International Infection, Immunity and Inflammation Conference (I4C)

In celebration of Dr. Bob Hancock's 70th Birthday and Research Career

May 14th & 15th 2019

Life Sciences Centre, University of British Colombia
Vancouver, BC Canada

Hancock Lab

THE UNIVERSITY OF BRITISH COLUMBIA

Welcome

Welcome from the organizing committee

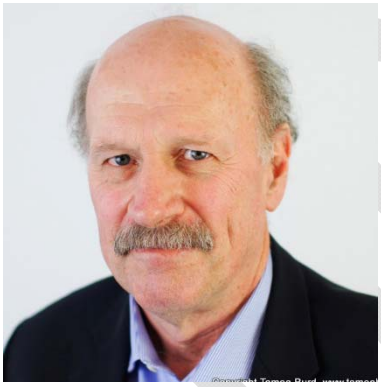
It is with great honour and privilege to welcome you to the first annual **International Infection, Immunity and Inflammation Conference (I4C)** at the University of British Columbia in Vancouver, Canada. We are pleased to bring together a diverse group of researchers, academics, and industry leaders to share with you the latest in the fields of *Pseudomonas*, Systems Biology, Peptides, New Therapeutic Discoveries and Innate Immunity.

We hope you will take this excellent opportunity to network, learn, and exchange ideas about the field with colleagues in the field from all over the world.

Organizing Committee,

Dawn Bowdish, McMaster University
Bob Hancock, University of British Columbia
Evan Haney, University of British Columbia
Neeloffer Mookherjee, University of Manitoba
Joerg Overhage, Carleton University

Welcome from R.E.W. “Bob” Hancock



The I4C is being held to celebrate the 70th birthday and 40-year research career of Bob Hancock at UBC. During his time at UBC he has made numerous break-throughs in the field of cationic host defence (antimicrobial) peptides and finding alternate treatments to antibiotic resistance.

Hancock is “considered a world leader in his field” and over his career he has published more than 720 papers and reviews, has 65 patents awarded, and is an ISI highly cited author in Microbiology with more than 72,000 citations and an h-index of 153. He has won several awards and is an Officer of the Order of Canada. He is a co-founder of Migenix, Inimex Pharmaceuticals, ABT Innovations, Sepset Biotherapeutics, and the Centre for Drug Research and Development.

Currently Hancock and his lab’s research interests include small cationic peptides as novel antimicrobials, broad-spectrum anti-biofilm agents, and modulators of innate immunity, the development of novel treatments for antibiotic resistant infections and inflammation, the systems biology of innate immunity, inflammatory diseases and *Pseudomonas aeruginosa*, and antibiotic uptake and resistance.

Support:

The organizing committee gratefully acknowledges the support of the following:

The University of British Columbia

Please note there is no food or drink in the lecture theatre.

Internet Access
Wifi Wireless internet is available by connecting to the ubcvisitor network, for free light browsing, no login required. If you are from another education institution that uses eduroam you can also access that network at UBC.

- Select the "ubcvisitor" wireless network on your wireless device.
- Open up a web browser, and you will be directed to the login page.

University of British Columbia (UBC)

Located on the traditional unceded territory of the Musqueam people, UBC's Vancouver campus is set at the edge of a peninsula overlooking the Strait of Georgia and the Salish Sea. The city of Vancouver is a short distance away and provides a sparkling backdrop for a university continually shaping its place as a world leader in research and teaching. From breathtaking ocean views to snow dusted mountaintops, world-renowned gardens and entertainment, the campus promises to welcome alumni and visitors at every step. We hope you left time in your travel schedule to explore UBC. Here are some interesting things to see on campus:

Museums and Galleries

Beaty Biodiversity Museum www.beatymuseum.ubc.ca

Irving K. Barber Learning Centre ikblc.ubc.ca

Morris and Helen Belkin Art Gallery www.belkin.ubc.ca

Museum of Anthropology www.moa.ubc.ca

Pacific Museum of the Earth pme.ubc.ca

Gardens

Nitobe Memorial Garden www.botanicalgarden.ubc.ca/nitobe

UBC Botanical Garden www.botanicalgarden.ubc.ca

UBC Welcome Centre

The UBC Welcome Centre is located in the Robert H. Lee Alumni Centre and is the perfect place to start your journey on the Vancouver campus. Their knowledgeable staff can answer your questions, provide maps and directions and let you know what events are happening during your visit. Located at 6163 University Blvd, or call: 604-822-3313

8:00 a.m. – 6:00 p.m. Monday to Friday

8:00 a.m. – 4:00 p.m. Saturday

10:00 a.m. – 4:00 p.m. Sunday

PROGRAM

Day 1: Tuesday May 14th 2019

Registration

08:00-08:30	Registration: Outside LSC 1

Symposium Opening

08:30-08:40	Welcome, instruction and general information **Dawn Bowdish** *On behalf of the organizing committee*
08:40-08:55	Symposium Introduction **Bob Hancock** Professor, University of British Columbia

Session One: *Pseudomonas*

Chair: Joerg Overhage

08:55-09:15	**Karl-Erich Jaeger** *University of Düsseldorf and Forschungszentrum Jülich*
09:15-09:30	Let's stick together – adaptation of *P. aeruginosa* to reactive chlorine stress **Joerg Overhage** *Carleton University*
09:30-09:45	A multi-host approach to identifying the origin of host association in *Pseudomonas* **Cara Haney,** *University of British Columbia*
09:45-10:05	**Fiona Brinkman** *Simon Fraser University*
10:05-10:25	Aminoglycoside-promoted changes to lipopolysaccharide in *Pseudomonas aeruginosa*: involvement of the MexXY multidrug efflux system **Keith Poole** *Queen's University*

10:25-10:45	Conversion of the pyrophosphate-specific OprO- into phosphate-specific OprP- porin of *Pseudomonas aeruginosa* by exchanging key amino acids at the channel constrictions **Roland Benz** *Jacobs University Bremen*
10:45-11:00	Discovery and Development of New Mechanism Novel Antimicrobials Enabled by the Discuva Platform **Elena Breidenstein** *Summit Therapeutics*
11:00-11:10	**Trainee talk**

11:10-11:30	Coffee Break

Session Two: Peptides

Chair: Evan Haney

11:30-11:55	Regulating Host Defence Against Infection: the Cathelicidin Fire Alarm **Donald J Davidson** *University of Edinburgh*
11:55-12:10	Exploring the Chemical Space of Multifaceted Host Defence Peptides **Evan Haney** *University of British Columbia*
12:10-12:30	 **Havard Jenssen** *Roskilde University*
12:30-13:30	**Lunch**
13:30-13:55	Synthetic antibacterial and antibiofilm peptides to combat infections and tumours **Peter Nibbering** *Leiden University Medical Center*
13:55-14:15	Strategies to mitigate antimicrobial peptide toxicity **Suzana K Straus** *University of British Columbia*
14:15-14:35	 **Cesar de La Fuente-Nunez** *Massachusetts Institute of Technology*
14:35-14:45	**Trainee talk**

14:45-15:15	Coffee Break

Session Three: Innate Immunity

Chair: Dawn Bowdish

15:15-15:50	**Stephen Stick** *Telethon Kids Centre for Respiratory Research*
15:50-16:10	**Dawn Bowdish** *McMaster University*
16:10-16:30	New strategies for prevention and treatment of *Pseudomonas aeruginosa* infections **Bernd H. A. Rehm** *Griffith University*
16:30-16:50	Utilising differentiated wild type and knockout human stem cells to investigate mechanisms of innate immunity in macrophages **Christine Hale** *Wellcome Sanger Institute*
16:50-17:10	Transgenerational immune protection in the pacific oyster *Crassostrea gigas* **Celine Cosseau** *Host Pathogen Environment interaction Laboratory*
17:10-17:30	Childhood vasculitis syndromes microscopic polyangiitis (MPA) and granulomatosis with polyangiitis (GPA) have different etiologies as indicated by integrating blood transcriptomic and clinical metadata **Kelly Brown** *University of British Columbia*

Day 2: Wednesday May 15th 2019

08:30-9:00	Coffee

Session Four: Systems Biology

Chair: Amy Lee

09:00-09:25	Studying emerging diseases through genomics and stem cells; Antibiotic resistant typhoid as an exemplar **Gordon Dougan** *University of Cambridge and Wellcome Sanger Institute*

09:25-09:45	Transcriptional Profiling of Stem Cell-Derived Macrophages Provide Functional Insights to Genome-wide Association Studies **Amy Lee** *University of British Columbia*
09:45-10:05	 **Andrew Currie** *Murdoch University*
10:05-10:25	The influence of microbiota in early-life on optimal vaccine responses **David Lynn** *South Australian Health & Medical Research Institute*
10:25-10:45	Towards Immersive Network-based Visual Analytics for Systems Biology **Jeff Xia** *McGill University*
10:45-11:05	Characterizing the molecular determinants underlying severe Ebola virus disease and post-recovery persistence: science under negative pressure **Jason Kindrachuk** *University of Manitoba*
11:05-11:15	**Trainee talk**

11:15-12:15	Lunch

Session Five: New Therapeutic Discoveries

Chair: Neeloffer Mookherjee

12:1512:40	Oral Blis- *Streptococcus salivarius* probiotics to promote a healthy oral microbiota **John Hale** *Blis Technologies*
12:40-13:00	 **Neeloffer Mookherjee** *University of Manitoba*
13:00-13:20	Small molecules that repress exopolysaccharide expression have antibiofilm and antivirulence activities against *Pseudomonas aeruginosa.* **Shawn Lewenza** *Athabasca University*
13:20-13:40	 **Melissa Brown** *Flinders University*

13:40-14:00	Bacterial chemotaxis and changing paradigms. **Victoria Korolik** *Griffith University*
14:00-14:20	Signaling heterogeneity in the conserved PhoPQ-PmrD-PmrAB regulatory cascade governing host-defence peptide resistance in *Escherichia coli* **Joe McPhee** *Ryerson University*
14:20-14:30	**Trainee talk**

14:30-17:00	Poster Session **Bob Hancock** *University British Columbia*

Abstracts

Day 1 | **Session one** | ***Pseudomonas***

Karl-Erich Jaeger

University of Düsseldorf
Forschungszentrum Jülich
Germany

Joerg Overhage

Carleton University
Ottawa, Canada

Let's stick together – adaptation of *P. aeruginosa* to reactive chlorine stress

Bacteria are able to survive under a variety of often harmful environmental conditions such as heat or cold, nutrient limitation or antimicrobial treatment due to a multitude of adaptation processes and stress responses. One important adaptation and survival strategy exhibited by a wide range of bacteria is the formation of biofilms. Biofilms are communities of microorganisms attached to a surface and embedded in a self-produced, polymeric matrix. Biofilm bacteria have been shown to possess unique characteristics including increased stress resistance and higher antimicrobial tolerance leading to failures in bacterial eradication in many technical and clinical settings including drinking water industries and hospitals.

Here, we investigated the adaptation of *P. aeruginosa* to reactive chlorine species including hypochlorite (HClO), a phagocyte-derived host defense compound and frequently used disinfectant (household bleach). We identified that reactive chlorine species strongly stimulated *P. aeruginosa* stress responses and increased biofilm formation at sublethal concentrations. This enhanced formation of biofilms was very specific to reactive chlorine species such as hypochlorite and chloramine, but did not occur in response to other tested oxidants likes hydrogen peroxide [H_2O_2] or the herbicide paraquat. Subsequent gene expression profiling, LC-MS analyses and mutant studies revealed a key role of the intracellular second messenger cyclic-di-GMP in HClO-induced biofilm development.

Day 1	Session one	*Pseudomonas*

Cara Haney

Michael Smith Laboratories
University of British Columbia
Vancouver, Canada

A multi-host approach to identifying the origin of host association in *Pseudomonas*

Members of the genus *Pseudomonas* are commensals and pathogens across diverse hosts including plants and animals. Plant and animal innate immune systems show functional conservation at a molecular level, and there are common virulence factors required for *Pseudomonas* to infect diverse hosts. Using comparative genomics and forward genetics, we identified genes involved in LPS modification and polyamine metabolism that predict host association and are required to evade plant and animal immunity. By using an accessible and high-throughput model of the plant root ("rhizosphere") microbiome coupled with validation in an opportunistic infection (mouse abscess) model, our goal is to identify conserved mechanisms by which commensals and pathogens can persist in association with a host.

Day 1 | **Session one** | ***Pseudomonas***

Fiona Brinkman

Simon Fraser University
Burnaby, Canada

Day 1 | **Session one** | ***Pseudomonas***

Keith Poole

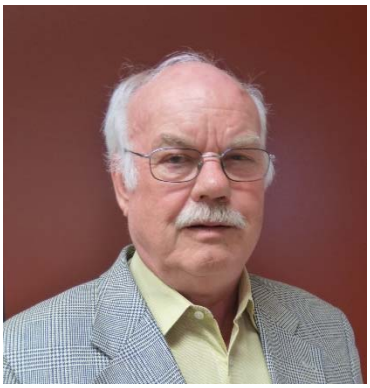
Queen's University
Kingston, Canada

Aminoglycoside-promoted changes to lipopolysaccharide in *Pseudomonas aeruginosa:* involvement of the MexXY multidrug efflux system

Keith Poole1, Kevin Rome1, Courtney E. Chandler2, Christie Gilmour1 and Robert K. Ernst2
1Department of Biomedical and Molecular Sciences, Queen's University, Kingston, ON, Canada
2 Department of Microbial Pathogenesis, University of Maryland, Baltimore, MD, USA

The Mg^{2+} antagonism of aminoglycoside activity in wild type (WT) *Pseudomonas aeruginosa* is dependent on the presence of the aminoglycoside (AG) resistance-promoting MexXY multidrug efflux system (Antimicrob Agents Chemother **45**:2001), and MexXY expression has been linked to changes in lipopolysaccharide (LPS) and susceptibility to the LPS-targetting polymyxin antimicrobials (Antimicrob Agents Chemother **59**:7276), indications that this efflux system has functional links to LPS. In agreement with this, treatment of *P. aeruginosa* with the *mexXY*-inducing AG, paromomycin (PAR), and the related antimicrobial, spectinomycin (SPC), yielded an increase in lipid A fatty acylation and increased hydroxylation of the fatty acids, and this was absent or markedly reduced in a MexXY- mutant strain. These results were consistent with an AG-promoted, MexXY-dependent decrease in activity of the PagL lipid A deacylase and increase in one or both of the LpxO1/LpxO2 lipid A hydroxylases. In support of this, PAR and SPC promoted a decrease in expression of the *pagL* gene and an increase in expression of the *lpxO1* gene in WT *P. aeruginosa* that was largely lost in the MexXY- mutant. These AG-promoted changes in gene expression were independent of the PhoPQ two-component system (TCS) that is known to regulate *pagL* expression in *P. aeruginosa.* The AG-promoted increase in *lpxO1* expression was, however, lost in a *pmrA* mutant, an indication that the PmrAB TCS mediated this effect. Given the importance of LPS for AG binding and entry into *P. aeruginosa* cells, MexXY-driven changes to this macromolecule may contribute to AG resistance, and the reduced AG accumulation typically associated with MexXY operation may, thus, reflect reduced binding and uptake vs. efflux-mediated exclusion.

Day 1 | **Session one** | ***Pseudomonas***



Roland Benz

Jacobs University
Bremen, Germany

Conversion of the pyrophosphate-specific OprO- into phosphate-specific OprP- porin of *Pseudomonas aeruginosa* by exchanging key amino acids at the channel constrictions

Roland Benz, Sonalli Ganguly, Anusha Kesireddy, Ulrich Kleinekathöfer

Pseudomonas aeruginosa is a major opportunistic pathogen that represents a considerable cause of nosocomial infections in humans. Its outer membrane has very low permeability for antibiotics caused by the presence of many specific porins. Among them are OprP and OprO that represent phosphate specific channels expressed in *P. aeruginosa* under phosphate starvation conditions. The crystal structures of both outer membrane channels show trimeric arrangements, where each monomer consists of 16 antiparallel β-strands connected by long extracellular loops and short periplasmic turns. Phosphate specific OprP and pyrophosphate specific OprO, show despite large homology, structural differences in their binding sites situated in the pore constriction region. Previously, it was shown that the mutation of amino acids in Y62F and Y114D of OprP, led to an exchange in substrate specificity similar to OprO. In order to support the role of these key amino acids in the substrate sorting of these specific channels, we created the reverse mutants for OprO (F62Y, D114Y and F62Y/D114Y) in this study. We studied the phosphate and diphosphate binding of the mutated channels in planar lipid bilayers. The experimental findings together with molecular dynamics simulations support the view that just a few strategically positioned amino acids are mainly responsible for the substrate specificity of OprP and OprO. The mutation of these amino acids in the channels allows interchanging their properties.

Day 1 | **Session one** | ***Pseudomonas***

Elena Breidenstein

Summit Therapeutics
Cambridge, UK

Discovery and Development of New Mechanism Novel Antimicrobials Enabled by the Discuva Platform

INTRODUCTION:

Increasing antimicrobial resistance among Gram-negative bacteria combined with the current antibiotic innovation gap highlights the need for novel antimicrobial agents. We have developed a tightly integrated set of proprietary technologies which, following phenotypic screening, reveal the molecular targets and resistance liabilities associated with antimicrobial compounds.

APPROACH AND RESULTS:

High density (typically every 7-15 bp) transposon mutant libraries are generated in key pathogenic bacterial strains. The engineered transposons can influence gene regulation across the entire genome (upregulation, disruption and down regulation) depending on the context of the insertion site. Next Generation Sequencing processing and analysis of surviving transposon mutants following exposure to antimicrobial compounds reveals the range of molecular mechanisms that the target pathogen can utilize to survive in the presence of the compound: key target signals and resistance drivers included. The Discuva Platform has been validated with established, marketed and clinical phase antibiotics. To exemplify the depth of the Discuva Platform, we present data generated on known antibiotics (such as fosfomycin) against *Pseudomonas aeruginosa* and *Escherichia. coli*. The analysis clearly reveals engagement with *murA* (cell wall synthesis target of fosfomycin) and a number of additional potential drivers of resistance including *ptsI, cyaA, uhpT/A/C, phnG-P* for *E. coli* and *glpT, glpR* and hypothetical protein with phosphohydrolase function for P. aeruginosa. More importantly we are using the Discuva Platform in our internal novel antibiotic research and development activities including in our programs targeting *Neisseria gonorrhoeae* and ESKAPE pathogens.

CONCLUSIONS:

The Discuva Platform provides high quality data on the mode of action and resistance liabilities of antimicrobial compounds and also allows the accurate triaging from hit selection, through chemical optimization, and best clinical candidate nomination. The rapid cycle time of the process permits integration into medicinal chemistry design and SAR rationalization. We believe our Discuva Platform opens up the pool of available antibiotic starting points, increasing the chance of generating new mechanism novel antibiotic drugs.

Day 1	Session two	Peptides

Donald J. Davidson

University of Edinburgh Centre for Inflammation Research
Edinburgh, UK

Regulating Host Defence Against Infection: the Cathelicidin Fire Alarm

The threat of antibiotic-resistant pathogens has been declared a global emergency, requiring the urgent development of novel approaches for the treatment of infectious diseases. Strategies aimed at augmenting effective host defence, by harnessing critical components of innate immunity, have the potential to bypass common resistance mechanisms.

Antimicrobial Host Defence Peptides (HDP) are key, evolutionarily conserved components of the innate immune system. Mammalian HDP are widely expressed throughout the body, with key, non-redundant roles in protection against infectious threats. In addition to direct microbicidal potential, HDP have pleiotropic modulatory properties that impact upon the inflammatory response, adaptive immunity, and repair. However, the relative importance of these properties to host defence against infection *in vivo*, remains to be determined.

HDP of the cathelicidin family are highly expressed in neutrophil granules and are inducible in other immune effector cells. Regulation of human cathelicidin (hCAP-18/LL-37) has been implicated in a range of disease processes, while mice deficient in cathelicidin have increased susceptibility to infections in the lung, skin, gastrointestinal tract, urinary tract and eye. Cathelicidin has been shown to modify the balance of inflammatory processes; both dampening potentially harmful pro-inflammatory cytokine responses and inducing protective cellular inflammatory responses.

We demonstrate *in vivo* that i) exogenously-applied cathelicidin promotes pulmonary clearance of the multi-drug resistant pathogen *Pseudomonas aeruginosa* primarily by inflammomodulation, and that ii) induction of endogenous cathelicidin in the lung is essential for an effective host response, via promotion of protective pulmonary neutrophil responses. We also present a novel intracellular, NLRP3-dependent mechanism for cathelicidin-mediated promotion of protective airway epithelial cell responses to *P. aeruginosa* infection, resulting in altruistic cell death and enhanced neutrophil recruitment.

These modulatory properties of HDP have the potential to inform new alternative and/or complementary interventions for the treatment of antibiotic-resistant infections.

Day 1	Session two	Peptides

Evan Haney

Center for Microbial Diseases and Immunity Research, University of British Columbia
Vancouver, Canada

Exploring the Chemical Space of Multifaceted Host Defence Peptides

Host defence peptides (HDPs) are short polypeptide sequences found ubiquitously in nature that have garnered significant attention as alternatives to antibiotics. Originally appreciated for their direct antibacterial effect, HDPs are now known to exhibit a wide range of biological activities including antibiofilm and immunomodulatory functions. Curiously, HDPs with potent activity in one arena may possess weak activity in other areas suggesting that the various activities of HDPs exist on independent but overlapping activity landscapes. In principle, synthetic peptides could be optimized for specific biological purposes provided sufficient sequence information were available to predict the activity of novel peptides. Unfortunately, beyond the generic properties of HDPs (eg. positive charge and amphipathicity), our current understanding of the chemical space occupied by active HDPs is limited. Using various peptide screening and activity-guided design strategies, we have begun to explore the various activity landscapes of synthetic HDPs in an effort to understand the peptide sequence requirements that govern these diverse biological functions. Ultimately, an improved understanding of the chemical space and activity landscapes of HDPs will be necessary to fully realize their therapeutic potential.

Day 1	Session two	Peptides

Havard Jenssen

Roskilde University
Denmark

Day 1	Session two	Peptides

Peter Nibbering

Leiden University Medical Center
Leiden, Netherlands

Synthetic antibacterial and antibiofilm peptides to combat infections and tumours

The efficacy of antibiotics is increasingly jeopardized by the emergence of antimicrobial resistant (AMR) bacterial strains, biofilms and persister formation. Obviously, there is an urgent need for novel agents and strategies to combat infections caused by such bacteria. Antimicrobial peptides are considered the most promising candidates for the development of such novel agents. Indeed, treatment of therapy-resistant, chronic suppurative otitis media patients with ototopical drops containing the synthetic antibacterial and antibiofilm peptide (SAAP) P60.4Ac was successful in 47% of the cases versus 6% in the placebo group. Unfortunately, resistance to this peptide was seen in several strains of *Staphylococcus aureus*. Triggered by these findings we first designed and tested novel peptides with increased antibacterial and antibiofilm activities (as compared to P60.4Ac) that hardly or not induce resistance. The lead peptide SAAP-148 is highly effective against bacteria, biofilms and persisters in vitro and bacteria on ex vivo human skin and superficially wounded mice. Modifications of this SAAP were designed to further improve peptide's functional characteristics. Secondly, the genome of various animal species was mined for novel antimicrobial peptides, which were synthesized and tested. Several peptides from e.g. snakes were highly effective against (AMR) bacteria (including persisters) whether or not residing in biofilms without inducing resistance. Interestingly, some of these peptides showed selective cytotoxicity to an array of tumours. Moreover, a modified SAAP-148 peptide was highly effective in redirecting the tumour-tolerating immune response to an anti-tumour response. Together, synthetic antibacterial and antibiofilm antimicrobial peptides may become novel agents in the fight against infections and tumours.

Day 1	Session two	Peptides

Suzana K. Straus

University of British Columbia
Vancouver, British Columbia, Canada

Strategies to mitigate antimicrobial peptide toxicity

Antibiotic resistance is projected as one of the greatest threats to human health in the future and hence there is a great need to find alternatives. Antimicrobial peptides (AMPs) have shown great promise, because bacteria develop no or low resistance to AMPs. However, only few antimicrobial peptides are used as therapeutics, due to problems such as toxicity, short circulation half-life, and rapid kidney clearance.

This contribution describes a number of strategies to circumvent such challenges by: 1) formulating AMPs with pegylated phospholipid micelles; and 2) conjugating the peptides to polymers to alter residence time and biodistribution in the body, without significant loss in activity. In the first instance, results will demonstrate how pegylated micelle formulated peptides have potential as therapeutic agents for treating high-density infections in a murine cutaneous abscess model. For the second strategy, results of conjugation to the natural aurein 2.2 and more active derivatives to hyperbranched polyglycerol (HPG) will be presented. Hyperbranched polyglycerol (HPG) has gained attention due to its excellent biocompatibility, multifunctionality and plasma half-life, which can be tuned by changing its molecular weight. HPGs have been used as scaffolds for the development of long circulating drug conjugates, anticoagulant neutralizing agents, for cell surface modification, as an osmotic agent in peritoneal dialysis and organ preservation, making them an excellent candidate to conjugate AMPs. Finally, release strategies from HPG will also be discussed.

Day 1 | Session two | Peptides

Cesar de la Fuente-Nunez

Massachusetts Institute of Technology
Cambridge, United States

Structure-function-guided exploration of an antimicrobial peptide identifies activity determinants and generates synthetic therapeutic candidates.

Antimicrobial peptides (AMPs) constitute promising alternatives to classical antibiotics for the treatment of drug-resistant infections, which are a rapidly emerging global health challenge. However, our understanding of the structure-function relationships of AMPs is limited, and we are just beginning to rationally engineer peptides in order to develop them as therapeutics. Here, we leverage a physicochemical-guided peptide design strategy to identify specific functional hotspots in the wasp-derived AMP polybia-CP and turn this toxic peptide into a viable antimicrobial. Helical fraction, hydrophobicity, and hydrophobic moment are identified as key structural and physicochemical determinants of antimicrobial activity, utilized in combination with rational engineering to generate synthetic AMPs with therapeutic activity in a mouse model. We demonstrate that, by tuning these physicochemical parameters, it is possible to design nontoxic synthetic peptides with enhanced sub-micromolar antimicrobial potency in vitro and anti-infective activity in vivo. We present a physicochemical-guided rational design strategy to generate peptide antibiotics.

Day 1	Session three	Innate Immunity

Stephen Stick

Telethon Kids Centre for Respiratory Research
Nedlands, Australia

Day 1	Session two	Peptides

Dawn Bowdish

McMaster University
Hamilton, Canada

Age-associated inflammation, macrophage function and longevity.

As we age levels of cytokines in the circulation and tissue increase. Individuals with higher than average levels of 'age-associated inflammation' are more likely to develop chronic conditions, to become frail and die prematurely. In contrast, those with lower than age-average levels are more likely to lead active, independent and healthy lives. Even though age-associated inflammation is a predictor of poor health and premature mortality, it is not clear what causes it. Using aged (2 yr) conventional and germ-free mice, we have demonstrated that age-associated inflammation does not occur in the absence of a microbiome. Furthermore, age-related changes in the composition of the gut microbiota also contribut to age-associated inflammation as transferring the microbiome from old mice leads to higher levels of intestinal permeability and systemic inflammation than that of young mice. This systemic inflammation, and specifically increasing levels of tumour necrosis factor alpha (TNF) result alter myeloid cell development and ultimately monocyte and macrophage function, which contributes to the development of age-related conditions (e.g. frailty, sarcopenia, chronic conditions) and impairs host defence against infection. These mechanistic observations are consistent with the epidemiological data on longevity, which show that a 'microbiome-friendly' diet high in fibre and exercise (which is an effective way of reducing systemic inflammation), are the most effective strategies for living a long and healthy life.

Day 1 | Session two | Peptides

Bernd H.A. Rehm

Griffith University
Brisbane, Australia

New strategies for prevention and treatment of *Pseudomonas aeruginosa* infections

Pseudomonas aeruginosa is one of the leading causes of nosocomial infections and causes serious life-threatening infections due to intrinsic and acquired antibiotic resistances [1]. Immuno-compromised individuals are most at risk, such as those with severe burns and wounds, infected by human immunodeficiency virus (HIV) as well as CF patients. The formation of characteristic biofilms coincide with antibiotic resistance and persistent infections ie successful evasion of the immune system. There is an unmet demand for vaccines to prevent infections and for anti-bacterial compounds for the treatment of acute and chronic *P. aeruginosa* infections.

Vaccines provide a strategy for prevention of the disease caused by *P. aeruginosa* [2-3]. We have developed a new strategy to design and produce multivalent particulate vaccines for induction of protective immunity. Antigens (epitopes/domains of outer membrane proteins such e.g. OprF, OprI, OprL and AlgE) were engineered to constitute chimeric proteins which include a functional polyester synthase to synthesize and assemble antigen-coated biopolyester inclusions in recombinant *E. coli* and/or *P. aeruginosa.* Such biopolyester beads (200-500 nm) coated with antigens of interest were previously shown to induce protective immunity against a range of bacterial pathogens and HCV [4]. The knockout of competing polymer biosynthesis pathway in *P. aeruginosa* enhanced carbon flux toward production of the desired polyester inclusions. The immunological properties of antigen (protein and carbohydrate) coated biopolyester beads were investigated *in vivo* up to challenge studies assessing protective immunity in an acute pneumonia model.

Small molecule drugs derived from large libraries (Compounds Australia, NatureBank Australia) were screened against *P. aeruginosa* biofilms grown in microtiter plates by using high content imaging combined with live/dead and biofilm matrix staining. The persistent *in vivo* biofilm were mimicked by using strains engineered to produce biofilms reflecting various adaptations. Hits have been subjected to omics analyses in order to identify new targets. Phenotypic characterisation (biofilm formation, EPS production etc) of cells exposed to sub-lethal concentrations of drug candidates provided insight into the mechanism of action.

Overall, I will present and discuss our recent advances in vaccine development and anti-bacterial drug discovery.

1. Moradali, M. F.; Ghods, S.; Rehm, B. H., Pseudomonas aeruginosa Lifestyle: A Paradigm for Adaptation, Survival, and Persistence. Front Cell Infect Microbiol **2017**, 7, 39.
2. Finco, O.; Rappuoli, R., Designing vaccines for the twenty-first century society. Frontiers in immunology **2014**, 5.
3. Priebe, G. P.; Goldberg, J. B., Vaccines for Pseudomonas aeruginosa: a long and winding road. Expert review of vaccines **2014**, 13 (4), 507-519.
4. Rehm, B. H., Bioengineering towards self-assembly of particulate vaccines. Curr Opin Biotechnol **2017**, 48, 42-53.
5. Lee, J. W.; Parlane, N. A.; Wedlock, D. N.; Rehm, B. H., Bioengineering a bacterial pathogen to assemble its own particulate vaccine capable of inducing cellular immunity. Sci Rep **2017**, 7, 41607.

Day 1	Session two	Peptides

Christine Hale

Wellcome Sanger Institute
Hinxton, UK

Utilising differentiated wild type and knockout human stem cells to investigate mechanisms of innate immunity in macrophages

Human induced pluripotent stem cells engineered via Cas9/CRISPR technology to bear a 49 base pair (bp) missense mutation in exon 5 of the SLC11A1 gene were differentiated to the macrophage lineage and compared phenotypically to their parental line, A1ATD-1. Differential expression data from RNAseq pathway analysis indicated that, as expected, genes involved with iron metabolism were statistically different between the parent and KO lines but also highlighted differences in key immune and phagosomal/lysosomal pathways. Subsequent in vitro experimentation revealed alterations in the resulting knockout macrophages in terms of numbers isolated, the process of differentiation, immune surface markers, phagocytic ability, metabolic state as well as increased susceptibility to Salmonella Typhimurium infection. We would suggest that the SLC11A1 mutated macrophages derived through the in vitro differentiation process are activated and/or polarised to a different lineage from the parental line and thus explain the altered phenotypic characteristics described within.

Day 1 | Session two | Peptides

Celine Cosseau

Host Pathogen Environment interaction Laboratory
France

Transgenerational immune protection in the pacific oyster *Crassostrea gigas*

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More and more studies show how the environmental parameters during the early stages of development of living organisms may lead to significant positive or negative carryover effects on their subsequent life stages and also on their offspring. In this sense, parental experience with parasites and pathogens can lead to increased offspring resistance to infection, through a process known as transgenerational immune priming (TGIP). In this study, we investigated if we can educate the innate immune system to induce enhanced survival capacities through immune shaping in the Pacific oyster *Crassostrea gigas*. This species is currently confronted of massive recurring mortalities, called the Pacific oyster mortality syndrome (POMS) without existing therapeutic treatment. This syndrome, of complex etiology, involves different types of pathogen including bacteria and a virus, the herpesvirus OsHV-1 µVar. An exposure to a microbiota-rich (non-infectious) water during larval development was compared to filtered and UV-treated water control. The exposure was applied on two full-sib families from 2 hours to 10 days post-fertilization, which is an important developmental window (e.g. immune system ontogenesis) during which epigenetic information might be integrated from the environment. This microbial exposure successfully led to increased survival capacities during oyster juvenile stages in response to the POMS disease, in laboratory conditions and in the field for the exposed generation as well as the subsequent one. This result clearly suggests transgenerational immune priming (TGIP), where parents enhance offspring immune defense based on their own immunological experience. Transcriptomic analysis further shows that TGIP elevates baseline expression of immune effectors in offspring and shapes offspring to induce immune-related genes more rapidly when faced to the disease. Microbiota influences as well as epigenetic determinants orchestrating these phenomena are currently being investigated to bring insight on the oyster capacities to build an innate immune memory.

Day 1 | Session two | Peptides

Kelly Brown

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Childhood vasculitis syndromes microscopic polyangiitis (MPA) and granulomatosis with polyangiitis (GPA) have different etiologies as indicated by integrating blood transcriptomic and clinical metadata

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Introduction Primary vasculitis encompasses several life threatening diseases with differing phenotypic clinical manifestations that are classified in part by the size of the predominantly inflamed blood vessels. Small vessel, anti- neutrophil cytoplasmic antibody (ANCA)-associated vasculitis (AAV) subtypes Microscopic Polyangiitis (MPA) and Granulomatosis with Polyangiitis (GPA) may benefit from different treatments. Yet overlapping clinical features in the absence of a mutually exclusive classification criteria make these subtypes of AAV difficult to differentiate.

Objective The purpose of this study is to determine if blood transcriptomic data from children with MPA and GPA can aid classification and provide insight into disease etiology.

Methods RNA sequencing (Illumina HiSeq 2500) was performed on whole blood from 30 pediatric patients at the time of initial diagnosis of GPA or MPA. Sequence data (fastq reads) were mapped to the human genome (STAR software) and differential expression (DESeq2) and pathway overrepresentation analysis (InnateDB and Reactome pathway annotation system) performed.

Results Hierarchical clustering based on Euclidean distances between samples placed patients in two main groups each consisting primarily of patients with an initial classification of either GPA or MPA. More than 3,000 genes were differentially expressed between the groups with MPA patients showing enrichment for T cell receptor signaling pathways, cell adhesion molecules and cytokine-cytokine receptor interactions, and GPA patients enriched, among others, for Toll-like, NOD-like, and B cell receptor signaling pathways and neutrophil activation suggestive of a bacterial stimulus.

Conclusion Differentiating signatures and preliminary etiologies for GPA and MPA support different treatment paradigms for their management and is a step towards improved molecular diagnostics for classification of vasculitidies and other diseases with overlapping clinical phenotypes.

Day 2	Session four	Systems Biology

Gordon Dougan

University of Cambridge
Wellcome Sanger Institute

Studying emerging diseases through genomics and stem cells; Antibiotic resistant typhoid as an exemplar

Infectious diseases remain a serious threat in the modern world with the emergence of new pathogens that can evade current therapeutic approaches. Antibiotic resistant bacteria are exemplars of such threats. An explosion in new technologies, such as genome sequencing (host and pathogen) and stem cell biology, are providing blueprints for the design of systems both for tracking disease and for exploring new interventions. Further, we are now understanding how even relatively avirulent microbes can influence health and disease in the shape of the microbiota.

Using Salmonella as an example I will describe how genomics can be used to monitor the evolution and spread of diseases, such as typhoid, that are still extremely common in resource poor settings and in travellers to such regions. Now forms of antibiotic resistant typhoid have spread globally and are still acquiring resistance even to the newest antibiotics. Salmonella Typhi, the cause of typhoid, normally only infects humans and cannot be studied effectively in animals. I will describe how controlled human challenge and stem cell biology are providing new opportunities to study this pathogen in ‘in vitro’ systems such as Induced Pluripotent Human Stem Cell-derived macrophages and organoids.

Day 2 | Session four | Systems Biology

Amy Lee

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Transcriptional Profiling of Stem Cell-Derived Macrophages Provide Functional Insights to Genome-wide Association Studies

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Genome-wide association studies have uncovered numerous genetic variants with potential impacts on complex human diseases such as autoimmune diseases. However, functional studies aimed at untangling the role of genetic variations and environment cues underlying these human diseases have lagged. To help decipher this puzzle, we developed a mouse embryonic stem cell-derived macrophage model and created 26 immune gene knock-outs to characterize their transcriptomic responses to two live pathogens (*Salmonella typhimurium* and influenza A) and four pathogen-associated molecular patterns (CpG oligodeoxynucleotides, lipopolysaccharide, peptidoglycan and polyinosinic-polycytidylic acid).

We used the weighted correlation network analysis (WGCNA) and the grade of membership (GoM) model to define biologically functional modules from >800 RNA-Seq samples. In WGCNA, modules are defined as groups of genes with similar expression, whereas GoM partitions each sample into biologically-distinct modules by allowing partial membership of each sample. Pathway over-representation analysis of both WGCNA and GoM modules confirmed biologically-meaningful functional enrichment. To identify human diseases associated with any particular module, we performed disease ontology semantic and enrichment analysis and identified mutants that impact the expression of those modules with human disease associations. We hypothesize that a mutation that impacts the gene expression profile of a particular module will provide a mechanistic underpinning for the associated diseases enriched within this module. Using this approach, we have identified that the dysregulation in VEGF ligand-receptor interactions and stimulator of IFN gene (STING)-mediated induction of host immune responses pathways provide a potential functional link between Ncf1 mutation and lupus.

Day 2	Session four	Systems Biology

Andrew Currie

Murdoch University
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Day 2 | Session four | Systems Biology

David Lynn

South Australian Health and Medical Research Institute
Adelaide, Australia

The influence of microbiota in early-life on optimal vaccine responses

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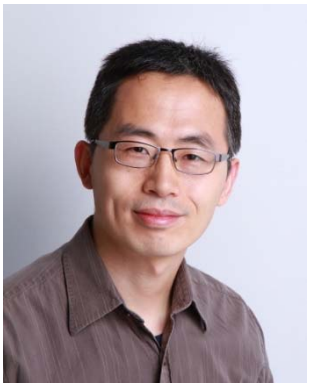
Antibody-mediated responses play a critical role in vaccine-mediated immunity. However, for reasons that are poorly understood, these responses are highly variable between individuals. We have recently found that antibiotic-driven intestinal dysbiosis, specifically in early-life, leads to significantly impaired antibody responses to five different adjuvanted and live vaccines. Restoration of the commensal microbiota following antibiotic exposure rescues these impaired responses. In contrast, antibiotic-treated adult mice do not exhibit impaired antibody responses to vaccination. Interestingly, in contrast to impaired antibody responses, immunized mice exposed to early-life antibiotics display significantly enhanced T cell cytokine recall responses upon *ex vivo* restimulation with the vaccine antigen. Our results demonstrate that, in mice, antibiotic-driven dysregulation of the gut microbiota in early-life can modulate immune responses to vaccines that are routinely administered to infants worldwide. While animal models are informative, we now require a better understanding of the relationships between the microbiota and vaccine responses in human infants. To do this, we have initiated a clinical study (the AIR study) of human infants who have either been exposed, or are unexposed, to antibiotics in the neonatal period. More than 100 infants have already been recruited. In this presentation, I will summarise our preclinical work to date and will present an overview of the AIR clinical study and the innovative systems vaccinology approach we are using to identify and validate the key microbial and host pathways through which the gut microbiota modulates immune responses to all routine infant immunisations.

Day 2	Session four	Systems Biology



Jianguo (Jeff) Xia

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Towards Immersive Network-based Visual Analytics for Systems Biology

Network analysis is a powerful approach in systems biology. Networks capture known relationships among different entities (molecules, diseases, *etc*.) of interest. Multiple algorithms can be applied to reveal important connections and “hot spots”. Researchers can then visually explore these relationships to gain insight or develop new hypothesis. The process is appealing, as networks intuitively engage and empower users to make more informed decision based on systems-level considerations.

The wide applications of different omics technologies necessitate generation and visualization of increasingly large networks. This once enjoyable experience in network analysis has now become a big challenge. In this talk, I will discuss our recent efforts in leveraging cloud technology, machine learning and virtual reality (VR) to develop a new-generation platform for network-based visual analytics directly accessible from web browsers. If conditions permit, audiences will have the opportunity to experience “immersive” network visualization by the end of my talk.

Day 2 | Session four | Systems Biology

Jason Kindrachuck

Laboratory of Emerging and Re-emerging Viruses,
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Characterizing the molecular determinants underlying severe Ebola virus disease and post-recovery persistence: science under negative pressure

Emerging and re-emerging viruses pose a significant threat to global public health. Outbreaks attributable to these pathogens, including ebolaviruses and influenza viruses, continue to increase in frequency as a result of changing socio-economic, environmental, and ecological factors. Many of these viruses result in severe illness and complex pathogenesis during the course of infection; however, the molecular processes underlying clinical illness are often poorly understood. To this end, an integration of basic research and clinical data can accelerate translational research for emerging and re-emerging viruses. Detailed molecular investigations of the severe clinical and pathologic manifestations associated with these viruses provides important insight into disease pathogenesis and may advance therapeutic discovery. Characterization of the global activation state of host cell kinases (the kinome) provides direct insight into cellular responses at the level of complex cell signaling networks and individual kinases. Further, kinome analysis may also guide patient management strategies and facilitate therapeutic discovery. The utility of kinome analysis and systems biology approaches for investigating emerging and re-emerging viral diseases will be discussed with a focus on Ebola virus pathogenesis throughout the course of nonfatal human clinical disease and convalescence. In particular, I will highlight: i) the relation of viral-mediated cell response dysregulation with clinical disease progression; and ii) the molecular mechanisms underlying asymptomatic Ebola virus testicular persistence and sexual transmission during convalescence.

Day 2	Session five	New Therapeutic Discoveries

John Hale

Blis Technologies
Otgao, New Zealand

Oral Blis- Streptococcus salivarius probiotics to promote a healthy oral microbiota

Streptococcus salivarius is a commonly-occurring commensal bacterium found both exclusively and ubiquitously in the human oral cavity. The well-characterized *S. salivarius* strain K12 was originally selected for development as a probiotic on the basis of its particularly strong, megaplasmid-encoded inhibitory activity against the important disease- associated species *Streptococcus pyogenes*. As such, its initial application was to provide school-aged children with protection against streptococcal pharyngitis. Clinical trials have shown exciting results and have led to reduced absenteeism from school and work associate with simple probiotic application. Other work identified additional health benefits linked to the regular use of probiotic preparations of oral probiotics including the reduction of acute otitis media episodes in young children and decreased severity of symptoms in halitosis-affected adults. This talk will present the story behind the development of a probiotic bacterium for a new application including an insight to the science, development and challenges face as well as discussion about new opportunities and applications not previously anticipated at the time of original discovery.

Day 2 | Session four | Systems Biology

Neeloffer Mookherjee

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Innate defence regulator (IDR) peptide in airway inflammation

Innate Defence Regulator (IDR) peptides, synthetic derivatives of cationic host defence peptides, can resolve both infections and regulate inflammation. Exogenous administration of IDR peptides can confer protection and control inflammation in a variety of infection models. We examined the effects of IDR peptides in a house dust mite-challenged murine model of airway inflammation, which is routinely used as a preclinical model for asthma. We showed that our lead IDR peptide significantly improves airway hyper-responsiveness (breathing capacity) and suppresses infiltration of inflammatory cells, in particular eosinophils and neutrophils, in the lungs. System-level analyses revealed that the peptide suppresses the expression of several molecular candidates within the inflammatory network activated in the lungs. Our studies demonstrate that an immunomodulatory IDR peptide controls the pathophysiology related to airway inflammation in a murine model of allergic asthma. Further interrogation of underlying mechanisms demonstrated that IDR peptides regulate airway inflammation by targeting the chronic inflammatory cytokine IL-33 in bronchial epithelial cells (in murine lung tissue and in human primary bronchial epithelial cells). As IL-33 is implicated in steroid-refractory severe asthma, our findings suggest that IDR peptides exhibit the potential to control steroid-refractory severe asthma. These studies provide the foundation for the development of IDR peptides as immunomodulatory therapy for chronic inflammatory respiratory diseases. The advantage of IDR peptide-based therapy is the ability to control inflammation without compromising resolution of infections.

Day 2 | Session four | Systems Biology

Shawn Lewenza

Athabasca University
Alberta, Canada

Small molecules that repress exopolysaccharide expression have antibiofilm and antivirulence activities against *Pseudomonas aeruginosa.*

Pseudomonas aeruginosa is an archetypal biofilm-forming organism that causes chronic lung infections in cystic fibrosis (CF) patients. Biofilm formation is a universal virulence strategy in which bacteria grow in dense microbial communities enmeshed within a polymeric extracellular matrix. Matrix-enclosed populations are protected from antibiotic exposure and the immune system. The main extracellular matrix polymers of *P. aeruginosa* are exopolysaccharides (EPS) and eDNA. Given the central importance of the EPS for biofilms, they are attractive targets for novel anti-infective compounds. We used a high-throughput gene expression screen to identify compounds that repress expression of the *pel* genes. The *pel::lux* repressors demonstrated antibiofilm activity against microplate and flow chamber biofilms formed by wild-type and hyperbiofilm-forming strains. To determine the potential role of EPS in virulence, *pel/psl* mutants were shown to have reduced virulence in feeding behavior and slow killing virulence assays in *Caenorhabditis elegans.* The antibiofilm molecules also reduced *P. aeruginosa* PAO1 virulence in the nematode slow killing model. Lastly, the combination of antibiotics and antibiofilm compounds increased killing of *P. aeruginosa* biofilms. These small molecules represent a novel anti-infective strategy for the possible treatment of chronic *P. aeruginosa* infections.

Day 2 | Session four | Systems Biology

Victoria Korolik

Institute for Glycomics,
Griffith University
Brisbane, Australia

Bacterial chemotaxis and changing paradigms.

Bacteria have evolved to sense changes in their environment and move to change their position in order to avoid unfavourable conditions or manoeuvre towards new niches using chemotaxis signal transduction pathway. Bacterial chemosensors respond to external stimuli with unique precision and sensitivity - a key survival trait in search for nutrients and locating a target host cell, and as such, are considered to be critical for bacterial colonisation and pathogenicity The well-researched E. coli chemotaxis system pathway (receptor-CheA/CheW-CheY-flagella) has previously served as a reference for the characterisation of chemotaxis in other bacteria. In recent years, however, our knowledge of chemotaxis pathways has progressed from a simple *E. coli* paradigm to a much more complex scenarios in other bacteria where similar, but more complex pathways exist. Gastrointestinal pathogen *Campylobacter jejuni* encodes a single chemosensory pathway relaying signal through eleven sensory receptors, seven of which sense external ligands. We have now characterised six of the seven *C. jejuni* external sensors, including the aspartate chemosensory receptor CcaA and the multi-ligand receptor CcmL, capable of responding to 5 repellents and 5 attractants, CcrG which respond to galactose and now a new class of chemosensor, Tlp10.

Day 2 | Session four | Systems Biology

Joe McPhee

Ryerson University
Toronto, Canada

Signaling heterogeneity in the conserved PhoPQ-PmrD-PmrAB regulatory cascade governing host-defence peptide resistance in *Escherichia coli*

Escherichia coli is a well-characterized model organism and also a significant cause of enteric and invasive infections in numerous populations. In order to successfully colonize the host and cause disease, *E. coli* must be able to respond to host signals and resist killing by effector molecules of the host innate or adaptive immune system. During inflammatory bowel disease, host-defense peptides are produced in a disease-specific manner, whereby patients with CD showed elevated levels of human beta-defensins while patients with Crohn's disease have elevated levels of LL-37. Here, we show that clinical isolates of *E. coli* vary greatly in their ability to resist molecules of the host immune system in a disease specific manner. We created transcriptional fusions to GFP to assess the level of PhoPQ or PmrAB signaling in a subset of these disease-associated strains. We observe large strain to strain variation in the ability of a particular strain to respond to a PhoPQ inducing signal and these difference are correlated with the ability of the strain in question to mount an appropriate response to those signals. We propose that regulatory heterogeneity in conserved signaling systems may be a critical feature of bacterial responses to a given host environment.

Posters

#	Title	Presenter
1	Antimicrobial molecules in platelets fight the Mycibacterial infection.	Flor de María Torres Juárez
2	Gallium disrupts bacterial iron metabolism and has therapeutic effects in mice and humans with lung infections	Richard Siehnel
3	Surfing motility: A conserved yet diverse adaptive phenotype	Evelyn Sun
4	Role of the Herpes Simplex Virus Protein UL21 in Regulating Nuclear Egress of Capsids	Renee Finnen
5	Multidrug adaptive resistance of *Pseudomonas aeruginosa* swarming cells	Shannon Coleman
6	Effect of treatment with metformin, insulin and glyburide on the expression of antimicrobial peptides during infection with Mycobacterium tuberculosis in vitro models.	Adrian Rodriguez-Carlos
7	Synthetic peptides as adjuvant therapy for acute and chronic *Pseudomonas aeruginosa* skin infections	Daniel Pletzer
8	Mechanisms underlying *Pseudomonas aeruginosa* susceptibility to antimicrobials in clinically relevant conditions	Corrie Belanger
9	Machine Learning Approaches to predict ER patient progression to sepsis.	Arjun Baghela
10	The Effect of Macrophage Activation State and Endotoxin Tolerance on resistance to Salmonella Infection	Kate Sedivy-Haley
11	Treating chronic rhinosinusitis by eradicating biofilms using antimicrobial photodynamic therapy and recolonizing the sinus with a healthy microbiome by sinonasal microbiota transplants.	Mike Trimble
12	The development of peptidomimetics with immunomodulatory and anti-biofilm activities.	Hashem Etayash
13	Novel Biofilm-Specific Targets to Fight Adaptively Resistant Infections	Melanie Dostert
14	RNA-Seq reveals inflammatory mechanisms of pediatric vasculitis before and after treatment.	Maren Smith
15	Bioinformatic identification of *Pseudomonas aeruginosa* stringent response regulon	Travis Blimkie
16	Influence of nitrogen source and metabolism on virulence of *Pseudomonas aeruginosa*	Morgan Alford

17	Unraveling the Role of Monocytes/Macrophages during Endotoxin Tolerance – a New Driver of Sepsis	Beverlie Baquir
18	Integrative Genomics and Systems Biology of *Pseudomonas aeruginosa:* Evolutionary Biology of an Opportunistic Pathogen	Roger C. Levesque
19	Direct *in Vivo* Studies of *Pseudomonas aeruginosa* Bacterial Diversity in Lung Infections.	Roger C. Levesque
20	Identification and characterization of crocodylian beta-defensin variants.	Felix Santana
21	Cdc42 Rho GTPase; the molecular switch regulating pro- and anti-inflammatory functions of the human host defence peptide LL-37	Mahadevappa Hemshekhar
22	Interplay of LL-37 and IL-17: differential expression of proteins associated with neutrophilic airway inflammation and remodeling	Anthony Altieri
23	Disruption of the central hydrophobic region mitigates the anti-inflammatory activity of an innate defence regulator (IDR) peptide, but not the ability to improve lung function.	Hadeesha Piyadasa
24	Antibiotics suppress intestinal antiviral responses in a Microbiota-independent manner	Andrew Sharon
25	The unusual convergence of steroid catabolic pathways in *Mycobacterium abscessus*	Jessica Chorolovski
26	Elucidating novel regulators of EPEC virulence through transcriptomic analysis.	Zakhar Krekhno
27	The Small RNA, SrbA, is Important for Biofilms and Pathogenicity in *Pseudomonas aeruginosa* Strain PA14	Patrick Taylor
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