

Abstracts book

Contents

Poster no.	Talk title	Presenter	Page
3	Typing of Salmonella species Prevalent Among Children Having Diarrhoea in Parts of North-Western Nigeria	Ignatius Mzungu	1
4	Isolation and characterization of novel bioactive compounds from marine rare actinomycetes	Jonathan Inetianbor	1
5	Biomaterial Modulation for Management of Catheter-Associated Urinary Tract Infection (CAUTI)	Mark Waters	2
6	Antibiogram and beta lactamase genes among cefotaxime resistant E. coli from wastewater treatment plant	Anthony Ayodeji Adegoke	2
7	Lignocellulose digestion by anaerobic rumen microbial consortia from sheep	Sandhya Jayasekara	3
8	Characterization of the gamma-glutamylpolyamine synthetase GlnA3 in <i>Mycobacterium tuberculosis</i> as a potential drug target	Sergii Krysenko	3
9	Evaluation of antifungal activities and antihaemolytic effects of Cinnamon essential oils from leaf and bark on <i>Candida albicans</i> and <i>Candida auris</i>	Hoang Tran	4
10	ORAL CANDIDIASIS IN HIV INFECTED PATIENTS VISITING SUKRARAJ TROPICAL AND INFECTIOUS DISEASE HOSPITAL(STIDH), TEKU, KATHMANDU AND ITS ANTIFUNGAL SUSCEPTIBILITY PATTERN BY DISC DIFFUSION METHOD.	Pankaj chaudhary	4
11	Surveillance of β -lactam, azithromycin and fosfomycin resistance in non-typhoidal <i>Salmonella</i> : Characterisation of an S. Infantis plasmid	Winnie Lee	5
12	Characterising the inhibition profile of a novel antimicrobial	Nathaniel Cole	5
13	Exploring Coastal Plants as a source of Plant Growth Promoting Endophytic Bacteria	Gareth Raynes	6
14	Isolation of Bacterial Strains From Compost with Biocontrol Ability Against <i>Burkholderia glumae</i> Infection in Rice Seedling	Abinubli Tariswafi Mawarid	6
15	Identification and characterisation of a novel SXT/R391 ICE-like mobile genetic element isolated from an Irish wastewater environment.	Shannon Slattery	7
16	Polysaccharide-Dependent Biofilm Formation is induced by Bile in Late Cystic Fibrosis Isolates of <i>Staphylococcus aureus</i> .	Mary B. Turley	7
17	Genomic and Proteomic Analysis of the Giant Acinetobacter Bacteriophage vB_AbyM_TRS5	Harriet Eaton	8
18	D-serine: trick or treat?	Natasha Turner	8
19	Household arthropods and their associated bacterial communities	Federica Boiocchi	9
20	The Diversity and Comparison of the Temperate Bacteriophages of <i>Pseudomonas aeruginosa</i> from the IPCD International Pseudomonas Consortium Database containing over 1000 <i>Pseudomonas aeruginosa</i> Genomes	Libby Duignan	9
21	Evaluation of the retention of clinically relevant pathogens on high touch environmental surfaces using the ATP Bioluminescence Monitoring system	Sladjana Malic	10

22	Acquisition of fluoroquinolone resistance leads to increased biofilm formation and pathogenicity in <i>Campylobacter jejuni</i> .	Matthew Whelan	10
23	Actinobacterial Diversity from Indonesian Extreme Environments As a Source of Novel Antimicrobial Drug Leads	Ali Budhi Kusuma	11
24	Application of ABDITE® support for nitrification for Anammox activity in Expanded Bed Biofilm Reactor (EBBR)	Comfort Anyanwu	11
25	Inactivation efficacy of four model bacteria in plasma activated water during cold storage	Yiming Zhao	12
26	<i>Staphylococcus aureus</i> targets corneodesmosin to colonise skin in atopic dermatitis	Aisling Towell	12
27	Analysis Of Qualitative Feedback Received By Means Of Modified 'Take Five' Antibiotic Audit Tool	Thomas Cronin	13
28	CYANOBACTERIA AS ONE OF THE MOST PROMISING BOTANICAL SUN PROTECTING AGENT; A WAY TOWARDS HEALTHY COSMETICS	Tharangika Bowange	13
30	Whole Genome Sequencing Reveals Genetic Diversity in <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> Population Circulating in Irish Cattle	Viktor Perets	14
32	Fibronectin Binding Proteins Mediate Adherence of <i>Staphylococcus aureus</i> to the corneocyte protein Loricrin	Thaina da Costa	15
33	Physicochemical Interactions between Silica Nanoparticles and EPS Biomolecules within the Biofilm Matrix of <i>Pseudomonas fluorescens</i> WCS365	Dishon Hiebner	15
35	Identification of genes that contribute to fitness of African and global clades of <i>Salmonella</i> Enteritidis during infection of macrophages	Wai Yee Fong	16
36	Investigating the fundamental interactions between nanoparticles and biofilms of <i>Pseudomonas</i> species	Henry Devlin	16
37	Multimerizing type IV pilus subunit of an oral pathogen binds human cytokines	Nelli Vahvelainen	17
38	Repurposing Old Drugs to do New Tricks – The use of Thioridazine to treat multi-drug resistant infections	Daniela Alves Ferreira	17
39	Unravelling the requirement for host chloride channels during HRSV infection	Hayley Pearson	18
40	Harnessing the <i>Klebsiella</i> : macrophage arms race	Brenda Morris	18
41	Macrophage Sabotage: Undermining Macrophage Signalling by <i>Klebsiella pneumoniae</i>	Daniel Moody	19
42	The putative multicopper oxidase of <i>Staphylococcus aureus</i> confers copper tolerance	Martin J. Sutton	19
43	Secretomic Analysis of Three Ubiquitous <i>Phytophthora</i> Species Threatening Global Forest Ecosystems	Jamie McGowan	20
44	An antibiotics mediated evolutionary arms race between Alexander Fleming's <i>Penicillium rubens</i> and a bacterium <i>Bacillus muralis</i> .	Ayush Pathak	20
47	The use of genotypic screening, PCR-based replicon typing, pulsed-field gel electrophoresis genotyping and whole genome sequencing to paint a fine transmission map of group 1 CTX-M β -lactamases in ESBL-producing <i>Escherichia coli</i> strains isolated from Croatian patients	Tomislav Mestrovic	20
49	Role of the exporter PptAB and the protease Eep in secretion and maturation of pheromones in <i>Streptococcus thermophilus</i>	Abarna LINGESWARAN	21

P13

corneodesmosin as a key ligand for *S. aureus* on AD corneocytes. We show that strain of *S. aureus* isolated from infected AD skin lesions adhere to recombinant corneodesmosin. Using surface plasmon resonance, we show that three cell wall anchored proteins expressed recombinantly bind to corneodesmosin with high affinity. Two of these proteins promote *S. aureus* adherence to corneodesmosin. High-resolution imaging of corneocytes from AD skin revealed that strong adhesive interactions are not uniformly distributed across the corneocyte surface but mostly concentrate on the tips of villus-like projections, consistent with corneodesmosin being a ligand. In summary this study identifies novel interactions between *S. aureus* and corneodesmosin and thus provides important new insights into the first steps in the establishment of *S. aureus* skin colonisation in AD patients.

27

Analysis Of Qualitative Feedback Received By Means Of Modified 'Take Five' Antibiotic Audit Tool

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Abstract

Objective: Appropriate antibiotic prescribing is essential for patient care. As a result, we set out to explore reasons behind antibiotic prescribing behaviour and how it might be optimised.

Method: Data were collected over a three month period using an online pre-formed questionnaire, which was disseminated monthly to different departments within our hospital. Our specific analysis focused on the free-text question: 'On reflection, are you aware of any opportunities that could have been taken to improve the quality of this antibiotic prescription'. Thematic analysis was performed to develop relevant codes.

Results: We received 62 free-text responses with suggestions for improvement. The top three categories of response related to: (1) missed opportunity to send appropriate specimen(s) to microbiology; (2) sub-optimal/conflicting documentation; and (3) duration of therapy inappropriately prolonged and/or not specified/justified.

Discussion: The feedback provided is valuable in its capacity to inform decision making at the Trust's Antimicrobial Steering Group, and optimising parts of the system in order to make it easier to do the right thing. Areas for potential improvement, highlighted by feedback received, included: (1) Implementation of reminders on our electronic prescribing system (EPS) to ask if blood cultures have been taken, before commencing antibiotics (2) Providing reminders on our EPS for antibiotic review (3) Documentation of discussions with an infection specialist on our EPS. This project is ongoing, and further data collection and analysis is planned following our implantation of suggested improvements.

28

CYANOBACTERIA AS ONE OF THE MOST PROMISING BOTANICAL SUN PROTECTING AGENT; A WAY TOWARDS HEALTHY COSMETICS

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Abstract

Ultra Violet light has adverse effects on skin including mutagenicity and accelerated skin aging. With the depletion of Ozone layer responsible in filtering harmful Ultra Violet rays, humans not only in temperate regions but also in tropical countries are more affected. Thus, use of sunscreens has been more demanded.

P14

Potential toxicity shown by synthetic Ultra Violet filters in humans directs the attention of consumer on natural Ultra Violet filters. Therefore, aim of this study was to determine Sun Protection Factor of naturally occurring cyanobacteria biomass. Biomass was diluted with alcoholic solutions and absorbance was recorded between 290-320 nm at 5 nm intervals using UV- spectrophotometry. Mansur equation was applied to determine Sun Protection Factor. *Oscillatoriales* sp. showed the highest Sun Protection Factor of 1.57 ± 0.002345 while *Croococcidiopsis* sp. showed the lowest Sun Protection Factor of 0.05 ± 0.033216 . All the tested strains showed considerable Ultra Violet protection capabilities compared to most of the well-known herbal extracts. Effective sun screen properties along with higher photosynthetic ability, rapid growth, less area and simple nutrient requirement for growth, less capital investment and zero environmental pollution, make these cyanobacteria one of the most promising botanical agents to be used as an effective sunscreen in cosmetic industry.

Keywords: Sun Protection Factor, Synthetic, Natural, Adverse effects

30

Whole Genome Sequencing Reveals Genetic Diversity in *Mycobacterium avium* subspecies *paratuberculosis* Population Circulating in Irish Cattle

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Abstract

Mycobacterium avium subspecies *paratuberculosis* (MAP) causes Johne's Disease (JD), a chronic enteritis, in cattle. Understanding the transmission dynamics of MAP will inform control of JD. Whole genome sequencing (WGS) has been applied to many pathogen systems, where its unprecedented resolution has greatly enhanced our understanding of the molecular epidemiology of pathogen transmission. However, WGS has seen limited application to MAP; here we report the first study of its kind in Ireland.

DNA was extracted from 150 MAP isolates collected from cattle across Ireland. Extracts were prepared into libraries and were sequenced on an Illumina NextSeq500. Sequencing data were processed and analysed using a bioinformatic pipeline.

The phylogeny obtained from sequencing data shows that the MAP population circulating in Irish cattle is diverse, which may partly have resulted from importation of MAP strains from Europe into Ireland. This shows similarity to a WGS MAP study in Canada that noted the impact of cattle imports on the Canadian MAP population. Furthermore, comparing our Irish isolates to a global MAP WGS study showed close similarity of some Irish isolates to European isolates, again suggesting intracontinental spread.

Comparison of WGS data with previously available VNTR data for our isolates indicates that VNTR typing has limited resolution for discriminating MAP strains, and often does not distinguish isolates correctly when compared with WGS SNP data.

The genomic data presented here provide the first comprehensive picture of genetic diversity of Irish MAP and a baseline for future studies into the spread and persistence of MAP in Irish cattle.