

College of Science, NUI Galway



National University of Ireland, Galway
Ollscoil na hÉireann, Gaillimh

RESEARCH DAY



Featuring Research by:

School of Natural Sciences

School of Chemistry

School of Physics

School of Maths, Statistics and Applied Maths

Regenerative Medicine Institute REMEDI

NCBES

Martin Ryan Institute

Environmental Change Institute

Monday, 20th April 2009

9.00 am – 5.15 pm

IT125, IT Building (Staff Oral Presentations)

Foyer, Orbsen Building

(Student Poster Presentations)

PRIZES AWARDED FOR THE BEST POSTER PRESENTATIONS

Topics covered include: Adult Stem Cell Research, Anti-Cancer Agents, Genetical Genomics, Climate Change and more

Admission to the event is free of charge and open to everyone!

For further information:

<http://www.nuigalway.ie/science/news.html>



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College of Science Research Day

Foreword -



Dr. Fawaz Aldabbagh
Vice Dean of Research

I would like to welcome postgraduates, researchers and academic staff across all disciplines of the College of Science, NUI Galway to the College of Science Research Day 2009. This is a unique day in the University calendar, since leading scientists across all disciplines in our College will get together, present and debate their research in a forum that is open to the public. Talks will be topical and aimed at a lay-audience. I therefore also welcome the general public and various dignitaries from industry, local education and others parts of our University to this important event.

The purpose of this event is to highlight research taking place within disciplines, schools and in our research centres. We hope the event will help to publicise important recent research achievements, new prominent academic appointments, as well as foster new collaborations across the College and the University.

A simultaneous Postgraduate Poster Competition will be held in the Orbsen Building Foyer. There are three poster prizes of €300 each for the best poster presentations. Students will be judged on (i) the quality of the poster & abstract presented, (ii) the scientific information provided and (iii) interaction between the student and the judging panel. Poster abstracts are presented in this book of abstracts in alphabetical order within Schools and Disciplines.

I thank all who will make this into a stimulating and interesting day, including speakers, poster presenters and judges, and the audience for listening and discussing the science. Special thanks go to Claire Mitchell and the Dean of Science for organization.

I am happy to receive feed back and comments regarding the day.

Fawaz Aldabbagh

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http://www.nuigalway.ie/chemistry/level2/staff/f_aldabbagh/Fawaz.htm

College of Science Research Day
Monday, 20th April 2009

IT125, IT Building
9.05 am – 5.15 pm

Time	Speaker	Discipline/School/Centre
9.05	Dr. Gerry Morgan <i>Welcome & Chairman</i>	Dean of Science
9.10	Prof. Colin O'Dowd <i>Atmospheric Composition & Climate Change</i>	ECI & C-CAPS
9.30	Dr. Petri Piironen <i>Discontinuities in Changing Systems</i>	Applied Mathematics
9.50	Dr. Emil Skoldberg <i>Applicable Algebra</i>	Mathematics
10.10	Dr. Andrew Shearer <i>Computational Physics - How we can do big science from the desktop?</i>	Physics
10.30	Coffee Break + Viewing of Student Posters, Foyer, Orbsen Building	
11.20	Prof. Lokesh Joshi <i>The Sweeter Side of Biological Communication</i>	NCBES
11.40	Dr. Fiona Kavanagh <i>From The Deep Sea to DNA: How to make a crustacean</i>	Zoology
12.00	Dr. Adrienne Gorman <i>Cell death and survival</i>	Biochemistry
12.20	Dr. Richard Fitzgerald <i>MRI Carna - Facilities, Projects and Opportunities</i>	MRI Carna
12.40	Viewing of Student Posters	To continue over lunch
1.00	Lunch + Viewing of Student Posters, Foyer, Orbsen Building	
2.20	Prof. Paul Murphy <i>Small Molecule Anti-Cancer Agents</i>	Chemistry
2.40	Prof. Brian McStay <i>The Nucleolus, A Paradigm for Genome Organization in Human Cells</i>	Biochemistry
3.00	Prof. Rhodri Ceredig <i>Bone-Marrow Understanding the Cell Factory</i>	REMEDI
3.20	Coffee Break + Viewing of Student Posters, Foyer, Orbsen Building	
3.50	Prof. Cathal Seoighe <i>Bioinformatic; Genetical Genomics and mRNA Splicing</i>	Mathematics, Statistics & Applied Mathematics
4.10	Dr. Peter Crowley <i>The Protein Surface: Structure and Interactions</i>	Chemistry
4.30	Dr. Zoë Popper <i>The Plant Cell Wall — Polysaccharides, Proteoglycans and Evolution</i>	Botany
4.50	Rosarie Coughlan <i>Research Support Librarian</i>	James Hardiman Library
5.10	Presentation of Student Poster Prizes	

Student Poster Presentations

Book of Abstracts

Division of Physical Sciences

School of Chemistry

School of Physics

STUDENT POSTER PRESENTERS

School of Chemistry

No.	ID Number	Surname	Name	Year/Programme
1.	06117864	Fahey	Karen	3PS1
2.	01718291	Frain	David	3PS1
3.	01031490	Gilchreest	Lorraine	4PS1
4.	01737694	Healy	Darren	4PS1
5.	03659585	Kirby	Fiona	2PS1
6.	02020408	Moriarty	Eóin	3PS1
7.	02844966	Nash	Maria	3PS1
8.	04359445	O'Toole	Peter	1PS1
9.	07233678	Saravanan	Rengaraj	2PS1
10.	07233288	Serinyel	Zeynep	2PS1

School of Physics

No.	ID Number	Surname	Name	Year/Programme
11.	02456311	Burke	Daniel	3PS1
12.	99465094	Fergus	Alan	5PS1
13.	05125367	Leahy	Conor	4PS1
14.	03997677	Logean	Eric	5PS1
15.	02307839	McCallig	Margaret	2MS1
16.	03484882	McDonagh	Ann	2MS1
17.	02127342	McDonnell	Patricia	2PS1
18.	03090892	Monahan	Ciaran	2MS1
19.	02378248	Murphy	Kevin	3PS1
20.	06117881	Nowakowski	Maciej	3PS1
21.	05118573	Rodríguez	Oscar	4PS1
22.	00326607	Smith	Arlene	4PS1
23.	07239000	Vaishya	Aditya	2PS1

SYNTHESIS OF FIVE TO EIGHT-MEMBERED [1,2-*a*] ALICYCLIC RING-FUSED BENZIMIDAZOLEQUINONE ANTI-TUMOUR AGENTS

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Mitomycin C (MMC, Figure 1), a naturally occurring indolequinone, is the archetypical bioreductive drug clinically used to treat solid tumours. Upon reductive activation, the activated form of MMC undergoes a cascade of reactions resulting in DNA cross-linking via alkylation at positions 1 and 10.¹ O'Donovan and Aldabbagh recently reported the novel *N*-methylaziridinebenzimidazolequinone (**1**) and evaluations of cytotoxicity towards normal human skin fibroblasts and Fanconi Anemia cells.² The latter cell-line was shown to be hypersensitive to MMC and (**1**). Since various alicyclic [1,2-*a*] ring-fused benzimidazolequinones have recently been shown to have cytotoxicity in the nanomolar range (10^{-9} M) with selectivity towards hypoxic solid tumour cells,^{3,4} we decided to synthesize new five to eight-membered [1,2-*a*] alicyclic ring-fused benzimidazolequinones with aziridine substituents on the quinone moiety. Furthermore the size of the alicyclic ring has been shown to influence the cytotoxicity of five and six-membered ring fused benzimidazolequinones containing an additional cyclopropane ring.^{3,4} In our most recent paper, we reported the synthesis of seven and eight-membered [1,2-*a*] alicyclic ring fused benzimidazoles by a one-pot catalytic hydrogenation/acetylation of 1-nitrophenyl-2-azacycloalkanes.⁵ This poster details this approach to alicyclic ring fused benzimidazolequinones containing an aziridinyl substituent on the quinone moiety.

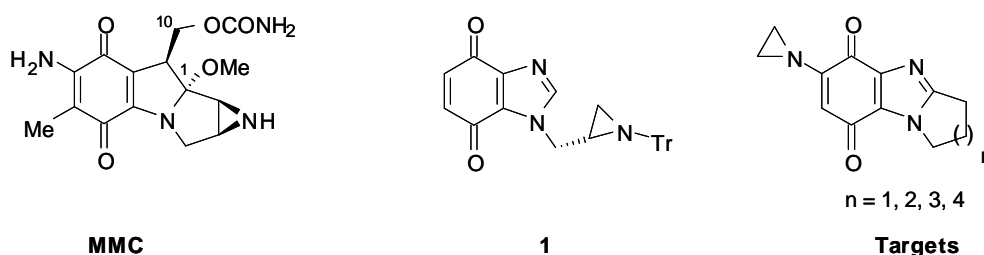


Figure 1

References

- ¹S. E. Wolkenberg, D. L. Boger, *Chem. Rev.*, **2002**, *102*, 2477-2495.
- ²L. O'Donovan, M. P. Carty, F. Aldabbagh, *Chem. Commun.*, **2008**, 5592-5594.
- ³S. Hehir, L. O'Donovan, M. P. Carty, F. Aldabbagh, *Tetrahedron*, **2008**, *64*, 4196-4203.
- ⁴M. Lynch, S. Hehir, P. Kavanagh, D. Leech, J. O'Shaughnessy, M. P. Carty, F. Aldabbagh, *Chem. Eur. J.*, **2007**, *13*, 3218-3226.
- ⁵K. Fahey, F. Aldabbagh, *Tetrahedron Lett.*, **2008**, *49*, 5235-5237.

NOVEL ARABOX LIGANDS: SYNTHESIS AND ENANTIOSELECTIVE CATALYTIC APPLICATION

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We have prepared novel type of Bis(oxazoline) ligand which when coordinated to a metal has two chiral centers within the metallocycle.¹ We will report on the synthesis and structure of these AraBOX Ligands and on their catalytic activity in transition metal catalysed reactions.

Metal complexes of 2,2-bis(oxazoline) ligands are well established asymmetric catalysts applicable to a wide variety of synthetically important reactions such as cyclopropanation, Diels-Alder cycloaddition, ene reactions, aldol reactions etc. Catalytically active complexes of these ligands have been reported using metals such as Fe, Cu, Co, Mg, Zn and Pd. A wide variety of ligands based on this structural motif have been reported. Such variations have largely concentrated on the functionalisation of the oxazoline rings and some variation at the bridgehead linkage.

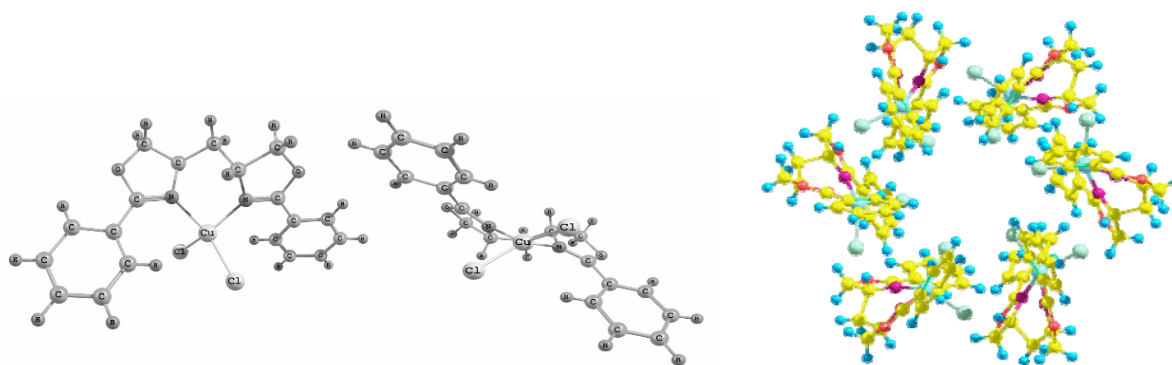


Figure 1: X-Ray crystal structure of Cu(II) phenyl AraBOX complex, “twist”, and unit cell.

Our aim was to create a new family of bisoxazoline ligands where the chiral centers were moved close to the bridgehead. This would have the consequence of introducing a twist into the ligand backbone which could have benefits in the catalysts’ activity in certain reactions. To that end we have successfully synthesised 4,4-bis(oxazoline) ligands which combine similar coordination chemistry to that of the 2,2-bis(oxazoline) ligands, with the intriguing feature of having the chiral centers of the ligand within the metallocycle in the catalytic complex.

We will present the synthesis of the ligand shown via a novel one-pot double deprotection/activation/ring-closure protocol, the ligand-metal complex crystal structure and its catalytic performance in standard test reactions, comparing its performance to that of established 2,2-BOX complexes.

- 1) '*The Synthesis of AraBOX, a New 4,4'-bis(oxazoline), from Novel Pentitol-Derived Bis β -Aminoalcohols.*' Frain, D.; Kirby, F.; McArdle, P.; O'Leary, P. *Synlett* **2009**, *in press*

THE GENERATION OF CARBON RADICALS FOR SYNTHETIC PURPOSES USING A SILICA SUPPORTED POLYOXOMETALATE AS A PHOTOMEDIATOR

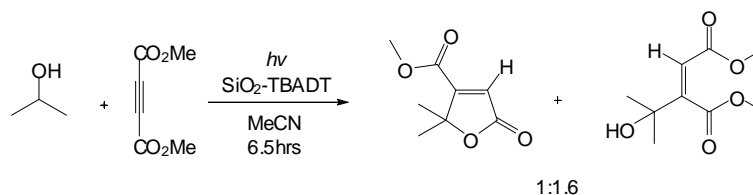
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Many of the current methods of generating carbon radicals for use in synthesis are problematic as they use AIBN, tin hydrides, peroxides, etc. An attractive alternative involves using a triplet state ketone as a photomediator to abstract hydrogen from a C-H bond, thus generating a nucleophilic carbon radical which reacts with alkynes¹ and alkenes² carrying electron withdrawing groups. Our previous work in this area has used photomediators such as benzophenone which suffer from a lack of reactivity and the need to use chromatography to remove them from the product mixture. An alternative approach involves polyoxometalates (POMs), such as tetrabutylammonium decatungstate (TBADT), which is readily produced by the reaction of tetrabutylammonium bromide with sodium tungstate dehydrate. We have now shown that TBADT is a more reactive photomediator, facilitating the reaction of cycloalkanes and cyclic ethers which are unreactive in the presence of benzophenone. It is also easily removed from the product mixture.



Scheme 1

The enhanced reactivity of TBADT comes at a price however, with oligomeric and di-alkylated by-products being formed in the reactions of cycloalkanes and cyclic ethers with alkynes. In addition to 1:1 addition products (Scheme 1), alcohols react with alkynes to give a variety of 2:1 adducts as by-products. Significantly we have now shown that the use of TBADT supported on silica results in a modulated reactivity and eliminates the formation of most of these by-products. In addition the SiO₂-TBADT can be easily recovered by filtration and recycled. The use of this supported POM in the reactions of alkynes with cycloalkanes, primary and secondary alcohols and cyclic ethers will be reported. A mechanistic framework for the reactions described will also be presented.

Acknowledgement: LMG is grateful to the Irish Research Council for Science, Engineering and Technology for an Embark Scholar Award.

¹ N.W.A. Geraghty, E.M. Herson, *Tetrahedron Lett.*, **2009**, 50, 570.

² D. Dondi, M. Fagnoni, A. Albini, *Chem.Eur.J.*, **2006**, 12, 4153.

NATURAL GAS: AUTOIGNITION OF C1 – C5 BLENDS

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Natural gas composition variations throughout the world can cause changes in the combustion chemistry and therefore changes the stability envelope of the combustion system. Fundamental measurements of the ignition delay time of synthetic mixtures, particularly at pressures and concentrations of interest to gas turbines, are therefore important for the design and operation of efficient engines. Rapid compression machine (RCM) and shock-tube facilities have been employed to study the oxidation of natural gas blends at high pressure and intermediate- to high-temperature conditions. The use of both of these devices allows a broad temperature envelope to be investigated and therefore encompass the complete range of temperatures and pressures applicable to gas turbines. A detailed chemical kinetic mechanism has been developed to simulate these results and will be used to approximate similar fuels.

Mixtures of CH₄/ C₂H₆ / C₃H₈ / nC₄H₁₀/ nC₅H₁₂ have been studied in the temperature range 630—1540 K, in the pressure range 8—30 atm, and at equivalence ratios of 0.5—2.0 in ‘air’. For shock-tube experiments the diluent gas was nitrogen whereas in RCM experiments the composition of the diluent gas ranged from pure nitrogen (at lower temperatures) to pure argon (at the highest temperatures). In addition, the combustion chamber in the RCM was fitted with a thermostat and heating tape to control and vary the initial temperature thereby varying the compressed gas temperature. Because the timescale of a rapid compression machine experiment is so long heat loss plays a significant role in both the experiment and the simulation. Therefore a series of non-reactive experiments were performed in order to account for the heat loss at each mixture composition and pressure. Figure 1 shows the experimental ignition profile for a blend of 2.09% CH₄/ 0.67% C₂H₆ / 0.033% C₃H₈ / 0.0167% nC₄H₁₀/ 0.0084% nC₅H₁₂ in ‘air’ where excellent agreement between both shock-tube and RCM results can be seen.

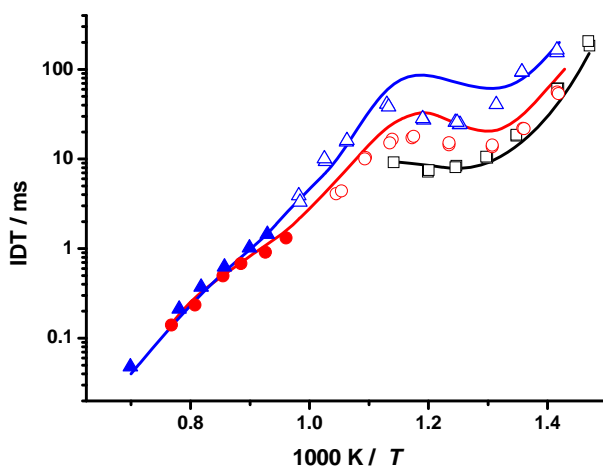
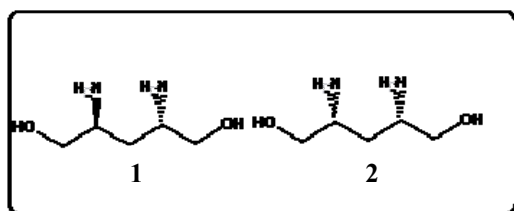


Fig. 1: 20 bar, RCM: □ 6.1% fuel, ○ 3.1% fuel, △ 1.6% fuel
ST: ● 3.1% fuel, ▲ 1.6% fuel, (lines): simulation

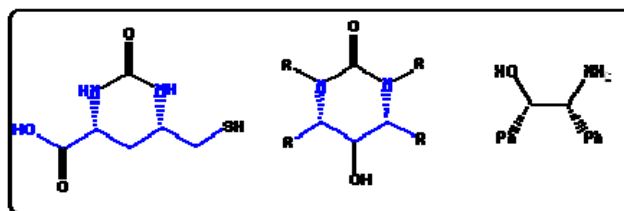
ENANTIOSELECTIVE SYNTHESIS OF DIAMINO DIALCOHOLS: KEY BIOACTIVE BUILDING BLOCKS

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The preparation of novel diamino dialcohols, (2R, 4R)-2,4-diaminopentane-1,5-diol and meso 2,4-diaminopentane 1,5-diol, from D-(+)-arabitol and xylitol respectively is described. Chiral amino alcohols, chiral aminodiols and their derivatives have found application in medicinal chemistry, organocatalysis, and as key building blocks in the synthesis of bioactive molecules.

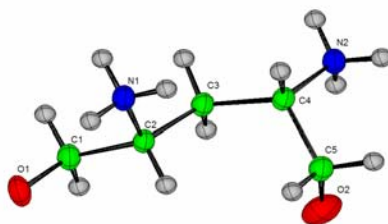


Diamino alcohols prepared in this study.



Molecules with medicinal and catalytic applications with the same structural motif.

A suitable starting point for the synthesis of the diamino dialcohols was identified as 3-deoxyarabitol and 3-deoxyxylitol. The preparation of which was achieved from D-(+)-arabitol and xylitol in 3 steps. It involves acetal protection of 4 alcohols, deoxygenation of the central carbon and deprotection to give the tetrol. Selective protection of the primary alcohols followed by activation of the secondary alcohols, S_N2 substitution with azide and reduction gave the TBS protected amine. Deprotection and isolation as the dihydrochloride salt gave diamino dialcohols 1 and 2.



X-Ray Crystal structure of diamino dialcohol 2.

We have successfully synthesised two stereoisomers of a key diamino dialcohol from readily available precursors. Our focus has now switched to their use as precursors to bioactive compounds such as pyrimidones, and their use as organocatalysts for aldol or Barbier type reactions.

References

- D. Frain, F. Kirby, P. McArdle, P. O' Leary, *Synlett*, **2009**.
B. Linclau, A. J. Boydell, P. J. Clarke, R. Horan, C. J. Jacquet, *J. Org. Chem.*, **2003**, 68, 8252

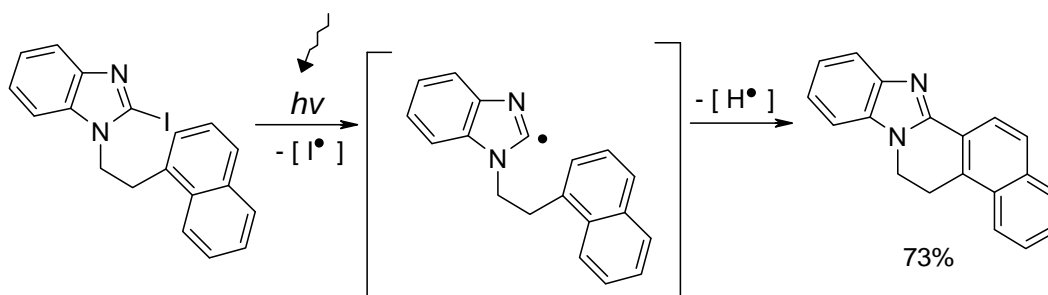
HOMOLYTIC AROMATIC SUBSTITUTIONS OF BENZIMIDAZOL-2-YL RADICALS BY PHOTOCHEMICAL METHODOLOGY

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The following presentation describes light-initiated homolytic aromatic substitutions of benzimidazol-2-yl radicals. These cyclizations are more efficient in terms of yield than literature $\text{Bu}_3\text{SnH/AIBN}$ mediated reactions.¹ Our methodology avoids the use of toxic and hazardous radical initiators (and associated waste disposal problems), and gives less incidence of competitive radical reduction than the Bu_3SnH -mediated reaction. For example (Scheme 1), on exposure to UV-light, 2-iodo-1-[2-(naphthyl)ethyl]-1*H*-benzimidazole was converted to the novel pentacyclic system 5,6-dihydrobenzimidazo[2,1-*a*]benzo[*f*]isoquinoline in very good yield.



Scheme 1

Previous work by our group^{2,3} has focused on the generation of imidazol-2-yl radicals using UV-light and their subsequent cyclization onto aromatics. We now expand the credentials of this methodology by applying these annulations towards the synthesis of new [1,2-*a*] alicyclic ring fused benzimidazolequinone anti-tumour agents containing additional fused aryl rings. Benzimidazolequinones containing [1,2-*a*] fused alicyclic rings have been shown to have cytotoxicity in the nanomolar (10^{-9} M) range with increased potency towards hypoxic (deoxygenated) regions of solid tumours.⁴ Selectivity towards the latter is determined by the ease of single electron reduction by enzymes such as cytochrome P-450 reductase. The increased conjugation of the diazoles presented may further facilitate reductive activation, thus increasing selectivity towards hypoxia.

References

1. S. M. Allin, W. R. Bowman, R. Karim, S. S. Rahman, *Tetrahedron*, **2006**, *62*, 4306-4316.
2. M. A. Clyne, F. Aldabbagh, *Org. Biomol. Chem.*, **2006**, *4*, 268-277.
3. F. Aldabbagh, M. A. Clyne, *Lett. Org. Chem.*, **2006**, *3*, 510-513.
4. M. Lynch, S. Hehir, P. Kavanagh, D. Leech, J. O'Shaughnessy, M. P. Carty, F. Aldabbagh, *Chem. Eur. J.*, **2007**, *13*, 3218-3226.

DEVELOPMENT OF NANOSCALE TEMPERATURE RESPONSIVE CULTURE SURFACES FOR CELL CULTURE AND RECOVERY

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Traditional methodologies employed for cell harvesting using proteolytic enzymes degrade cell surface receptors, consequently impairing subsequent function. A cell harvesting technique using thermoresponsive polymer films as a platform for cell growth, offers a viable alternative for recovering cells and cell sheets. In aqueous solution poly-N-isopropylacrylimide (pNIPAm) has a lower critical solution temperature of 32°C. It is this phenomenon that is exploited in temperature controlled cell harvesting. It has been shown that pNIPAm surfaces are generally non-conductive to reasonable cell growth¹. This issue has been overcome using two different approaches; Okano et al. have grafted pNIPAm using electron beam polymerisation to yield an ultra-thin layer of pNIPAm². It is hypothesised that a low concentration of grafted polymer density allows for seeded cells to interact with the underlying substratum¹. Alternatively, the addition of an over-layer of cell adhesion promoting proteins onto a pNIPAm film negates pNIPAm's adverse effect on cell adhesion³. This body of work seeks to offer a more simple and economic protocol to fabricate pNIPAm coatings for cell harvesting. We propose that coating thickness has a significant bearing on how well cells adhere and proliferate. This research focused on the biocompatibility of coatings deposited using three methods; ultra-thin films were simply adsorbed, the solvent casting technique was used to yield films of 4-5µm thickness and a spin coating film deposition technique was developed to yield sub-micron thick films. Since film thickness seems to have an effect on cell response, it is imperative that this parameter can be evaluated. Sub-micron film thickness cannot be evaluated trivially and a system of thin film appraisal was developed from which we can measure films of 50-500nm in thickness. AFM, SEM-3D-MeXTM and profilometry analysis estimated the film thickness of the spin coated films to be approximately 100nm; the results attained were in very good agreement. We believe such a measurement system can have many uses outside the biotechnology remit. Cells seeded on sub-micron and adsorbed pNIPAm coatings adhered and proliferated to monolayer with cell morphology similar to cells grown on TCP. Casted films did not support cell growth, with most cells seeded remaining in suspension. PicoGreen® and Alamarblue® assays quantitatively confirmed this result. Upon temperature reduction cells detached from the sub-micron and adsorbed coatings in 5-15 minutes. Due to the thin nature of the 100nm and adsorbed films, polymer dissolution is minimised. Ultra-thin adsorbed coatings facilitate cell-to-underlying TCP contact thus encouraging cell biocompatibility similar to TCP. It is unclear how the 100nm spin coated films exude a similar cellular response, as the film thickness exceeds what is hypothesised to be the maximum distance for cell substratum TCP interaction¹. We propose that local micromechanical characteristics affect the manner in which cells interact with the thin film. Sub-micron and adsorbed coatings of pNIPAm offer a viable alternative to technologically complex methods for temperature modulated cytotechnology.

References: 1. V.P. Gilcreest, et al., *Langmuir*, 2004, 23, pp 10138-10145. 2. T. Okano, et al., *Langmuir*, 2004, 20, pp 5506-5511. 3. M. Moran et al., *J. Biomed Mat. Res A.*; 2007, 81A(4), pp 840-876

INVESTIGATION OF ISO-OCTANE DATA

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Iso-Octane and n-Heptane are primary reference fuels (PRF), with an octane rating of 100 and 0, respectively. For example, a petrol fuel with an octane rating of 87 will exhibit the same ignition characteristics as an 87/13 mixture of Iso-Octane and n-Heptane. Many different research groups have studied the oxidation of both these fuels experimentally and computationally, as they are essential to understanding the combustion of petrol. Rapid Compression Machine (RCM) and Shock Tube facilities are among the main instruments used to better understand fuel combustion at various temperatures, pressures and equivalence ratios.

Recently, it has emerged that there are inconsistencies with the available data, in particular with the RCM data. Some researchers' have reported ignition delay times (IDT) that vary considerably. One possible explanation to this is condensation of fuel during the compression phase, causing the fuel mixture 'in air' to become leaner than planned. Condensation within the mix tank is also a possible cause. Figure 1 shows some of the available data (at $\phi=1$) and the discrepancies between each set, particularly at pressures of approximately 14 atm.

A number of fuel mixtures 'in air' were made up. This time, a reference fuel was added. n-Heptane was used at a set proportion to Iso-Octane. These mixtures were then investigated, using a Gas Chromatography-Mass Spectrometer (GC-MS). The aim was to observe whether or not the fuels remained proportional to one another. At lower fuel concentrations, there were consistent results. At $\phi=1$, there were significant differences in the data points, showing that condensation is a possible cause for the inconsistency.

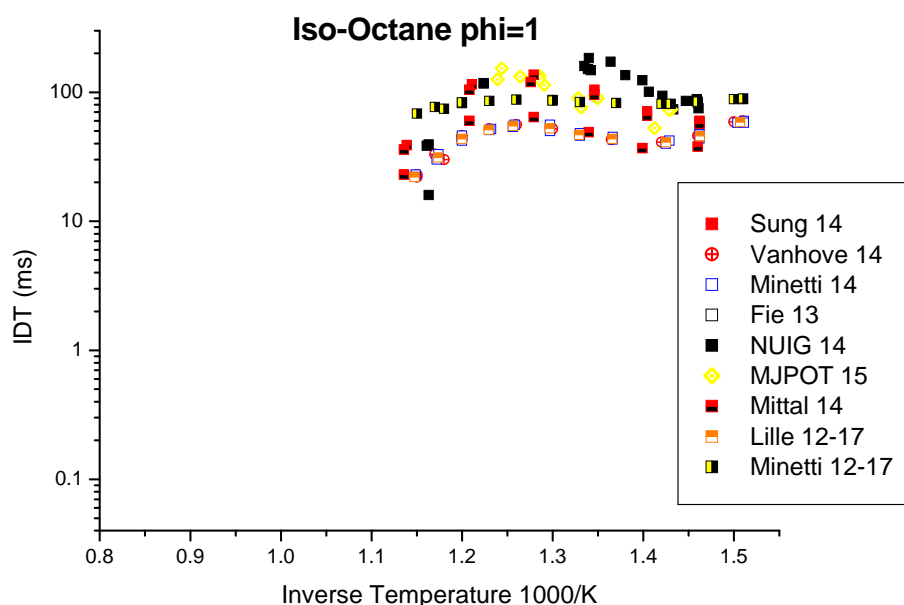


Fig. 1: RCM data at $\phi=1$, from various research groups

CHARACTERIZATION OF REDOX MEDIATORS WITH GLUCOSE OXIDASE (GOX) FOR BIOFUEL CELL OPERATION

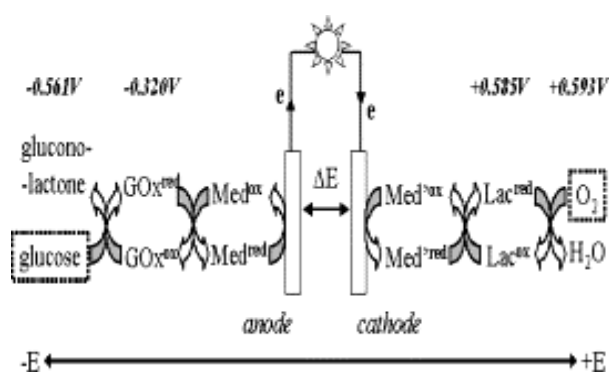
Rengaraj Saravanan, Paul Kavanagh, Susan Boland, Peter Jenkins and Donal Leech

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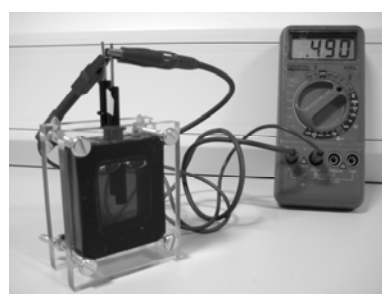
E-mail: donal.leech@nuigalway.ie

http://www.nuigalway.ie/chemistry/staff/donal_leech/personnel.html

Biofuel cells (BFC) using purified redox enzymes for bioelectrocatalytic oxidation / reduction to produce electrical power are gaining an increased interest among researchers due to the possibility of powering implantable or miniaturized electronic devices. Electron transfer can be achieved using redox mediators that shuttle electrons between the active site of an enzyme and an electrode. In our research, osmium based complexes are used as these electron shuttling mediators and can form building blocks for bioelectrocatalytic layers. Mediator performance can be compared by evaluation of solution-phase pseudo first-order rate constants (k_f) for mediator / enzyme electron transfer. This evaluated parameter was exploited to select the most appropriate mediators for operation of a glucose/ O_2 biofuel cell and the complexes were subsequently co-immobilized with appropriate enzymes to produce prototype BFCs.



Schematic depiction of a mediated biocatalytic glucose/oxygen biofuel cell using glucose oxidase and laccase as biocatalysts.



Model of assembled biofuel cell

SHOCK-TUBE IGNITION DELAY TIME MEASUREMENTS AND CHEMICAL KINETICS MODELLING FOR MIXTURES OF DIMETHYL ETHER AND METHANE IN AIR

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Abstract

Dimethyl ether (DME) appears as an alternative biofuel/ignition enhancer for diesel fuel in compression ignition engines thanks to its high cetane number (~55) comparable to that of diesel fuel, low auto-ignition temperature, high oxygen content (34.8%) and the absence of C–C bonds, which altogether result in low soot and particulate matter emissions. It has been experimentally shown that the addition of even a small amount of DME into methane increases reactivity of the system significantly^{1,2}. DME has been investigated experimentally and computationally by many groups and various chemical kinetic mechanisms have been developed based on these studies covering both low- and high-temperature DME oxidation chemistry. Among computational studies, Zhao *et al.*³ reports DME unimolecular decomposition rate constant expressions calculated at certain pressure intervals between its low- and high-pressure limits for both nitrogen and argon as diluent gases, through theoretical computation.

This study constitutes an experimental and modelling study of ignition delay times of CH₄/DME mixtures in "air", and re-estimation of the pressure-dependant unimolecular decomposition reaction rate constant of DME, and shows that this calculation was needed to reproduce the experimental results at high pressures. Ignition delay times for the mixtures were measured behind reflected shock waves at pressures varying from 1.3 atm to 35 atm over the temperature range from 900 K to 1650 K. Eight sets of mixtures have been investigated with equivalence ratios of 0.3, 0.5, 1.0 and 2.0 and with varying DME contents in fuel from 20% to 40%. The rate constant for the unimolecular decomposition reaction $\text{CH}_3\text{OCH}_3 (+\text{M}) \leftrightarrow \text{CH}_3\text{O} + \text{CH}_3 (+\text{M})$ has been re-estimated and a nine-parameter Troe fit is generated to describe the reaction as a function of temperature and pressure. The resulting rate expression agrees well with that recently reported by Cook *et al.*⁴ in the temperature range 1300–1700 K at 1.5 atm and is faster than that of Zhao *et al.*³ for temperatures up to 1700 K, by about a factor of two. A chemical kinetics mechanism consisting of 118 species and 667 reactions was used to simulate the experimental data. Model comparisons with the experiments are presented. Overall, the mechanism captures the experimental trends and is mostly in good agreement with the data.

References:

¹ T. Amano and F.L. Dryer, *Proc. Comb. Inst.*, **1998**, 27, 397–404

² Z. Chen, X. Qin, Y. Ju, Z. Zhao, M. Chaos, F.L. Dryer, *Proc. Comb. Inst.*, **2007**, 31, 1215-1222

³ Z. Zhao, M. Chaos, A. Kazakov and F.L. Dryer, *Int. J. Chem. Kinet.*, **2008**, 40, 1–18

⁴ R.D. Cook, D.F. Davidson, R.K. Hanson., *Proc. Comb. Inst.*, **2009**, 32, 189–196

OPTIMAL PHOTOMETRY OF FAINT COMPANIONS

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We propose a new approach to differential astrometry and photometry of faint companions in adaptive optics images. It based on a prewhitening matched filter, also called the Hotelling observer in the literature. We focus on cases when the companion's signal is located within the bright halo of the parent star. Using real adaptive-optics data from the 3m Shane telescope at the Lick Observatory we compare the performance of the Hotelling algorithm with other estimation algorithms currently used for the same problem.

The real single-star data is used to generate artificial binary objects with a range of magnitude ratios and separations. Using this data we find that the Hotelling algorithm provides the lowest astrometric error and photometric error in all cases.

In the case of high Strehl ratio data ($SR \approx 0.5$) the differential photometry of a binary star with a $\Delta m = 4.5$, and a separation of 0.6 arc seconds, is better than 0.1 magnitudes; a factor of two lower than the other algorithms considered.

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SIMULATION OF PARTICLE DEPOSITION AND RESUSPENSION THROUGH THE INTEGRATION OF ACTIVE TRACERS INTO AN EXISTING CFD FORMULATION

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Introduction: The phenomenon of aerosol transport in turbulent flows has been studied extensively using Direct Numerical Simulation over the past few decades. One of the most useful DNS approaches is Lagrangian simulation. Lagrangian simulations of aerosols in turbulent flows have provided much information regarding aerosol deposition to surfaces and aerosol-turbulence interactions. Because individual aerosol trajectories are calculated in Lagrangian simulations, details of aerosol motion are accessible that are unattainable by experiment. Thus making Lagrangian Modelling a highly powerful tool in aerosol transport simulation.

Model Development: A Computational Fluid Dynamic program called OpenFOAM[1] is used as a base and modified to incorporate wall collisions, bounce and re-entrainment. To model such behaviour, aerosols' potential functions for population of aerosols are developed governing sticking and re-entrainment of aerosols. When an aerosol strikes a surface under most existing models the aerosol adheres to the surface (perfect sink). In this work there are two outcomes that occur which are dependent on the velocity of the aerosol when it impacts with the surface. At low impact velocities the aerosol adheres but as the impact velocity increases the aerosol may bounce if the velocity of impact is greater than a critical velocity defined

as:- $V_c = \left[\frac{2E_a}{m} \right]^{\frac{1}{2}}$ where E_a is the surface adhesion as detailed by Johnson *et al* [2],

m is the mass of the aerosol. $E_a = E_m + E_s$ Where E_m is the mechanical energy at impact and E_s is the surface energy at contact.

While the phenomenon of resuspension has been studied extensively on its own, very little work has been done including resuspension into a standard Lagrangian model. In the present work, E_a is equal to E_s and the critical velocity is calculated. If the critical velocity is less than the velocity of the flow at position of the particle, the aerosol is resuspended into the flow at velocity dependent on the aerosol properties and energy remaining after the aerosol has over the adhesion energy.

Preliminary Results: The initial test case being run has 200 aerosols with a diameter of 90 μ m injected at a velocity ranging between 0.1 and 2 m/s. The fluid velocity at the inlet is 5 m/s. As expected from experimental data and other simulations predictions, the aerosol concentration is greatest in the near wall region and depositing aerosols have settling velocities inline with expected values (for larger aerosols gravitational effect becomes dominate). Aerosols are depositing with deposition velocities less than their injection velocities and when they resuspend, they tend to deposit again within a few time steps. The simulation results include aerosol bounce and are in agreement with experimental data and theoretical model predictions.

References

1. <http://www.opencfd.co.uk/openfoam>
2. K. L. Johnson, K. Kendall, and A. D. Roberts, *Proc. R. Soc. London, A* 324, 301 (1971).

TEMPORAL DYNAMICS AND STATISTICAL CHARACTERISTICS OF THE MICROFLUCTUATIONS OF OCULAR WAVEFRONT ABERRATIONS

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Microfluctuations of accommodation have been the subject of many studies¹. Few of them have looked at the effect that they have on the overall wavefront aberrations, or at the statistical description of their dynamics. New technology developments permit now to address these issues with unprecedented resolution and accuracy. We aim at studying the dynamics of the wavefront aberrations introduced by microfluctuations of accommodation and characterising their temporal statistics at different target distances during steady state accommodation.

A custom-built aberrometer was implemented (5.4mm diameter pupil, 250 μ m spatial sampling and 150Hz frame rate). We conducted measurements on the right eye of 5 healthy subjects (25 to 40 years old). For each subject we collected 9 trials at each of 3 fixation target distances (far point, near point, and mid-point between them). Each trial was 26 seconds in duration (4,000 data points per trial, 36,000 data points in total). The time series of the wavefront RMS and its derivative were calculated for each trial (RMS was estimated from a 5th order Zernike polynomial expansion). Probability density functions (PDF) for the time series and their derivatives were found.

The PDFs of the time series were found to be non-Gaussian, exhibiting heavy tails and skewness. We found that the degree of the heavy-tailed effect is dependent on the level of accommodation, in that the heavy tails are more apparent at fixation distances corresponding to the near point and mid-point than at the far point. In many cases the derivative of the RMS under accommodation exhibits a Lévy-type stable PDF.

We have shown that the dynamics of aberrations show non-Gaussian statistics and that they present heavy-tailed and in some cases, skewed PDFs. We noted that the heavy tails were more apparent during active accommodation. This leads us to suggest that the observed PDFs of the RMS wavefront resulting from microfluctuations of accommodation may be the result of the coupling between the RMS wavefront aberration and the accommodative control system. Lévy-like statistics are often related with optimal control strategies^{2, 3}, hence we propose for future work to investigate this matter further.

References

¹ W.N. Charman, G. Heron. *Ophthalmol. Physiol. Opt.*, 1988, 8, 153-164.

² J.L. Cabrera, J.G. Milton. *Chaos*, 2004, 14 (3), 691-698.

³ C.W. Eurich, K. Pawelzik. *Int. Conf. on Artificial Neural Networks*, 2005, 2, 365-370.

THE EFFECT OF THE RETINA ON THE OCULAR DOUBLE-PASS INTENSITY POINT-SPREAD FUNCTION

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INTRODUCTION. Objective assessments of the quality of the eye optics have been obtained since 1950 from the double-pass image of a point source, the point-spread function (PSF) [1,2] assuming that the contribution from the retina is negligible. Using the same assumption, we expect that the double-pass PSF obtained after adaptive optics correction of the ocular aberration is close to the diffraction limit. This work has been published [3].

METHOD. A custom-made fundus camera that incorporates a close-loop adaptive optics system was built. This system probes the ocular aberrations over a 6.7mm pupil using a beam at 675 nm and an Hartmann–Shack wavefront sensor with 97 lenslets. A computer controlled 35-element bimorph deformable mirror cancels the measured aberrations in real-time. The images of the double-pass PSF with 0.2 arcmin resolution are obtained using a 1-second flash from a point source emitting at 543 nm (HE-NE laser). Two through focus series were obtained, one after adaptive optics correction of the ocular aberrations, and the other without adaptive optics correction (at measured optimum focus), in four subjects aged between 25 to 36 years (two subjects with dark pigmented eyes and two with light pigmented eyes).

RESULTS. The mean wavefront aberrations measured after correction was 0.097, 0.085, 0.097, 0.072 μm root mean square (without tip, tilt) for each subject. The shape of the doublepass PSF closely follows a Lorentzian distribution. The width (half-width at half-maximum) of the double-pass PSF (at best focus) after correction of the ocular aberrations was 1.1, 1.2, 1.7, 1.7 arcmin and the width without correction was 2.3, 1.8, 3.2, 2.3 arcmin. The width of the double-pass PSF reconstructed from the wavefront aberration measurements after correction are all close to 0.2 arcmin. The diffraction limit is 0.19 arcmin.

CONCLUSION. After adaptive optics correction of the ocular aberrations, the double-pass PSF is more compact than without correction. The width of the double-pass PSF after correction is about 6 times for dark pigmented eyes and 9 times for light pigmented eye wider than the width expected for a diffraction limited eye. The magnitude of the remaining aberrations measured by the wavefront sensor is too small to explain these results. The pigments being concentrated in the retinal pigment epithelium layer and in the choroid, the measured width reflects the influence of the eye fundus on the double-pass PSF.

REFERENCES

- [1] F. Flamant, *Rev. Opt. Theor. Instrum.* **34**, 433 (1955).
- [2] P. Artal, J. Santamaría, and J. Bescós, *J. Opt. Soc. Am. A* **5**, 1201 (1988).
- [3] E. Logean, E. Dalimier, and C. Dainty, *Opt. Express* **16**, 17348 (2008).

AN EVALUATION OF COMMON SOURCES OF HAND ARM AND WHOLE BODY VIBRATION IN THE IRISH CONSTRUCTION AND ENGINEERING INDUSTRY

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The introduction of the Safety, Health & Welfare at Work (General Application) Regulations 2007¹ presented challenges for the Irish Construction and Engineering Sectors in terms of vibration exposure assessment and management. The aim of this project was to evaluate worker exposure to vibration and recommend an exposure management system to aid in the selection of 'low risk' equipment, and help schedule work activities so as to minimise worker exposure when using 'high risk' tools.

Hand arm (HAV) and whole body vibration (WBV) was measured on a variety of vibrating equipment in accordance with ISO 5349:2001 and ISO 2631:1997 respectively. Study measurements of both hand arm and whole body vibration were found to be comparable with existing published data²⁻⁴. A questionnaire survey was utilised to collect information on vibrating equipment use and exposure times. Worker's exposure estimations were then verified using workplace observations. Two exposure management systems were piloted at two sites based on vibration emission values recorded, both worker and management feedback on the usability of both systems was sought using a short questionnaire survey.

Study results show that in most cases, tool age had a statistically significant effect on the vibration emission values recorded for hand tools ($p < 0.05$). Terrain and unit operation had a statistically significant effect on the vibration emission level recorded on vehicles such as mini dumpers ($p = 0.01$, $p = 0.05$) and excavators ($p = 0.01$, $p = 0.01$).

Worker 8 hour exposure estimates for HAV and WBV calculated using the median vibration emission values, and the exposure times recorded during workplace observations, were compared to the Exposure Action and Exposure Limit values cited S.I. 299 of 2007. Study results also show that there was a statistically significant difference between A(8) exposure estimates calculated using exposure times self reported by the worker compared with exposure times recorded during workplace observations for both (HAV ($p = 0.001$) and WBV ($p = 0.00$)). In all cases the exposure estimates (A(8)) calculated using the self reported exposure times were greater. For the purposes of carrying out a reliable risk assessment, direct measurements of worker exposure time are preferable to self-estimate methods such as questionnaire surveys.

The vibration exposure management system should be implemented across the organisation, and should include measures to ensure old or damaged equipment is replaced as necessary. Procurement policies should be revised to ensure that equipment with low vibration emission levels are purchased where possible.

References

1. Safety, Health and Welfare at Work (General Application) Regulations 2007 (SI 299 of 2007)
2. Ikeda, K., Ishizuka, H., Sawada, A., Urushiyama, K. (1998) Vibration Acceleration Magnitudes of Hand-Held Tools and Workpieces. *Industrial Health* **36**: 197-208
3. Paddan, G.S., Griffin, M.J. (2002) Evaluation of Whole-Body Vibration in Vehicles. *Journal of Sound and Vibration* **253**: 195 – 213
4. Jang, J.Y., Kim, S., Park, S.K., Roh, J., Lee, T.Y., Youn, J.T. (2002) Quantitative Exposure Assessment for Shipyard Workers Exposed to Hand-Transmitted Vibration From a Variety of Vibration Tools. *AIHA* **63**, 305 – 310.

AEROSOL PARTICLE RESUSPENSION STUDIES FROM HUMAN BODY SURFACES FOR EXPOSURE ASSESSMENT

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In the current climate, a threat not only exists from accidental releases of artificial radioactive material, but there is also a real risk of deliberate release in the course of terrorist attacks on major population centres. In preparing for this latter scenario, accurate estimates of whole body exposure, arising from all exposure pathways is necessary in order to design effective countermeasures. In assessing population exposure to radioactive aerosol particles following a nuclear accident, research up to the early 1990s^{1,2}, focussed on inhalation as the only important route of exposure. One exposure pathway that merits investigation, and for which no comprehensive experimental data are available, is that of exposure to contaminant material that was formerly deposited on the human skin, hair and clothing. This is especially important in the case where a person might be unwittingly contaminated and might spread this contamination to others via the process of resuspension from their skin, hair and clothing. This exposure pathway may also have significance for airborne pollutants that are non-radioactive, e.g. infectious aerosol that becomes re-entrained from disturbance of hospital bedding, etc.

Within the Centre for Climate & Air Pollution Studies, NUI, Galway, tracer labelled particles are generated in representative size ranges, using monodisperse silica. As in earlier experiments in this research group^{3,4}, neutron activatable tracers and fluorescent labels are used. "Contamination" of clothing materials with these particles takes place within a 2.25m³ aluminium deposition chamber, where a small 2W fan is to simulate real room mixing conditions. An open face filter air sampler is operational during deposition events. Using this experimental set up, a wide range of clothing fabrics will be "contaminated", incorporating rough, smooth, synthetic and natural etc. Samples will be generated with low and high particle loadings, and using sub-micron and super-micron particle size distributions. Experiments will then be carried out in a test room, whereby volunteers will have the "contaminated" clothing attached to them, and they will then participate in one of several pre-defined activity patterns (which include remaining stationary, walking at a pre-defined rate, vigorous activity, etc). Isokinetic sampling of the room air will allow the collection of filters, which can later be analysed by neutron activation analyses to determine the mass of resuspended tracer particles. In addition, real-time particle size spectrometry equipment will be present in the room, to allow an assessment of any shift, relative to the deposited particles, in size distribution of the resuspended particles.

Following data analysis and in collaboration with scientists in the Nuclear Safety Section of the Riso National Laboratory, Denmark, Monte-Carlo simulations will be carried out to assess the importance of the dose contribution arising from resuspended particles.

References

¹ *Airborne contamination in the indoor environment and its implications for dose.* Andersson, Roed, Byrne et al. Riso Report R-1462(EN).

² *Radiation Dose Implications of Airborne Contaminant Deposition to Humans.* Andersson, Fogh, Byrne, et al. Health Physics, 82, No.2, 2002, pp. 226-232.

³ *Stable Tracer Aerosol Deposition Measurements in a Test Chamber.* Byrne et al. Journal of Aerosol Science, Vol. 26, Issue 4, 1995, Pages 645-653.

⁴ *Measurement of contaminant removal from skin using a portable Fluorescence Scanning System.* Hession, Byrne et al. Journal of Environmental Radioactivity, Vol. 85, Issues 2-3, 2006, pp. 196-204.

MODELLING EXPOSURE TO PHARMACEUTICAL AEROSOLS

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Introduction

In the pharmaceutical sector occupational exposure to active pharmaceutical ingredients (APIs), with exposure limits as low as $1\text{ng}/\text{m}^3$, arises in research, development and manufacturing. Occupational Health and Safety legislation, specifically the European Council Directive 98/24/EC and the Registration Evaluation and Authorisation of Chemicals (REACH) Regulations 2006, requires that manufacturers of chemical demonstrate that their products are manufactured, controlled and used in a manner that is safe for their workers, consumers and environment. This can prove difficult as in most instances it is only possible to make small numbers of exposure measurements and given the variability between and within workers it is often difficult to obtain sufficient objective data to make reliable exposure conclusions. Validated occupational exposure models are useful tools in the exposure assessment process and can provide a way of estimating workers' exposure in the absence of sufficient measurement data. This research project aims to further develop and validate an existing deterministic occupational exposure model^{1,2} to predict airborne exposure of workers in the pharmaceutical industry.

Methods

Workplace exposure assessment data from the pharmaceutical industry, containing all the worker and workplace information required for the exposure model was collated and inputted into the exposure model. The measured exposure levels ranged from 0.001 to $10,000\ \mu\text{g}/\text{m}^3$ and included a range of handling activities, control measures and abnormal operating conditions. Model predictions of exposure were then compared to the measurement results for each exposure assessment. Regression analysis (SAS statistical Software) will be employed to calibrate the model predictions against measurement data and improve exposure predictions for a range of situations representative of the pharmaceutical industry.

Results

Initial results indicate that the exposure estimates are of comparable accuracy and precision to measurement data. The correlation between the log-transformed predictions and actual measured values for the exposure assessments was 0.77, with a positive bias of 3.6 (n=453). Individual estimates were at most an order of magnitude different from the average measured value, but this was comparable to the variation in the measurement data for the same exposure scenario.

Future work

Further data on model input parameters, particularly the dustiness of pharmaceutical powders and on exposure control measures used in the industry will further aid the accuracy of the predictions. Subsequent to calibration, the exposure model will be validated with a second exposure assessment data set. The model will be extended to incorporate Bayesian statistics, allowing model predictions of exposure to be updated with measurement data.

References

- ¹ J. Cherrie, T. Schneider, S. Spankie, M. Quinn, *Occup. Hyg.*, **1996**, 3, 75-83.
- ² J. Cherrie, T. Schneider, *Ann. Occup. Hyg.*, **1999** 43(4), 235-245.

MODELLING THE IMPACT OF IODINE OXIDE NUCLEATION OVER THE OPEN OCEAN

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Abstract

Halogens influence the oxidising capability of the Earth's troposphere, and recently, it was demonstrated that condensable iodine oxide vapours can nucleate very efficiently to form particles, which may have an impact on cloud cover and hence on climate as a whole. Here a one dimensional eulerian microphysical aerosol dynamics model was used to perform analysis of nucleation and growth mechanisms in a marine environment that included iodine oxides as well as condensable organic vapours. The iodine oxides and condensable vapours were considered to originate from the photolytic production of condensable iodine-containing compounds arising from the biogenic emissions of marine flora.

Throughout the simulations, four different schemes to simulate particle formation were used: the sulphuric acid driven nucleation scheme developed by Kulmala, Laaksonen, and Pirjola 1998, iodine driven nucleation ($K_1 \times [I_xO_x]$), sulphuric acid – iodine oxide driven nucleation ($K_2 \times [H_2SO_4]$), and particle formation deriving from cluster activation theory ($A \times [H_2SO_4]$). Results showed that there was a significant enhancement to the number concentration of aitken mode particles (5nm – 50nm), and a considerable increase in the average particle radius for aitken mode particles as well as small increase in the radii of accumulation mode particles (50nm – 500nm).

It was concluded that the presence of iodine oxide vapours as well as other condensable vapour species in a marine environment, would lead to a net increase in number concentration of nucleation mode particles with the potential to lead to an increase in larger particles that could participate in climactic processes.

EXPERIMENTAL DETECTION OF PHASE SINGULARITIES FOR A TURBULENT ATMOSPHERE

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A laser beam in a line-of-sight (LOS) optical communication system propagating over a horizontal path near the Earth's surface experiences heavy distortion due to atmospheric turbulence. An adaptive optics (AO) system can be used to correct for this distortion, however the presence of phase singularities will limit its effectiveness. Phase singularities are caused by the atmospheric distortion and can be seen as zeros of intensity in the cross-section of the laser beam at the receiver. They cause a 2π radian discontinuity in the phase of the optical wavefront. An experimental lab set up is being used to detect phase singularities in simulated atmospheric turbulence. Some results from this set up will be presented.

OCULAR ABERRATIONS IN THE CENTRAL 10-DEG VISUAL FIELD OF THE HUMAN EYE

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We explore the impact of different types of ocular aberrations in the central 10-deg visual field, using a dedicated aberrometer that measures the total wave aberration in terms of the first 20 Zernike polynomials. The strength of each aberration term is assessed in relation to the total RMS wavefront error. We analyzed the contribution of the lower-order and high-order aberrations for the horizontal and vertical meridians in 15 young healthy human eyes. We found that astigmatism and field curvature (focus error off-axis) have the largest contributions to the field-dependence of the wavefront error. Our theoretical and experimental findings show the significance of astigmatism and field curvature contribution to ocular aberrations and their rapid change even at small off-axis angles (3-5 deg). We emphasize the importance of correcting these field aberrations in the future retinal imaging instruments.

VECTORIAL POLARIMETRY

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We propose a method to study the interaction of the three-dimensional electric field in the focal region of a high numerical aperture (NA) microscope objective [1] with a sub-resolution specimen as a means to retrieve sub-resolution information about the specimen.

Fig. 1 is a diagram of the proposed method known as vectorial polarimetry. The high NA focusing lens focuses the incident field, $\mathbf{E}^{(0)}$, creating a three-dimensional field distribution in the focal region, where the sub-resolution specimen is positioned. In the most general case, a three-dimensional scattered field, $\mathbf{E}^{(s)}$, is produced after the interaction of the focused field with the specimen. $\mathbf{E}^{(s)}$ then propagates to the high NA collector lens where it is collimated, projecting the longitudinal component, $E_z^{(s)}$, over the transversal components, $E_x^{(s)}$ and $E_y^{(s)}$, to obtain a beam-like field $\mathbf{E}^{(2)}$. Since the projection of the longitudinal component is a function of the scattering angle, the polarisation state of the scattered light is analysed at different positions across the exit pupil of the collector lens to obtain the scattering-angle-resolved distribution of polarisation states. This distribution contains information on the transversal and longitudinal components of the scattered field.

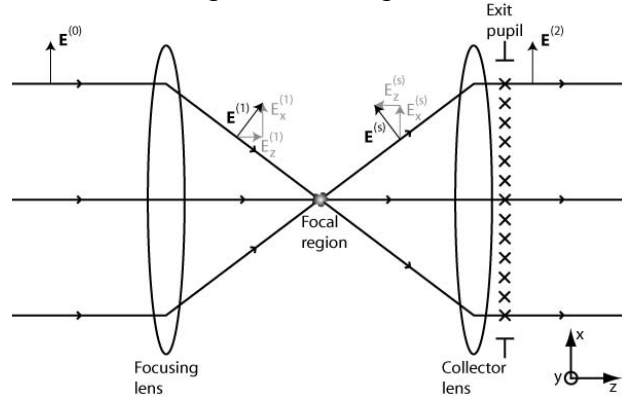


Figure 1: Diagram of the vectorial polarimetry method. The crosses represent sample positions, within the exit pupil of the collector lens, where the polarisation state is analysed.

Our numerical modelling of the system shows that it is possible to determine if a sub-resolution specimen has undergone sub-resolution displacements, within the focal region of the lens, by looking at the polarisation distribution in the exit pupil of the collector lens.

We have built a vectorial polarimeter, based on the system introduced by Lara and Dainty [2], to obtain an experimental proof of concept. Experimental work is underway.

References

1. B. Richards and E. Wolf, “Electromagnetic diffraction in optical systems II. Structure of the image field in an aplanatic system”, *Proc. R. Soc. A*, **253** (1274), 358–379, 1959
2. D. Lara and C. Dainty, “Axially resolved complete Mueller matrix confocal microscopy”, *Appl. Opt.*, **45** (9), 1917-1930, 2006

NUMERICAL PARTIALLY COHERENT IMAGING USING ELEMENTARY FUNCTIONS

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Coherence can be defined as the degree to which electromagnetic radiation or any sort of oscillating quantity maintains a near-constant phase relationship, both temporally and spatially. The theory of coherence and propagation of light through imaging systems is well established. For coherent and incoherent sources, the intensity in the image plane can be predicted numerically using a straightforward convolution calculation. Image formation becomes more complicated when dealing with partially coherent light, as treating two-dimensional intensity fields (described by the four-dimensional; mutual coherence function in the time domain or cross-spectral density in the frequency domain) requires evaluating four-dimensional integrals. These calculations are complex, slow to process and place demands on system memory. A 1000 by 1000 pixel image therefore requires one tera-word of storage, large even by modern standards. Modal expansions of various kinds can speed up the computation time and complexity, but still require a four-dimensional calculation to find the modes themselves.

We present a variation on a method recently introduced [1], in which elementary functions are used to reduce the integrals to two dimensions for light of relatively high degree of coherence. Instead of an exact modal expansion of the mutual coherence function or cross-spectral density, an approximate expansion is used, into what we call in this paper “elementary functions” (to distinguish them from true modes). Recently, we have placed this method on a more rigorous basis [2], in particular paying attention to issues such as sampling [3].

In this paper, we outline the method and show some numerical results. This approach has applications in modelling of photolithographic systems in which partially coherent excimer lasers operating in the Deep Ultra-Violet (DUV) regime have been used for the last decade. An accurate numerical model of such systems could prove useful in solving the classic inverse imaging problem of lithography reticle design.

- [1] M Wald et al, “Design of a microscopy illumination using a partial coherence light source”, Proc SPIE **5962** 59621G (2005)
- [2] A Burvall, A Smith and J C Dainty, “Elementary functions: propagation of partially coherent light”, submitted January 2009.
- [3] M Unser, “Sampling – 50 years after Shannon”, Proc IEEE **88** 569-587 (2000)

RELATIVE HUMIDITY EFFECTS ON AEROSOL LIGHT SCATTERING PROPERTIES

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Aerosols are highly variable component of the atmospheric system, both in space and time and hence exhibit diversity in their optical and microphysical properties. Effect of humidity on aerosol particle depends on the hygroscopic nature of aerosol. More hygroscopic aerosol means increase in effects of humidity which in turn can alter their size¹, mass concentration, chemical composition² as well as their radiative properties and visibility reduction. Light scattering techniques³ are useful tool for studying the hygroscopic and deliquescent nature of aerosol.

Aerosol light scattering coefficient measurements were made during a recent field campaign (from 16/01/2009 to 16/02/2009) at Mace Head (Co. Carna) using two TSI Integrating Nephelometers- one running freely and the other (from PSI, Switzerland) under controlled humidity cycle. Significant difference in the scattering coefficient values has been found at high relative humidity as compared corresponding measurements for low relative humidity. Scattering enhancement factor of up to ten has been found for a four fold increase in relative humidity.

A new aerosol humidification system will be made which will enable continuous measurements of aerosols under controlled relative humidity conditions.

References

¹I.N. Tang, *Journal of Geophy. Res.*, **1996**, *101(19)*, 19,245–19,250.

²D.S. Covert, R.J. Charlson, N.C. Ahlquist, *Journal of App. Met.*, **1972**, *11(6)*, 968-976.

³T.L. Anderson, D.S. Covert, S.F. Marshall, M.L. Laucks, R.J. Charlson, A.P. Waggoner, J.A. Ogren, R. Caldow, R.L. Holm, F.R. Quant, G.J. Sem, A. Wiedensohler, N.A. Ahlquist, T.S. Bates, *Journal of Atmos. Ocean Tech.*, **1996**, *13(5)*, 967-986

**School of Mathematics, Statistics
and Applied Mathematics**

STUDENT POSTER PRESENTERS

School of Mathematics, Statistics and Applied Mathematics

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25.	07233005	Bishop	Marcus	2PS1
26.	02344238	Geeleher	Paul	1PS1
27.	05768888	Humphries	Neil	1MS1
28.	00468444	Hurley	Daniel	3PS1
29.	08233245	Lacerda	Miguel	1PS1
30.	01843621	Naughton	Liam	3PS1
31.	02101840	O'Shaughnessy	Jessica	4PS1
32.	07231272	Pfeiffer	Kirsten	2PS1
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QUIVER PRESENTATIONS FOR DESCENT ALGEBRAS

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Following the recent article [3] of Gotz Pfeiffer that describes a mechanism for producing a quiver presentation of the descent algebra of a finite Coxeter group, we apply the method in the case of the Coxeter group of type A by representing the elements of Pfeiffer's presentation as sequences of binary trees. We intend to use the same method to calculate quiver presentations for the other infinite families of Coxeter groups.

References

[1] Ibrahim Assem, Daniel Simson, and Andrzej Skowronski. *Elements of the Representation Theory of Associative Algebras*. Cambridge University Press, 2006.

[2] Reutenauer Christophe. *Free Lie Algebras*, volume 7 of London Mathematical Society monographs (new series). Oxford University Press, 1993.

[3] Gotz Pfeiffer. A quiver presentation of solomon's descent algebra. *Adv. Math.*, 220:1428-1465, 2009

BIOCONDUCTORBUNTU - A LINUX DISTRIBUTION THAT IMPLEMENTS A WEB-BASED DNA MICROARRAY ANALYSIS SERVER

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BioconductorBuntu is a custom distribution of Ubuntu Linux that automatically installs a server-side DNA microarray processing environment, and provides a user friendly web-based GUI to many of the tools developed by the Bioconductor Project, which can then be accessed either locally or across a network. Installation is simply based on booting off the installation CD or by using a debian package provided to upgrade an existing Ubuntu installation. Because of the levels of reconfiguration required to run the system a clean install is recommended. In its current version, several microarray analysis pipelines are supported including oligonucleotide, dual or single dye experiments. BioconductorBuntu is designed to be extensible, by server side integration of further relevant Bioconductor modules as required, facilitated by its straightforward underlying Python-based infrastructure. BioconductorBuntu offers an ideal environment for the development of processing procedures to facilitate the analysis of next-generation sequencing datasets.

The Bioconductor Project's suite of genomic analysis software is perhaps the best known and most widely used open source data processing platform for a wide variety of data, particularly for the analysis of microarray data. Its unique strength lies in the large dynamic community of developers and the constant evolution of novel analytical and statistical techniques, freely accessible to the user community - recent developments include modules devoted to the processing of next-generation sequencing data. However its R based command line environment can make its usability intimidating for many potential users. BioconductorBuntu aims to bridge this gap by providing in the first instance a user friendly web-based microarray processing platform utilising relevant Bioconductor modules, and facilitating its installation on a local server by bundling it into a custom Ubuntu linux port.

The project is entirely based on open source software which is free to redistribute, use and alter. Ubuntu Linux is the operating system upon which the server is built. All analysis of gene expression microarray data are performed in R, specifically using Bioconductor. Pipelines facilitating the analysis of other microarray platforms are potentially available to the user community by coding additional functionality in R and Python, which is made easier because of the generalized framework implemented to facilitate the existing analysis pipelines. The CGI scripts which run on the server are written in Python. These scripts handle input and output to and from the xHTML, CSS and JavaScript based user interface, as well as writing to and from the database and making calls to R and Bioconductor via the RPy interface; RPy being a robust Python interface to the R Language.

DYNAMICS & GEOMETRY OF AN IMPACT OSCILLATOR

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An impact oscillator is a fundamental mathematical model that can be applied in a wide variety of real-world systems. There are two components, an oscillator (well-studied and usually deterministic for all time) and an impacting surface with a reset rule, which introduces discontinuities into the system. Therefore impact oscillators are fundamentally discontinuous systems, which are usually simulated numerically rather than solved analytically.

The traditional ways to present results in oscillatory systems are phase-space and bifurcation diagrams. Bifurcation diagrams show changes in the long-term behaviour of the system under parameter variation and phase-space diagrams represent the trajectory in line with our instinctive view of how the world works – “trajectories are curved and walls are straight”. These forms have limitations:

- There is no global view – the effect of changes to the initial conditions cannot usually be predicted without re-simulating the system.
- Neither the time to the next impact nor whether an impact is missed are immediately obvious.

In an attempt to address these limitations, we are beginning an exploration of a new approach as outlined in ‘Discontinuity Geometry for an Impact Oscillator’¹, in which the phase-space for presenting results is re-defined and topologically distorted in a such a way that our instinctive view is now reversed – “trajectories are straight and walls are curved”. The basic form in this new approach is the “Impact Surface V_c ”, which is defined in terms of 3 co-ordinates;

- v - the initial velocity of the current trajectory
- τ - the initial phase-time of the current trajectory
- t - the time since the last impact

If $x_c(v, \tau; t)$ denotes the solution to the underlying dynamical system with initial data (position, velocity, time) = (c, v, τ) , then for fixed c the impact surface is defined to be $V_c = \{ (v, \tau, t) \mid x_c(v, \tau; t) = c \}$. Thus V_c is the set of all those points where a trajectory will impact at some future time. Within this framework, not only is V_c fixed for all initial velocities and times, but some of the dynamical properties of the system can be directly linked to specific details of the shape and curvature of V_c . Thus this is a significant step towards an explanation of the global dynamic properties.

This study is at an early stage & so far only a simple 1-variable system has been considered, but results to date indicate that this method deserves further investigation.

Reference

¹ Chillingworth D.R.G., *Dynamical Systems*, **2002**, 4, 389-420.

VIRASORO CORRELATION FUNCTIONS FOR VERTEX OPERATOR ALGEBRAS

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A vertex operator algebra¹ (VOA) is a quadruple $(V, Y, \mathbf{1}, \omega)$ consisting of a \mathbf{Z} -graded complex vector space, a linear map for formal parameter z and a pair of states, the vacuum vector $\mathbf{1}$ and the conformal vector ω . For each state v the image under the Y map is the vertex operator $Y(v, z) = \sum v_n z^{-n-1}$ and in particular for the conformal vector ω it is defined as $Y(\omega, z) = \sum L_n z^{-n-2}$ where L_n satisfies the Virasoro Algebra.

We are interested in Virasoro n -point correlation functions for Vertex Operator Algebras on Riemann surfaces of genus zero and one. For the (genus zero) sphere the Virasoro n -point function is defined as an inner product² $\langle \mathbf{1}, Y(\omega, z_1) \dots Y(\omega, z_n) \mathbf{1} \rangle$ and is a symmetric rational function of $z_{ij} = z_i - z_j$. Using a recursive reduction formula the n -point function this can be expressed as the sum of certain weights of graphs with n vertices labeled by z_i and where each vertex has exactly 2 edges. Thus the Virasoro 2-point function $C/(2(z_{12}))^4$ has graphical expansion



For the genus one torus, the Virasoro n -point function can be calculated using Zhu's reduction formula³. This also has a symmetric graphical expansion (because a certain elliptic function satisfies a non-linear ordinary differential equation) as the sums of the weight of graphs with n vertices where each vertex is labeled by z_i and has 0, 1 or 2 edges. Thus the two point function

$$F((\omega, z_1), (\omega, z_2)) = \eta^{-c} ((q d_q)^2 + c E_2 q d_q + ((c/2) E_2)^2 + 2 P_2(z_{12}) q d_q + (c/2) P_2^2(z_{12})) Z$$

is given by the sum of weight of 6 graphs.

References

¹V. Kac, Vertex Operator Algebras for Beginners, *University Lecture Series* Vol. **10** (AMS 1998).

²Mason, G. and Tuite, M.P.: Torus chiral n -point functions for free boson and lattice vertex operator algebras, *Commun.Math.Phys.* **235** (2003) 47-68.

³Y. Zhu, Modular invariance of characters of vertex operator algebras, *J.Amer.Math.Soc.* **9** (1996) 237-302.

A PHYLOGENETIC HIDDEN MARKOV MODEL FOR DETECTING POTENTIAL HLA-RESTRICTED EPITOPES IN HIV-1 GAG

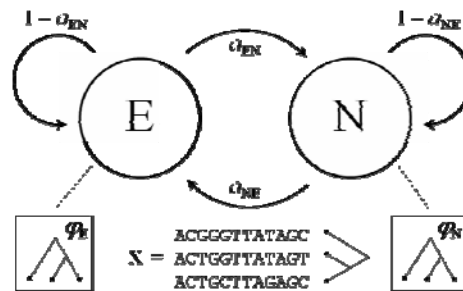
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The human immune system is designed to recognise, eradicate and recall invading viruses. An effective cellular immune response depends upon the presentation and recognition of viral peptides called epitopes, which are cleaved from viral proteins and presented on the cell surface by specific human leukocyte antigen (HLA) molecules. The epitope/HLA complex is subsequently detected by cytotoxic T lymphocytes (CTLs) which mount an immune response to eliminate the virus-infected cell.¹ The human immunodeficiency virus (HIV) escapes the immune system by acquiring mutations at critical sites within epitopes that inhibit processing, HLA interactions and/or CTL recognition. Robust correlations between some mutations within HIV epitopes and the HLA genotype of the host provide clear evidence of immune-mediated selection pressure. Such mutational patterns may be utilised to identify novel epitopes in the viral genome.²

This poster presents a phylogenetic hidden Markov model (phylo-HMM) for the detection of HLA-restricted epitopes in the Gag polyprotein of HIV Type 1. In this context, a phylo-HMM is defined as the four tuple $\Theta = (S, \varphi, A, b)$ consisting of a set of two states $S = \{E, N\}$ corresponding to epitope (E) and non-epitope (N) regions of the viral genome, a set of associated phylogenetic models $\varphi = \{\varphi_E, \varphi_N\}$, a state transition probability matrix $A = \{a_{ij}\}$ $i, j \in S$ and a vector of initial state probabilities $b = (b_E, b_N)$.



Each phylogenetic model is in turn defined as a continuous time Markov stochastic process $\varphi_i = (Q_i, \pi_i, \tau_i, t_i)$ $i \in S$ with an appropriately parameterised codon substitution matrix Q_i , equilibrium frequencies π_i , a tree topology τ_i and a set of branch lengths t_i . By allowing φ_E to depend on the known HLA genotypes of the individuals, it is hypothesised that the posterior probability $p(S_k = E | X, A, b, \varphi)$ of the epitope state at position k in a sequence alignment X will be large for codon sites where selection

¹ T. Bhattacharya *et al.*, *Science*, **2007**, 315, 1583-1586

² Z. L. Brumme *et al.*, *Journal of Virology*, **2008**, 82(18), 9216-9227

pressure favours mutations offering an immune escape, indicating a potential epitope.³

SUBGROUPS OF SYMMETRIC GROUPS, THEORY AND APPLICATIONS

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The study of the subgroup lattice of the symmetric group is one of the oldest areas of research in Group Theory. Since every group can be viewed as a subgroup of a symmetric group it serves as a unique tool to better understand many finite groups. The development of computer algebra packages such as GAP⁴ has enabled a new approach to this problem in recent times.

The table of marks¹ of a finite group is a matrix of numbers which completely describes the subgroup lattice. The objective of this research is to develop new methods for the computation of tables of marks.

In 1929 Lunn and Senior³ outlined how tables of numbers obtained from the subgroup lattice of a symmetric group could be used to investigate the possible configurations of a molecule. The matrix of numbers which they used was in effect the table of marks. Of course at that time calculations could only be carried out by hand, and so very few tables of marks were known. The dawn of the computer age breathed new life into this area and breathed new life into this area of research.

In 1989 Labelle and Yeh² closely highlighted the link between tables of marks and *Combinatorial Species*. The theory of molecular and atomic species expressed the configuration of a molecule in the language of combinatorics. This new theory bridged the gap between pure mathematics and organic chemistry.

Kerber et al subsequently developed a software package MOLGEN⁵ which uses these mathematical ideas to produce all possible configuration of a given molecule. The production of new tables of marks will enable further study to be carried out into this area.

References

¹G. Pfeiffer, *The Subgroups of M_{24} or How to Compute the Table of Marks of a Finite Group*, *Ex. Math* 6, **1997**

²J. Labelle, Y.N. Yeh, *The Relation between Burnside Rings and Combinatorial Species*, *J. Combin. Th.* **1989**

³A.C. Lunn, J.K. Senior, *Isomerism and Configuration*, *Journal of Physical Chemistry*, **1929**

⁴The GAP Group-Groups, Algorithms and Programming, <http://www.gap-system.org>, **2008**

⁵MOLGEN 4.0, <http://molgen.de>, **1996**

³ A. Siepel and D. Haussler, *Statistical Methods in Molecular Evolution*, R. Nielsen (Editor), **2005**, 325-350

CONVOLUTIONAL CODES FROM GROUP RINGS

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Convolutional codes have many applications. The original uses were in deep space communications, while others include mobile phone networks and ATM networks. Finding convolutional codes that have desirable properties and are easy to decode is often a challenge.

Quick Look In (QLI) convolutional codes were discovered by Massey and Costello in 1971 and proved to have several desirable properties¹. These convolutional codes were considered further by several other authors and improved on over time. They were more recently used to construct turbo codes².

We have found that using group ring methods to construct convolutional codes allows us to precisely construct QLI convolutional codes. The QLI convolutional codes we are able to construct have better free distances than those in the original paper, and they are comparable to those in papers published since the original. They also simulate better than those in the original paper. Importantly, they are constructed in an algebraic way which is an advantage. In particular, an algebraic construction reduces the storage space necessary to implement the code.

Interestingly, Bahl introduces another type of convolutional code called Complementary Convolutional Codes³. These convolutional codes have complementary generators. While not all of the convolutional codes in this category may be constructed through group ring methods, we are able to guarantee that all convolutional codes constructed through group ring methods to produce complementary convolutional codes will be noncatastrophic. This is something that Bahl cannot guarantee.

Group ring convolutional codes are constructed by taking units in the group ring⁴. The above papers specifically discuss (2,1) convolutional codes, which may be constructed from the group ring $Z_2 C_2 C_\infty$. In the poster, we describe two different group ring constructions along with the comparisons to the papers mentioned above.

¹ Massey, J. , Costello, D. Jr, *IEEE Transactions on Communication Technology*, 1971, 19, 806-813.

² Massey, P., Costello, D. Jr, *IEEE International Symposium on Information Theory*, 2001., 141.

³ Bahl, L., Jelinek, F., *IEEE Transactions on Information Theory*, 1971, 17, 718-727.

⁴ Hurley, T., *International Journal on Pure and Applied Mathematics*, 2009, 50, 431-463.

HOW DO FIRST YEAR MATHEMATICS STUDENTS VALIDATE MATHEMATICAL ARGUMENTS?

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The study of proofs is a major obstacle in the transition from school to university mathematics. Given the importance of argumentation and proof in the spectrum of mathematical activities, the incoming students' understanding, appreciation and knowledge of the nature and role of proof must be considered.

Proof is a difficult mathematical concept for students. Research shows that most university students do not know what constitutes a proof² and experience difficulties not only in constructing proofs but also in determining whether a proof is valid⁴. Selden and Selden see the *lack of validation skills as linked to beginning university students' well-documented inadequate conceptions of proof*³.

We describe the results of an exploratory study of first years mathematics undergraduates' criteria when validating mathematical arguments or proofs. The study is based on several tests and interviews with first year honours mathematics students at NUI Galway. We confronted the students with numerous (correct and incorrect) proposed proofs of mathematical statements, and asked them to evaluate and criticize those.

The first year students' comments on different and partly incorrect 'proofs' of mathematical statements gave us a clear picture about the student's criteria when validating mathematical arguments. We see on the positive and encouraging side that most of the students recognize the difference between a demonstration by example and a proof as well as the importance of mathematical definitions and convincing mathematical arguments. On the negative side we have to note the students' formalic and inflexible picture of valuable proofs. Structure and 'mathematical-looking' formalism seem more important to some students than the ideas comprising the argument.

In recently held interviews with eight randomly chosen students we focussed on some questions which arose after analysing the written test results.

References

- ¹Alcock, Lara and Weber, Keith: How do mathematicians validate proofs?
Paper presented at the annual meeting of the North American Chapter of the International Group for the Psychology of Mathematics Education, Toronto, Canada, **2004**.
- ²Recio, A.M. and Godino, J.D. : Institutional and Personal Meanings of Proof.
Educational Studies in Mathematics, **2001**, 48(1), 83-99.
- ³Selden, A. and Selden, J. :Unpacking the logic of mathematical statements.
Educational Studies in Mathematics, **1995**, 29(2), 123-151.
- ⁴Selden, A. and Selden, J. Validations of proofs written as texts: Can undergraduates tell whether an argument proves a theorem? *Journal for Research in Mathematics Education*, **2003**, 34(1), 4-36.

MODELLING OF DRUG DIFFUSION IN STENTS

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Application of drug eluting stents for prevention of restenosis is a popular approach. The stent acts as a source of drug, from a polymer coating or from reservoir, which is transported into and through the artery wall. In this poster, the reversible binding of drug to the vascular tissue is modelled.

$$\frac{\partial c}{\partial t} = D \frac{\partial^2 c}{\partial x^2} - k_r bc + k_l a$$

$$\frac{\partial a}{\partial t} = k_r bc - k_l a$$

$$\frac{\partial b}{\partial t} = -k_r bc + k_l a$$

where c is concentration of free drug, b is concentration of free binding sites, a is concentration of activated drug, D is diffusion coefficient of drug, k_r is association constant between drug and binding sites and k_l is dissociation constant.

Numerical as well as analytical solutions of this system are described. Besides, a model for the water transfer into and drug release from polymer matrix is presented. One of the major challenges in the future is considering polymer swelling using moving boundary condition.

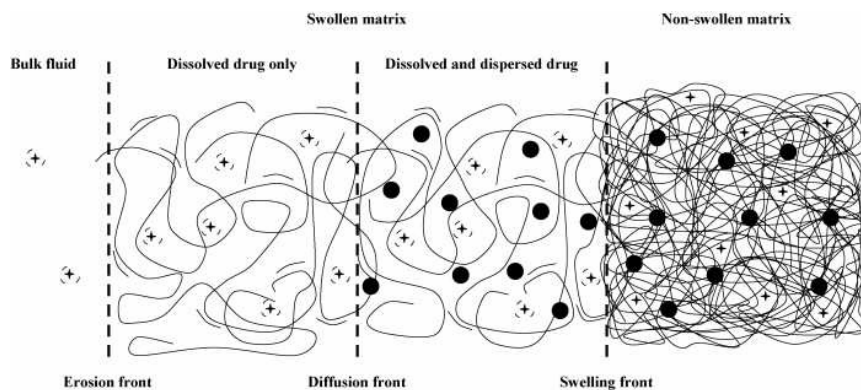


Fig. A swelling controlled drug delivery system containing dissolved and dispersed drug.

References

- [1] J. Crank, *The Mathematics of Diffusion*, Oxford University Press (1975).
- [2] J. Crank, *Free and Moving Boundary Problems*, Oxford University Press (1984).
- [3] A. Borghi, E. Foa, R. Balossino, F. Migliavacca and G. Dubini, *Computer Methods in Biomechanics and Biomedical Engineering*, **2008**, *11*, 367-377.
- [4] J. Siepmann, F. Siepmann, *International Journal of Pharmaceutics*, **2008**, *364*, 328-343.

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Biochemistry
Botany
Earth and Ocean Sciences
Microbiology
Zoology

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38.	00093181	Lowery	Deila	4PS1
39.	06123741	Mnich	Katarzyna	3PS1
40.	03025063	O'Donoghue	Yvonne	2PS1
41.	01921398	Read	Danielle	4PS1
42.	01921398	Read	Danielle	4PS1
43.	07233829	Simila	Janika	2PS1
44.	07233689	Tikhanovich	Irina	2PS1
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50.	01700715	Sullivan	Caroline	4PS1
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56.	04031717	Finn	Rebecca	1PS1
57.	08233162	Gill	Aileen	1PS1

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59.	01047965	Kelly	Olivia	3PS1
	02758211	Hughes	Dermot	3PS1
60.	04010566	O'Boyle	Nicholas	1PS1
61.	08233026	Olszak	Marta	1PS1

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REGULATION OF CDC45 IN THE CELL CYCLE AND AFTER DNA DAMAGE.

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The Cdc45 protein is involved in the regulation of eukaryotic chromosomal DNA replication¹ and is the main target for a Chk1-dependent Cdc25/Cdk2-independent DNA damage checkpoint following low dose UV damage². We aim to investigate the molecular basis of this DNA damage signal transduction pathway of which Cdc45 is a target.

To this end, HeLa S3 cells have been synchronized in the cell cycle and fractionated. Moreover, the chromatin association of Cdc45 post-UV treatment and throughout the cell cycle has been analyzed by western blotting and immunoprecipitation of Cdc45 from HeLa S3 cells.

These studies show that Cdc45 chromatin-association is reduced in response to UV damage in HeLa S3 cells in a dose-dependent manner. Moreover, Cdc45 chromatin-association is maximal in the S phase of the cell cycle and Cdc45 can be immunoprecipitated from soluble and chromatin-associated fractions in HeLa S3 cells. Immunofluorescence microscopy of Cdc45 in HeLa S3 cells revealed a time-dependent rearrangement of Cdc45 in response to UV treatment. Currently we examine the sub-cellular localization of Cdc45 in HeLa S3 cells pre- and post-UV treatment in more detail and demonstrate a UV-damage dependent co-localisation between Cdc45 and the Promyelocytic Leukemia protein (PML), a protein with a well characterised role in DNA damage response.

¹C. Bauerschmidt, S. Pollok, E. Kremmer, H.P. Nasheuer and F. Grosse, *Genes to Cells* **2007** 12: 745–758.

²P. Liu, L.R. Barkley, T. Day, X. Bi, D.M. Slater, M.G. Alexandrow, H.P. Nasheuer and C. Vaziri, *J Biol Chem* **2006** 281(41): 30631–30644.

SENSITIZATION OF BREAST CANCER CELLS TO APOPTOSIS BY RO-08-2750, AN ANTAGONIST OF NGF-P75^{NTR} BINDING

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In contrast to normal breast cells, approximately 80% of breast cancer cells produce nerve growth factor (NGF)¹. In addition, breast cancer cells express NGF receptors, TrkA and p75^{NTR}, through which NGF can promote breast cancer cell proliferation and survival, respectively in an autocrine manner^{2,3}. Thus, inhibition of NGF signalling represents a valid therapeutic target for treatment of breast cancer, since resistance of breast tumours to chemotherapy may be due pro-survival NGF signalling.

Here we show that NGF can protect MCF-7 and MDA-MB-231 breast cancer cells from apoptosis induced by DNA-damaging agents. Cells were treated with 50 ng/ml NGF for 24 h prior to treatment with either 200 µg ml⁻¹ etoposide or 5 µM doxorubicin for a further 24 h. Apoptosis was measured by DEVDase caspase activity assay, Annexin V assay and morphological assessment. NGF pre-treatment of cells completely blocked apoptosis induction by both of these chemotherapeutic agents. Since the anti-apoptotic effects of NGF are reported to be via p75^{NTR} signalling, we hypothesized that inhibition of endogenous NGF binding to p75^{NTR} could sensitise the cells to apoptosis. In order to test this, we used a novel NGF-binding compound, Ro 08-2750, that prevents NGF interaction with p75^{NTR}⁴. Cells were treated with 0.5 µM Ro 08-2750 for 1 h prior to treatment with 200 µg/ml etoposide. Treatment with Ro 08-2750 alone does not induce apoptosis. However, there was a statistically significant sensitization of the cells to induction of apoptosis by etoposide as measured by methods outlined above. Thus, anti-NGF therapy holds the possibility of increasing the effectiveness of cyto/genotoxic drugs used as adjuvant therapies in breast cancer treatment.

References

¹E. Adriaenssens et al., *Cancer Res*, **2008** 68(2), 346-351.

²S. Descamps et al., *Journal of Biological Chemistry*, **2001** 276(21), 17864-17870.

³L. Dollé et al., *Oncogene*, **2003**. 22, 5592-5601.

⁴O. Niederhauser et al., *Journal of Neuroscience Research*, **2000** 61(3), 263-272.

EFFECT OF PROTEASOME INHIBITION ON THE DNA DAMAGE RESPONSE IN CISPLATIN-TREATED HUMAN CELLS LACKING DNA POL η

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The chemotherapeutic platinum-based drug cisplatin acts through the formation of platinum-DNA adducts, intrastrand crosslinks and interstrand crosslinks, blocking DNA replication. Human cells express a number of specialised polymerases, including DNA polymerase η (pol η), capable of carrying out DNA replication in the presence of damage. DNA replication arrest activates the DNA damage response, involving post-translational modifications of downstream effector proteins. Among the major types of post-translational modifications are protein phosphorylation and protein ubiquitination. Phosphorylation, in particular by the PI-3 kinase-related protein kinases (PIK kinases) ATM, ATR and DNA-PK plays an important role in the cellular response to DNA damage. Protein ubiquitination includes monoubiquitination, which usually modifies protein function but does not lead to degradation, and polyubiquitination, which targets proteins for proteasome-mediated degradation. To provide insight into the interplay between phosphorylation and ubiquitination in the response of human cells to cisplatin, the effect of proteasome inhibition on cisplatin-induced protein phosphorylation and ubiquitination was investigated in pol η -deficient XP30RO cells. XP30RO cells were treated with 0-5 μ g/ml cisplatin, in the presence or absence of the proteasome inhibitor MG-132. The levels and post-translational modifications of three key DNA damage response proteins, RPA2 and FANCD2 were investigated using western blotting and phosphospecific antibodies. This analysis demonstrates that (i) the proteasome inhibitor MG132 alters the pattern of cisplatin-induced RPA2 phosphorylation at a number of sites in the N-terminal; (ii) compared to normal cells, cisplatin-induced FANCD2 monoubiquitination is increased in cells lacking DNA pol η . This data demonstrates that cisplatin-induced modification of individual DNA damage response proteins by protein phosphorylation and ubiquitination can be modulated by proteasome inhibition.

STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF RAD9 PROTEIN.

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DNA damage checkpoints are triggered in response to DNA insults. Once activated, these pathways prevent replication and segregation of the damaged DNA. In addition to cell cycle delays they regulate repair, transcription and the apoptotic response to DNA damage. Budding yeast *RAD9* was the first checkpoint gene identified. The checkpoint activity of this protein has been reported in all phases of the cell cycle. Loss of this gene impairs checkpoint-activated cell cycle arrests and increases genomic instability. Mutational analysis of this protein has provided important information about the different regions of Rad9 participating in different DNA damage functions. Despite intensive research by many laboratories, the complete function of this protein is not fully understood. In particular, the role of Rad9 extensive phosphorylation during cell cycle remains to be investigated.

This work will present the generation and analysis of novel *rad9* mutants designed to understand the role of Rad9 cell cycle phosphorylation in its functions. In particular role in regulating Chk1, will be investigated a downstream checkpoint effector.

PRIMASE-DNA BINDING IS MODULATED BY IRON

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The eukaryotic DNA polymerase- α -primase is an essential protein for the initiation of DNA replication. It consists of four subunits, p180, p68, p58 and p48 and is highly conserved from yeast to human. Initiation requires the function of the specialised dimeric primase (p58 and p48), which synthesises de novo the RNA primers (required by DNA polymerases for replication). The p58 C-terminus has been shown to exhibit a 4Fe-4S cluster. UV/Vis spectra data of the purified p58CT indicate that it is essentially in a Fe(II) state of bound iron, which can be oxidized into a Fe (III) state by ferricyanide. Binding analysis of p58CT to ϕ X174 ssDNA shows that reduced iron content does not affect p58CT binding. However binding of the polypeptide to dsDNA pUC18, both plasmid and linearised forms, were significantly affected by the presence of iron. Additional studies to analyse further the effect on binding that iron exhibits to primase is currently under way.

EFFECT OF NERVE GROWTH FACTOR ON THE INHIBITION AND DEGRADATION OF ACTIVE CASPASE-3

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INTRODUCTION: Degenerative diseases often involve excessive cell death due to apoptosis, of which the main biochemical hallmark is the activation of caspase proteases. Activation of effector caspase-3 leads to cell death due to proteolysis of many cellular substrates. This is recognized as the 'point of no return' for cell death, since the cells cannot be rescued once caspases are activated. Caspase inhibitors have the potential to be therapeutic agents in the treatment of diseases characterized by excessive apoptosis. Nerve growth factor (NGF) pro-survival signaling can induce changes in protein expression as well as post-translational modification of proteins, resulting in the inhibition of apoptosis³. Here, we investigate the ability of NGF treatment to mediate direct inhibition of caspase-3, which results in PC12 cells survival¹⁻².

METHODOLOGY: techniques employed were induction of apoptosis by 1.5 μ M thapsigargin (TG) treatment for 24 h, survival signaling pathways were activated using 100 ng/ml NGF for indicated periods of time, Western blotting, DEVDase caspase activity assay.

RESULTS: treatment of PC12 cells with TG results in caspase-3 activation (i.e., cleavage to the p17 active form) and induction of DEVDase activity. We have found that exposure of PC12 cells to NGF either before or after TG treatment significantly reduced DEVDase activity and this corresponded to a decrease in protein levels of active caspase-3. However, XIAP protein expression was unaffected by NGF treatment, indicating that NGF does not regulate caspase-3 activity through XIAP induction. Furthermore, the general protein translation inhibitor cycloheximide did not prevent NGF-mediated loss of cleaved caspase-3, indicating that new protein expression is not required.

CONCLUSION: These studies show that at times when caspase-3 is activated, NGF treatment leads to both the inhibition and degradation of active caspase-3. There are no changes in XIAP levels after NGF or TG treatment, ruling out a role for XIAP in the caspase degradation. New protein synthesis is not required for the loss of p17.

REFERENCES

1. HR. Stennicke, CA. Ryan and GS. Salvesen, *Trends Biochem Sci.*, **2002**, 94-101.
2. E. Szegezdi, KR. Herbert, ET. Kavanagh, A. Samali and AM. Gorman, *J. Cell. Mol. Med.*, **2008**, 12, 2482-2496.
3. A. Brunet, SR. Datta, ME. Greenberg, *Curr Opin Neurobiol.*, **2001**, 11, 297-305.

NKT-CELL AND $\gamma\delta^+$ T-CELL POPULATIONS IN NORMAL AND *HELICOBACTER PYLORI*-INFECTED GASTRIC MUCOSA

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Although the immune response to *Helicobacter pylori* (*HP*) is considered to primarily involve classical T-cells, innate T-cell populations such as natural killer T- (NKT-) cells and $\gamma\delta^+$ T-cells are likely to play central roles in infection with this gastric pathogen.² NKT-cells express an invariant T-cell receptor (TCR) alpha chain, V α 24J α 18, and also NK cell surface markers³ while T-cells bearing the $\gamma\delta$ -TCR display the V γ 9 δ 2 rearrangement and lack of CD4 and CD8 receptor expression. The aims of this study were to quantify these T-cell populations in the epithelium and lamina propria layers of normal gastric mucosa, and to compare their numbers in *HP* infection. Biopsies were obtained from the antral mucosa of 33 subjects (eight *HP*-positive and twenty five *HP*-negative subjects as determined by the CLO[®] test). Single cell suspensions from the epithelial and lamina propria layers were prepared from the biopsies using EDTA/DTT and collagenase treatments. The cells were surface labelled with fluorochrome-conjugated antibodies, and the percentages of CD3⁺V α 24J α 18⁺ (NKT-cell) and CD3⁺V γ 9V δ 2⁺ ($\gamma\delta^+$ T-cells) populations were quantified using flow cytometry. In the epithelial layer of the normal gastric mucosa, the median level of NKT-cells was 1.47% (range, 0-8.12%) with markedly higher numbers in *HP*-positive subjects (median, 2.47%; range, 0.7-3.12%). In contrast to the epithelial layer, NKT-cells were lower in the lamina propria layer in *HP*-positive compared with *HP*-negative subjects (median, 0.49%, range, 0-1.35% vs. 0.8%, 0-4.95%). As regards $\gamma\delta^+$ T-cells, the median level of $\gamma\delta^+$ T-cells was lower in the epithelial layer (median, 6.94%, range, 0.24-16.58% vs. 4.36%, 2.96-10.44%) and in the lamina propria layer of *HP*-positive compared with *HP*-negative controls (median, 1.6%, range, 1.07-2.91% vs. 2.97%, 0.86-5.51%). In conclusion, differences were found in the numbers of innate T-cells in gastric layers in *HP*-infection. Altered numbers of innate T-cells are likely to be important in the *HP*-associated immune response.

References

¹D. Velin, P. Michetti, *Digestion* **2006**, 73,116-23.

²J. O'Keeffe, A. P. Moran, *Helicobacter* **2008**, 13,1-19.

³E. Tupin, Y. Kinjo, M. Kronenberg, *Nat. Rev. Microbiol.* **2007**, 5,405-17.

HEAT SHOCK ENHANCES NGF-INDUCED NEURITE ELONGATION WHICH IS NOT MEDIATED BY HSP25 IN PC12 CELLS

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INTRODUCTION: neuronal differentiation and neurite outgrowth are key processes during development of the nervous system. Understanding the regulation of neurite outgrowth is crucial to developing therapies to promote axon regeneration after injury or in neurodegenerative diseases. Here, we sought to determine whether heat shock (HS) affected nerve growth factor (NGF)-induced neurite outgrowth, since the signaling pathways overlap¹⁻².

METHODOLOGY: techniques employed were HS treatment at 42 °C for 1 h, Western blotting, reverse transcription-PCR, stable overexpression of human heat shock protein 27 (Hsp27), siRNA knockdown of Hsp25 and inhibition of Hsp25 phosphorylation with SB202190 (20 μM).

RESULTS: treatment of PC12 cells with NGF stimulates them to differentiate into a sympathetic neuron-like phenotype. We have found that exposure of PC12 cells to HS significantly enhanced NGF-induced neurite elongation, but not branching. This HS treatment led to induction of Hsp25 and Hsp70. The morphological changes induced by NGF were accompanied by increased Hsp25 mRNA levels, in addition to elevation in Hsp25 protein expression and phosphorylation, without a concomitant increase in Hsp70. Thus, a possible role for Hsp25 in NGF-stimulated neurite outgrowth was investigated. However, quantification of NGF-induced neurite elongation and branching revealed that neither of these features are altered in PC12 cells which stably overexpressed human Hsp27 (to mimic HS induction of Hsp25). Similarly, knockdown of Hsp25 using siRNA had no effect on NGF-induced neurite outgrowth. Inhibition of p38 MAPK signalling with SB202190 blocked phosphorylation of Hsp25 without affecting NGF-induced neurite outgrowth or the HS-dependent enhancement of elongation. However, inhibition of MEK1/2 with U0126 (10 μM) partially reduced the HS-enhancement of NGF-stimulated neurite elongation.

CONCLUSION: these findings indicate that Hsp25 is not required for NGF-induced neurite outgrowth, which is in contrast to findings in dorsal root ganglion neurons differentiated with laminin³. Nor is Hsp25 responsible for the HS-enhancement of NGF-induced neurite elongation in PC12 cells, instead occurring in part through MEK signaling, which is a major signaling pathway for both NGF and HS.

REFERENCES

¹EJ. Huang and LF. Reichardt, *Annu Rev Biochem.*, **2003**, 72, 609-642.

²SI. Nadeau and J. Landry, *Adv Exp Med Biol.*, **2007**, 594, 100-113.

³K. Williams, M. Rahimtula and KM. Mearow, *J Neurosci Res.*, **2006**, 84, 716–723.

IDENTIFICATION OF A CASPASE-12 SPLICE VARIANT IN THE RAT AND UPREGULATION DURING ER STRESS-INDUCED APOPTOSIS

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INTRODUCTION: stress in the endoplasmic reticulum (ER) can induce apoptosis¹, which is a significant form of cell death during neurodegenerative disorders. ER stress involves processing of the ER-localised caspase-12², which contains a caspase-recruitment domain (CARD) and p20/p12 domains. However, the role of caspase-12 is yet to be fully characterised during ER stress-induced apoptosis³. This study investigates the expression of caspase-12 mRNA and a novel splice variant during ER stress-induced apoptosis in rat PC12 cells.

METHODOLOGY: ER stress-induced apoptosis was induced in rat adrenal PC12 cell line by thapsigargin (Tg; 1.5 µM) or tunicamycin (Tm; 2 µg/mL). For comparison, apoptosis by alternative death mechanisms was induced by etoposide (Etop; 50 µg/mL) or staurosporine (Sts; 1 µM). Other techniques used were Dounce tissue homogenisation, RNA extraction, reverse transcription-PCR and TOPO-Blunt vector cloning.

RESULTS: the expression of the variant was much greater than normal caspase-12, and the mRNA levels of both were significantly increased following treatment of PC12 cells with Tg or Tm over a 24 h time-course. Furthermore, we have shown an absence of caspase-12/variant induction following the initiation of apoptosis with Etop or Sts. The caspase-12 variant has been fully cloned and sequenced to reveal a 26 amino acid insert situated after the CARD domain. This does not interrupt the reading frame nor introduce a premature stop codon. We have investigated the mRNA levels of the variant in a range of adult rat tissues, revealing that it is widely expressed and always at a higher level than normal caspase-12. Tissues which demonstrate particularly high levels of normal and variant caspase-12 include the adrenal gland, stomach, rectum and liver, while the spleen, small intestine and kidney have low expression. Moreover, *in vitro* transcription/translation has revealed that recombinant active caspase-12 (Δ CARD mutant) is capable of cleaving the variant as effectively as it cleaves pro-caspase-12 itself.

DISCUSSION: these data reveal the existence of a highly expressed splice variant throughout a range of rat tissues which is induced by ER stress and can be cleaved *in vitro*. The insert may confer an advantageous role to the protein in order for cells to widely express the variant so highly compared with caspase-12.

REFERENCES

¹S. Kumar, *Cell Death Differ*, **2007**, *14*, 32-43.

²M. Lamkanfi, M. Kalai and P. Vandenabeele, *Cell Death Differ*, **2004**, *11*, 365-368.

³E. Szegezdi, U. Fitzgerald and A. Samali, *Ann N Y Acad Sci*, **2003**, *1010*, 186-194.

INVESTIGATING THE BIOLOGICAL EFFECT OF FALCARINOL TYPE POLYACETYLENES ON MAMMALIAN CELLS

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Secondary metabolites are important compounds synthesised by plants. Although they are not essential for growth and reproduction, they have important functions including: protection against stress caused by pathogens, herbivores and environmental factors; serving as attraction cues for pollinators and seed dispersing animals; and delivering signals between and within cells. These chemicals have been extensively utilised by humans as a source for dyes, fibres, glues, oils, flavouring agents, etc and they are also an important source for discovering new drugs, pesticides and herbicides. In human nutrition, secondary metabolites have traditionally been thought to be undesirable because of their potential toxicity. Recently this view has been changed, since it has been noted that high consumption of fruit and vegetables seem to reduce the risk for certain types of cancer and chronic diseases. It has been proposed that long term intake of certain secondary metabolites could be behind this protective effect. Polyacetylenes are a group of secondary metabolites which have at least one carbon-carbon triple bond (alkynyl) as a functional group. They are widespread in nature and can be found in plants, fungi, marine algae and invertebrates, insects, and frogs. Today over 2000 polyacetylenes are known, and from these more than 1100 are from the plant family Asteraceae (formerly Compositae)¹. Falcarinol, falcarindiol and falcarindiol are the main polyacetylenes found in human food, carrots being their primary source. They are also found in other food plants such as celery, parsnip, parsley, tomato and aubergine². The study of polyacetylenes has been complicated by their unstable nature since they easily undergo degradation by oxidative, photolytic and pH dependent factors¹. However, many of them have found to possess several interesting biological activities such as being highly toxic against fungi, bacteria, and other microbes. They are also cytotoxic against several cell lines, cancer cells being more sensitive than normal cells. This cytotoxic effect has been noted to be biphasic, the lower concentrations being beneficial and the higher being cytotoxic^{3,4}. The three falcarinol type polyacetylenes previously extracted from carrot by AFRC, Teagasc, Dublin, are to be assayed for their antioxidant activity and used in cell based assays to investigate their effect on gene expression and possible protective effect against oxidative stress with polyacetylene concentrations that are present in plasma after ingestion.

¹R. Minto & B. Blacklock, *Progress in Lipid Research*, **2008**, *47*, 233-306.

²K. Brandt, L. Christensen, J. Hansen-Møller, S. Hansen, J. Haradlsdottir, L. Jespersen, S. Purup, A. Kharazmi, V. Barkholt, H. Frøkiær & M. Kobæk-Larsen, *Food Science & Technology*, **2004**, *15*, 384-393.

³L. Christensen & K. Brandt, *Journal of Pharmaceutical and Biomedical Analysis*, **2006**, *41*, 683-693.

⁴V. Dembitsky, *Lipids*, **2006**, *41*, 883-924.

DNA REPLICATION OF HUMAN BK VIRUS IN MURINE AND HUMAN CELL EXTRACTS

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The human polyomavirus BKV causes persistent and asymptomatic infections in most humans¹ and is the etiologic agent of polyomavirus associated nephropathy (PVAN) and other pathologies². Unfortunately, there are no animal models with which to study activation of BKV replication in the human kidney and the accompanying PVAN. A sensitive in vitro replication assay was developed with purified BKV TAg that supported robust BKV DNA replication in human cell extracts, but not murine cell extracts. In vitro assays revealed differences in replication specificity between BKV TAg and the TAg of simian virus 40 (SV40) and human polyomavirus JC (JCV) and their respective origins; and unlike SV40 TAg, addition of human replication proteins, DNA polymerase α -primase, replication protein A, or topoisomerase I to BKV TAg did not rescue BKV DNA replication in murine extracts³. Notably, addition of murine extracts to BKV TAg in human extracts inhibited BKV DNA replication at a step prior to or during unwinding of BKV DNA. These results implicate features of BKV TAg distinct from SV40 TAg and JCV TAg, that restrict replication in murine cells and that may modulate BKV replication in human cells.

References

¹S.D. Gardner, A.M. Field, D.V. Coleman, B. Hulme, *Lancet*, **1971**; *1*, 1253–1257.

²D. Fioriti, M. Videtta, M. Mischitelli, A.M. Degener, G. Russo, A. Giordano, V. Pietropaolo, *J. Cell Physiol.*, **2005**; *204*, 402-406.

³C. Mahon, B. Liang, I. Tikhanovich, J.R. Abend, M.J. Imperiale, H.P. Nasheuer, W.R. Folk, *J Virol.* **2009**, in the press.

TRAIL RESISTANCE IN NON-TRANSFORMED CELLS IS PROVIDED BY MULTIPLE FACTORS

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Tumour necrosis factor-related apoptosis-inducing ligand (TRAIL) is a member of the tumour necrosis factor family of death ligands. TRAIL is able to bind to two death inducing receptors, DR4 and DR5, and to two decoy receptors, DcR1 and DcR2. Through binding to DR4 and DR5, TRAIL can induce apoptosis selectively in tumour cells. Normal, untransformed cells are resistant to TRAIL, however, very little is known about the mechanism of their resistance. Approximately 50-60% of tumour types are also resistant to TRAIL. To sensitise these tumours to TRAIL without causing toxicity to normal cells, the mechanism that protects non-transformed cells from TRAIL should be identified.

As a typical non-transformed cell type, primary human dermal fibroblasts were used. We have shown that expression of the decoy receptors is not necessary for TRAIL resistance. Inhibition of protein synthesis could sensitise the cells to crosslinked TRAIL-induced apoptosis, indicating that there is a block in the intracellular TRAIL signalling pathway. Further examination of the TRAIL-induced signal transduction pathway revealed that multiple factors contribute to TRAIL resistance. Treatment of the cells with crosslinked TRAIL failed to induce detectable level of caspase-8 processing, however partial caspase-3 cleavage to its p20 fragment was observed, indicating that there is a block at the level of the DISC (Death Inducing Signalling Complex). Down-regulation of cFLIP, a known short-lived anti-apoptotic protein that inhibits pro-caspase-8 activation at the TRAIL DISC, could not sensitise the cells to crosslinked TRAIL-induced apoptosis, but resulted in enhanced caspase-3 cleavage to its p20 fragment. Lack of PARP processing in the same samples confirmed that caspase-3 was not active probably due to the presence of further inhibitors acting downstream of the DISC.

TALAROMYCES EMERSONII ENZYMES; THEIR APPLICATION IN CEREAL BASED FUNCTIONAL FOOD

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The fungus *Talaromyces emersonii* is known to produce a wide assortment of thermostable xylanolytic and cellulolytic enzymes¹. This is important when seeking to improve or create texture using enzymes in cereal processing. In the baking industry, hemicellulases are important for improving dough machinability, increasing the dough stability, allowing even crumb formation and as dough improvers, resulting in a larger volume with improved crumb texture.

The isolation and characterisation of novel enzymes can be used to improve food quality and nutrition. Many fungal enzymes with potential functions in this area have been identified including hemicellulases, cellulases and proteases².

A range of assays were also performed on various *T. emersonii* cocktails. The results showed that, when grown on certain carbon sources, *Talaromyces emersonii* produces a broad spectrum of enzymes with potential use in the baking industry. These include xylanase, esterase, amylase, peptidase and oxidase activities³. These enzyme cocktails have been characterized with regards to their temperature and pH optima and are in baking trials for sourdough, rye, oat and wheat breads in collaboration with UCC.

References

¹ Moloney A, Considine PJ, Coughlan MP, *Biotechnology Bioengineering*, 1983, 25, 1169-1173

² Lyons TP, *Biochemistry Soc. Trans.*, 1982, 10, 287-90

³ Murray P, Aro N, Collins C, Grassick A, Pentilla M, Saloheimo M, Tuohy M, *Protein Expression and Purification*, 2004, 38, 248-257

AN EVALUATION OF THE EFFECTS OF PREDICTED CLIMATE CHANGE ON *ASCOPHYLLUM NODOSUM*

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Abstract

Ascophyllum nodosum (Linnaeus) Le Jolis (Phaeophyceae) is an ecologically important intertidal keystone species on sheltered rocky shores on the Irish west coast, which supports up to 75 other marine species¹ but it is also harvested commercially. Ecological effects of harvesting include loss of epi-fauna and -flora, increased desiccation and danger of photodamage/bleaching in harvested habitats, increased erosion and morphological alterations such bushy *Ascophyllum* growth². In addition, predicted impacts of global change, e.g. an increase in UV-radiation levels and rising temperatures, could change the productivity of *A. nodosum*³.

One objective of this project is to predict potential changes in productivity due to environmental pressures including elevated UV-radiation, increased temperature and nutrient enrichment. Further, the impact of harvesting on these areas and their recovery are monitored here with the aim to ensure sustainable exploitation of the species. The present study thus assesses productivity of *A. nodosum* under current conditions *in situ*, and attempts, in lab and field experiments, to predict the change in productivity under different environmental conditions.

Using different field sites in Cos. Clare and Galway, *in situ* growth in harvested and non-harvested sites is being measured, and morphological and structural changes in *A. nodosum* populations in response to harvesting evaluated. Additionally physiological differences between plants from harvested and non-harvested sites are investigated on a seasonal basis using CO₂-assimilation and PAM-fluorescence. Considerable differences were observed between sampling sites with regard to standing crop, patterns in associated vegetation, responses to nutrients loading as well as growth and morphology of *A. nodosum*. Whether the observed differences were caused by harvesting or by the ambient environmental conditions, requires further investigations.

References

¹ **E. Wells and M. Wilkinson**, In: *Marine Biodiversity in Ireland and adjacent waters*. Ed: J.D.Nunn. Ulster Museum, **2001**, 15-26.

² **P.J.S. Boaden & M.T. Dring**, *Helgolaender Meeresuntersuchungen*, **1980**, 33, 700-710.

³ **M. Keser, J.T. Swenarton, J.F. Foertch**, *Journal of Sea Research*, **2005**, 54, 211-220.

DIVERSITY AND ABUNDANCE OF LICHENS ACROSS AN ALTITUDINAL GRADIENT IN SWAZILAND, SOUTHERN AFRICA

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Lichens play an integral role in the ecological value of a habitat and are commonly accepted as reliable indicators of environmental quality. As a result, the mapping of lichen abundance, diversity and distribution is becoming routine across the globe, as such surveys are generally fast and inexpensive. However, large parts of Africa remain unexplored in terms of lichenological research. For example, no published records of lichen distribution, diversity or abundance exist for Swaziland, southern Africa. This current study aims to document the diversity and distribution of epiphytic lichens in two protected nature reserves of Swaziland to serve as a baseline database for epiphytic lichens for the country. Lichens were collected across an altitudinal gradient in Swaziland. Over 170 lichen samples were collected and are currently being identified; distribution throughout the country was mapped and species restricted to Highveld and Lowveld sites were noted. The importance of lichens for passerine birds was also analysed by examining nests for the presence/absence of lichens, whilst paying particular attention to the types of nests which commonly incorporate lichen into their design. Distinct trends were noticed in the type of nests that included lichens; specific traits suggested that birds more than likely use lichen as a form of camouflage, deterring predators as opposed to ascertaining any structural benefit from the lichen thallus.

A STUDY OF THE PLANT COMMUNITIES OF OCEANIC HEATH IN THE WESTERN IRISH MOUNTAINS AND THEIR POTENTIAL RESPONSE TO CLIMATE CHANGE

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The mountains of western Ireland have a strongly oceanic climate, with equable temperatures and high year-round rainfall. This distinctive climate leads to the occurrence of plant communities unique to oceanic areas. The heath vegetation of the higher mountain ranges contains many communities and species which are restricted to oceanic regions¹. Among the most important of these is a rare community of large leafy liverworts, known as ‘mixed northern hepatic mat’ vegetation². It only occurs in mountainous regions along the west coast of Ireland and Scotland, where the climate is highly oceanic, but has recently been recorded as extinct in Connemara, due to heavy grazing³. The species of this community are of northern distribution and reach the southern limit of their range in southwest Ireland.

The northern hepatic mat community, as well as a number of other oceanic and northern communities and species of montane heath habitats may be potentially threatened by the impacts of global climate change. The climate is expected to become warmer, with less summer and more winter rainfall, leading to distinct changes in many Irish plant communities⁴. The decrease in summer rainfall is likely to have a strong impact on the distribution and frequency of hepatic mat vegetation, as liverwort species are dependant on constant high humidity. Ireland’s already rare and limited Arctic-montane plant communities are also likely to be threatened by climate change. It is projected that increases in temperatures will lead to an expansion of the range of more competitive lowland species to higher altitudes, which will out-compete slow growing Arctic-montane species.

In order to predict changes in occurrence of these already vulnerable species and communities, it is important to document the climatic range where they currently grow, within the mountains of western Ireland. Detailed mapping of plant communities and their regional variation will also provide useful baseline data for monitoring change in relation to future climate oscillations.

References

¹Averis, A.M. Averis, A.B.G. Birks, H.J.B. Horsfield, D. Thompson, D.B.A. Yeo, M.J.M. *An Illustrated Guide to British Upland Vegetation*. **2004**, Joint Nature Conservation Committee, Peterborough.

²Ratcliffe, D.A. *New Phytologist*, **1968**, *67*, 365-439.

³Holyoak, D.T. *Proceedings of the Royal Irish Academy*, **2006**, *106B*, 225-236.

⁴Jones, M.B. Donnelly, A. Albanito, F. *Proceedings of the Royal Irish Academy*, **2006**, *106B*, 323-334.

LOWLAND GRASSLANDS IN AGROECOSYSTEMS; ARE THERE GRASSLANDS OF HIGH NATURE VALUE ON CONVENTIONAL FARMS?

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Unimproved species-rich grasslands were once widespread across Western Europe. Losses of these habitats have been incurred largely through agricultural intensification, especially in lowland areas. The conservation of the biodiversity that remains on farmed landscapes is a European Union (EU) objective. This study has surveyed grassland habitats, the dominant habitat on Irish farms, with the aim of assessing the High Nature Value of the farms. Plant species data were gathered from 600 fields in east Co. Galway along with management, ecological and spatial descriptors, to examine the diversity of lowland grasslands on farms in this region and to test the application of the current habitat classification system. Using the latter, over 70% of fields were classified as Improved Agricultural Grassland. Results of more detailed analyses demonstrate a range of grasslands, varying in species richness from Semi-natural to Improved Agricultural Grasslands. However, a large number of fields were of intermediate species richness, and suggests the inclusion of an intermediate grassland category, i.e. Semi-improved Grassland to the classification system. Accurately describing the grassland habitats that occur on conventional farms will give a better assessment of a farm's High Nature Value status. It will also aid targeting of agri-environmental biodiversity options and grassland restoration initiatives.

IMPLICATION OF ENVIRONMENTAL FACTORS ON GROWTH, PRODUCTIVITY AND PIGMENTATION OF ALGAE

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Algae play a key role in biogeochemical cycling in coastal and off-shore waters, with their basic photosynthetic functions controlled by light, nutrients and temperature¹. They form the base of most aquatic food webs and impacts on these organisms have enormous implications for the higher trophic levels. Algal-environment interactions are complex and recent research has focused on algal physiological and chemical responses to environmental impacts, in particular climate change². Additionally, emissions of iodocarbons from algae have been documented and are of significance in aerosol formation³. As part of an EPA STRIVE-funded project, this research aims to quantify algal responses to environmental conditions like UV-radiation, temperature and salinity, and to evaluate the release of chemicals like I₂, Dissolved Organic Matter (DOM) and Particulate Organic Matter (POM) exudation from algae under different regimes. This work will provide input to the biological component of the ocean-atmosphere coupled climate model which will elucidate our understanding of air-sea exchange processes of aerosol and ozone and its impacts on climate.

Optimum growth conditions for selected species of microalgae (including representatives of diatoms, dinoflagellates and coccolithophores) were determined. Impacts of different levels of irradiance, temperature and nutrient regimes on the growth cycle of two strains of *Emiliania huxleyi* were studied. Depending on the growth phase of the cultures, a relationship between the two biomass indices (cell number and chlorophyll *a*) was investigated. In the case of macroalgae, significant species in terms of known iodine emission potential (*Laminaria digitata*, *Saccharina lattissima*, *Laminaria hyperborea*, *Ascophyllum nodosum*, *Fucus* spp. and *Porphyra* spp.) are being cultured under different environmental conditions. This study will also provide productivity estimates and assess impacts of PAR & UV, temperature and salinity on selected algal organic compounds and photoprotective pigments. Furthermore, impact of environmental stress on potential emissions of molecular iodine and volatile organic compounds (VOC) from micro- and macroalgal species will be undertaken. Analysis of dissolved organic carbon (DOC) and particulate organic carbon (POC) in seawater and culture media of micro- and macroalgal species will also be carried out.

References

1. Y. Suzuki and M. Takahashi, *Journal of Phycology*, **1995**, 31, 880-888.
2. J. Beardall and J. Raven, *Phycologia*, **2004**, 26-40.
3. J. Greenberg, A. B. Guenther and A. Turnipseed, *Environmental Chemistry*, **2005**, 2, 291-294.

DEVELOPMENT OF METHODS FOR, AND DETERMINATION OF ARSENIC IN IRISH MARINE BIOTA.

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Arsenic occurs naturally in both organic and inorganic forms in marine waters (c.2 $\mu\text{g L}^{-1}$)[1] and sediments (c.40 mg kg^{-1})[2], and is taken up from them and incorporated into the food web by a range of marine biota. As a result, the concentrations of total arsenic in some finfish, shellfish and seaweed may be over one hundred times greater than maximum permissible concentrations applied to other foods under Irish legislation[3]. The majority of marine species consumed by humans have complex uptake and metabolic systems which concentrate, but also detoxify, arsenic to the extent that the predominant form (arsenobetaine in fish) is considered to be virtually non-toxic. However, this natural safeguard is insufficient to protect public health as highly toxic inorganic forms persist alongside over thirty further metabolites of intermediate toxicities. The complete separation and quantification of each arsenical is necessary for risk evaluation, but routine monitoring requires a higher rate of sample turnover through the analysis of the most toxicologically relevant inorganic form. With correct sample pre-treatment, hydride generation and spectroscopic detection provide a number of solutions. Results for total arsenic are presented for various species in Irish waters, following the development and validation of a highly accurate method applicable to routine analysis. A novel method for the rapid detection of the inorganic fraction has been selected for validation and is also discussed.

References

1. Smedley, P.L. and D.G. Kinniburgh, *United Nations Synthesis Report on Arsenic in Drinking Water*, in *Water and Sanitation*, WHO.
2. Francesconi, K.A. and J.S. Edmonds, *Arsenic in the sea*. Oceanographic marine biology annual review, 1993. **31**: p. 111-151.
3. *S.I. No. 44/1972 — Health (Arsenic and Lead in Food) Regulations, 1972.*, O.o.t.A. General, Editor. 1972.

AN EVALUATION OF THE BIODIVERSITY OF IRISH UPLANDS: ARE CURRENT POLICIES DELIVERING IN TERMS OF BIODIVERSITY AND ECOSYSTEM FUNCTION?

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EU agri-environmental schemes aim to encourage “environmentally friendly” farming practices and in Ireland the main scheme currently in operation is the Rural Environmental Protection Scheme (REPS). Although €2.45 billion has been invested in REPS between 1994 and 2007, relatively little research has assessed the effectiveness of REPS in promoting biodiversity and any studies undertaken to date have produced ambiguous results. It is likely that a range of factors determine the effectiveness of agri-environmental schemes including socio-economic factors and in particular, farmers’ attitudes to and implementation of the scheme. It is in this context that this study is being undertaken whereby upland farms in the west of Ireland will be studied to assess the effectiveness of REPS and the Commonage Framework Plans (introduced by the National Parks & Wildlife Service (NPWS) in 1999 to control grazing). This will be achieved by mapping the major habitats of upland farms and evaluating these farms in terms of their contribution to biodiversity and ecosystem function. The latter will be achieved by plant surveys and vegetation condition scoring using NPWS guidelines, in addition to assessing ground beetle communities as bioindicators of habitat quality. The results of this project will then be correlated with a sister project which will be examining farmers’ management practices and attitudes towards biodiversity through interviews and questionnaires. The assessment of the effectiveness of agri-environmental schemes in promoting biodiversity is necessary to ensure that measures that work are encouraged while those which have little positive effect are discontinued. It is expected that this investigation will provide a good indication of the biodiversity of upland farms within the context of the socio-economic factors affecting it.

Keywords: Biodiversity, Uplands, Rural Environmental Protection Scheme, Commonage Framework Plans, Carabidae

DEVELOPMENT OF A TARGETING MECHANISM FOR REGENERATION OF THE INTERVERTEBRAL DISC

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Introduction

Low back pain (LBP) is a crippling condition with a lifetime incidence rate estimated to be in excess of 70% in industrialised nations. The cause of LBP remains elusive but degeneration of the intervertebral disc (IVD) has been identified as a leading factor of LBP based on imaging studies¹. The IVD consists of a soft gelatinous nucleus pulposus (NP) rich in ECM proteins in the centre of the disc, bound peripherally by an annulus fibrosis (AF) fibrocartilage subunit. Disc degeneration is characterised by an ingrowth of blood vessels and nerves into the avascular and aneural tissue and secondly, by increased degradation of the extracellular matrix². Current therapies alleviate the pain temporarily but do not restore disc function.

The objective of this study is the development of a targeting mechanism for disc regeneration using phage display technology and nanotechnology. IVDs are avascular and without lymphatic drainage, this contained environment provides an ideal setting for intradiscal injection of genes/growth factors as a potential therapy. Nanoshells containing genes or growth factors will be therefore be targeted to specific cells within the disc using scFv fragments generated through phage display.

Experimental Approach

Candidate target genes were chosen based on microarray and RT-PCR analysis of patients with varying degrees of degeneration, as defined by the Thompson scale. This led to identification of NCAM, which was cloned in two forms: one a single domain and the second a homodimer derived from the full-length protein. The constructs were generated using overlap PCR and an N-terminal signal peptide was added to direct the peptide to the periplasm. A C-terminal hexahistidine tag was incorporated to facilitate protein purification and detection³. DNA sequencing confirmed the constructs and was followed by subcloning into an expression vector, protein production and purification of the recombinant protein using immobilised metal affinity chromatography (IMAC).

Results

Soluble NCAM protein was extracted from the *E. coli* periplasm. Coomassie staining and Western blotting revealed the presence of minor protein contaminants in IMAC column eluates after one-step affinity chromatography. Further purification was used to clean up the eluted protein, which was detected using an anti-hexahistidine reporter antibody. Panning of a phage scFv combinatorial library will commence shortly to identify NCAM-binding proteins for use in delivery of nanoshells to NP cells.

References

1. Luoma K, et al. *Spine*, **2000**, 25, 487-492.
2. Purmessur D, Freemont AJ, Hoyland JA. *Arthritis Res. Ther.*, **2008**, 10, R99-108.
3. Hu X, O'Dwyer R, Wall JG. *J. Biotechnol.*, **2005**, 120, 38-45.

DIFFERENCES IN DEVELOPMENT OF RESISTANCE TO THE ANTIBIOTIC CIPROFLOXACIN AND THE BIOCIDES BENZALKONIUM CHLORIDE IN *CAMPYLOBACTER JEJUNI* NCTC 11168

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Campylobacters remain highly important zoonotic pathogens and are recognized as major causes of human gastroenteritis worldwide. In Ireland, campylobacteriosis is mainly a food-borne infection, in which foods of animal origin, and in particular is the handling and consumption of poultry meat. The use of fluoroquinolone in poultry flocks, demonstrated unequivocally to select for ciprofloxacin-resistant campylobacters in commercially-reared poultry, potentially compromises treatment of infection by antibiotic therapy. Good hygiene practices are paramount in preventing infection routinely employ the use of biocides. This work used an *in vitro* chemostat model to characterise emergence of resistance in *Campylobacter* to the fluoroquinolone antibiotic ciprofloxacin (broth MIC: 0.06 mg l⁻¹, agar MIC: 0.125mg l⁻¹) and biocide benzalkonium chloride (BKC) (broth MIC: 0.64 mg l⁻¹, agar MIC: 8 mg l⁻¹). Chemostats were run with antibiotic and disinfectant selective pressures over 1500h. Sub-minimum inhibitory concentrations (Sub-MIC) of ciprofloxacin resulted in the development of resistant mutants with resistance between 2- and 4-fold greater than the wild type strain. However, the majority (> 95%) of the population was still susceptible to ciprofloxacin. Eventually, when the ciprofloxacin concentration was increased up to 12 mg l⁻¹ in the chemostat, hyper-resistance strains (agar MIC: 128 mg l⁻¹) were detected within the population. In contrast, exposure to Sub-MIC concentrations of BKC induced a slow stepwise increase in resistance to BKC. A doubling of MIC was observed for every 8-fold increase in BKC selective pressure. The trend continued even after exposure to MIC and Supra-MIC concentrations of BKC. These results confirm that campylobacter readily acquires resistance to ciprofloxacin and suggests that residual concentrations of disinfectant containing BKC may increase the tolerance of *C.jejuni* and may compromise the effectiveness of disinfectants in controlling campylobacter infection.

ROLE OF JNK ACTIVATION IN THE PATHOGENESIS OF *VIBRIO PARAHAEMOLYTICUS*.

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Infection with *Vibrio parahaemolyticus* following consumption of contaminated seafood poses a huge health risk. Infection is characterised by widespread destruction of the intestinal mucosa with epithelial cell damage and inflammation caused by high levels of pro-inflammatory cytokines¹. This study will investigate the mechanisms by which *V. parahaemolyticus* causes activation of the human JNK signalling pathway and how this activation promotes and stimulates host responses. *V. parahaemolyticus* contains two Type Three Secretion Systems, TTSS-1 and TTSS-2². It is these secretion systems that are implicated in the infection process associated with *V. parahaemolyticus*. While TTSS-1 is the principle mediator of cytotoxicity, TTSS-2 is associated with enterotoxicity. The Type Three Secretion Systems enable the bacteria to secrete various effector proteins into the cytosol of the human epithelial cells and in this way cause infection. Three main effectors have been shown to interfere with cell signalling pathways within the epithelial cells; VP1686, VopT and VopA (VopP)³. VP1686 is cytotoxic to macrophages while VopA targets epithelial cells. VP1657 is a translocator protein required for translocation of the effector proteins into the host cells. The effects of *V. parahaemolyticus* TTSS-effector proteins on the JNK signalling cascade was assessed by analysing the effects induced in Caco-2 cells upon co-incubation with the bacteria. Immunoblotting was carried out to determine which MAPK proteins are activated in response to *V. parahaemolyticus*. We observed that all three MAPKs (p38, p42/44 and JNK), are activated. It also illustrated that TTSS-1 plays an important role in each case. TTSS-1 mutants (Δ VscN1) did not lead to MAPK activation following co-incubation with Caco-2 cells. VscN1 is required for the secretion of the effector proteins. These results suggest that TTSS-1 is vital for *V. parahaemolyticus* cytotoxicity. Results obtained for the double mutant (Δ TTSS-1, Δ TTSS-2) suggest the presence of an inhibitory effect. MAPKs were activated in the presence of both the double mutant and the TTSS-2 (Δ VscN2) mutant however no activation occurred on co-incubation with the TTSS-1 mutant. This suggests that the TTSS-1 mutant may also play an inhibitory role in *V. parahaemolyticus* infection. Immunoblotting was carried out on samples obtained from Caco-2 cells treated with various MAPK inhibitors. These inhibitors target either the MAPK directly or proteins located upstream in the cell signalling cascade. In the future these inhibitors will be employed in barrier studies to determine the ability of *V. parahaemolyticus* to influence epithelial barrier function.

References

- ¹F. Qadri, M. S. Alam, M. Nishibuchi, T. Rahman, N. H. Alam, J. Chisti, S. Kondo, J. Sugiyama, N. A. Bhuiyan, M. M. Mathan, D. A. Sack, G. B. Nair, *J. Inf. Dis.*, **2003**, *187*, 1085-96.
- ²K. S. Park, T. Ono, M. Rokuda, M. H. Jang, K. Okada, T. Iida, T. Honda, *Infect. Immun.*, **2004**, *72*, 6659-65.
- ³R. N. Bhattacharjee, K. S. Park, Y. Kumagai, K. Okada, M. Yamamoto, S. Uematsu, K. Matsui, H. Kumar, T. Kawai, T. Iida, T. Honda, O. Takeuchi, S. Akira, *J. Biol. Chem.*, **2006**, *281*, 36897-904.

INVESTIGATION OF DEEP MEDITERRANEAN SEA MICROBIAL COMMUNITY STRUCTURES

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The total number of prokaryotic cells in the ocean has been estimated to be in the order of 10^{30} cells¹, representing 54 to 84 % of all prokaryotic cells on Earth. Understanding the abundance and diversity of marine prokaryotic communities represents the first step in elucidating the enormous contribution they make towards the biogeochemical cycles of planet Earth.² The deep-sea remains largely unexplored and poorly understood due to the remote nature of the environment and challenges associated with collecting samples.

Water samples were taken aboard the N/O Urania from depths between 150m and 5100m from a number of sites in the central region of the Mediterranean Sea. Bacterial biomass was collected by filtration using 0.2µm pore filters. Enumeration of microorganisms was carried out by epifluorescence microscopy.

Bacterial community structure was studied by means of DGGE (Denaturing Gradient Gel Electrophoresis)³ analysis of 16S rRNA genes. Primers complementary to the conserved portion of the V3 region were used to amplify a fragment of the 16S rDNA from the community. Variations in community structure was most obvious at all sites when comparing the deep communities with those in intermediate and surface waters. Differences between sampling sites will also be discussed.

Future work will involve the excision and sequencing of prominent bands thought to reflect the keystone members of the community. This work will contribute to understanding the biodiversity and ecosystem functioning in contrasting Southern European Deep-Sea Environments.

References

¹ W. B Whitman., D. C. Coleman, & W. J. Wiebe, *Proceedings of the National Academy of Sciences*, **1998**,95, 6578-6583.

² D. M. Karl, *Nature Reviews: Microbiology*, **2007**, 5, 759-769

³ A. E. Murray, C. M. Preston, R. Massana, L. T. Taylor, A. Blakis, K. Wu, & E. F. DeLong, *Applied & Environmental Microbiology* **1998**, 64, 2585-2595.

ELUCIDATION OF THE RESPONSES TO WEAK ACIDS IN THE HUMAN PATHOGEN *LISTERIA MONOCYTOGENES* USING GENE MICROARRAYS.

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Contamination of processed food by the pathogen *Listeria monocytogenes* is a major human health risk. *L. monocytogenes* causes the gastrointestinal food infection listeriosis, a rare but extremely severe systemic infection in humans. Food preservation methods include the use of weak organic acids to reduce microbial growth. However, *L. monocytogenes* has been identified in foods that use organic acids as preservatives. Although the response of *L. monocytogenes* to strong acids has been investigated, there little is known on how *L. monocytogenes* responds to weak acids, particularly at the molecular level. The objective of this study was to investigate the molecular response of *L. monocytogenes* to five food-grade organic acids, acetic, lactic, sorbic, citric and benzoic acid. Growth experiments were carried out to investigate the effects of weak acid effects on *L. monocytogenes*. Microarray and quantitative RT-PCR were performed to elucidate the molecular responses of the organism to weak acids. The response mechanisms of *L. monocytogenes* to weak acids, is different from the response to strong acids; σ^B and the glutamate decarboxylase system are not utilized in response of *L. monocytogenes* to weak acids. Weak acid stress affects all functional categories of the genome of *L. monocytogenes*. Overall a small number of genes showed altered expression in response to weak acids. No changes were shared by all five acids. However, 26 genes showed altered expression in response to at least two acids and nine genes were down regulated in response to three acids; benzoic, lactic and sorbic.

**PIONEERING COLD DIGESTION:
FEASIBILITY AND ECOPHYSIOLOGY OF LOW
TEMPERATURE (10 AND 15°C) ANAEROBIC TREATMENT OF
RAW SEWAGE**

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Sewage is almost always treated in aerobic reactors, followed by a mesophilic (c.35°C), anaerobic, sludge-reduction process. A polyphasic experimental approach, based on novel environmental engineering and targeted molecular microbial ecophysiology, was adopted to address our two-fold objective: to (1) investigate the feasibility of anaerobic digestion of raw (without aerobic pre-treatments) sewage under temperate conditions, and (2) study the community – and architectural – structure-function relationships of the consortia in the granular biofilms underpinning the process. Custom-designed, continuous, up-flow bioreactors were employed at 37, 15 and 10°C. Separate trials demonstrated (1) efficient and stable chemical oxygen demand (COD) removal (c.90%), and biogas production (300 ml CH₄/l-reactor/d; 60-72% CH₄), from synthetic sewage ('SYNTHESES'; 750 mg COD/l) applied at an organic loading rate (OLR) of 3 kg COD m³/d; and (2) COD removal c.60% from dilute sewage (250 mg COD/l). Additionally, up to 55% removal of total nitrogen was achieved. Temporal digestibility and specific methanogenic activity (SMA) batch assays, with SYNTHES or various direct and indirect methanogenic substrates, indicated a shift in microbial activity at each temperature from acetoclastic to hydrogenotrophic methanogenesis. Propionate degradation was rate-limiting at 15 and 10°C. 16S rRNA gene clone library, terminal restriction fragment length polymorphism, denaturing gradient gel electrophoresis and fluorescence in situ hybridization (FISH) analyses of sewage-degrading biomass supported SMA data and indicated the predominance of Methanomicrobiales and Methanobacteriales. Microautoradiography (MAR)-FISH – applied for the first time to raw-sewage-degrading anaerobic sludge – enabled the link between single-cell ecophysiology and *in vitro* SMA data from multi-species consortia.

GENERATION OF A GENOMIC LIBRARY IN ORDER TO IDENTIFY NOVEL *Vibrio parahaemolyticus* ADHESINS AND INVASINS.

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Vibrio parahaemolyticus is a food-borne pathogen which is capable of inducing acute inflammation of the gastro-intestinal tract¹. The organism forms part of the commensal micro-flora of many species of shellfish and disease symptoms in humans usually arise due to consumption of heavily contaminated fish. One of the principle virulence mechanisms employed by *V. parahaemolyticus* during pathogenesis is the secretion of effector proteins into host cells via a Type Three Secretion System (TTSS)². Intimate association between the bacterium and the host cell is required in order for this process to occur. *V. parahaemolyticus* is also capable of invading epithelial cells and surviving in the intracellular environment³. This study will focus on the adhesins and invasins utilised by the bacterium during pathogenesis. A random genomic library was constructed using the pWEB-TNC™ cosmid cloning kit supplied by EPICENTRE ®. *V. parahaemolyticus* genomic DNA was randomly sheared by passage through a narrow bore syringe. Insert fragments of approximately 40 kb were selected for ligation by electrophoresis. Following end-repair, this insert DNA was ligated into a cosmid vector and subsequently packaged into T1 phage. The packaged library was then titered by adsorption on to a T1 resistant strain of *E. coli* and selection on a medium containing an appropriate antibiotic. The packaged library was then stored in aliquots, each containing a desired level of coverage of the *V. parahaemolyticus* genome. This library will be expressed in a non-adherent, non-invasive strain of *E. coli* and subsequently screened for the ability to adhere to and invade Caco-2 epithelial cells by incubation with Caco-2 cells followed by the gentamicin protection assay. Insert DNA from adherent/invasive clones will then be sequenced, revealing *V. parahaemolyticus* sequences which play a role in the adhesion and invasion process.

References

¹ K.S. Park, T. Ono, M. Rokuda, M.H. Jang, T. Lida, T. Honda, *Microbiol. Immunol.*, **2004**, 48, 313-318.

² T. Honda, T. Lida, Y. Akeda, T. Kodama, *Microbe*, **2008**, 3, 462-466.

³ Y. Akeda, K. Nagayama, K. Yamamoto, T. Honda, *J. Infect. Dis.*, **1997**, 176, 822-824.

DEVELOPMENT OF A POLYCLONAL ANTIBODY AGAINST OpuCA IN CHICKENS FOR MEASURING THE ACTIVITY OF σ^B IN *Listeria monocytogenes*

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Effective multiplication in many different environments and resistance at the early stages of infection within the host are crucial to the transmission and invasion of the foodborne pathogen *Listeria monocytogenes*. The alternative sigma factor (σ^B) plays a significant role in listerial stress tolerance and many components of σ^B regulon have been identified. Using Western blotting, we observed that individual mutations of four genes under σ^B control with unknown function (*lmo0796*, *lmo0913*, *lmo2391* and *lmo2748*) do not have any influence on the levels of σ^B and also on the levels of two proteins predicted to participate in σ^B regulation - RsbW and RsbV. However, the proposed σ^B regulation system suggests that the activity of σ^B could still be affected. Growth experiments with a range of concentrations of NaCl confirmed the presence of an alternative defence against osmotic stress controlled by σ^B as growth of the $\Delta sigB$ strain is impaired while the $\Delta opuCA$ strain is not affected by salt concentrations up to 1.8 M. OpuCA which is responsible for the uptake of compatible solute carnitine and whose expression is controlled by σ^B , may be a good candidate protein to act as reporter of σ^B activity. Two chickens were immunized with the purified OpuCA protein to produce polyclonal antibodies. Chicken sera were tested for specificity by Western blotting and used for investigating the activity of σ^B during osmotic stress. We will present data that suggest this antibody will be the useful tool in determining the activity of σ^B in the stress response of *L. monocytogenes*.

K. R. Fraser, D. Harvie, P. J. Coote, C. P. O'Byrne, *Appl Environ Microbiol*, **2000**, 66, 4696-704.

J. Marles-Wright, R. J. Lewis, *Curr Opin Struct Biol*, **2007**, 17, 755-60.

C. P. O'Byrne, K. A. Karatzas, *Adv Appl Microbiol*, **2008**, 65, 115-40.

THE STUDY OF SEGMENTATION GENES IN THE CENTIPEDE *STRIGAMIA MARITIMA*

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The origin of animal segmentation has been debated by generations of scientists. The three main groups of segmented animals are the Arthropods (e.g. insects), the Annelids (e.g. “earthworms”) and the Vertebrates (e.g. humans), representing the two different kinds of segmentation, inner and outer segmentation. The traditional view of three independent origins in the three different lineages has been questioned recently after the employment of arthropod models other than the fruit fly *Drosophila*, with its extremely derived segmentation process. Similarities in the molecular pathways responsible for segment formation in vertebrates and less derived arthropods, like spiders¹ were discovered and fuel the discussion about a common origin of segmentation processes. This shows that the main questions in evolutionary developmental biology can’t be resolved by focussing just on the standard model organisms, which nonetheless have proved very valuable to our understanding of developmental mechanisms in the past.

Centipedes became a new model for the study of the evolution of segmentation processes about six years ago². Like in spider segmentation, centipedes show similarities to vertebrate segmentation with oscillating expression of the *notch* gene³. This puts centipedes in the focus of evolutionary and developmental (“evo-devo”) research. Furthermore, the amount of segments, sequentially formed in the centipede embryo, provide an ideal timeline to observe the segmentation process.

We work mainly on segmentation genes of the well conserved group of segment polarity genes (*wingless*, *hedgehog*, *cubitus interruptus*). These genes establish the boundaries between the newly formed segments in the embryo. Their expression is analysed through *in situ* hybridization. By comparing the expression of these genes in the centipede with the expression in other arthropods we learn about the way gene expression is shaped in the evolution of animal body plans.

References

- ¹ Stollewerk, A., Schoppmeier, M. & Damen, W. G. Involvement of Notch and Delta genes in spider segmentation. *Nature* **423**, 863-865 (2003).
- ² Kettle, C., Johnstone, J., Jowett, T., Arthur, H. & Arthur, W. The pattern of segment formation, as revealed by engrailed expression, in a centipede with a variable number of segments. *Evolution & Development* **5**, 198-207 (2003).
- ³ Chipman, A. D. & Akam, M. The segmentation cascade in the centipede *Strigamia maritima*: Involvement of the Notch pathway and pair-rule gene homologues. *Dev Biol* (2008).

INFILLING OF WETLANDS WITH CONSTRUCTION AND DEMOLITION (C & D) WASTE IN THE WEST OF IRELAND – IMPLICATIONS FOR WETLAND CONDITION USING HYDROLOGICAL PARAMETERS AND INVERTEBRATE BIOINDICATORS.

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Wetlands are important components of watersheds and provide useful ecosystem services including the transfer and storage of water, plant and animal production, organic decomposition, habitat provision, flood control, filtering and cleansing of water, erosion control and recreation. Despite these valuable ecosystem services, many wetlands, particularly those in the west of Ireland, have been or are currently being infilled with C & D waste because of the rapid increase in development in recent years. Very little is known about the impact of infilling on wetland ecosystem function in Ireland and this provided the incentive for this project (based in county Galway), the aims of which are to: a) determine the occurrence and land cover of licensed and unlicensed C & D infill sites on wetlands throughout County Galway b) quantify the impact of C & D waste on water quality and quantity using hydrological analyses c) develop a bioassessment methodology for wetlands affected by C & D infilling using plant and invertebrate bioindicators. For the hydrological component of this study, the Water Framework Directive (WFD) database and the recent study of wetlands in County Galway undertaken by Galway County Council will be accessed to provide existing information regarding water bodies in the county which will then be used for site selection. Water flows to and from each site will be determined using standard measurement techniques and this will be coupled with predictive methods to determine extreme flows. Water will be sampled up-gradient and down-gradient of sites for analysis and the impacts of flood protection from the infilling of the wetlands will also be conceptually modelled using FSR (Flood Studies Report) and FEH (Flood Estimation Handbook) methods. For the bioassessment component, marsh flies (Diptera: Sciomyzidae) which have already proven to be useful bioindicators of change in turloughs and callows, will be sampled using a variety of techniques in conjunction with plant community composition and structure.

Cognate Disciplines

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SURVIVAL AND IMMUNOGENICITY OF MESENCHYMAL STEM CELLS FROM THE GREEN FLUORESCENT PROTEIN TRANSGENIC RAT IN THE ADULT RAT BRAIN

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Background: A major technical limitation in pre-clinical cell replacement research has been the ability to discriminate between donor and host tissue post-transplantation. This has been substantially improved by the availability of transgenic animals which express ‘reporter’ genes such as green fluorescent protein (GFP). *Objective:* This experiment sought to determine the usefulness of one such transgenic reporter rat to assess the survival of bone marrow-derived rat mesenchymal stem cells (MSCs) following direct transplantation to the intact adult rat brain. We also sought to determine if the expression of GFP in the brain impacted on the survival of the MSCs or affected the host’s neuro-immune response to the cells. *Methods:* Rats received intrastriatal injections of sterile transplantation medium, 100,000 normal MSCs or 100,000 GFP-MSCs and were sacrificed 1, 4, 7, 28 and 42 days post-transplantation for astrocyte and microglial immunohistochemical staining. *Results:* GFP-MSCs were evident at all time points examined although their survival declined over time. Graft volume estimates comparing normal and GFP-MSCs revealed that GFP expression did not adversely affect the survival of the stem cells in the brain. Furthermore, immunostaining for astrocytes and microglia revealed that expression of the reporter protein did not affect the immunogenicity of the stem cells. *Conclusions:* Overall, these data indicate the usefulness of GFP for investigating the survival of MSCs following transplantation to the brain. However, the mechanisms responsible for the poor survival of the stem cells must be elucidated if these cells are ever to become truly useful for cell-based therapies for neurodegenerative disorders.

DESMOSOMAL PROTEINS IN ZEBRAFISH DEVELOPMENT

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Desmosomes are integral to maintaining tissue integrity and strength, and are particularly important in tissues which undergo routine mechanical stress such as the skin and heart. Defects in various desmosomal proteins have been linked to Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC) and sudden death. Loss of the desmosomal armadillo proteins, plakophilin 2 (PKP2) and plakoglobin (PG), in mice leads to cardiac instability and embryonic lethality^{1,2}.

We have successfully cloned the zebrafish plakophilin 2 cDNA and have shown that the putative protein is similar to the human plakophilin 2. The mRNA is expressed throughout zebrafish embryonic development and it is present in epidermal and cardiac tissue at the later stages examined.

Knockdown of zebrafish plakophilin 2 by morpholino antisense technology has resulted in morphant embryos with cardiovascular defects accompanied by stage dependent anterior neural and tail defects. At 24 hours post fertilization (hpf), plakophilin 2 morpholino injected embryos had disrupted borders in anterior neural structures along with disruption of the tail. At 48 hpf and 72 hpf morpholino injected embryos showed pericardial oedema and blood pooling on the yolk prior to entering the heart.

Loss of plakoglobin results in a similar morphant phenotype in zebrafish embryos. Structural analysis of these morphants using transmission electron microscopy showed altered adhesion and cellular morphology in their cardiac valves along with reduced numbers of junction in the heart as a whole.

These data show the importance of desmosomal armadillo proteins in zebrafish embryonic development.

References

¹K.S. Grossmann, C. Grund, J. Huelsken, M. Behrend, B. Erdmann, W.W. Franke, W. Birchmeier, *J. Cell Biol.* **2004**, 167, 149-160.

²C. Bierkamp, K.J. McLaughlin, H. Schwarz, O. Huber, R. Kemler, *Dev. Biol.* **1996** 180, 780–785.

COGNITIVE BEHAVIOURAL CHARACTERISATION OF A RAT MODEL OF NEUROPATHIC PAIN

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Chronic pain, in particular neuropathic pain, impacts negatively on cognition, with neuropathic pain patients showing impaired performance on standardised cognitive tests (Povedano et al. 2007). However, the neural mechanisms mediating this pain-related cognitive impairment are poorly understood, due in part to the lack of a well validated animal model. The aim of this experiment was to compare cognitive performance in rats that have undergone spinal nerve ligation (SNL) surgery, as a model of neuropathic pain, and sham-operated control rats. Male Sprague-Dawley rats underwent tight ligation of the left L5 and L6 spinal nerves, under isoflurane anaesthesia. In sham animals, these nerves were exposed but not ligated. Nociceptive behaviour was assessed with von Frey hair testing for tactile allodynia and Hargreave's test for thermal hyperalgesia. Spatial learning was assessed in the Morris water maze, and spatial memory in both the Morris water maze and the T-maze. Recognition memory was tested in a novel-object-recognition paradigm. Animals were sacrificed by intracardiac perfusion and spinal cords were removed, sectioned and stained with FITC-conjugated isolectin B4 (IB4), a marker of primary afferent C-fibre nociceptors. Sections were visualised using fluorescent microscopy. IB4 showed a qualitative decrease in staining intensity in laminae 1-2 of the spinal cord on the ipsilateral side to ligation, as compared with the contralateral side and with sham controls, which indicates the surgery was successful. SNL rats developed tactile allodynia, and thermal hyperalgesia was observed 10 days post-surgery. SNL surgery had no effect on spatial learning in the acquisition phase of the Morris water maze test or on spatial memory assessed in both the Morris water maze probe trial and the T-maze test of spontaneous alternation. Recognition memory was also unaffected in the nerve-ligated group as compared with the sham control group. SNL surgery successfully modelled symptoms characteristic of neuropathic pain, allodynia and hyperalgesia, but was not associated with cognitive impairment in any of the tests used.

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Reference:

Povedano M, Gascon J, Galvez R, Ruiz M, Rejas J. Cognitive function impairment in patients with neuropathic pain under standard conditions of care. Journal of pain and symptom management 2007;33(1):78-89

CANNABINOID CB₁ RECEPTOR EXPRESSION IS DIFFERENTIALLY ALTERED FOLLOWING AXONAL OR TERMINAL LESION OF THE NIGROSTRIATAL PATHWAY IN THE RAT

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The endocannabinoid system is emerging as a potential therapeutic target for the treatment of movement disorders affecting the basal ganglia¹, such as Parkinson's disease. This is partly based on the finding that the highest level of the CB₁ subtype of cannabinoid receptor in the brain is in the basal ganglia, particularly within the substantia nigra (SN). Moreover, changes in CB₁ receptor expression have been reported in the post-mortem Parkinsonian brain² and in rodent models of the disease. This experiment sought to determine if expression of the receptor is altered in the two most commonly-used rat models of Parkinson's disease – those in which the catecholamine neurotoxin 6-hydroxydopamine is injected into the axons or terminals of the nigrostriatal pathway.

Parkinsonian lesions were induced in male Lister Hooded rats by stereotaxic injection of 6-hydroxydopamine into either the medial forebrain bundle (MFB) (n=19) or the nigrostriatal terminals (n=16) under isoflurane gaseous anaesthesia (2-5% in oxygen). On days 1, 3, 7, 14 and 28 post-lesion, rats were sacrificed by terminal anaesthesia (50 mg/kg pentobarbital) and transcardially perfused with saline and 4% paraformaldehyde. The brains were then processed for immunohistochemistry. Density of staining in the SN and striatum was quantified using Image J software.

The CB₁ receptor was very strongly expressed in the *pars reticulata* region of the SN (SN_{pr}) and did not overlap with tyrosine hydroxylase immunoreactivity in the *pars compacta* (SN_{pc}). Following the MFB lesion there was an initial, transient increase in CB₁ receptor expression in the SN_{pr} (Day 1= 159 ± 17.5%; Day 3= 198.4 ± 48.8%; Day 7= 158.8 ± 16.3%; Day 14 = 140.7 ± 25.6%; Day 28 = 99.8 ± 5.3%, data expressed as a percentage of the intact side; n=3/4 rats at each time point). Following the nigrostriatal terminal lesion, there was a progressive decline in CB₁ receptor expression in the SN_{pr} on the lesioned side of the brain (Day 1= 99.7 ± 7.9%; Day 3= 70.8 ± 10.5%; Day 7= 64.5 ± 2.3%; Day 14 = 55.5 ± 4.4%; Day 28 = 51.6 ± 15.7%, data expressed as a percentage of the intact side; n=3/4 rats at each time point). DARPP 32 immunohistochemistry was carried out on striatal sections from the terminal lesion model to determine if the loss of CB₁ receptor expression in the SN_{pr} was related to non-specific toxic effects of 6-hydroxydopamine. Injection of the neurotoxin at this site resulted in decreased striatal volume over time (Day 1= 11.83 ± 0.72; Day 28= 8.40 ± 0.72, data expressed as striatal volume of lesioned side (mm³), n=3/4 rats per time point) which correlated significantly with the decrease in CB₁ receptor expression in the SN_{pr} (r=0.595, P<0.05).

This experiment has established that expression of the CB₁ cannabinoid receptor is downregulated in the terminal lesion model of Parkinson's disease, apparently caused by non-specific damage by 6-hydroxydopamine of striatonigral

neurons, on which CB₁ receptors are located pre-synaptically in the SN_{pr}³. CB₁ receptor expression is transiently elevated in the MFB lesion model and is maintained over the 28 day period in this study. Therefore, the MFB lesion model may be more suited to investigating drugs targeting the cannabinoid system in an effort to identify novel therapies for Parkinson's disease.

¹Brotchie JM, *Curr Opin Pharmacol* **2003** 3(1), 54-61

²Lastres-Becker I, Cebeira M, de Ceballos ML, Zeng BY, Jenner P, Ramos JA, Fernández-Ruiz JJ. *Eur J Neurosci.* **2001** 14(11), 1827-32.

³Herkenham M, Lynn AB, de Costa BR, Richfield EK. *Brain Res* **1991** 547(2), 267-74

IMPORTANCE OF OXYGEN IN *IN VITRO* OVARIAN FOLLICLE CULTURE

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In vitro ovarian follicle culture provides a tool to investigate the processes that control folliculogenesis. Recent work from our laboratory has shown that the standard 5% CO₂ in air gas phase (20% O₂) does not supply sufficient O₂ to support optimal development of *in vitro* cultured murine ovarian follicles. The central hypothesis here is that optimal delivery of oxygen to follicles *in vitro* improves follicular development.

Follicles were isolated and cultured as described previously (Wycherley *et al.*, 2004). Preantral follicles (180-220 µm in diameter) were cultured for 6 days in either 20% or 40% O₂. Growth was assessed on alternate days by follicle diameter measurement. Follicles were treated with superoxide dismutase (SOD; 100 IU/ml), Trolox (100 µM) or haemoglobin (10, 100 mg/ml) on culture days 0, 2 and 4.

Follicles exposed to 40% O₂ reached a significantly greater ($P < 0.05$) terminal diameter than those cultured in 20% O₂ (353 ± 4.2 µm, 406 ± 11 µm; mean \pm s.e.m.). Trolox and SOD had no beneficial effect on follicle growth under all culture conditions. The addition of haemoglobin to follicles cultured in 20% O₂ significantly improved growth ($P < 0.01$) from control diameters of 365 ± 8.5 µm to 408 ± 6.3 µm at 10mg/ml and 400 ± 5.7 µm at 100mg/ml haemoglobin. Addition of haemoglobin to follicles cultured in 40% O₂ resulted in improved follicle growth from control diameters of 417 ± 16.7 µm to 448 ± 9.2 µm at 10 mg/ml and 443 ± 14.2 µm at 100 mg/ml, but this effect was only significant ($P < 0.05$) at 10 mg/ml haemoglobin.

From these data it is concluded that follicles cultured under conditions of improved oxygenation show improved growth and development.

INVESTIGATION OF PROSTAGLANDIN TRANSPORTER IN UTERINE EPITHELIAL CELLS

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Prostaglandin transport is a carrier-mediated system that transports prostaglandins (PGs) coupled to obligate lactate exchange and displays an affinity profile $\text{PGE}_2 = \text{PGF}_2\alpha > \text{PGD}_2 \gg \text{Arachidonic Acid}$ ¹. In the uterus the prostaglandin transporter (PGT) is necessary to control local PG transport (specifically PGE_2 and $\text{PGF}_2\alpha$). PGT is a member of the 12-transmembrane organic anion transporting polypeptide (OATP) superfamily of transporters, which facilitate the movement of a variety of organic compounds independently of Na^+ , Cl^- or H^+ ². In line with work from this lab (unpublished data) and recent studies by Banu et al., 2008³, it has been shown that PGT is not constitutively expressed in uterine epithelial cells (UECs). Maximum PGT expression has been shown in UECs at the dioestrous and proestrous stages of the cycle.

This study investigates the localization of PGT in rat uterine tissue following oxytocin challenge, to replicate the *in vivo* dioestrous stage of the cycle. Uterine horn tissue from rat was obtained and treated with 5IU oxytocin for 5, 15, and 30 minutes prior to immunohistochemical staining for PGT.

The results conclusively show that PGT is not constitutively expressed in rat uterine tissue. Treatment with oxytocin results in a time dependent increase in the expression of PGT increasing dramatically from 5 to 15mins post treatment with reduced expression at 30 minutes.

From these data we concluded that PGT is not constitutively expressed in uterine tissue and may depend on hormonally controlled cycle stage.

References

¹Brenda S. Chan, Shinichi Endo, Naoaki Kanai, and Victor L. Schuster
'Identification of lactate as a driving force for prostanoid transport by prostaglandin transporter PGT'

Am J Physiol Renal Physiol 2002 Vol. 282, Issue 6, F1097-F1102

² VL Schuster 'Molecular mechanisms of prostaglandin transport'
Annual Review of Physiology 1998 Vol 60 221-242

³ SK Banu, JA Arosh, P Chapdelaine, and MA Fortier
'Molecular cloning and spatio-temporal expression of the prostaglandin transporter: A basis for the action of prostaglandins in the bovine reproductive system'
PNAS 2003 100:11747-11752;

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THE SPATIAL AND TEMPORAL CHANGES OF MACKEREL (*SCOMBER SCOMBRUS*) EGG DENSITIES IN THE NORTH EAST ATLANTIC USING CENTRE OF GRAVITY AND INERTIA METHODS.

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Atlantic mackerel (*Scomber scombrus*) are a renowned migratory species spawning along the continental shelf from the Cantabrian Sea to the Hebrides between March and July¹. Feeding occurs in the North and Norwegian Sea during the autumn months and wintering grounds are to the north of Ireland and Scotland, although this can be variable¹. Mackerel make up a large part of the Irish fisheries catch and provides one of the most valuable European fisheries².

Individual statistics such as probability distribution can be very helpful in determining changes in density and variance of marine populations over time³. Data collected from the ICES triennial egg survey provides records of mackerel egg densities and distributions since 1977 which have been used to assess the dynamics of spawning behaviour and recruitment. Results demonstrate a northward shift of stage 1 mackerel eggs throughout the spawning season from the southern Bay of Biscay to the north of Scotland, with a flux of stage 1 eggs in the southern Bay of Biscay during July. It is possible to visually detect a northward shift of stage 1 eggs through time since 1977 to 2004 with increasing latitude associated with increasing temperature. An increase in the inertia or the variance of the egg distributions during egg development is also apparent, indicating a dispersal of the eggs over the continental shelf. The results add to the growing literature that spawning of Atlantic mackerel is undergoing a northward shift.

¹ A. Uriarte, P. Lucio, *Fisheries Research*, **2001**, 50, 129-139

² *ICES Working Group on the Assessment of Mackerel Horse Mackerel, Sardine and Anchovy*, **2007**

³ N. Bez, J. Rivoirard, *Fisheries Research*, **2001**, 50, 41-58

ESTROGEN INDUCED DIFFERENTIAL EXPRESSION OF GENES IN HUMAN UTERINE SMOOTH MUSCLE CELLS – A GLOBAL ANALYSIS.

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Objective: The two steroid hormones – progesterone and estrogen, regulate myometrial growth and contractility. During pregnancy, progesterone maintains myometrial quiescence while estrogen induces its contractility. Hence, in most mammalian species, parturition is associated with a decrease in the circulating progesterone levels and an increase in estrogen, which leads to the transformation of myometrium from a dormant stage to the contractile stage¹. However, the circulating human estrogen levels increases during mid gestation and ascends gradually until birth². Therefore, estrogen activation during labor is believed to be occurring more at the functional level with an increase in the myometrial responsiveness to estrogen. The molecular mechanism by which this is achieved is still vague. In the present study we identify differentially expressed genes in human uterine smooth muscle cells (hUtSMC) treated with 17-beta Estradiol (E2) compared to untreated cells.

Materials and Methods: hUTSMC (Lonza) were grown in complete Dulbecco’s modified essential medium (DMEM) and the medium was changed to phenol red free DMEM supplemented with 2% charcoal stripped serum (Biosera), treated with 10nM of E2 (Sigma Aldrich) and harvested after 24hrs and 72hrs (n=3) along with the corresponding controls. Total RNA was isolated, amplified, labeled and hybridized in OpArray human microarray chips (Operon). The image was analyzed using GenePix Pro 6.0 (Molecular Devices) and Genespring7.0 (Agilent Technologies). After data normalization, genes showing significant up or down regulation (two fold) across the desired conditions were identified and validated using real-time fluorescence RT-PCR.

Results: After 24hrs E2 treatment, 108 genes were identified and analyzed, of which 56 genes were up regulated and 52 down regulated. After 72 hrs E2 treatment 121 genes (82 – up and 39 - down) were identified, of which 12 genes (6 - up and 6 - down) were corroborated using real-time fluorescence RT-PCR.

Conclusion: Significant numbers of genes were differentially expressed with the E2 treatment and many of them have been previously linked to known estrogen pathways. Further analysis needs to be performed to help us understand the link between these genes and to the molecular mechanism of estrogen activation at labour.

References

1. Challis *et al.* The physiology of reproduction. New York: Raven Press: 1994. p. 985 – 1031
2. Tulchinsky *et al.* Am J Obstet Gynecol 1972;112:1095-100.

REDUCED REDUNDANCY IN DE NOVO PREDICTION OF TRANSCRIPTION FACTOR BINDING MOTIFS THROUGH MULTIPLE MOTIF ALIGNMENT

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Many algorithms exist which can predict binding motifs for sequence specific transcription factors. These algorithms typically model binding motifs as a matrix of probabilistic base frequencies known as a Position Specific Scoring Matrix (PSSM) or a Position Weight Matrix (PWM). A fundamental problem with many of these *in silico* motif predictors lies in the redundant nature of their predictions, with several predicted motifs essentially representing the same underlying biological signal or binding site. In order to address this problem, we have developed a Genetic Algorithm (GA) which performs a weighted multiple alignment of Position Weight Matrices resulting in a single representative motif for the redundant group.

We represent the alignment problem as finding the optimum offset (position relative to other motifs in the alignment) and orientation (forward or reverse) for a set of PWMs, with the goal of minimizing the total pairwise column-by-column sum squared distance between the matrices. In the GA model, each individual in the population represents a complete multiple alignment allowing for the simultaneous evaluation of many candidate alignments. The best alignments from each generation are subjected to selection, recombination and mutation, allowing the GA to iteratively improve on the initial alignments.

Recently, we have also applied this technique to the creation of Familial Binding Profiles (FBPs). Familial Binding Profiles represent the average binding specificity of a group of structurally related transcription factors. Aligning these known motifs allows us to provide a useful bias for *ab initio* motif finders – for example, in searching for binding sites for transcription factors of a given structural class. FBPs also allow us to make inferences about the evolution of particular binding sites and can be used in the classification of novel proteins.

Science Related Research

College of Arts, Social Sciences and Celtic Studies

College of Engineering and Informatics

**College of Medicine, Nursing Studies and Health
Sciences**

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THE COCYCLIC HADAMARD MATRICES OF ORDER 36

Author: Pádraig Ó Catháin

Abstract

The theory of cocyclic development was developed in the early 1990s to provide an algebraic framework within which combinatorial problems could be explored. The theory draws on ideas from group cohomology, abstract algebra and computational group theory. One area in which it has been profitably employed is in the theory of Hadamard matrices. These matrices are widely used in science and engineering, having applications in areas as diverse as communications, and spectroscopy.

In this poster, we will outline details of our search for the cocyclic Hadamard matrices of order 36. This problem was first addressed by Noburo Ito in the early 1990s; we complete his classification. Our method uses a result of de Launey on the equivalence of CHMs and 2 -($4t, 2, 4t, 2t$) Relative Difference Sets. We search for all such RDSs and use these to construct the relevant Hadamard matrices. The results obtained are new, and are currently being written up for publication.

AUTOMATED RIB AND VERTEBRA SEGMENTATION IN 3D THORACIC CT IMAGES

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In this paper we present an automated method to accurately segment the ribs and vertebra across 3D thoracic CT scans. Rib and vertebra structures are very useful landmarks in that they accurately delineate the lung outer wall and can be used to initialise adaptive curve models or constrain region growth leakage. Many medical imaging segmentation algorithms are limited in application due to anatomical variance across patient datasets. In the case of pathology, anatomical variation is increased, thus complicating the ability of an algorithm to initialise or perform. Segmentation techniques which incorporate ground truths offer increased robustness to variability and can often decrease the number of steps required for processing. Automated approaches to landmark identification are preferred, as they reduce operator intervention and allow greater focus on achieving segmentation accuracy.

HOMOGENOUS DRUG LOADING OF MESOPOROUS SILICA MCM-41 AND REPRODUCIBLE RELEASE OF ACTIVE DRUG: IBUPROFEN AS A CASE STUDY

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INTRODUCTION

Novel drug delivery systems (DDS) to improve the pharmacokinetic profile of hydrophobic drugs following oral administration is an area of keen interest in drug research. Vallet-Regí et al. (2001)¹ first reported the potential of mesoporous silica MCM-41 (MCM-41) as a candidate for drug delivery using ibuprofen as the model drug. High variation in the degree of drug loading (11-41 % wt/wt) reported^{1,2,3,4,5}, points to a need to develop a procedure that will yield a reproducible degree of drug loading, such that a reliable therapeutic dose of ibuprofen can be administered within the MCM-41 matrix. This study aims to investigate the effect of drug to carrier ratio on the degree of drug loading and to examine ibuprofen drug activity after release from MCM-41.

EXPERIMENTAL METHODS

Ibuprofen-loaded MCM-41 (Ibu-MCM) was prepared according to the method of Vallet-Regí et al. (2001)¹, ibuprofen to MCM-41 (wt/wt) ratios were 1:1, 0.6:1, 0.4:1 and 0.3:1. The amount of ibuprofen loaded in the MCM-41 material was quantified using HPLC analysis. Ibu-MCM samples were analysed using Shimadzu FTIR-8300 and Siemens Diffraktometer. *In vitro* release studies of Ibu-MCM (0.3:1 ratio) were performed in phosphate buffered saline (PBS) pH 7.4 at 37°C. Drug activity of ibuprofen released from Ibu-MCM was investigated using the COX inhibition assay (Caymen Chemicals).

RESULTS AND DISCUSSION

The reproducibility of ibuprofen loading into MCM-41 is dependent on the ratio of drug to carrier. FTIR and XRD analysis confirms pore loading of ibuprofen as opposed to surface adsorption. *In vitro* release of ibuprofen from MCM-41 achieves approx 90 per cent release within 2 hours. Drug activity of ibuprofen released from MCM-41 investigated using COX-1 inhibition indicated that the activity is similar to that of ibuprofen standard. The results of this study corroborate reports in the literature investigating MCM-41 as a DDS for ibuprofen.^{1,2} In addition, our data suggest the interaction between drug and carrier does not adversely affect the inhibitory activity of ibuprofen on COX-1. This finding requires further investigation of COX-2 inhibition.

REFERENCES

1. Vallet-Regí et al. *Chem. Mater.* **2001**, 13, 308-11
2. Horcajada et al. *Micro. Meso. Mater.* **2004**, 68, 105-09
3. Andersson et al. *Chem. Mater.* **2004**, 16, 4160-67
4. Charnay et al. *EJPB* **2004** 57, 533-40
5. Heikkila et al. *Drug Delivery* **2007** 14, 337-47

ACTIVITY OF TIGECYCLINE AGAINST EXTENDED SPECTRUM B-LACTAMASE (ESBL) PRODUCING *ENTEROBACTERIACEAE*

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Background: Tigecycline is the first glycylglycine antibiotic approved for therapeutic use and has reported activity against Extended Spectrum Beta-Lactamase (ESBL) producing *E. coli* and *Klebsiella pneumoniae*¹. This study examines the activity of Tigecycline against 150 ESBL producing *Enterobacteriaceae* collected from 14 hospitals throughout Ireland.

Methods: ESBL production was confirmed in all isolates collected in accordance with Clinical Laboratory Standards Institute (CLSI) disk diffusion criteria using cefpodoxime (10µg) and cefpodoxime plus clavulanic acid or by ESBL Etest using ceftazidime/ceftazidime plus clavulanic acid (TZ/TZL); cefotaxime/cefotaxime plus clavulanic acid (CT/CTL); and cefepime/cefepime plus clavulanic acid (PM/PML) in accordance with the manufacturers' instructions. Isolates were screened for the presence of *bla*_{CTX-M}, *bla*_{TEM} and *bla*_{SHV} by PCR using specific primers and protocols as previously described^{2,3}. The MIC of Tigecycline was determined for each isolate by Etest in accordance with the manufacturer's instructions.

Results: The *bla*_{CTX-M Group1} gene was detected in 60 isolates, *bla*_{CTX-M Group9} in 79 isolates, *bla*_{TEM} in 122 isolates, and *bla*_{SHV} in 25 isolates. Seven isolates possessed a *bla*_{CTX-M}, *bla*_{TEM} and *bla*_{SHV} variant. Tigecycline MICs between 0.25 and 6µg/ml were recorded for the 150 isolates, with 147 (98%) isolates susceptible, 3 (2%) intermediate and 0 resistant.

Conclusion: Tigecycline was active against 98% of diverse group of ESBL producing *Enterobacteriaceae* from a number of hospitals throughout Ireland and may be a useful agent for the treatment of infection with these generally multidrug resistant organisms. Activity was consistent regardless of the particular enzyme present.

References:

1. Townsend, M.L., Pound, M.W., and Drew, R.H. 2006. Tigecycline: a new glycylglycine antimicrobial. International Journal of Clinical Practitioners. 60(12): p1662-1672
2. Woodford, N., Fagan, E.J., Ellington, M.J. 2005. Multiplex PCR for rapid detection of genes encoding CTX-M extended spectrum β-lactamases. Journal of Antimicrobial Chemotherapy. p154-155.
3. Essack, S.Y., Hall, M.C., Pillay, D.G., Mcfayden, M.L., and Livermore, D. 2001. Complexity and Diversity of *Klebsiella pneumoniae* Strains with extended spectrum β-lactamases isolated in 1994 and 1996 at a Teaching hospital in Durban, South Africa. Antimicrobial Agents Chemotherapy. 45(1): p88-95

AN EVALUATION OF PHENOTYPIC AND MOLECULAR METHODS FOR TYPING A COLLECTION OF *SALMONELLA ENTERICA* SEROVAR TYPHIMURIUM (HUNTER'S DISCRIMINATION INDEX)

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Background: The aim of this work was to compare methods for evaluating the degree of similarity between isolates of a collection of *S. Typhimurium* (17 collected in Kenya, 1 collected in Ireland). In order to determine the most discriminatory typing method of those applied, Hunter's generalised formula was used to calculate the discrimination index (DI)¹. The DI is based on the probability that two unrelated strains sampled from the test population will be placed into different groups. A DI value of 0.0 indicates that the technique applied offers no discrimination. A DI value of 1.0 indicates that the technique applied is completely discriminatory.

Methods: Relatedness of isolates was determined by antimicrobial susceptibility testing (AST)²; pulsed field gel electrophoresis (PFGE)³ and variable number tandem repeat (VNTR) analysis⁴. Susceptibility to a panel of 21 antimicrobial agents was performed in accordance with Clinical Laboratory Standards Institute disk diffusion methods. PFGE using *XbaI* and *BlnI* and VNTR were performed in accordance with previously described protocols. Hunter's generalized formula was used to calculate the DI for all methods.

Results: AST, *XbaI* PFGE, *BlnI* PFGE and VNTR analysis identified 5, 14, 8 and 13 profiles respectively. A DI value of 0.641 was calculated for AST, 0.974 for *XbaI* PFGE, 0.752 for *BlnI* PFGE and 0.967 for VNTR. AST was the least discriminatory and *XbaI* PFGE was the most discriminatory of the methods applied.

Conclusions: PFGE using *XbaI* gave the highest level of discrimination for this collection of *S. Typhimurium*. This contrasts with our experience of the relative discriminatory power of VNTR and *XbaI* PFGE for discrimination between isolates of *S. Typhimurium* DT104 and related phage types which are highly clonal.

References:

1. Hunter, P. R. and M. A. Gaston (1988). "Numerical index of the discriminatory ability of typing systems: an application of Simpson's index of diversity." Journal of Clinical Microbiology. 26(11): 2465-2466.
2. CLSI Performance Standards for Antimicrobial Susceptibility Testing; Seventeenth International Supplement. CLSI Document M100-S17 Vol 27 No.1 (ISBN 1-56238-625-5).
3. Lindstedt, B.-A., T. Vardund, et al. (2004). "Multiple-locus variable-number tandem-repeats analysis of *Salmonella enterica* subsp. *enterica* serovar Typhimurium using PCR multiplexing and multicolor capillary electrophoresis." Journal of Microbiological Methods 59(2): 163-172.
4. Swaminathan, B., T. Barrett, et al. (2001). "PulseNet: the molecular subtyping network for foodborne bacterial disease surveillance, United States." Emerging Infectious Disease. 2001 May-Jun;7(3):382-9.

OCCURRENCE OF ANTIMICROBIAL RESIDUES AND ANTIMICROBIAL RESISTANT ORGANISMS IN WATERS AND EFFLUENT FROM A NUMBER OF SITES.

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Background: The impact of the environment on the emergence and dissemination of antimicrobial resistance is of increasing concern. This study assesses the presence of antimicrobial residues and antimicrobial resistant bacteria in waters and effluent from a number of sites.

Methods: Between April 2006 and June 2007, 189 samples from various sources (hospital effluent (HE), city sewage, rural group water supplies, sea water, outflow from a secondary wastewater treatment plant, city surface water, rivers and lakes) were collected. All samples were tested for E.coli and Enterococci by quantitative culture in the presence and absence of cefotaxime (CTX), ciprofloxacin (CIP), cefoxitin (FOX), ampicillin (A), streptomycin (S), tetracycline (T), sulphonamides (Su) and vancomycin (V) as appropriate. Samples were examined for aminoglycoside, tetracycline, quinolone, penicillin and macrolide residues by bioassay (the five plate method).

Results: Hospital effluent contained higher proportions of antimicrobial resistant organisms compared with other samples (e.g. average proportion of quinolone resistant E. coli in HE ~ 8% compared with ~ 0.5% for other samples). City sewage downstream of the hospital discharge showed a higher proportion of antimicrobial-resistant E. coli (e.g. CIP 45% v 0.3%) compared with upstream. Resistant E. coli are not completely removed by secondary wastewater treatment. E. coli resistant to A, S, T, and Su were observed in rural samples, with additional resistances to FOX, CIP, and CTX predominantly observed in urban samples. Antimicrobial residues (particularly quinolones) were present at biologically significant levels only in HE and in city sewage following discharge of HE.

Conclusions: Hospital effluent may contribute antimicrobial-resistant bacteria and antimicrobial residues to the environment. The implications of these findings for the emergence and spread of antimicrobial resistance merit further investigation.

ELEVATED SERUM LEVELS OF INTERLEUKIN-17 IN *HELICOBACTER PYLORI* INFECTION AND INFLAMMATION

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Background & Aims: Interleukin-17 (IL-17) is a pro-inflammatory cytokine produced by activated T-cells which is strongly associated with the development of tissue inflammation.¹ Infection with the gastroduodenal pathogen *Helicobacter pylori* (Hp) induces an inflammatory mucosal response characterized by infiltration of multiple cell types.² The aim of this study was to determine serum levels of IL-17 in patients with dyspepsia attending for diagnostic upper endoscopy to assess whether this cytokine was associated with gastric inflammation.³ **Methods:** This prospective study included 62 patients [28 (45%) female; 34 (55%) male; mean age: 46 years] attending an open-access endoscopy unit for oesophago-gastro-duodenoscopy. Patients receiving antibiotics, NSAIDs, or immunosuppressants, or with alcohol abuse, previous gastric surgery, other chronic inflammatory diseases and co-morbidities were excluded from the study. Voluntary written consent was obtained from each participant, confidentiality maintained, and institutional ethical guidelines maintained. Clinical data including age, background history, medication history, symptom record with alarm score, smoking history, brief physical examination and endoscopy results were recorded. As a part of the endoscopy procedure, an antral biopsy was subjected to the CLO test to establish Hp infection status, which was confirmed in histological examination of a second biopsy. Peripheral blood was collected before the endoscopy procedure. Serum was prepared and stored at -70 degrees centigrade before subsequent analysis of IL 17 by a quantitative sandwich enzyme-linked immunosorbent assay (R & D systems, MN. USA). The lower detection level of IL-17 was 8 pg/ml. **Results:** In healthy subjects without gastritis, IL-17 was not detectable in serum. In the Hp-positive group (n=19), 47.3% (n=9) of patients had significantly (P = 0.005, Pearson χ^2) elevated levels of serum IL 17 compared to 13.9% (n=6) in the *H. pylori* negative group (n=43), with an odds ratio of 5.55. All patients with increased levels of serum IL 17, irrespective of Hp status (n=15), had endoscopically and histologically proven inflammation. In this cohort 24% (n=15) subjects were smokers and out of these 20% (n=3) had elevated serum IL 17.

Conclusions: Production of IL-17 that is detectable in serum is strongly associated with inflammation in the gastroduodenal compartment. There is a significant likelihood of Hp-positive patients having elevated levels of IL 17 in serum.

References

¹T. A. Wynn, *Nat. Immunol.* **2005**, *6*, 1069-1070.

²R. Caruso, F. Pallone, G. Monteleone, *World J. Gastroenterol.* **2007**, *13*(42), 5547-5551.

³J. O'Keefe, A. P. Moran, *Helicobacter* **2008**, *13* (1), 1-19.

ULTRASENSITIVE MULTIPLEXED DETECTION OF CANCER BIOMARKERS USING MICROFLUIDIC DEVICE

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Development of point-of-care protein arrays to measure multiple protein cancer biomarkers in clinical samples holds great promise for reliable early cancer detection and could achieve effective cancer prevention for millions. In this study, a microfluidic device was designed and tested by detecting H₂O₂ based on horseradish peroxidase (HRP) enzyme bioelectrocatalysis. This prototype consists of a single microfluidic channel made from poly(dimethylsiloxane) coupled to an injector and incorporating a sensing electrode, Ag/AgCl reference electrode and Pt counter electrode. The sensing electrode utilizes a gold wire (500 μm) coated with 5 nm glutathione-decorated gold nanoparticles (AuNPs) to which HRP was covalently linked using EDC protocols. Direct electrochemistry of HRP enzyme was used to detect the H₂O₂ at high sensitivity with a detection limit of 5 nM. Current microfluidic immunosensor prototype employs two strategies, a carbon array electrode which were coated with multiple primary antibodies (Ab1) in a microfluidic channel and a magnetic bead bioconjugate featuring multiple enzyme labels (HRP), multiple detecting antibodies with acquired prostate cancer biomarkers which include prostate specific antigen (PSA), prostate-specific membrane antigen (PSMA), platelet factor 4 (PF4), and interleukin 6 (IL-6). The magnetic bead bioconjugate can then be injected into channel and could be captured by corresponding primary antibodies (Ab1) on the array electrode to form the sandwich immunoassay. H₂O₂ was pumped to the channel, at applied potential, HRP labels reduced H₂O₂ to provide electrical signals, which is proportional to the concentration of biomarkers. This microfluidic immunoassay array required less sample volumes and gave superior mass sensitivity to commercial assays for detection biomarkers, such as classical enzyme-linked immunosorbent assay (ELISA).