

PCR Research Bazaar

Programme
&
Abstracts

30 June 2025



PBS PGR RESEARCH BAZAAR PLANNING COMMITTEE

Professor Linda Seton

Professor Francesca Giuntini

Adam Crockett

Cherene de Bruyn

Jamie Williams

Paul Riley

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Liverpool,
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School of Pharmacy and Biomolecular Sciences

9:30AM - 10:00AM

Registration

10:00AM - 10:20AM

Welcome

Bazaar Bingo

10:20AM - 11:20AM

Research Communication Science Talks

Adam Crockett

Improving chronic skin healing via RNA nano therapies

Cherene de Bruyn

More or less? A mini study comparing soil and forensic DNA extraction kits using variable soil inputs

Elliot Mbeta

Social determinants of health and adverse clinical outcomes among patients with hypertension A real-world analysis using a global federated database

BREAK

11:30AM - 12:30PM

Suleiman Fatimoh Ozavize

Identification of substrate protein S-acyl transferase 10 involved in salt stress

School of Pharmacy and Biomolecular Sciences

Data Exchange

Paul Riley

Showing the impact of using different STR Kits by forensic practitioners when scoring canine genotype profiles for mixed samples.

Suleiman Fatimoh Ozavize

Method of using protoplast to determine subcellular location

Cherene de Bruyn

Student research excellence: something to ASPIRE to

LUNCH

Molecules and Mocktails Networking
Poster Session

13:30AM - 14:00PM

The Doctoral Academy
LJMU Library

14:00AM - 14:40PM

Bazaar Banter: From lab to listener Workshop

CLOSING

Feedback from the Judging Panel
Prize Giving
Thank you



RESEARCH COMMUNICATION TALKS ABSTRACTS

Improving chronic skin healing via RNA nano therapies

Adam Crockett

The project is to produce a therapy to enhance the wound healing process in those with chronic skin wounds. To achieve this requires developing a delivery system to insert a specific strand of micro-RNA (miR-21-5p) into fibroblast cells. The delivery system will compose of a combination of nanomaterials (rhamnolipids and phospholipids) to produce micelle nanoparticles decorated with cell penetrating peptides to increase entry in the cell. The next step will be to insert the micro-RNA into the nanoparticles, introduce them to healthy and chronic fibroblast cells and examine their growth.

More or less? A mini study comparing soil and forensic DNA extraction kits using variable soil inputs

Cherene de Bruyn, Dr Kirstie Scott, Dr Heather Panter, Dr Frederic Bezombes, Dr Cathrine Bie Petersen, Dr Elena Zavala and Dr Komang Ralebitso-Senior

Soil is a common component of terrestrial environments and a valuable source of trace evidence in forensic investigations. However, extracting high-quality DNA from soil, especially from low-biomass, inhibitor-rich samples such as those associated with clandestine graves, remains a significant challenge. This study aims to evaluate the effectiveness of four commercial DNA extraction kits in recovering microbial and human DNA from soil samples collected from an urban park Denmark. Four DNA extraction protocols were assessed including: the FastDNA™ SPIN Kit for Soil (MP Biomedicals), Chelex/Amicon protocol, DNA Investigator/EZ2 system, and the PrepFiler/Automate Express. DNA yield was quantified using a Qubit fluorometer, while the Quantifiler™ Trio kit was used to evaluate DNA presence, degradation, and PCR inhibition. Both 100 mg and 250 mg soil inputs were tested to assess the impact of sample mass on DNA recovery.



RESEARCH COMMUNICATION TALKS ABSTRACTS

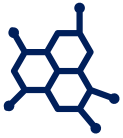
The FastDNA™ SPIN Kit consistently produced the highest microbial DNA yields, with the 250 mg input yielding nearly twice as much DNA as the 100 mg input. Internal positive control (IPC) Ct values (~27) indicated minimal PCR inhibition for the FastDNA™ SPIN Kit. The other three kits, which are optimized for human biological materials, yielded little to no detectable DNA, which aligns with the expected absence of human DNA in the soil samples. In the Quantifiler Trio qPCR assay, samples from all 4 kits plotted with Ct values above 40 on the standard curve indicate extremely low or undetectable levels of human DNA, suggesting degradation, inhibition, or absence of target material. These findings highlight the importance of selecting DNA extraction methods tailored to the sample type and intended analysis. The FastDNA™ SPIN Kit for Soil is well-suited for forensic applications involving microbial DNA in soil, while the other kits optimized for human DNA are less effective in such contexts. This study underscores the need for method-specific considerations in forensic analysis.

Social determinants of health and adverse clinical outcomes among patients with hypertension A real-world analysis using a global federated database
Elliot Mbeta, Rajiv Sankaranarayanan, Philip Austin, Peter Penson, Gregory Y.H. Lip and Garry McDowell1

Background: Hypertension remains one of the most prevalent and modifiable cardiovascular risk factors for heart failure (HF) and other cardiovascular diseases. It's estimated that hypertension affects an estimated 1.3 billion people globally, contributing to approximately 10.8 million deaths annually.

Despite public health efforts, its management remains challenging, influenced by social determinants of health (SDoH). This study examines the association between SDoH and adverse cardiovascular events in hypertensive patients, excluding HF.

Methods: A retrospective cohort study was conducted using the TriNetX global federated health research network. Patients were classified as socially deprived based on ICD-coded indicators of four SDoH factors: extreme poverty, unemployment, problems associated with living alone, and low income.



RESEARCH COMMUNICATION TALKS ABSTRACTS

The primary outcome was the 5-year risk of a composite measure including all-cause mortality, ischemic heart disease (IHD), cerebrovascular accident (CVA), heart failure (HF), angina pectoris, acute myocardial infarction (AMI), atrial fibrillation/flutter, and cerebral infarction. Secondary outcomes assessed individual components of the composite outcome. To account for baseline characteristic variations between groups, we included covariates such as demographics (age, sex, race/ethnicity) and cardiovascular medications. Cox proportional hazards regression was used to estimate hazard ratios (HRs) and 95% confidence intervals (CIs) after 1:1 propensity score matching (PSM).

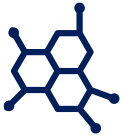
Results: After propensity score matching, the study included 39,307 socially deprived (68.6 ± 13.5 years; 55.3% female) and 21,806 non-deprived (68.6 ± 13.5 years; 55.3% female) hypertensive patients. Socially deprived individuals had a significantly higher risk of the primary composite outcome (HR 1.58, 95% CI 1.53–1.63), and were at increased risk for IHD (HR 1.46), angina pectoris (HR 1.29), AMI (HR 2.30), HF (HR 2.92), atrial fibrillation/flutter (HR 1.39), and all-cause mortality (HR 1.58, 95% CI 1.53–1.63).

Conclusion: Social deprivation is strongly associated with increased risk of adverse major cardiovascular events among hypertensive patients. Future prospective studies are needed to address potential unmeasured confounders and validate these findings.

Identification of substrate protein S-acyl transferase 10 involved in salt stress

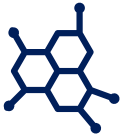
Suleiman Fatimoh Ozavize and Dr. Qi Baoxiu

Breeding of salt-tolerant crops has contributed to sustainable agriculture, leading to food security, helping alleviate poverty worldwide. By 2050, food production must increase by over 50%, particularly in developing countries, as the population is expected to reach 9.7 billion. However, plants sensitivity to soil salinity limits its production.



RESEARCH COMMUNICATION TALKS ABSTRACTS

However, plants sensitivity to soil salinity limits its production. Developing salt-tolerant varieties of plant could significantly enhance plant tolerance and yield under abiotic stress, ensuring food security. Previous study of our group showed that protein S-acyltransferase 10, AtPAT10 is involved in salt stress response via targeting substrate proteins to tonoplast. However, the exact number and type of proteins are currently unknown. Due to the membrane localization of both PAT10 and its substrate proteins, as well as the transient nature of S-acylation, we employed the biotin ligase-mediated proximity labelling and mass spectrometry (PL-MS) assay to identify proximal proteins of AtPAT10. These proteins will be further verified to confirm whether they are related to AtPAT10, establishing AtPAT10-S-acylated substrate protein network. PL-MS has been effective in other species, such as the fruit fly, but has yet to be applied in plants to identify novel substrate proteins for PATs. So far, we have identified 1,122 AtPAT10 proximal proteins, subsequent analysis of these proteins put them to signal transduction, development, and salt tolerance. These studies provide a foundation for further investigating PAT10's role in salt tolerance in crop plants, aiming to create novel salt-tolerant varieties, enhancing food security for the future.



DATA EXCHANGE ABSTRACTS

Showing the impact of using different STR Kits by forensic practitioners when scoring canine genotype profiles for mixed samples.

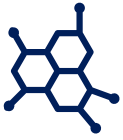
Paul Riley

Three graphs showing the difference in ability to accurately score canine genotypes of various mixed samples from multiple forensic practitioners across different institutions. The commercially accepted STR kit used for forensic casework involving canine DNA, Canine Genotypes 2.1 kit, performed worse the more extreme the mixtures became with participants being unable to score most of the canine profiles at all. In comparison, the CaDNAP kit made up of panels 1 and 2, displayed a complete success rate in panel 1 and only a small room of error in panel 2.

Method of using protoplast to determine subcellular location

Suleiman Fatimoh Ozavize, Dr. Qi Baoxiu

Protoplasts, which are plant cells with their cell walls removed, are a valuable tool for various research applications in Arabidopsis. They can be isolated from leaves, roots, or other tissues using enzymatic digestion and then used for transfection, fusion, or other studies. A common method involves using a "Tape-Arabidopsis Sandwich" to isolate protoplasts from leaf mesophyll cells, followed by PEG-mediated transfection with DNA or RNA for transient gene expression.



DATA EXCHANGE ABSTRACTS

Student research excellence: something to ASPIRE to *Cherene de Bruyn, Sarah Klingberg and Samantha Barker*

Excellent student research at undergraduate and Masters level should be recognised and celebrated. Moreover, students should be given the opportunity to develop these research projects into publishable formats. Postgraduate Researchers (PGRs), on the other hand, often lack hands-on experience with the peer review and editorial processes that underpin academic publishing. ASPIRE is a PGR-led, open-access, multidisciplinary journal at Liverpool John Moores University that addresses both of these needs. As a student focused and managed journal it provides a platform for publishing outstanding student research while offering PGRs the opportunity to serve as Editors, Reviewers, and Mentors. Through this involvement, PGRs gain valuable experience in research governance, impact, and engagement, all of which are key components of the Researcher Development Framework. In this session I will provide a brief introduction to the LJMU ASPIRE Journal and some of its key features.



Functional Peptide-Based Nanomaterials for Delivery of microRNA to Medulloblastoma

Danielle Holmes, Touraj Ehtezazi¹, Alister Fielding, Kehinde Ross and Alice McCloskey

Background: Medulloblastoma (MB) is the most common malignant brain cancer in children, with 50 new diagnoses each year in the United Kingdom (UK). Treatments include chemotherapy, radiotherapy and surgery, but result in devastating side effects including later-in-life cancers, poor quality of life and neurological/mental health conditions. These side effects, as well as the development of chemoresistance in MB tumours, have resulted in the need for new therapeutics. Specific microRNAs (miRNAs) containing a toxic 6-mer seed sequence exhibit tumour suppression properties on the RNA-induced silencing complex (RISC) protein, via death induced by survival gene elimination (DISE). However, the potential of DISE-dependent miRNA action in MB has not been established. Furthermore, several tumour suppressor miRNAs appear to be downregulated in MB, but mechanisms for miRNA-replacement therapy in MB have not been defined. The development and progress of new MB therapeutics is hindered by blood brain barrier (BBB); a selective, semi-permeable membrane between the brain's interstitium and surrounding tight blood junctions, acting as an immune defence. Nonetheless, peptide and peptide-based nanoparticles have emerged as promising agents for small RNA delivery across the BBB. We therefore hypothesised that peptide-based nanoparticles may be suitable vehicles for miRNA delivery into MB cells.

Methods: We analysed three DISE miRNAs (hybrid and wild-type) from the miR-34, miR-124 and miR-204 families for their effects on MB cell lines (DAOY and HD-MB03) through in vitro studies including cytotoxicity assays and eventually confocal microscopy. The self-assembling formation of complexes between the miRNA and the group's novel peptide (TY-28, with a sequence of GGGWGPIACDIFTNSRGKRA) was examined by agarose gel electrophoresis.



POSTER ABSTRACTS

Results: Agarose gel electrophoresis indicated an optimum positive value (~25) for nitrogen/phosphorus ratio for each peptide/miRNA nanoparticle. This was further shown by dynamic light scattering. Cytotoxicity assays showed cell viability was significantly reduced when the chosen miRNAs were introduced into DAOY and HD-MB03 cell lines, respectively with up to 61 and 51% a reduction in cell viability.

Conclusions: The work conducted to date shows promise and contributes to addressing the gaps in MB management. Next steps will further characterise the physicochemical properties of the nanoparticles and demonstrate their ability to deliver miRNAs into MB cells in monolayer and 3D culture settings, in a functionally relevant manner.

A parallel approach to forensic investigation: Leveraging UAVs and eDNA in clandestine grave detection

*Cherene de Bruyn, Dr Kirstie Scott, Dr Heather Panter, Dr
Frederic Bezombes and Dr Komang Ralebitso-Senior*

A variety of biotic (microbes, scavengers and insects) and abiotic (soil pH, moisture and temperature etc.) factors impact the decomposition process. In terrestrial environments, these factors vary considerably and can complicate the identification and detection of human remains and clandestine graves. Unmanned aerial vehicles (UAVs) equipped with imaging sensors have been used to support grave detections. A limitation of current experimental designs is that they often investigate isolated factors impacting decomposition or employ surface or shallow sub-surface burials, with either multiple mammalian or human cadavers or single burials without cadaver material. This approach limits the creation of validated and reliable predictive models for single burials. This research proposes a parallel framework that integrates remote sensing with forensic ecology approaches to enhance the identification and detection of human remains and single clandestine graves.



POSTER ABSTRACTS

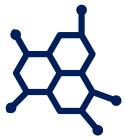
Through simulated shallow burials, this research seeks to develop more reliable methods for grave detection including the estimation of time since intervals. With the addition of environmental DNA (eDNA) sequencing shifts in soil microbial communities can be monitored to develop a “microbial clock”, specifically for post-burial and post-translocation interval estimation by analysing changes in microbial landscapes. By leveraging cutting-edge drone technology to explore changes in terrestrial landscapes and linking them to shifts within the soil microbial communities, this project has the potential to enhance forensic investigations through a more comprehensive and reliable approach. This multidisciplinary approach has the potential to significantly refine grave detection techniques, fostering more sustainable and inclusive advancements in forensic science.

The Impact of Stress on Concordance to Antihypertensive Medications: A Systematic Review and Meta-Analysis

K. Williams, J. Yates, E. Mbeta, A. Morrow, R. Latham, R. Lotto, I. Jones, P. Penson

Background and Aims: Despite effective pharmacological treatments, hypertension control remains suboptimal, with only 35% of treated individuals achieving target blood pressure. Poor medication concordance is a key contributing factor. Psychosocial influences – such as stress – may affect concordance, but findings across the literature have been mixed. This review aimed to evaluate whether stress is associated with concordance to antihypertensive medication.

Methods: A systematic search was conducted in PsycINFO, MEDLINE, CINAHL and Web of Science, following PRISMA AND JBI guidelines. Studies were included if participants were ≥ 18 years, had been prescribed antihypertensive medication, reported measurable indicators of both stress and concordance, and employed quantitative methods. Twelve studies met the inclusion criteria: six were included in the meta-analysis, and six were synthesised narratively.



POSTER ABSTRACTS

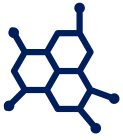
Results: The meta-analysis found a significant negative association between stress and concordance (OR =0.57, 95% CI: 0.45-0.74, $p < .001$), indicating that higher stress is associated with lower medication concordance. Substantial heterogeneity was observed (I^2) = 97.1%, likely due to differences in how stress and concordance were measured across studies. Narrative synthesis findings were mixed, with two studies supporting the association.

Conclusion: These findings highlight the importance of recognising stress as a potential barrier to medication concordance. Addressing stress in patients with hypertension may help improve concordance and, in turn, blood pressure control. Future research should focus on real-world application and explore why stress impacts concordance.

Extracellular Vesicles: A Novel Tool In The Prenatal Diagnosis of Congenital Heart Disease

Lesley Sloan

Congenital heart disease (CHD) is the most common birth defect, occurring in almost 1% of births. CHD is diagnosed prenatally, during a routine 20-week anomaly ultrasound scan but this method has limitations, and subsequently, as many as 50% of CHD cases fail to be diagnosed until birth (Singh et al., 2015). We are investigating novel biomarkers in maternal blood which could form the basis of a prenatal blood test. Extracellular vesicles (EVs) are small, membrane-bound particles that are released from most cell types and involved in endocrine signalling. EVs released by the foetus can cross the placental syncytiotrophoblasts (Fig 1) and are detected in maternal blood. (Adamova et al., 2023). These are therefore a potential source of biomarkers for foetal disease, with the ability to be isolated from maternal blood samples. EVs express a number of potential biomarkers (Fig 2). Micro RNA is carried in the cargo whilst the vesicle surface expresses proteins including tetraspanins as well as glycans. The ultimate goal of this work will be to identify EV biomarkers of CHD in maternal blood with which to develop a prenatal diagnostic test.



POSTER ABSTRACTS

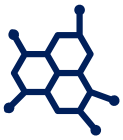
Our specific aims are as follows:

- To develop in vitro models to study the mechanisms of EV trafficking across the placenta.
 - To develop methods to identify biomarkers in the EV cargo (micro-RNA; miR) and expressed on the surface (glycans) using a rat model of pregnancy
 - To apply these methods to clinical samples obtained from diseased and healthy pregnancies (the ExoChase study)
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MicroRNA Approaches to Preserving Hair Follicle Function in Scarring Alopecia

Lauren Tonge, Adel Mohamed, Francesca Giuntini, Imran Saleem, Alun Hughes, James Baker, Talveen Purba, Matthew Harries and Kehinde Ross

Frontal fibrosing alopecia (FFA) is a scarring alopecia characterised by permanent hair loss due to inflammation-driven damage to hair follicle (HF) stem cells. Epithelial-mesenchymal transition (EMT) and fibrosis have also been implicated in the pathology of FFA, but the mechanisms are poorly understood. While nucleic acid therapies (NATs) have shown much promise for several complex diseases, their potential in scarring alopecia has received limited attention. MicroRNAs (miRNAs) represent one such framework for the development of NATs given that miRNA dysregulation occurs in a wide range of disorders. Therefore, this study aims to determine whether miRNA levels are dysregulated in FFA, how such dysregulation may contribute to FFA pathogenesis and explore the potential of miRNAs as nucleic acid therapeutics for FFA. Using RNA sequencing approaches, several miRNAs whose expression was downregulated in FFA in patients were identified. Of these, five downregulated miRNAs (miR-17-3p, miR-20a-5p, miR-135b-5p, miR-423-3p and miR-484) were bioinformatically predicted to target the LEPTIN gene (LEP), a proinflammatory adipokine implicated in HF regulation and EMT.



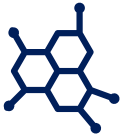
POSTER ABSTRACTS

For functional studies, immortalised primary keratinocytes were transfected with a fluorescently labelled miRNA and visualised by fluorescence microscopy, revealing a transfection efficiency of 63%. Consistent with this, an increase in miRNA expression was observed upon analysis by RT-qPCR. Elevation of miRNA levels by transfection of immortalised primary keratinocytes will enable initial validation of LEP as a target for the identified miRNAs of interest. We will subsequently develop and characterise miRNA mimic formulations with the aim to restore miRNA levels in the HF and potentially to improve patient outcomes. The distribution of the most promising miRNA mimic will be examined in healthy and FFA HFs using RNAScope approaches. The miRNA mimic and appropriate control oligonucleotides will be loaded into chitosan nanoparticles conjugated to a cell-penetrating peptide, IMT-P8, known to reach the HF.

Unveiling the Microbiome, Micronutrient and Metabolite Profile of Panta Bhat, a Traditional Soaked Cooked Rice

Sadia Afrin, Mosharraf Hossain Sarker, Glyn Hobbs, Ismini Nakouti

Malnutrition is the single largest underlying cause of mortality in children and women in low and middle-income countries (LMICs), affecting 3 billion people worldwide. Recently, the trend in fermented food research has increased in popularity due to the capacity of probiotic microbes to improve food nutritional values. “Panta Bhat”, the overnight soaking cooked rice, is a traditional preservation method that makes it more nutritious and delicious. Anecdotal evidence and our preliminary data on simulated soaked rice suggests that soaking cooked rice in water overnight causes a mild, but consistent fermentation of the rice and this process also improves its micronutrient contents. Our previous study identified two Gram-positive probiotic bacteria, *Leuconostoc lactis* and *Weissella confusa*, and mineral analysis showed significant increases micronutrients in soaked rice compared to unsoaked rice. Significantly, there was a notable reduction in glycaemic response after consuming soaked rice ($P < 0.01$). Little scientific research has been done in this tradition food.



POSTER ABSTRACTS

The findings could offer a low-cost strategy to combat malnutrition and electrolyte imbalances in vulnerable groups. Furthermore, this research aligns with the UK government's food strategy on "healthier and sustainable dietary choice", promoting better public health outcomes. In this study, we will investigate the microbiome composition in traditional soaked rice, along with the bioavailability of micronutrients, metabolites and suppression of pathogen growth and potential health benefits to humans.



RESEARCH IN ACTION PHOTOS

Focus and Precision in the Lab

Ismail Al-Saadi

I took this photo of my friend while he was working in the lab. It shows how focused and careful he is when doing an experiment. The picture captures a quiet moment where every drop and measurement is important. It reminds us how much hard work and patience goes into research. Even small steps in the lab can help make a big difference in science and medicine. This photo shows the hard work behind discoveries that can help people in the future.

Davood in the depth of research

Mohammad Fattahi

I visualize my nanoparticles using microscopic technique.

Thoughts and reflections from the Sun

Cherene de Bruyn

The sun is a symbol of renewal. It's golden glow marks the start of a new day. In Cape Town, South Africa, this sunrise symbolised the start of an exciting research collaboration - a journey. As the sun travels across the sky, its rays brighten everything. And while mountains can block the light, it is only momentary. PGR journeys can be full of tall, unavoidable mountains. But the sun is persistent. Even the tallest mountains can't escape its radiance. With determination, patience and grit, we can journey to the summit of the PhD mountain and bask in the brilliance of the sun.

Planets and petri dishes

Cherene de Bruyn

Discovery is driven by curiosity, just like the search for planets. As researchers, we don't need to travel to the edge of the galaxy to study the extraordinary. With our pipettes and microscopes in hand, we explore uncharted territory, finding the remarkable in the lab. In a sphere that crosses many disciplines, we circumvent the mundane and remain positive, because gram for gram, our vista is vast. Training at BioGrad reminded me that there is no such thing as a small science, even a little can tell us a lot. Like a molecular cosmos can be contained within a petri dish – and isn't that exciting!



Liverpool John Moores University

