Abstracts book

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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.

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

Thomas Cronin[1], Amy Belfield[2], Daniel Weiand[2]
[1]Newcastle University, Newcastle, United Kingdom. [2]Newcastle upon Tyne Hospitals NHS Foundation Trust, Newcastle, United Kingdom

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.

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

Tharangika Bowange[1], Md. Fuad Hossain[1,2,3], Wasantha Kumara[2], Renuka Ratnayake[1]

[1]National Institute of Fundamental Studies, Kandy, Sri Lanka. [2]Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna, Matara, Sri Lanka. [3]Department of Biochemistry and Molecular Biology, Gono Bishwabidyalay (University), Savar, Dhaka, Bangladesh

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.

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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

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

Viktor Perets[1], Sophie Cassidy[1], John Browne[1], Kevin Kenny[2], Jim O'Mahony[3], Joseph Crispell[1], Stephen Gordon[1]

[1]School of Veterinary Medicine, University College Dublin, Dublin, Ireland. [2]Central Veterinary Research Laboratory, Backweston, Co. Kildare, Backweston, Ireland. [3]Department of Biological Sciences, Cork Institute of Technology, Cork, Ireland

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.