PRECISION MEDICINE

The University of the Western Cape,
Ghent University and the University of Missouri's
joint symposium on Precision Medicine:

Therapeutic Targets

Promoting focused Trans-institutional
Collaborative Research

27-30 March 2023
The University of the Western Cape
Cape Town South Africa

UNIVERSITY of the WESTERN CAPE

AFRICA PLATFORM
Ghent University Association

GHENT UNIVERSITY

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Promoting focused Trans-institutional Collaborative Research

Precision medicine has been defined as “an emerging practice of medicine that uses an individual’s genetic profile to guide decisions made about the prevention, diagnosis and treatment of disease. Knowledge of a patient’s genetic profile can help doctors select the proper medication or therapy and administer it using the proper dose or regimen”. In other words, each person’s unique clinical, genetic, genomic, and environmental information influences the nature of diseases, their onset, their course, and their response to medications in very individualized ways.

Translating findings from genomics, pharmacogenomics and related -omics fields into clinical applications capable of reducing the burden of chronic diseases remains an enormous challenge. To address this, precision health research must ensure the fit of genomic medicine with the key approach of whole-person care through personalization; targeting areas that will see early benefits such as pharmacogenomics and novel therapeutic targets; ensuring that appropriate clinical decision support is available; supplementing genomic information with patient information including EMRs, and looking to the future for areas of development such as the intersection of population health and genomics.

This symposium has been designed to bring together researchers from UWC, Ghent and the University of Missouri to share their current work, brainstorm on needed resources including innovative data sharing and co-create opportunities for collaboration and competitive funding applications. Ultimately, we hope to provide precision medicine interventions that are more cost-effective than population-based measures and will improve health care in Africa, Europe and the United States.

Zoom Webinar Registration Link: https://bit.ly/3ZJITWP

Symposium Organisers:

- Umesh Bawa, Psychologist & Director of the International Relations Office – University of the Western Cape
- Mary Stegmaier, Associate Professor & Vice Provost for International Programs – University of Missouri
- Rod Uphoff, Elwood Thomas Missouri Endowed Professor Emeritus of Law, University of Missouri School of Law & Director, University of Missouri South African Education Program, Extraordinary Professor – University of Western Cape Law Faculty
- Annelies Verdoolaege, Policy Advisor Internationalisation Ghent University & Coordinator of the Africa Platform of Ghent University Association & Extraordinary Professor – University of the Western Cape

PROGRAMME

Monday, March 27

8:00 - 8:55 Arrival tea/coffee/bakery

9:00 - 13:00 UGent Presentations - each 30 minutes with 15 minutes for questions

- Camelid single domain antibodies (Nanobodies): principles and applications in (bio)medical research by Prof. Jan Gettemans
- Toward targeted therapies for medication-resistant epilepsy by Prof. Robrecht Raedt
- Integrative gene regulatory network biology for precision medicine: elucidation of molecular mechanisms and pinpointing key regulators in complex diseases by Prof. Vanessa Vermeirssen
- Pharmacogenetics in Belgium: from high expectations towards more clinical applications by Prof. Lies Lahousse **(virtual)**
- Biomarker identification and profiling in heterogeneous prostate tumors by Prof. Kathleen Marchal **(virtual)**

13:00 - 14:45 Lunch for symposium attendees

15:00 - 15:30 Welcoming Remarks

- Rector Tyrone Pretorius
- President Mun Choi
- Vice-rector Mieke Van Herreweghe

15:30 - 16:30 Presentation by group #1

- Hypoxia enhances the secretion of Cancer Paracrine factors and Exosomes and is crucial to the progression of metastasis across the Blood-Brain Barrier by Prof. David Fisher (UWC)
- Sleep Apnea End-Organ Morbidity: Exosomes as Diagnostic and Prognostic Phenotypic Markers by Prof. David Gozal (MU) & Prof. Abdelnaby Khalyfa (MU)

16:30- 18:00 Presentation by group #2

- Presentation 1: Development of Neuroprotective Agents and the Implementation of an African Specific Disease-Gene Variant Data Analytic Platform with a Focus on Alzheimer's Disease by Prof. Jacques Joubert (UWC) and Prof. Xiaoqin Zou (MU) **(virtual)**
- Presentation 2: Alzheimer's disease mitigation: AI, neuroimaging and gut-brain axis by Prof Ai-Ling Lin (MU) **(virtual)** and Prof. Jacques Joubert (UWC)

Tuesday, March 28

10:00 - 13:00 Small group meetings

13:00 - 14:45 Lunch for symposium attendees

15:00 - 16:00 Presentation by group #3

- Developing a multimodal, integrative, in-silico, multiomics data science approach to early detection of HPV-based biomarkers of oropharyngeal head and neck cancer by Prof. Henry Adeola (UCT), Prof. James Bashkin (UM St. Louis), Prof. Haly Holmes (UWC), Prof.Amir Afrogeh (UWC), Prof. Badri Adhikari (UM St. Louis) and Dr Hocine Bendou (UWC).

16:00 - 17:00 Presentation by group #4

- Precision nanomedicine for tuberculosis therapy by Prof. Admire Dube (UWC) and Prof. Raghuraman Kannan (MU) **(virtual)**

17:00 - 18:00 Presentation by group #5

- Patient Data standardization and collection for UWC; benefits of collaborations and partnerships by Prof. Gerald J Wyckoff and Prof. Jennifer-Anne Chipps (UWC) **(virtual)**

Wednesday, March 29

8:00 - 8:55 Arrival tea/coffee/ bakery

9:00- 13:00 Group Presentations - each 25 minutes with 10 minutes for questions.

- Utilization of the African Genome Project for Africa-focused Precision Medicine and Precision Drug Discovery: A Case Study of Statins by Prof. Samuel Egieyeh (UWC)
- Precision medicine: Pharmacogenomics and Development of Individualised Drug Therapy for Diabetes and Hypertension Patients by Prof. Mongi Benjeddou (UWC)
- Application of metabolomics and DNA adductomics to further unravel the impact of the exposome in health and disease by Dr. Lieselot Hemeryck (UGent)
- FLEXiGUT: Investigating the life-course impact of dietary and environmental exposure on chronic low-grade gut inflammation by Dr. Roger Peró-Gascón, Prof. Dr. Marthe De Boevre, Prof. Dr. Sarah De Saeger, and the FLEXiGUT consortium **(virtual)**
- The prognostic role of M2-type tumor associated macrophages in oropharyngeal squamous cell Carcinoma by Dr. Tijl Vermassen (UGent) and Mr. Mathieu Struys (UGent)
- The role of human papilloma virus and tumor-infiltrating lymphocytes in oral and oropharyngeal cancer microenvironment: a tricontinental study by Dr. Tijl Vermassen (UGent) and Mr. Mathieu Struys (UGent)
- Creating Precision Medicine Education for Future Pharmacists: Challenges and Opportunities for the UM/UWC Partnership by Ms. Nicole Keuler (UWC) and Prof. Jerry Wyckoff (UMKC)
- Smart Sensing and Analytics for Cognitive Health Care by Prof. Sajal Das (Missouri Science & Technology)

13:00 - 14:45 Lunch for small groups

15:00 - 18:00 Small group meetings

Thursday, March 30

Open day for group meetings or social activities.
All morning sessions will be recorded for circulation at UM, UGent & UWC. The afternoon sessions on Monday and Tuesday will be webinar style to provide the opportunity for UM and Ghent researchers to participate virtually.

Camelid single domain antibodies (Nanobodies): principles and applications in (bio)medical research by **Prof. Dr. Jan Gettemans (UGent)**

Nanobody lab, Dept. Biomolecular Medicine, Faculty of Health Sciences Ghent University, Belgium
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Abstract

Nanobodies from llamas or alpacas have attracted increased attention during the previous decade due to their versatility in biomedical research. These small (15 kDa) single chain recombinant antibodies are routinely cloned and expressed in bacteria, yeast or mammalian cells at high yield. Nanobodies can be used for a variety of purposes, including blocking enzymatic activity, perturbing protein-protein interactions, intracellular expression as intrabodies, site-specific insertion of unnatural amino acids in their primary structure for antibody drug complex (ADC) development, site specific coupling of fluorophores, quantum dots, gold nanoparticles, etc. This talk will highlight how nanobodies can further our understanding of proteins and their role in desease, and discuss how nanobodies can contribute as a research instrument, diagnostic or therapeutic in cancer, neurodegenerative diseases and orphan disorders. Our lab specializes in raising nanobodies against proteins considered potential drug targets. We have expertise in knocking out protein functions using nanobodies and have shown that using nanobodies cancer cell migration, invasion and metastasis can be countered, as well as proteolytic degradation of an amyloidogenic protein using a novel approach.

Biography

Jan Gettemans studied biochemistry at Ghent University in Belgium and is currently a full professor at the same university. Teaching assignments include protein structure and function, metabolism, cell and gene technology for students in medicine, biomedicine and dentistry. He was a member of the VIB institute for 15 years. He is also member of the American Society for Cell Biology (ASCB) since 2006 and the American Association for Cancer Research (AACR) since 2014. He serves as a board member of the Belgian Society for Biochemistry and Molecular Biology (BSBMB) since 2013 and was appointed secretary of the same society since 2014. In 2018, Jan founded Gulliver Biomed by, a Ghent University spin-out company developing a portfolio of single domain antibodies as well as custom nanobodies for academics and biotech and pharmaceutical companies, and since its inception serves as its CEO. In 2016 he was awarded the Janine and Jacques Delruelle prize, Queen Elisabeth medical foundation, Belgium, for research on Gelsolin Amyloidosis (Familial Amyloidosis of the Finnish type). Current research projects aim at using single domain antibodies to perturb proteins involved in Alzheimer's Disease, inherited retinal eye disorders, and cancer (invadosomes and metastasis).

Jan Gettemans

Toward targeted therapies for medication-resistant epilepsy by Prof. Dr. Robrecht Raedt, 4BRAIN (UGent)

Associate Professor, Faculty of Medicine and Health Sciences
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Abstract

Standard of care treatment for epilepsy involves daily oral intake of anti-epileptic drugs (AEDs). This form of therapy influences the complete nervous system although, in most cases, a limited part of the brain generates the epileptic seizures. As a consequence AED treatment is frequently associated with severe off-target side effects. Also, about 30% of patients with epilepsy still have epileptic seizures despite therapy with AEDs. These patients are called to have drug-resistant epilepsy. Research at the 4BRAIN focuses on the development of new therapies for drug-resistant epilepsy, with less side effects and higher efficacy. Strategies are explored which specifically target the seizure focus, i.e. the neural network in the brain responsible for the generation of epileptic seizures. These strategies include electrical deep brain stimulation (DBS) of epileptogenic brain regions, but also more experimental approaches such as chemogenetics, optogenetics and photopharmacology. Chemo- and optogenetic approaches involve injection of AAV viral vectors in the seizure focus to render excitatory neurons sensitive for inhibition with respectively drugs or light. In case of photopharmacology, a coumarin-caged adenosine A1 receptor (A1R) agonist (DEACM-CPA) has been synthetized which uncages in response to illumination with 405 nm light. This allows light-control over A1R-mediated inhibition of neurotransmission and neuronal excitability. While deep brain stimulation (DBS) is translated from the bench to the bedside, chemogenetics, optogenetics and photopharmacology are still being investigated ex vivo and in vivo in rodent models for temporal lobe epilepsy but with the goal to translate it to the clinic. Besides our endeavours in developing new therapies, we are also interested in understanding the mechanisms of action of vagus nerve stimulation (VNS), the most frequently used neuromodulatory therapy for drug-resistant epilepsy. Some years ago, we discovered that VNS-induced release of norepinephrine by the locus coeruleus, a small nucleus in the brain stem plays a crucial role in the seizure-suppressive effects of VNS. Currently our aim is to further understand how this release of norepinephrine mediates seizure suppression using photometry, opto- and chemogenetic techniques allowing to measure and control norepinephrine release with high spatiotemporal specificity. Through this improved understanding we aim to further optimize the efficacy of vagus nerve stimulation for epilepsy. Although most of the 4BRAIN research is done in animal models and patients with epilepsy, targeted therapies and vagus nerve stimulation have therapeutic potential in other (focal) brain diseases such as multiple sclerosis, stroke, brain cancer, Parkinson's disease, Alzheimer disease, depression, etc.

Biography

Robrecht Raedt was born September 19, 1980 in Kortrijk (Belgium). He obtained his Master's degree in Biology at Ghent University (Belgium) in 2002. In 2007, he successfully completed his PhD research at the Faculty of Medicine and Health Sciences of Ghent University. The topic of his PhD research was 'Cell Therapy for Epilepsy'. This work implicated isolation and culture of stem cells, biochemical characterization of cell clones, cell grafting in various epilepsy models, immunohistochemistry, etc. He worked as a postdoc at the Laboratory for Clinical and Experimental Neurophysiology, Neurobiology and Neuropsychology at Ghent University (LCEN3) on unravelling the mechanism of action of neurostimulation therapies for epilepsy (vagus nerve stimulation and deep brain stimulation) both in animal models as in patients with epilepsy. It involved techniques such as microdialysis and intracranial electrophysiology in rats and single-unit recording in humans. Since he was appointed as an Assistant Research Professor at Ghent University in 2011, Robrecht Raedt is doing research on the neural basis of behavioural control (cognitive and emotion control) using intracranial recording and neuromodulatory techniques during cognitive testing both in humans as in animal models. Robrecht Raedt was also associated to the University of Lethbridge (Dr. McNaughton lab) from 2012 to 2014 to investigate the neural dynamics leading to the development of spontaneous epileptic seizures using high density recordings in the hippocampus of rodent models for epilepsy. Currently, he is appointed as Associate Research Professor at Ghent University focusing on glioma-associated epilepsy, modulation of epileptic brain networks using opto- and chemogenetics and photopharmacology. Since January 2018, he is appointed as Department Head of Animal Facility of the Faculty of Medicine of Ghent University.

Robrecht Raedt

Integrative gene regulatory network biology for precision medicine: elucidation of molecular mechanisms and pinpointing key regulators in complex diseases by

Prof. Dr. ir. Vanessa Vermeirssen (UGent)

Lab for Computational Biology, Integromics and Gene Regulation (CBIGR), Department of Biomedical Molecular Biology and Department of Biomolecular Medicine, Ghent University, Ghent, Belgium – Cancer Research Institute Ghent, Ghent, Belgium
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Abstract

Technological advancements have led to a wealth of omics data in bulk, but also more and more at single cell level: (epi) genome, transcriptome, proteome, metabolome, ... The capacity to integrate multi-omics data, to something more than the sum of the existing data, is key to elucidating the causes of complex diseases. Gene regulation and signaling control development, homeostasis and disease. Integrated gene regulatory networks are a valuable tool to map systems-wide the molecular interactions between different biomolecules across omics types in a specific disease context. They allow to obtain systems biological insights into complex diseases: what are key pathways and regulators at play, and what are potential drug targets and mechanisms of therapy failure? Gene regulatory networks represent regulatory or functional molecular interactions between regulators such as transcription factors and their target genes, providing an overview of the regulatory programs at play. Uncovering these molecular interactions in a given biological context through the computational process of network inference comes down to unraveling statistical dependencies. This generally requires transcriptome or other omics data for many patients. We and others have shown that different network inference methods reveal complementary aspects of the underlying gene regulatory networks and that integrating different omics data provides a more accurate, multi-modal view of gene regulation. For personalized medicine, gene regulatory networks of individual patients are attractive and these can be constructed by single-sample network inference methods on population-level data. Recently, we moved into the field of single-cell network inference, which allows to chart regulatory programs specific for an individual patient and distinct cell states. In this talk, I will give an overview on our research projects in precision medicine.

The CBIGR (pronounce “see bigger”) team aims to unravel mechanisms of complex diseases by acquiring a functional understanding of gene regulation and signaling towards personalized medicine, using statistics, bioinformatics and machine learning, as well as high-throughput biological approaches. We are applying, benchmarking and optimizing methods in transcriptomics, (epi)genomics, single-cell analysis, multi-omics data integration, gene regulatory network inference and drug response prediction. The application focus of the lab is on disorders of the nervous system. In glioblastoma and neuroblastoma tumors, we identify novel driver genes and pathways, and we investigate plasticity and regulatory heterogeneity as responsible factors for drug escape and therapeutic failure. Tumors often show heterogeneity and the identification of key regulators that drive cancer transcriptional reprogramming can be used to therapeutically interfere in precision oncology. In neurological disorders, we study mechanisms of pan-neuroinflammation and gut-brain communication in search for novel preventive and therapeutic opportunities.

Biography

Vanessa Vermeirssen graduated from Ghent University with a Master of Science and a PhD in Bioscience Engineering. She conducted postdoctoral training in functional genomics, systems biology, bioinformatics and computational biology at the University of Massachusetts Medical School, the Center of Plant Systems Biology of VIB, and the Center for Medical Genetics Ghent. For her doctoral and postdoctoral training, she was awarded fellowships from the Research Fund Flanders, D. Collen Research Foundation for Biomedical and Biotechnology Research from the Belgian American Educational Foundation and the Belgian Science Policy Office. She was part-time visiting professor at Odisee. In 2019, she obtained a research professorship (BOF-ZAP) at Ghent University within the inflammatory gut-brain axis consortium. She started the Laboratory for Computational Biology, Integromics and Gene Regulation (CBIGR) at the Department of Biomedical Molecular Biology and the Department of Biomolecular Medicine. She also became a group member at the Cancer Research Institute Ghent (CRIG). She has internationally recognized expertise in systems biology and bioinformatics, more specifically in gene regulatory networks, regulatory genomics, transcriptomics, epigenomics, network inference and multi-omics data integration.

Vanessa Vermeirssen

Pharmacogenetics in Belgium: from high expectations towards more clinical applications by **Prof. Dr. Lies Lahousse (UGent)**

Department of Bioanalysis, Pharmaceutical Care Unit, Faculty of Pharmaceutical Sciences, Ghent University, Belgium, Department of Epidemiology, Erasmus Medical Center, Rotterdam, The Netherlands
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Abstract

Precision medicine integrates genotypic, endotypic and phenotypic data in health-care to optimize prevention and treatment of human diseases. The PREPARE study demonstrated that the chance for clinically relevant adverse drug reactions is 30% lower when patients received genotype-guided drug treatment. However, large-scale clinical implementation of pharmacogenetics (PGx) to optimize drug safety and effectiveness has yet to be rolled out. Therefore to guide future implementation initiatives, we investigated the current level of knowledge, applications, and expectations of local pharmacists and physicians towards PGx and determined the factors that influence healthcare professionals' knowledge. In addition, we surveyed the public opinion on pharmacogenomic research and testing to foster integration within Belgian health care. Finally, we investigated whether PGx could also increase effectiveness of inhaler therapy in respiratory disease based on population-based health data. While half of participating citizens ever experienced side effects or treatment failure and the majority was convinced that pharmacogenomic tests could help doctors to prescribe them the right drugs, the knowledge of, and experience with PGx was rather low among healthcare professionals. The care provider's profession, practice setting, and level of prior education significantly affected their PGx knowledge, independent of their years of experience. Potential clinical applications are broad since we showed that genetic variants could predict response to inhaled corticosteroids in patients with asthma, and to inhaled 2-agonists in patients with COPD. In conclusion, the prediction of treatment response based on a person's genetic makeup could improve drug effectiveness besides drug safety. While citizens and care providers show high expectations from PGx, the clinical applications to move this field within precision medicine forward, are still scarce in Belgium.

Biography

Lies Lahousse's research line in pharmacoepidemiology combines aspects of clinical pharmacology and clinical epidemiology and studies drug use and (side)effects in large numbers of people to support rational drug use thereby improving health outcomes in the population. Her research group focuses on therapy adherence and precision medicine including optimizing the benefit risk ratio of approved drugs by studying heterogeneity among phenotypes, endotypes and underlying genetics with the ultimate goal of improving care of patients with chronic complex diseases e.g. asthma and COPD. By deep phenotyping and international collaboration in population genomics, her group aims heritability and novel genetic variants of pulmonary function traits by genome-wide association studies. Her group aims to further investigate these and other omics-data in interaction with approved drugs and translate pharmacogenomics into clinical practice.

Lies Lahousse

Biomarker identification and profiling in heterogeneous prostate tumors by **Prof. Dr. Kathleen Marchal (UGent)**

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Abstract

identification and application of biomarkers for patient stratification is complicated by the spatial heterogeneity of the primary tumor: in PCa the primary tumor contains multiple cancer lesions of which only some will have the proper molecular signature to drive metastatic disease. Usually one tumor sample per patient (e.g. biopsy) is profiled for biomarker assessment. This sample, selected by the pathologist usually corresponds to the lesion with the highest Gleason score and tumor percentage (index lesion). However, we recently showed that the index lesion, despite having the highest Gleason score, not always corresponds to the lesion, seeding the metastasis. If the index lesion does not correspond to the lesion with the highest metastatic potential, profiling the index lesion only might result in missing the biomarker and underestimating the aggressive status of the tumor. This complicates the identification of good biomarker combinations and their subsequent validation in clinical studies. In this presentation we show how we want to cope with this tumor heterogeneity by exploiting a unique mulifocal cohort in combination with the potential offered by digital pathology.

Biography

Kathleen Marchal obtained a PhD in Molecular Microbiology in 1999 (FWO fellow). From 1999-2004, she contributed as postdoctoral fellow FWO (ESAT-SCD, KU Leuven, Faculty of Engineering) to the set-up of one of the first Belgian bioinformatics labs. From 2004-2014 she was, first assistant and later associate professor bioinformatics (Fac of Bioscience Engineering) at KU Leuven. Since 2011, she joined UGent (Fac of Sciences) where her research group is physically located in the engineering department (IDLab/ IMEC). The group published more than 200 peer reviewed publications, of which >50 as last author, K. Marchal was responsible for the design and organization of the Master of Science in bioinformatics at both KU Leuven and UGent and still is chair of the educational commission of the Master of Science in Bioinformatics at UGent. The main expertise of the group consists of developing computational methods for outstanding problems in systems genetics. Hereto, advanced statistics and machine learning are combined with adequate biological assumptions to design conceptually new methods. This approach resulted in in seminal work on Gibbs sampling-based motif detection and internationally renowned expertise in network inference. When genome sequencing became more main stream, the group pioneered in developing graph-based methods for genotype-phenotype mapping in clonal systems, with applications on both microbial and cancer-related datasets. The group has internationally recognized expertise in cancer-genomics/ bioinformatics and ample of expertise with machine learning.

Kathleen Marchal

Hypoxia enhances the secretion of Cancer Paracrine factors and Exosomes and is crucial to the progression of metastasis across the Blood-Brain Barrier by **Prof. David Fisher Ph.D. (UWC)**

Deputy HOD of Medical Bioscience, Head of the Neurobiology Research Group, University of the Western Cape, Adjunct Professor - School of Health Professions, University of Missouri
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Abstract

Cancer cells have been reported to use the secretion of paracrine factors and exosomes to compromise the endothelial barrier to prepare for their passage into the brain parenchyma. As cancer cells are known to act differently under conditions of hypoxia, we investigated how conditional media (CM) derived from breast and glioblastoma cells incubated under conditions of normoxia and hypoxia would affect the proliferation of brain endothelial cells (bEnd.3). Brain endothelial cells (BECs: bEnd.3) were cultivated with normoxic and hypoxic CM generated from breast cancer MCF7 cells and glioblastoma U-87 cells. Cell proliferation was evaluated using the trypan blue exclusion assay and phases of the cell cycle were evaluated using flow cytometry. bEnd.3 proliferation was suppressed more aggressively with hypoxic CM after 72 and 96 h; cell cycle analysis showed that paracrine treatment tended to prevent BECs from entering the G2 phase, thus suppressing cell division. Conclusions: MCF7 and U-87 cells induce suppressed proliferation of BECs deferentially under hypoxia by blocking cell cycle progression to the G2 phase through the secretion of exosomes and paracrine factors. Our data points conclusively to how monitoring cancer paracrine factors as diagnostic markers can assist clinicians in treating cancer more precisely for individual patients. In future studies, we will investigate how intermittent hypoxia will affect the progression of cancer by studying the secretion of exosomes and their cargoes.

Biography

Professor David Fisher graduated from UWC with a BSc (Van der Horst Prize for best overall student), He obtained his BSc (Hons) and MSc from the University of Cape Town followed by his PhD from UWC. He was appointed as an adjunct professor in the School of Health Professions at the University of Missouri, Columbia, USA. Prof Fisher has held several administrative positions ranging from Chairperson of the Medical Bioscience Department, acting Dean and Deputy Vice-Chancellor to the Deputy Dean of Science faculty (UWC). In this regard, his achievement has been recognized by UWC, and in 2007 presented him with the "Distinguished Administrators Award". He is a physiologist with a research background in the neurobiology field of the blood-brain barrier. Neurobiology Research: Blood-brain Barrier: The capillaries of the brain are particularly special, as they are not simply conduits for blood, but are primarily responsible to ensure that the neurons function in a strictly regulated homeostatic environment. The endothelium of these capillaries forms the central component of the blood-brain barrier (BBB). The pathologies emanating from compromised permeability across the BBB have been implicated in psychiatric disorders, epilepsy, multiple sclerosis, neuroinflammation, stroke, and traumatic brain injury (Greene, et al., 2019 for a review). Thus, the regulation of permeability across the BBB is of interest from a physiological, pharmaceutical, psychological, and clinical perspective. Since 2014, we have embarked on a series of research projects aimed at understanding the physiological and narcotic underpinning of the BBB function and although these have been successful from a personal research point of view, concretized collaboration from colleagues across the Faculty of Science and indeed across faculties, have ramped up the potential of a novel research niche at UWC. In this regard, he has recently launched the new Neurobiology Research Group at UWC. This research group concentrates on the effects of novel pharmaceuticals designed to affect the progression of Alzheimer's disease, narcotics (Methamphetamine, alcohol, phytocannabinoids, and endocannabinoids), oxidative stress, and reductive stress on the "Blood-Brain Barrier". He supervises several research students and has an ongoing collaboration with the Universities of Missouri, Buffalo, and Wyoming (USA), as well as locally with the Universities of Stellenbosch, Pretoria, and UNISA.

Professor David Fisher

Sleep Apnea End-Organ Morbidity: Exosomes as Diagnostic and Prognostic Phenotypic Markers by **Prof David Gozal (MU) and Prof Abdelnaby Khalyfa (MU)**

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Abstract

Obstructive sleep apnea (OSA), the most severe form of sleep-disordered breathing, is characterized by intermittent hypoxia during sleep (IH), and sleep fragmentation (SF). OSA is associated with increased risk for morbidity and mortality affecting cardiovascular, metabolic, and neurocognitive systems, and has been recently implicated in cancer incidence and mortality. Substantial variability in OSA outcomes suggests that genetically-determined and environmental and lifestyle factors affect the phenotypic susceptibility to OSA. Furthermore, OSA and obesity often co-exist and manifest activation of shared molecular end-organ injury mechanisms that if properly identified may represent potential therapeutic targets. A challenge in the development of non-invasive diagnostic assays in body fluids is the ability to identify clinically relevant biomarkers. Exosomes, a class of extracellular vesicles (EVs), are very small membrane vesicles that are secreted and released by a variety of cells. These exosomes play important roles in mediating cell-cell communication via their cargo that includes lipids, proteins, mRNAs, miRNAs, and DNA. We have recently identified a unique cluster of exosomal miRNAs in both humans and rodents exposed to intermittent hypoxia as well as in patients with OSA with divergent morbid phenotypes. We will present recent findings regarding exosomal cargos including microRNAs, involved in intercellular communication relevant to OSA, endothelial and metabolic dysfunction, and neurocognitive impairments as well as their potential utility as diagnostic and prognostic biomarkers.

Biography

David Gozal is currently the Marie M. and Harry L. Smith Endowed Chair and the Chairman of the Department of Child Health at the University of Missouri, as well as Physician-in-Chief of the University of Missouri Health Children's Hospital. Prof. Gozal's research interests include projects such as gene and cellular regulation in hypoxia and sleep disruption, murine models of sleep disorders, and genomic and proteomic approaches to clinical and epidemiological aspects of sleep apnea in both adults and children. In addition, he has pioneered biomarker discovery and machine learning approaches for the diagnosis of sleep apnea across the lifespan. More recently, he has begun exploration of the role of the gut microbiome and circulating exosomes as mechanistic effectors and biomarkers in sleep disorders and associated morbidities. He is Past President of the American Thoracic Society, the world leading organization for pulmonary, critical are and sleep medicine, was a member of the Board of Directors of the Sleep Research Society 2014-2016 and is Deputy Editor-in-Chief for the journal Sleep, and Associate Editor for ERJ, Pediatric Pulmonology, and Frontiers in Neurology and Frontiers in Psychiatry. He has been the recipient of the ATS Amberson Lecture in 2002 and was awarded the William C. Dement Academic Achievement Award by the American Academy of Sleep Medicine in 2013, and the 2016 Lifetime Achievement Award of the National Sleep Foundation. He has also received two honorary doctorates from the University of Barcelona and University of Lleida in Spain. His research work has been continuously supported by grants from the NIH since 1992, and he has published over 835 peer-reviewed original articles carrying a H index of 135 and >75,000 citations (one of the top 1,000 most ever cited biomedical scientists in the world), along with more than 175 book chapters and reviews, edited 6 books, presented more than 1,000 scientific abstracts, and has extensively lectured all over the world.

David Gozal

Biography

Abdelnaby Khalyfa, MS, PhD, is associate professor in the Department of Child Health, and a member of Ellis Fischel Cancer Center at the University of Missouri (MU). Dr. Khalyfa is also a representative for the School of Medicine to Faculty Council. Dr. Khalyfa is a renowned sleep researcher who studies the metabolic and vascular consequences of sleep disorders. He has conducted groundbreaking research relating to obstructive sleep apnea (OSA) in children, linking the disorder to genetic disruptions that lead to inflammation, organ dysfunction and metabolic dysfunction using multi-omics approaches including single cells, metabolomic, gut microbiota, lipidomic, and transcriptomics. Dr. Khalyfa developed research around how extracellular vesicles (exosomes) can change cell phenotypes based on disease state, and his research is focusing on circulating exosomes in obstructive sleep apnea as phenotypic biomarkers and mechanistic messengers of end-organ morbidity. Dr. Khalyfa research seeks to identify genetic markers in children and adults with sleep disorders that could predict the onset of long-term medical conditions such as obesity, hypertension and cancer. He believes defining how a specific exosome miRNA profile relates to disease pathogenesis will engender a new, clinically feasible opportunity to examine the miRNA content of exosomes in a patient blood sample for early diagnosis and as a gauge of response to therapy. One of the most important aspects of exosomal miRNAs is that they represent a potential valuable tool for non-invasive early diagnosis, treatment selection and prediction of therapy resistance. miRNA-based therapy aims to restore aberrantly expressed miRNAs to a physiological level, either by administering synthetic miRNAs that mimic them, or by administering anti-miRNAs that reduce their abundance. The blood-brain barrier (BBB) is composed of brain microvascular endothelial cells (BMEC), pericytes and astrocytes. Dr. Khalyfa developed a 3D-BBB system that reproduces many of the characteristics of the human BBB, which can be useful as a high-throughput evaluation tool to facilitate the development of central nervous system (CNS) drug and precision medicine. Dr. Khalyfa holds three patents.

Abdelnaby Khalyfa

Presentation 1

Development of Neuroprotective Agents and the Implementation of an African Specific Disease-Gene Variant Data Analytic Platform with a Focus on Alzheimer's Disease by **Prof. Jacques Joubert, Ph.D. (UWC) and Prof. Xiaoqin Zou Ph.D. (MU)**

Jacques Joubert, Drug Design and Discovery lab, School of Pharmacy, Faculty of Natural Sciences, University of the Western Cape, South Africa
Xiaoqin Zou, Departments of Physics and Biochemistry and programme affiliations in Biochemistry, Bioinformatics and Computational Biology, University of Missouri, MO, USA

Abstract

Dementia, with Alzheimer's Disease (AD) being the most common form, is a condition that affects a significant number of people worldwide and is projected to increase in the future. Recently, our group has developed edaravone-based pyridinium derivatives (EBPDs) that show potential as neuroprotective agents. The EBPDs have a variety of biological activities such as acetylcholinesterase inhibition, free radical scavenging, modulating amyloid- plaque formation, inhibiting the -secretase enzyme, and protecting neuronal cells and Zebrafish larvae against neurotoxicity. However, there is also formation of EBPD radical adducts in biological media observed in in vitro blood-brain barrier (BBB) pilot studies. Therefore, we have developed solid-lipid nanoparticle delivery systems to improve the absorption, stability and penetration of EBPDs across the BBB. We are currently validating our in vitro findings through rodent in vivo behavioural toxicity studies and will further evaluate the AD therapeutic potential of the EBPDs using a 3xTg-AD mouse model in collaboration with Dr. Ai-Ling Lin. In another related study we are focussing on the tau protein and its role in the formation of neurotoxic neurofibrillary tangles as a potential cause of AD. The specific targets that we are studying are the glycogen synthase kinase 3 beta (GSK3) and the sirtuin-1 (SIRT1) enzymes, as both have been reported to play a role in the accumulation of hyperphosphorylated tau proteins. Our team, in collaboration with Dr. Xiaoqin Zou, has commenced with a virtual high-throughput screening and computer-aided drug design (CADD) study to identify hit compounds that could inhibit GSK3 and/or promote SIRT1 activity. In parallel with these studies, we are in the process of developing a new interactive platform for drug discovery and precision medicine in Africa by leveraging bioinformatics and computational methods. The platform will feature a database of 3D protein models from identified African protein variants and will be validated with the GSK3 enzyme using in-vitro studies on wild-type and African variant GSK3 proteins. The project will provide a proof-of-concept for the utilization of the platform for African precision drug discovery endeavours. This talk will therefore focus on the development of the EBPDs, the shift from Aß to the tau protein in AD research, and the use of CADD studies to identify novel inhibitors of the GSK3 and SIRT1 enzymes. Additionally, it will cover the implementation of a web-based platform for studying genetic variants in African populations and its potential to address underrepresentation in genetic research.

Presentation 2

Alzheimer's disease mitigation: AI, neuroimaging and gut-brain axis by

Prof. Ai-Ling Lin (MU) and Prof. Jacques Joubert, Ph.D. (UWC)

Jacques Joubert, Drug Design and Discovery lab, School of Pharmacy, Faculty of Natural Sciences, University of the Western Cape, South Africa
Ai-Ling Lin, Vice Chair for Research, Radiology Professor of Radiology, Biological Sciences, and Institute for Data Science & Informatics, University of Missouri, MO, USA

Abstract

Alzheimer's disease (AD) is the most common form of dementia and currently there are no effective therapeutics to reverse the course once the clinical symptoms developed. Early identification of risk factors for AD and effective interventions thereof would be critical to mitigate AD pathological development and prevent the onset of clinical symptoms. In the presentation, I will demonstrate how we used artificial intelligence approach to identity the risk factors from clinical data, and determined the effectiveness of pharmacological and nutritional interventions in an animal model with human APOE4 genes, the strongest genetic risk factor for AD. Our methods include in vivo MRI brain imaging, gut microbiome analyses, metabolomics, and behavioural assessments. Future direction on translational/clinical applications and precision medicine will also be discussed.

Biography

Jacques Joubert is an Associate Professor of Pharmaceutical Chemistry with 15 years of experience in drug design, medicinal chemistry, biological assay development, virtual screening and protein-ligand docking studies. His laboratory is well established in the field of drug design and discovery and has the necessary facilities and licenses to conduct organic synthesis, advanced biological assays and computational drug design studies. Jacques's group has designed and evaluated novel compounds for diseases such as malaria, tuberculosis and neurodegenerative disorders. Jacques is currently the PI for projects funded by the South African Medical Research Council and the Perivoli Africa Research Centre, which is focused on the biological evaluation and drug development of lead compounds for use against neurodegenerative disorders, inflammatory diseases and/or stroke. He has a strong record of publications (62 papers, H-index: 19), funding administration and student supervision and is currently an NRF C-rated scientist.

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Jacques Joubert

Biography

Xiaoqin Zou is a professor of bioinformatics and computational biology with over 25 years of experience on computational modelling of biomolecules. Xiaoqin's laboratory is well established in the fields of protein-protein and protein-peptide structure prediction and protein-ligand docking. My group develops state-of-the-art algorithms on molecular docking/scoring and applies the methods to real applications in collaboration with experimentalists. She has published a total of 98 peer-reviewed journal papers and book chapters. Xiaoqion is a former recipient of the NSF CAREER Award, an American Physics Society Fellow, and an National Academy of Inventors Senior Member. She is also a recipient of the NIH MIRA grant award, a funding mechanism by NIGMS that helps "distribute funding more widely among the nation's highly talented and promising investigators."

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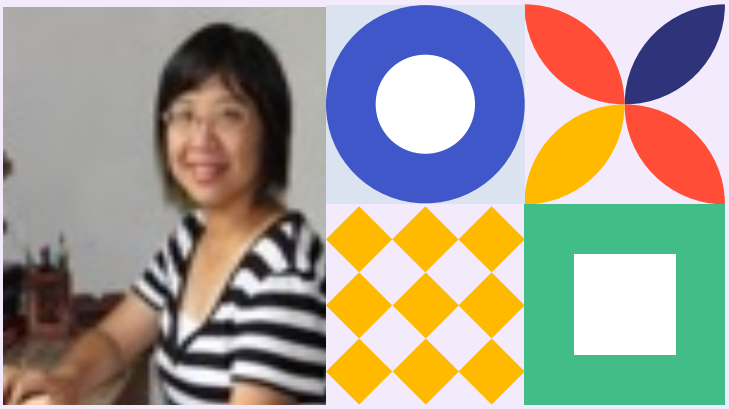

Xiaoqin Zou

Biography

Ai-Ling Lin completed her PhD and Postdoctoral training as a medical physicist from the University of Texas Health Science Center in San Antonio, TX. In 2014, she began her independent research career as an Assistant Professor at the University of Kentucky and promoted to Associate Professor with tenure in 2019. She joined University of Missouri as a Full Professor with tenure in August 2021. Dr. Lin is a well-known expert on translational neuroimaging of brain vascular and metabolic function in aging, Alzheimer's disease (AD), stroke and traumatic brain injury (TBI). She developed and applied magnetic resonance imaging and spectroscopy, and positron emission tomography to test nutritional and pharmacologic approaches for protecting the brain from aging, TBI and AD. She is also an expert on artificial intelligence (AI) and multi-omics (such as metabolomics, transcriptomics, and gut microbiome). She has applied AI to identify markers that are highly predictable for AD development and progression, and applied gut microbiome analyses to study gut-brain interaction underlying brain aging, stroke, TBI, and AD. Dr. Lin has been successful in securing NIH funding, including KL2, K01, R01s, and administration supplement awards, and several Foundation grant awards. She has served on many grant review panels, including being a charter member on the Clinical Translational Imaging Science (CTIS) study section for NIH, as well as for NASA and several private foundations. Her reputation has been recognized internationally by being frequently invited to be a speaker, to organize international conferences and chair symposia related to neuroimaging, aging, AD and gut microbiome.

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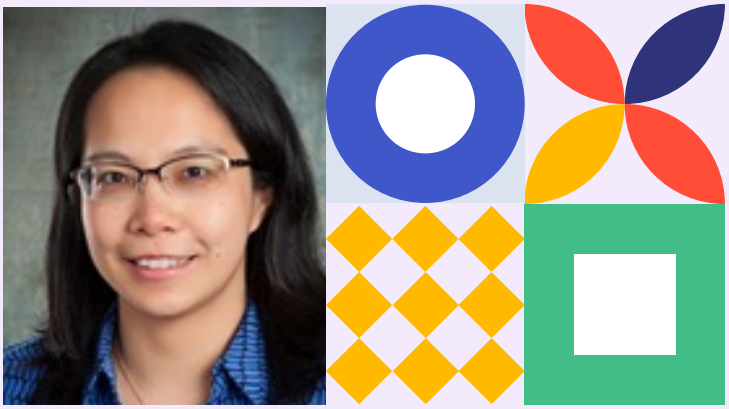

Ai-Ling Lin

Developing a multimodal, integrative, in-silico, multiomics data science approach to early detection of HPV-based biomarkers of oropharyngeal head and neck cancer by

Prof. Henry Adeola (UCT), Prof. James Bashkin (UM St. Louis), Prof. Haly Holmes (UWC), Prof.Amir Afrogeh (UWC), Prof. Badri Adhikari (UM St. Louis) and Dr Hocine Bendou (SANBI, UWC)

Email: henry.adeola@uct.ac.za ; bashkinj@umsl.edu; hholmes@uwc.ac.za ; amir.afrogheh@nhls.ac.za

Abstract

Head and neck cancer (HNC) has a high burden in Africa. Poor oral health constitutes a significant burden of disfigurement, discomfort, social isolation, and NCD-related deaths in this region. A result is that patients with HNC have 55% five-year survival, high post-treatment relapse rates, and limited treatment/diagnostic options. Despite the high burden of infection and increasing incidence of Human Papillomavirus (HPV)-induced oropharyngeal HNC (OHNC) in Africa, epidemiological and genetic risk factors have not clearly explained a reasonable proportion of variation in OHNC risk and site predilections. In Africa, the dentist-to-patient ratio is about 1:150,000, compared to 1:2000 in the industrialized world, translating to ca. 8,000 dentists per 1.2 billion people in Africa. Hence, this study aims to develop a sustainable and rapid multimodal artificial intelligence (AI)-aided tool for OHNC detection in resource-limited settings. This will be achieved by leveraging publicly available eHealth and African database resources. A team of clinical oral scientists, biochemists, and computer science data experts from UWC and UMSL will deploy computational models, pipelines, and algorithms, using a mined data set of over 2500 anticipated retrospective generated multiomics coupled with eHealth records. This research addresses a critical need for early detection and risk stratification of OHNC. The conventional diagnostic standard for suspicious oral lesions is histopathology, which an expert pathologist carries out. However, the critical shortage of oral pathologists in the African region often leads to diagnostic delays and increased morbidities and mortalities. In addition to challenges posed by low agreement among pathologists and risk-based discriminatory grading schema for various OHNC entities, funding and infrastructural support are limited in many African countries. Hence, developing a robust, data-driven, cost-effective tool that can risk-stratify OHNC will be of significant benefit to patients in Africa. The high prevalence of head and neck cancers and many clinical eHealth records is highly conducive to artificial intelligence (AI) approaches.

AI-enhanced multiomics has been used successfully for precision biomarkers identification in various related diseases. This study aims to establish and sustain a multimodal integrative in-silico database biomarker mining with a multiomics approach for HPV-based OHNC biomarker discovery. The central hypothesis of this research is that an AI-enhanced multiomics approach will improve the automated detection and risk stratification of OHNC. Furthermore, combining multiomics with environmental and lifestyle data offers a powerful tool for understanding HPV+ OHNC risk in Africans. To accomplish the project's aim, we will (i) integrate multiomics data curated from publicly available multiomics databases, (ii) infer HPV status from unsupervised learning in TGCA, (iii) use curated eHealth records inferences to develop a multimodal biomarker and classification algorithm for OHNC in Africans. These deep/machine learning models have the potential to inform treatments, minimize unnecessary diagnostic interventions, and improve oral health care on the African continent.

Biography

Henry Adeola has recently completed his Ph.D. in cancer proteomics and genomics at the University of Cape Town through an International Centre for Genetic Engineering and Biotechnology (ICGEB) fellowship. Specifically he used mass spectrometry and protein microarray techniques to identify novel potential urinary and serological biomarkers of prostate cancer. He trained as a Dental Surgeon at the University of Ibadan Medical School and completed his postgraduate residency training in Oral and Maxillofacial Pathology/Biology at the Lagos University Teaching Hospital in Nigeria. He then spent a year at the Niigata University Medical and Dental Hospital in Japan as a molecular oral cancer research fellow. Whilst completing his PhD Henry worked as a part-time Lecturer at the Department of Oral and Maxillofacial Pathology, University of the Western Cape/ Tygerberg Hospital. Henry is firmly committed to addressing the cancer burden in Africa through transdisciplinary collaborative team science. He is currently an Associate Professor is in the Department of Medicine, University of Cape Town and the Department of Oral and Maxillofacial Pathology, University of the Western Cape, South Africa. He is a clinician-scientist who has a strong background in molecular oral pathology, proteomics, cancer research, in-silico bioinformatics, and systems biology.

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Henry Adeola

Biography

James K Bashkin, is a Professor of Chemistry and Biochemistry at the University of Missouri, St Louis, USA. He has over two decades of experience in HPV drug discovery, drug development, and mechanism of action research, with seven issued US patents and numerous publications in the area.

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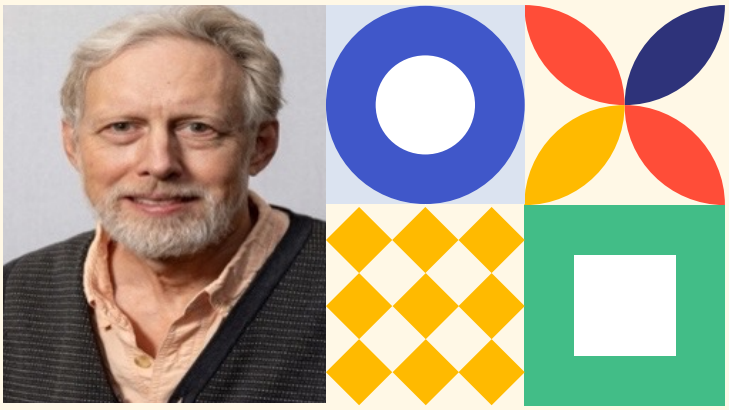

James K Bashkin

Biography

Haly Holmes is a certified periodontist who practices her clinical speciality as a staff member in the Department of Oral medicine and Periodontology Department (OMP) at the University of the Western Cape Dental Faculty and is responsible for undergraduate and postgraduate teaching and research supervision. Haly's exposure to the oral medicine clinics highlighted the increasing unmet challenges that oral pathologies pose on the African continent, particularly with regards to the need for early detection, understanding the pathophysiology, risk stratification. Thus, her research interest includes all aspects of oral medicine, employing a wide range of approaches from molecular to population-based research, in efforts to improve the understanding of the pathobiology, diagnostics and therapeutics of oral soft tissue pathologies. To this end, she has initiated the establishment of an oral medicine registry (ORMSA) to establish oral soft tissue lesions prevalence and trends. In addition, she is the PI of a newly-established working group to develop a saliva biorepository to determine the potential role of salivary biochemistry parameters and OMIC signatures (genomics, lipidomics, proteomics, etc) on the African continent. She is currently registered for a PhD in the department of Oral Pathology to establish the HPV-related oral cancer disease burden in South Africa with the anticipation of increasing the evidence-base for formulating diagnostic guidelines and recommendations for disease surveillance. Passionate about research, Haly serves on the departmental research committee, having supervised eleven students to successful completion of postgraduate degrees. Nationally, Haly has served as an external examiner for the College of Medicine of South Africa. Previously, she served as secretary and a member of ExCo of the SA Society of Periodontology, Implantology and Oral Medicine.

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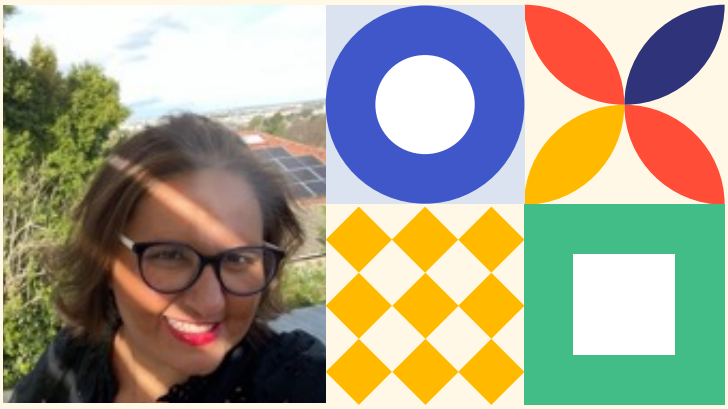

Haly Holmes

Biography

Amir Afrogheh is an Associate Professor at the University of the Western cape at Tygerberg Hospital and a Principal Specialist in Oral and Maxillofacial Pathology at the National Health Laboratory Service (NHLS) and. He is the current Head of the Department of Oral and Maxillofacial Pathology at the University of the Western Cape (UWC), Cape Town, South Africa. His PhD focused on HPV-induced cancers of the head and neck.

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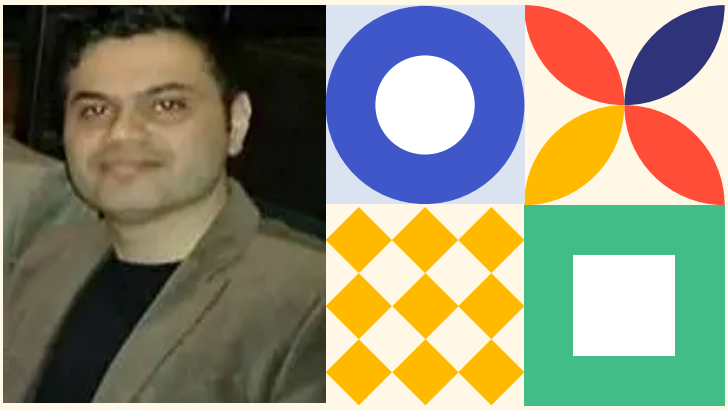

Amir Afrogheh

Biography

Badri Adhikari is an Assistant Professor of Computer Science at the University of Missouri, St Louis, USA. He is an expert in developing deep learning methods for bioinformatics problems.
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Badri Adhikari

Biography

Hocine Bendou is a senior researcher at the South African National Bioinformatics Institute, based at the University of the Western cape, South Africa. His research group focuses in developing data science solutions in the area of genomics and bioinformatic identification of genetic abnormalities driving the pathogenesis and progression of human cancer.
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Hocine Bendou

Precision nanomedicine for tuberculosis therapy by **Prof. Admire Dube (UWC) and Prof. Raghu Kannan (MU)**

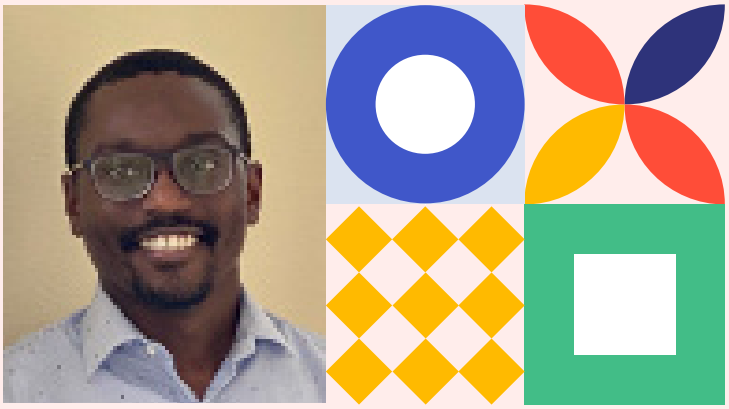
Email: adube@uwc.ac.za & KannanR@health.missouri.edu

Abstract

Tuberculosis (TB) caused by Mycobacterium tuberculosis (Mtb) is a major global public health concern and is a leading cause of death globally, and moreso in South Africa. Although relatively effective antibiotic drug regimens are available, treatment failure remains a major roadblock to TB control. Genetically encoded antibiotic drug resistance is a major concern. In our laboratory, we have been investigating nanoparticle-based host directed therapies. These systems are designed to activate host macrophages (the primary host cells of M.tb) to achieve eradication of M.tb without the use of antibiotics. This talk will discuss aspects of nanoparticle design and results obtained in in vitro and in vivo models of M.tb infection. Future directions will also be presented including formulation of lung targeted nanoparticle systems.

Biography

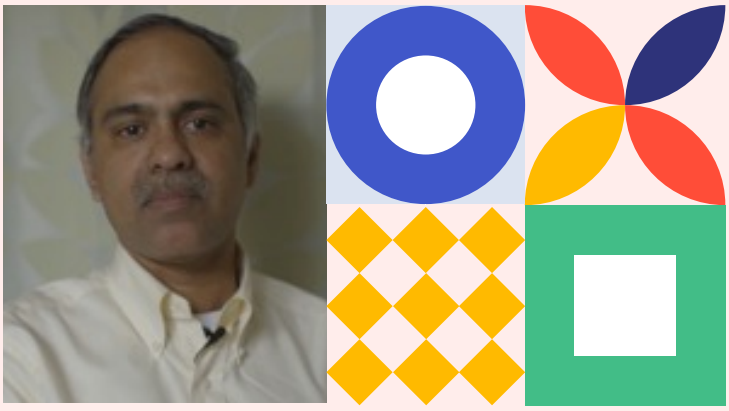
Admire Dube is a pharmaceutical scientist and Associate Professor in Pharmaceutics at the School of Pharmacy, University of the Western Cape. He is a pharmacist by training and holds a PhD in Pharmaceutical Sciences from Monash University Australia and post-doctoral training in nanomedicine from the University at Buffalo, USA. He previously held a position as Senior Researcher at the Council for Scientific and Industrial Research in Pretoria where he was involved in research and commercialization of nanoparticle delivery systems for infectious diseases. His research group at UWC supported by at least two NIH grants, focuses on the application of nanoparticles towards the treatment of tuberculosis, especially to achieve immunotherapy, targeted drug delivery and/or access across biological barriers. He has published several articles on nanomedicine in high impact factor journals and supervised several postgraduate students.



Admire Dube

Biography

University of Missouri, Columbia, MO. Dr. Kannan is a faculty of Radiology at University of Missouri (MU) and has been a faculty member at MU since 2005. He leads the program on clinical translation of nanomaterials at MU. He received his M.S. degree in chemistry from the Indian Institute of Technology at Madras in 1993 and his Ph.D. degree in chemistry, with a gold medal, from the Indian Institute of Science in 1999. Dr.Kannan has been actively involved in the design and development of nanomedicine drugs and metal based radioactive pharmaceuticals for over 23 years. Dr Kannan's research program is focused on developing gene and drug delivery vehicles to treat resistant tumors. Specifically, his research is focused on understanding the mechanisms of drug resistance in lung and ovarian cancers and identify therapeutic targets. Based on the targets identified, his team develop develops nanoparticle based therapeutic agents to overcome the resistance. Dr. Kannan has published over 70 peer-reviewed publications and have secured over 20 US patents. Dr. Kannan's research is funded by both NIH-R01 grants and the translational aspect funded by private pharmaceutical companies. His groups is currently funded over $5 million grants. Dr. Kannan is a co-founder of four start-up companies at MU and areas of research include Nanomaterials, Personalized Diagnostics, Molecular Imaging, Targeted Therapy.



Raghuraman Kannan

Patient Data standardization and collection for UWC; benefits of collaborations and partnerships by **Prof. Gerald J Wyckoff (UMKC) and Prof. Jennifer-Anne Chipps (UWC)**

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Abstract

The collection and use of patient data- whether it is limited to demographic data, includes health status information, or even includes tissue or genetic data- should be standardized across UWC entities for maximal value moving forward. This includes IRB and ethics reviews, standard questionnaires, shared electronic medical record systems across UWC clinical settings, trainings for health care personnel collecting information, and as possible, biobanking facilities.The ability to perform large scale, longitudinal studies on patient populations in the Western Cape, across South Africa, and in Africa generally, hinges on our ability to come together around these shared tasks. UWC is at an inflection point for this effort. Under the UMSAEP, we can harness expertise across the US and South Africa for this effort. The collection and use of data across our sites can empower GWAS, health outcomes studies, studies into transitions of care, and large-scale studies on population health. We will discuss the goals and needs of this effort; the shared opportunities and threats this effort faces; plans for pilot projects that utilize collected data; and funding sources that could help launch and sustain.

Biography

Gerald J Wyckoff, Ph.D., Professor and Chair, DPPS, UMKC School of Pharmacy

Modern drug discovery using in silico techniques is about sifting through large amounts of data to find signal in a sea of noise, and developing methodologies that do this efficiently. My educational background is as a molecular evolutionary geneticist, finding faint signatures of positive selection in a sea of genomic noise. This led me to become involved with large scale genomic, and later proteomic, projects utilizing a bioinformatic framework. At UMKC I have developed collaborations with structural biology faculty, in part to extend my knowledge of how to apply large-scale screening techniques to structure-based problems. This has been fruitful and allowed me to extend my knowledge in drug discovery towards chemical information signatures useful for high-throughput screening of compounds. All of these problems have as a common theme the development of tools to make sense out of large scale data where noise is high and signal is low. I also have the demonstrated ability to work with people in diverse fields, including structural biology and within medicinal chemistry. shared effort for this project over the next two decades.

Gerald J Wyckoff

Biography

Jennifer-Anne Chipps, Ph.D., Associate Professor, UWC, Faculty of Community and Health Sciences, School of Nursing: BSC Nursing Hon (WITS, South Africa), BSc Psychology Hon (UNISA, South Africa), Grad Dip Nursing Administration (WITS, South Africa), Grad Dip Nursing Education (WITS, South Africa), Masters in Public Health (UNSW, Australia), Grad Dip Applied Epidemiology (VETAB, Australia), Ph.D. Telemedicine (UKZN, South Africa)

Jennifer-Anne Chipps

Utilization of the African Genome Project for Africa-focused Precision Medicine and Precision Drug Discovery: A Case Study of Statins by Prof. Samuel A. Egieyeh (UWC)

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Abstract

The African genome contains the most genetic variants in the world. In 2020, a study published by the Human Heredity and Health in Africa focusing on single nucleotide polymorphism, found that the genotype of 426 African individuals contained more than 3 million variants that were not previously described. A review of the PharmKGB revealed missense mutations that led to clinically relevant effect both on metabolism and efficacy of many medications. Polymorphisms in drug transporters have been may contribute to the observed diversity in the response to some drugs in African patients. Specifically, the solute carrier organic anion transporter family member 1B1 (SLCO1B1) gene which encodes a membrane-bound sodium-independent organic anion transporter protein (OATP1B1) has been implicated as a determinant of efficacy and toxicity of HMG-CoA reductase inhibitors (statins). SLCO1B1 rs4149056 (also known as c.521T>C, Val174Ala or V174A which reduce uptake/transport activity of the OATP1B1) has been found at markedly higher frequencies in African population than in non-African populations. This might lead to increased risk of statin-related myopathy or myalgia when such patients are treated with statins. Furthermore, polymorphism in HMG-CoA reductase (HMGCR), a rate-limiting enzyme involved in cholesterol biosynthesis has been reported as determinants of the efficacy of statins.

Firstly, we used computational modeling to explore and compare the interaction and of rosuvastatin with the wild type and rs4149056 SNP of the OATP1B1 transmembrane transporter protein to gain insight into the potential rate of the drug transportation. We expect to quantify the extent of reduction in the uptake/transport of rosuvastatin by the OATP1B1 protein. This might guide dose adjustment for rosuvastatin in African population with rs4149056 SNP. Secondly, we used recently reported missense SNPs of HMGCR gene rs147043821 and rs193026499 as a foundation for precision drug discovery. We examined the effect of the SNPs on the predicted inhibitors of the mutated HMG-CoA reductase using computational modeling. Overall, we demonstrated the value and potential of the output from the African Genome Project to drive Africa-focused precision medicine and precision drug discovery.

Biography

Samuel Ayodele Egieyeh is a seasoned and highly experienced pharmacist with Bachelors and Master's degrees in Pharmacy, and PhD in Bioinformatics. He also has a post-graduate diploma in clinical research and drug development from the University of Basel, Basel

Samuel Ayodele Egieyeh

Precision medicine: Pharmacogenomics and Development of Individualised Drug Therapy for Diabetes and Hypertension Patients by **Prof. Mongi Benjeddou (UWC)**

Department of Biotechnology, Faculty of Natural Sciences,
University of the Western Cape, South Africa
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Abstract

Type 2 diabetes mellitus (T2DM) and hypertension represent two common conditions worldwide. They frequently occur in the same individuals in clinical practice. The presence of hypertension does increase the risk of new-onset of diabetes, as well as diabetes does promote development of hypertension. Comorbid hypertension and diabetes mellitus are associated with high rates of macrovascular and microvascular complications. T2DM is commonly accompanied by other cardiovascular disease (CVD) risk factors, such as hypertension, obesity, and dyslipidemia. CVDs are the most common cause of death in people with T2DM. Due to the frequent association with cardiovascular diseases, the management of hypertensive patients with T2DM is an important clinical priority. Metformin is often the first drug used to treat newly diagnosed type 2 diabetic patients, and it is widely prescribed worldwide. Metformin is effective as monotherapy and in combination with nearly every other therapy for type 2 diabetes, and its utility is supported by data from a large number of clinical trials. However, despite its exceptional efficacy and safety profile, about 40% of type 2 diabetes patients who have taken metformin failed to reach target fasting glucose level. Recent studies suggest that interpatient variability in response to metformin therapy could be related to polymorphisms in the organic cation transporter (OCT) genes and/or the multidrug and toxin extrusion (MATE) genes. In the case of hypertension, several genetic biomarkers for antihypertensive drug response have been also identified, which might be used in treatment selection and optimization for hypertension. Research in the field has also enhanced our understanding of hypertension and the mechanisms by which the various drugs produce efficacy. There are several examples of genes in the literature and databases with relatively strong data on associations of genetic polymorphisms with antihypertensive response; the data on ADRB1, CACNB2, and NEDD4L are detailed as examples. In this talk, we will present the main findings of a 12-year precision medicine project in South Africa with a special focus on admixed and indigenous Sub-Saharan African populations, as well as the main challenges and future directions for the project. The contribution of this project towards the development of an individualised drug therapy for patients with diabetes and hypertension will be highlighted.

Biography

Mongi Benjeddou a full professor in the Department of Biotechnology at the University of the Western Cape (UWC). His research interests and publications in the last few years cover human population genetics, forensic genetics, genetic ancestry studies, and more recently pharmacogenomics and precision medicine. The aim of his precision medicine research is to develop and validate individualized (drug) therapies for patients with diabetes, hypertension and other non-communicable diseases such as cancer, and suitable for indigenous and admixed populations from South Africa in particular, and the Sub-Saharan African region in general.

Mongi Benjeddou

Application of metabolomics and DNA adductomics to further unravel the impact of the exposome in health and disease by **Dr. Lieselot Y. Hemeryck (UGent)**

Lab. of Integrative Metabolomics, Dept. of Translational Physiology, Infectiology and Public Health Faculty of Veterinary Medicine, Ghent University, Belgium
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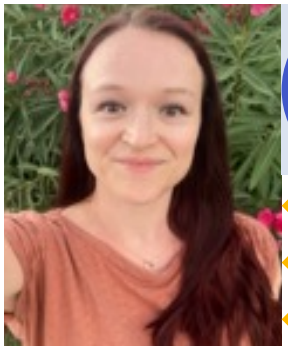
Abstract

The Laboratory of Integrative Metabolomics (LIMET, Prof. Lynn Vanhaecke) has developed extensive expertise in the optimisation and implementation of mass spectrometry (MS) based metabolomics and DNA adductomics methodologies. For many conditions, personalized preventive strategies and diagnostic, prognostic or predictive biomarkers of disease are lacking today. It is our belief that unravelling the molecular basis by which the exposome (diet, gut microbiome, etc.) impacts the human metabolome may address this hurdle. Therefore, our research aims to 1) develop true molecular high-resolution MS based metabolomics and DNA adductomics platforms to discriminate metabolic phenotypes of healthy vs. diseased individuals, and 2) unravel the impact of the exposome on the host metabolome in relation to disease (e.g. study the effect of red meat consumption on the digestive metabolome in relation to colorectal cancer (CRC) risk, follow-up during therapeutic intervention, etc.). In this context, in 2015, the Laboratory of Integrative Metabolomics LIMET was the first to develop untargeted polar metabolomic approaches for the analysis of fecal samples, which have been applied successfully in studying many food-related diseases, like e.g. food allergy, type 2 diabetes, CRC and inflammatory bowel disease. Complimentary to polar metabolomics, a novel and unique HRMS-based fecal lipidomics platform was developed and applied successfully to metabolic diseases in 2017. Both platforms have been refined in recent years, for metabolomic fingerprinting of urine, blood and tissue, plus more recently also saliva and cerebrospinal fluid. In addition, in 2015 we also developed a (full scan) HRMS based DNA adductomics platform. DNA adductomics is a highly promising tool for human biomonitoring and systems toxicology, which has been applied successfully to e.g. demonstrate that significant differences in DNA adduct formation (= DNA damage) occur according to ongoing endogenous processes (i.e. tissue type) as well as external influences, like e.g. exposure to pollutants, diet and lifestyle. It may be noted that the use of conventional MS applications is not that straightforward in a more practical and/or clinical (vs. laboratory) setting. Nevertheless, the introduction of Rapid Evaporative Ionisation MS (REIMS) offers compelling perspectives as REIMS can significantly reduce the time and workload required for metabolomics analyses, but enhance research output and efficiency by eliminating various sample preparation steps and chromatographic separation. In light of this, at LIMET, a REIMS platform for the rapid on site or point of care translatable diagnosis and prognosis of a variety of (patho)physiological changes has been optimized, considering a large spectrum of matrices (e.g. feces, blood, urine, saliva).

Biography

Lieselot Hemeryck is a senior FWO postdoctoral fellow, holding a Master in Veterinary Medicine (2012) and a Ph.D. in Veterinary Sciences (2017). During her Ph.D., Dr. Hemeryck's work focused on the development of a DNA adductomics platform to study the genotoxic effects of both endo- and exogenous chemicals. At that time, the DNA adductomics methodology was applied for the investigation of the carcinogenic effects of red meat consumption in relation to CRC, but is currently being implemented in a much broader exposomics setting. Dr. Hemeryck has won several awards, among which the prestigious Academy Award for Scientific Research in Veterinary Medicine by the Belgian Royal Academy of Medicine in 2019, for her contribution to the field of Veterinary Public Health. As a postdoc, Dr. Hemeryck's research interests include the further development and application of both metabolomics and DNA adductomics workflows.



Lieselot Hemeryck

FLEXiGUT: Investigating the life-course impact of dietary and environmental exposure on chronic low-grade gut inflammation by

Dr. Roger Peró-Gascón (UGent), Prof. Dr. Marthe De Boevre (UGent), Prof. Dr. Sarah De Saeger (UGent), and the FLEXiGUT consortium

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Abstract

Environmental factors contribute towards the risk for adverse health manifestations against a background of genetic predisposition. The exposomics research field aims to discover the non-genetic drivers of health and disease measuring environmental influences and associated biological responses throughout the lifespan. These include lifestyle, diet, exposure to environmental toxicants, and endogenous processes such as the gut microbiome metabolism among others. A personal exposome approach could be a valuable and complementary approach to pharmacogenomics and pharmacometabolomics in precision medicine. In this talk I will present the Flemish exposome project, FLEXiGUT, the first large-scale exposomics study focused on chronic low-grade gut inflammation. To characterize human life-course environmental exposure to assess and validate its impact on gut inflammation and related biological processes and diseases, we combine exposure science and high-throughput -omics technologies with epidemiological studies. We use three main sources of data: 1. available metadata on location, dietary intake and lifestyle; 2. biomonitoring of dietary and environmental contaminants in biofluids and tissues such as urine, blood and placenta; 3. analysis of associated biological responses by -omics techniques, including metagenomics, DNA adductomics and metabolomics, as well as the assessment of telomere length (as a marker for accelerated biological ageing) and measurement of inflammatory markers. An integrative multi-omics data processing approach will be applied to uncover associations between the exposures and diseases, but also provide insights into the mechanisms by which the exposure might be exerting its effects.

Biography

Roger Pero-Gascon is a postdoctoral researcher from the Flanders research foundation (FWO) working at the Centre of Excellence in Mycotoxicology and Public Health (CEMPH) of Ghent University, Belgium. In 2021, he joined the CEMPH to work on the FLEXIGUT exposome project. In October 2022, Dr. Pero was appointed principal investigator of MYCOGUT, a FWO-funded three-year research project to investigate the impact of chronic multiple mycotoxin exposure on gut inflammation using a biomonitoring approach. Dr. Pero did his PhD in Analytical Chemistry at the University of Barcelona (Spain) and received the PhD award from the Spanish Society of Chromatography and Related Techniques (SECyTA) for the best doctoral thesis defended in 2020. He extensively investigated on-line solid-phase extraction capillary electrophoresis-mass spectrometry using different affinity sorbents for the analysis of protein and microRNA biomarkers of neurodegenerative diseases and cancer in biological fluids.

Roger Pero-Gascon

The prognostic role of M2-type tumor associated macrophages in oropharyngeal squamous cell Carcinoma by **Dr. Tijl Vermassen (UGent) and Mr. Mathieu Struys (UGent)**

Email: Tijl.Vermassen@UGent.be & Mathieu.Struys@UGent.be

Mathieu Struys 1,2,3, Tijl Vermassen 3,4,5

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Background:

Oropharyngeal squamous cell carcinoma (OPSCC) is an immunogenic cancer characterized by a rapidly increasing incidence in various parts of the world. It is becoming increasingly clear that the tumor microenvironment (TME) and its associated immune cells play a pivotal role in both diagnosis and treatment of patients with OPSCC. Previous research from our group has indicated that patients with a high abundance of tumor infiltrating lymphocytes (TILs), and more specifically CD8+ cytotoxic lymphocytes, have a prolonged overall survival compared to patients with only limited numbers of TILs. Next to TILs, tumor-associated macrophages (TAMs) are one of the most abundant cell types in the TME. TAMs are characterized by a heterogeneous appearance, meaning they can occur in different forms with M1-like TAMs and M2-like TAMs as extremes of their spectrum. While M1-like TAMs present with anti-tumoral features, M2-like TAMs are associated to immune evasion, tumor progression, metastasis and poor prognosis. However, the prognostic value of individual M2-like TAM subsets in OPSCC remains unclear. The aim of our study is to determine the prognostic value of CD163, CD206 and CD68 expressing TAMs in OPSCC and to compare their relative prognostic accuracy.

Methods:

We examined the expression of TAM markers CD163, CD206 and CD68 in tumor samples from 65 patients with OPSCC using immunohistochemistry. TAM evaluation was correlated to TIL assessment and patient outcome. The relative prognostic accuracy of all individual markers was assessed. Sub-analysis was made based on patient HPV status.

Results:

Preliminary data will be shown at the conference.

The role of human papilloma virus and tumor-infiltrating lymphocytes in oral and oropharyngeal cancer microenvironment: a tricontinental study by Dr. Tijl Vermassen (UGent) and Mr. Mathieu Struys (UGent)

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Background:

It is indicated that human papilloma virus (HPV)-related head and neck cancer (HNC) has different tumoral characteristics to HPV negative HNC. For instance, patients diagnosed with HPV-positive tumors have better survival rates, when compared to patients with HPV-negative tumors. Prior studies have shown that HPV-related HNCs are mostly seen in the oropharynx, and that in contrast to HPV-types, these tumors have a different composition of tumor-infiltrating lymphocytes (TILs) in their tumor microenvironment (TME). However, limited research has been conducted into the actual role of HPV in the increased influx of TILs in the TME of tumors originating from the oral cavity. Furthermore, although the incidence of HPV-related head and neck cancer appears to be highest (and on the rise) in high-income countries, more epidemiological data from low- and middle-income countries are warranted. The aim of our study is therefore to evaluate the prevalence and TME-modulating role of HPV in oral and oropharyngeal cancer in different demographic regions of Africa, Europe, and North America.

Methods:

An international multicentric retrospective cohort (2013 - 2022) will be established through a collaborative partnership between the University of the Western Cape (UWC), Ghent University (uGent) and the University of Missouri St Louis (UMSL). Following ethical approval, archival FFPE tissue blocks will be retrieved for serial sectioning. First, we will evaluate the p16 and consequent HPV positivity in all oropharyngeal and oral cancer samples. One slide will be stained with hematoxylin-eosin (H&E, if no archived slide is available). A second slide will be used to assess the p16 status (surrogate marker for HPV) via p16 CINtec Histology on a BenchMark XT automated system (Ventana Medical Systems, USA). In case of p16 positivity, a third slide will be used to determine the HPV strain via high-risk HPV in situ hybridization (ISH), again on a BenchMark XT. The high-risk HPV ISH test is considered positive if a discrete, blue colored, precipitate is observed in the tumor cells. All stained slides will be digitized, providing the opportunity to share and remotely view images and allow discovery and quantification of image biomarkers using digital pathology and artificial intelligence analyses. Next, TILs in the TME will be quantified on H&E sections according to the standardized methodology stipulated in the IIBWG guidelines. Association between TILs and HPV positivity and subtype will be determined. Finally, the effect of HPV positivity and TILs on patient outcome parameters will be estimated.

Results:

None available yet.

Biography

Mathieu Struys (MD, PhD student) was born in 1997. In 2022, he obtained his master's degree in medicine at the Ghent University. In October 2022, he started his medical residency at the Department of Otorhinolaryngology and Head and Neck Surgery at the University Hospital Ghent along with his doctoral degree program at the Department of Head and Skin at the Ghent University. His research focuses on tumor immunology, tumor biomarkers and the potential of the tumor microenvironment to modify tumor progression and response to immunotherapy, with a particular interest in head and neck squamous cell carcinoma (HNSCC). Mathieu Struys and the research team he is affiliated to are conducting innovative research into describing the tumor microenvironment of HNSCC in order to identify novel biomarkers with a diagnostic and/or therapeutic potential.

Links: https://www.crig.ugent.be/en/dr-mathieu-struys-md
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Mathieu Struys

Biography

Tijl Vermassen was born in 1988. In 2011, he obtained his Master in Biomedical Sciences at the Ghent University. In 2016, he successfully completed his PhD in which he demonstrated that the total urine N-glycome of prostate proteins can assist in the diagnosis of prostate cancer. Since he obtained his PhD, Dr. Tijl Vermassen is affiliated as a postdoctoral scientist to the dept. Medical Oncology of the University Hospital Ghent and the research group Biomarkers in Cancer, dept. Basic and Applied Medical Sciences of the Ghent University. His primary research aim is the assessment of novel biomarkers for disease diagnosis, prognosis, and therapy response in various tumor indications (renal cell cancer, bladder carcinoma, prostate cancer and head and neck cancer). In his research, dr. Tijl Vermassen has a dual focus. Firstly, dr. Tijl Vermassen is carrying on the work of his PhD project by focusing on protein biology, more specifically on N-glycomics. As aberrant N-glycosylation is a typical feature in cancer, glycomics can be applied as biomarker for diagnosis and prognosis of various cancer types. As a postdoctoral scientist, he is continuing this research in order to develop a test that can be implemented in routine clinical practice in the near future. Secondly, dr. Tijl Vermassen has a high interest into immune-oncology. In this research, he explores how the tumor micro-environment can modify the response to targeted therapies, e.g. immunotherapy with check-point inhibitors. In this matter, he conducts innovative research into describing the tumor micro-environment of various solid carcinoma, through pathological approaches, genetic testing as well as protein biochemistry, to identify novel biomarkers with diagnostic or therapeutic potential.

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Tijl Vermassen

Creating Precision Medicine Education for Future Pharmacists: Challenges and Opportunities for the UM/UWC Partnership by

Ms. Nicole Keuler (UWC) and Prof Gerald J Wyckoff (UMKC), Professor and Chair, DPPS, UMKC School of Pharmacy

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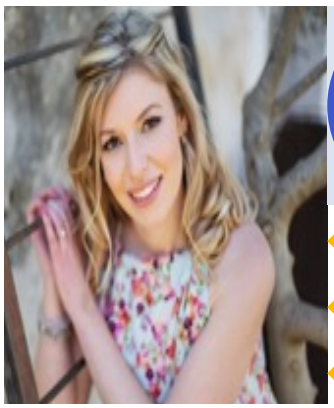
Abstract

Clinical application of pharmacogenomics (PGx) in practice can promote rational medicine use by following a personalised medicine approach, ultimately reducing adverse effects, and achieving patient health outcomes. Pharmacists are considered the most accessible healthcare professionals for patients and are ideally placed to lead PGx in practice but require the necessary knowledge and skills to fulfil this purpose. As patients are more exposed to genetic information, and as more therapeutics are developed with pharmacogenomic (PGx) recommendations, we need to ensure that pharmacogenetic and PGx competencies are not only included within pharmacy education but evaluated and revised continuously. At the UMKC School of Pharmacy, the only public School of Pharmacy in the state of Missouri and one of only two pharmacy schools in the state, a dedicated course in pharmacogenomics was added in 2019 to ensure students would be prepared for the challenges of interpreting pharmacogenetic guidance from evidence-based resources. Relying in part on didactic instruction as well as case-based examples, the course is meant to enable students to engage with the kind of questions patients will have from direct-to-consumer kits that are often sold in chain pharmacy stores and understand where FDA guidance comes from. It also deals with how drug approval is changing, the rise of companion diagnostics, and the concept of precision medicine in pharmaceutical settings. UWC School of Pharmacy is the only provider of pharmacy education in the Western Cape. PGx education is not included in the current B. Pharm degree curriculum. A core group of academic staff at UWC have expertise and interests in PGx, incorporating PGx through guest lectures or as part of kinetics lectures. A curriculum framework and competency standards can assist South Africa's universities to incorporate PGx into the B. Pharm degree to deliver pharmacists with the necessary knowledge and skill to lead PGx in practice. At all levels of education, building student cultural competence is important in this area of pharmacy education, and not just meeting but exceeding regulatory guidance for pharmacogenetic and genomic topics to "future-proof" student understanding of the material is critical. The long-term partnership between the UM System and UWC enables an exchange of research competence, but also coursework, teaching expertise, and opportunities for engaged learning between professional students. We will discuss the opportunities, both short- and mid-term, within the educational aspects of PGx and precision medicine for this collaboration. We will discuss course sharing opportunities, potential research on scholarship and learning, and future funding sources.

Biography

Nicole Keuler is a lecturer at the School of Pharmacy at the University of the Western Cape. She coordinates the Master of Clinical Pharmacy Programme and is involved in postgraduate and undergraduate teaching. Nicole has a special interest in pharmacogenomics and the clinical application in practice to optimise patient care. She is a Clinical Pharmacogenomics and Implementation Consortium (CPIC) Pharmacogenomics Global Research Network member. Nicole is embarking on her PhD journey to develop a pharmacogenomics curriculum framework for the B. Pharm degree in South Africa.



Nicole Keuler

Biography

Gerald J Wyckoff, Ph.D., Professor and Chair, DPPS, UMKC School of Pharmacy

Modern drug discovery using in silico techniques is about sifting through large amounts of data to find signal in a sea of noise, and developing methodologies that do this efficiently. My educational background is as a molecular evolutionary geneticist, finding faint signatures of positive selection in a sea of genomic noise. This led me to become involved with large scale genomic, and later proteomic, projects utilizing a bioinformatic framework. At UMKC I have developed collaborations with structural biology faculty, in part to extend my knowledge of how to apply large-scale screening techniques to structure-based problems. This has been fruitful and allowed me to extend my knowledge in drug discovery towards chemical information signatures useful for high-throughput screening of compounds. All of these problems have as a common theme the development of tools to make sense out of large scale data where noise is high and signal is low. I also have the demonstrated ability to work with people in diverse fields, including structural biology and within medicinal chemistry. shared effort for this project over the next two decades.

Gerald J Wyckoff

Smart Sensing and Analytics for Cognitive Health Care by **Prof. Sajal K. Das (UM S&T), IEEE Fellow**

Curators' Distonguished Professor, Daniel St. Clair Endowed Chair, Department of Computer Science, Missouri University of Science and Technology, Rolla
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Abstract

The rapidly growing elderly population in many parts of the world has started to impact people – emotionally, socially and economically. Current demography, medical and social trends in the U.S. indicate a large population of older adults are at risk of mild cognitive impairment (MCI) and dementia leading to Alzheimer's and Parkinson's diseases. This motivates us to design innovative non-invasive technology solutions for cognitive health assessment, care management, and well-being in people's own environments of daily life. A significant challenge in such technology-assisted solutions is collecting multi-modal sensing data and their analytics on resource-constrained wearables and IoT devices, in presence of uncertainty and noise. Another challenge is how to translate the extracted knowledge into actionable information for effective use by family members, doctors and caregivers. This talk will present our ongoing research on recognition of complex at-home activities of daily living (ADLs) with smartphones and wearables, and cognitive behaviour detection with the help of a smart chair that we built. For activity recognition, our innovative methodology can detect up to 21 fine-grained at-home activities, as opposed to typical 6-12 activities recognized by existing works. The smart chair based novel framework can detect user's functional and emotional activities, in addition to static and movement based sedentary postures, thus differentiating between MCI and dementia. In collaboration with a local hospital, our proposed solutions are tested and validated with pre-clinical data and a large number of real patient studies.

Biography

Sajal K. Das is a Curators' Distinguished Professor of Computer Science, and Daniel St. Clair Endowed Chair at the Missouri University of Science and Technology, Rolla, where he was the Chair of Computer Science Department during 2013-2017. He is also the co-founder of Smart Health Beacons, LLC. During 2008-2011, he served the National Science Foundation as a Program Director in the Computer and Network Systems Division. His research interests include wireless and sensor networks, mobile and pervasive computing, smart environments (smart city, smart health, smart agriculture, smart grid, smart transportation), cyber-physical systems and IoT, mobile crowdsensing, machine learning, data analytics, cloud computing, cyber-security, biological and social networks. He has contributed significantly to these areas, having published over 350 articles in high quality journals, over 475 peer-reviewed conference papers, and 56 book chapters. A holder of 5 US patents, Dr. Das has directed numerous funded projects totaling over $22 million, and coauthored four books. According to DBLP, Dr. Das is one of the most prolific authors in computer science. His h-index is 97 with 37,800+ citations according to Google Scholar. He is the founding Editor-in-Chief of Elsevier's Pervasive and Mobile Computing journal and serves as Associate Editor of several journals including the IEEE Transactions on Mobile Computing, IEEE Transactions on Dependable and Secure Computing, IEEE/ACM Transactions on Networking, and ACM Transactions on Sensor Networks. A founder of the IEEE PerCom, WoWMoM, SMARTCOMP and ACM ICDCN conferences, Dr. Das has served as General and Program Chair of numerous conferences. He is a recipient of 12 Best Paper Awards in prestigious conferences, and received numerous awards for teaching, mentoring and research including the IEEE Computer Society's Technical Achievement award for pioneering contributions to sensor networks and the University of Missouri System President's Award for Sustained Career Excellence. Dr. Das graduated 50 Ph.D. and 31 MS thesis students. He is a Distinguished Alumnus of the Indian Institute of Science in Bangalore. He is an IEEE Fellow.

Sajal K. Das