuppressants.

Biopsies from 48 paediatric patients (2-16 years of age) were collected during colonoscopy. Of these, 23 experienced relapse within 6 months (PUCAI 10+). Next-generation sequencing of V3-V4 hypervariable region and 16S qPCR provided data on relative and absolute bacterial abundances. Taxa differential abundance between relapse and remission groups was identified with zero-inflated Gaussian and negative binomial mixed-effect models. Meta-variables relevance to microbiome composition was assessed with VpThemAll package. XGBoost-based machine-learning models were used to predict relapse.

Diversity and species richness were diminished in the relapse group. 23 and 10 differential taxa were differential in negative binomial and Gaussian models respectively. Differential taxa included probiotic bacteria (*Bifidobacterium* genus, elevated in remission group) and pro-inflammatory species (from *Veilonella* and *Fusobacterium* genus, elevated in relapse). Patient treatment status ranked as third most relevant variable in explaining variance in the microbiota. Models based on ascending colon samples microbiome and demographic data reach AUC above 0.7.

Gut microbial composition is linked to treatment response in paediatric UC. Differential taxa include probiotic bacteria (*Bifidobacterium* genus, elevated in remission group) and pro-inflammatory species (from *Veilonella* and *Fusobacterium* genus, elevated in relapse). Microbiome-based models achieve good performance in predicting relapse.

59

Airborne Treasure Hunt: Optimising Aerosol Microbial Recovery from the Farm Environment

Anita Grasso, Sinead Corr, Marta Martins, Julie Renwick

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Abstract

Antimicrobial resistance (AMR) is one of the most challenging **global health and food security problems** facing society. Left un-tackled, AMR is predicted to cause more than 10 million deaths and an 11% decrease in livestock production annually by 2050. The use of antimicrobials in the agricultural setting poses an increased risk in the transmission of antimicrobial resistance (AMR). Medically important antimicrobials are being used to treat/prevent animal infections and control crop spoilage. For these reasons, AMR can only be addressed and faced with the "One Health" approach.

Despite several studies reporting on the impact of agricultural antimicrobial usage on soil, crops, wastewater treatment plants, and farm animals, there is a significant gap in our understanding of how **air** contributes to the transmission of AMR in these settings. The Environmental Protection Agency (EPA) gap analysis (2021) identified air and aerosols as the least investigated mode of transmission of antimicrobial-resistant organisms (ARO) and antimicrobial-resistant genes (ARG).

This research investigates the role of aerosols in the transmission of AROs and ARGs in the farm. Using the AirPrep™ Cub Sampler-ACD210, optimal methods for bioaerosol recovery were evaluated. This is fundamental when studying samples of low bioburden. Air sampling volume, duration and locations were compared. Sample processing using filter-washing and sonication steps were explored. Processing methods were assessed using CFU counts, DNA quantification and quality measurements and 16s-rRNA bacteria, fungal(ITS) and human(GADPH) qPCR DNA levels. The data generated will enable the ResistAMR project to perform optimal sample processing to maximize the recovery of airborne DNA for future sequencing.

64

Lung Microbiota analysis of asthmatics reveals pathogenic microbial blooms corresponding to lung inflammation and reduced microbial diversity.

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[1]Cork University Hospital, Cork, Ireland. [2]University College Cork, Cork, Ireland

Abstract

The existence of the lung microbiota has in recent years become to be appreciated. The lung microbiome by the nature of the lung function and mucociliary clearance is believed to be dynamic and diverse. We sought to characterise the lung microbiota in severe and non-severe asthmatics and investigate if the microbiota provided an insight into the pathology of severe asthma. Bronchoalveolar lavage (BAL) samples from 44 patients with a known diagnosis of asthma were collected. BAL cell counts and cytokine levels in both the lavage sample and matched serum samples were analyzed. Following DNA extraction, the microbial community of the BAL was analyzed using whole genome sequencing followed by analysis using the OneCodex platform and confirmation by qPCR.

The lung microbiome is dynamic but does have consistent microbial species such as Micromonospora and Prevotella (90 % of all samples) with an average Shannon diversity of 3.5. Severe asthmatics who smoke and have reduced FEV-1 displayed less abundance of *Prevotella pallens* and those with a Body mass Index (BMI) > 30 had reduced presence of Micromonospora species. Several samples displayed the presence of reduced microbial diversity and pathogenic blooms of *Haemophilus influenzae, H. parainflunezae*, *Staphylococcus* and *Streptococcus pneumoniae*. These blooms correlated with increased BAL neutrophils, lymphocytes and raised BAL IL1b, IL-8, IL-17 and TNFa and serum neutrophils. The lung microbiota is reflective of asthmatic severity and screening for decreased microbial diversity and microbial blooms could provide a useful tool for asthma stratification but also targeted therapeutics during episodes of exacerbation.

66

Regulation of *Acinetobacter baumannii* virulence by second messenger signalling systems

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Abstract

The role of second messengers in mediating virulence has been well-established in different bacterial pathogens. However, despite *Acinetobacter baumannii* being the top critical-priority pathogen, its regulation of virulence-related phenotypes by these signalling systems is elusive. In this work, we used high-throughput screening of the *A. baumannii* AB5075 transposon mutant library to identify novel biofilm formation regulators. A clean deletion mutant of the candidate gene was created and we analysed its effect on the transcriptome using dRNA-Seq. Subsequently, the transcriptomic results were phenotypically validated. We identified a previously uncharacterised predicted adenylate cyclase (AC), CavA, as a central regulator in *A. baumannii*. CavA was confirmed to be a functional AC synthesizing cAMP. Uncovering the CavA-mediated cAMP regulon showed that cAMP upregulated type IV pili while downregulating Csu pili and exopolysaccharide production genes transcription. In addition, we provide evidence that Vfr function is cAMP-dependent. We demonstrate for the first time that, cAMP is atop of a hierarchical signalling cascade. It controls inter- and intrabacterial signalling by modulating quorum sensing and c-di-GMP systems at transcriptional level, ultimately governing virulence *in vivo* and adaptive antibiotic resistance in *A. baumannii*. We challenge the established norm of high c-di-GMP leading to increased biofilm formation, as our results show that this paradigm is dependent on intracellular cAMP concentrations in *A. baumannii*. Overall, we demonstrate the central role of cAMP in modulating key virulence related phenotypes and suggest a possible hierarchy of the signalling systems in *A. baumannii*. This highlights cAMP as a potential target for novel therapeutic development.

77

Linking Knowledge to Employment: Core Skills in Education of TUS Microbiology Graduates

Andy Fogarty, Paulina Flannery, Dawn Howard, Cormac O'Shea

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Abstract

This presentation explores the integration of key employment skills within the BSc (Hons) Microbiology course at the Technological University of the Shannon (TUS) Athlone campus. Establish in 2017, the program aims to equip students with both classical and modern microbiological techniques benefiting from a small class size to help students achieve their full academic potential. Practical skills such as asepsis, microscopy, isolation, enumeration, and identification of microorganisms are heavily emphasized across various fields such as environmental, food, and industrial microbiology.

The development of employability skills—critical thinking, teamwork, problem-solving, communication, and adaptability—is fostered through a combination of innovative pedagogical approaches. These include enquiry-based learning (EBL), team-based learning (TBL), problem-based learning (PBL), and universal design for learning (UDL). In addition, a mandatory 20-week work placement in the country or abroad is a key component of the curriculum.

To date, over 60 graduates have successfully completed the programme, all of whom have secured employment or pursued postgraduate studies. Feedback from both students and employers has been instrumental in refining course content and delivery. For instance, the inclusion of a **Quality and Compliance** module was directly influenced by industry feedback or cross-modular assessment was also incorporated to reduce overassessment of students.

This presentation highlights how an integrated teaching approach and feedback-driven curriculum design enhance student employability. By bridging the gap between academic theory and industry practice, the BSc (Hons) Microbiology program ensures that graduates are well-prepared for the demands of the microbiology workforce.

Offered talk (15 minutes)

4

Adaptations and community changes in milk and water kefir microbiomes in response to environmental parameters (Kefir4All-Citizen Science Project)

Liam Walsh[1,2], Samuel Breselge[1,3], Guilherme Martin[4], Mairead Coakley[1], Paul Cotter[5,1,3], Fiona Crispie[1], Paul O'Toole[2,3]

[1]Teagasc Food Research Centre, Moorepark, Cork, Ireland. [2]School of Microbiology, Cork, Ireland. [3]APC Microbiome Ireland, Cork, Ireland. [4]Microbiology of Fermented Products Laboratory (FERMICRO), Viçosa, Brazil. [5]VistaMilk SFI Research Centre, Cork, Ireland

Abstract

Milk kefir and water kefir are fermented beverages traditionally produced by inoculating milk or a sugar-rich solution with a symbiotic microbial ecosystem contained within kefir grains. While these beverages have been consumed in certain regions for centuries, their global popularity has surged recently, prompting more research into their microbiomes. Kefirs are also studied as interesting model microbial communities.

We applied genome-resolved metagenomic analysis to milk and water kefir metagenomes, derived from the same initial microbial population, to study compositional change and microbial evolution at the species and strain level. Citizen scientists contributed by fermenting kefir using different substrates and growth conditions for up to 21 weeks, starting with a common source of kefir grain.

Our findings showed a period of rapid compositional change from weeks one to nine (wk01-wk09) in both milk and water kefir liquid and grain microbiomes. This period was followed by greater stability for many, though not all, metagenomes from weeks 13 to 21 (wk13-wk21). We documented evolutionary changes in several prevalent species, revealing higher mutation rates during the initial weeks compared to later stages. Both milk and water kefir metagenomes frequently contained bacteria not typically associated with kefir communities, likely acquired from the environment.

Although no potentially pathogenic species persisted in the kefir grains throughout the 21-week study, some did persist over extended periods. Ultimately, our findings provide new insights into how microbial ecosystems change and evolve over successive fermentations.

53

Generative AI and 360 mapping: opportunities to virtually redefine industrial site visits for microbiology undergraduates.

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Abstract

In Plato's *Phaedrus* (~370 BCE), Socrates laments the use of written accounts of great orations. The failing, in his view, lies in the inability of the written word to capture and convey the passion, virtue and context that underpin a lived performance. In this dialogue Plato presents perhaps the first critique of a "learning technology" (i.e. writing), and the limitations of the technical artifacts produced. Millenia later, modern educators are faced with the challenge of generative AI, a system trained solely on artifacts and lacking in passion, virtue or any sense of context or lived experience. Generative AI has the potential to undermine students' depth of engagement and capacity for synthesis of theory and concepts by providing ready-made content which students may not be in a position to interrogate for accuracy. However, herein we demonstrate the use of this technology to create learning opportunities that shift the focus from artifacts to authentic, contextually relevant experiences for students.

The VISTA project, funded via the Higher Education Authority of Ireland SATLE fund, explored technological advances in non-expert user 360 cameras, image manipulation software, generative artificial intelligence, and virtual tour to transform both the concept and the experience of industrial site visits. We report the design and deployment of this novel approach with undergraduate students in the School of Microbiology at UCC, to provide photorealistic, interactive, multiplatform, virtual access to industrial sites, together with AI based manipulations to create unique experiential learning opportunities. Aspects of scalability, sustainability and adaptability are also highlighted.

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