NUS National University of Singapore

Department of Biological Sciences
Faculty of Science

Amgen Scholars Asia Symposium

4 – 5 August 2022

AMGEN® Scholars Program

Discover Your Potential

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Amgen Scholars Asia Symposium 2022

A signature component of the summer program is the symposium where students hear first-hand from leading scientists working in industry and academia. Over the course of the symposium, scholars have the chance to share their summer research projects with their peers and deepen their understanding of various fields of science.

Each year, Amgen Scholars meet at the National University of Singapore to network with other Amgen Scholars as well as interact with leading industry and academic scientists. In early August 2019, Amgen Scholars from around the world participating in the Asia Program met in Singapore for a two-day symposium. There, they got a chance to present their summer research and to meet scientific leaders in industry and academia. The symposium is a unique feature of the program, allowing participants to gain exposure to the myriad career paths available in science.

After a year of hiatus due to the global pandemic, the Amgen Scholars Asia Symposium is back in Singapore this year to be held as a hybrid event with scholars and delegates from the other three host institutions joining in virtually.

Amgen Scholars Program Partners

NUS National University of Singapore

東京大学 THE UNIVERSITY OF TOKYO

京都大学 KYOTO UNIVERSITY

清華大學 Tsinghua University

Event Organizer

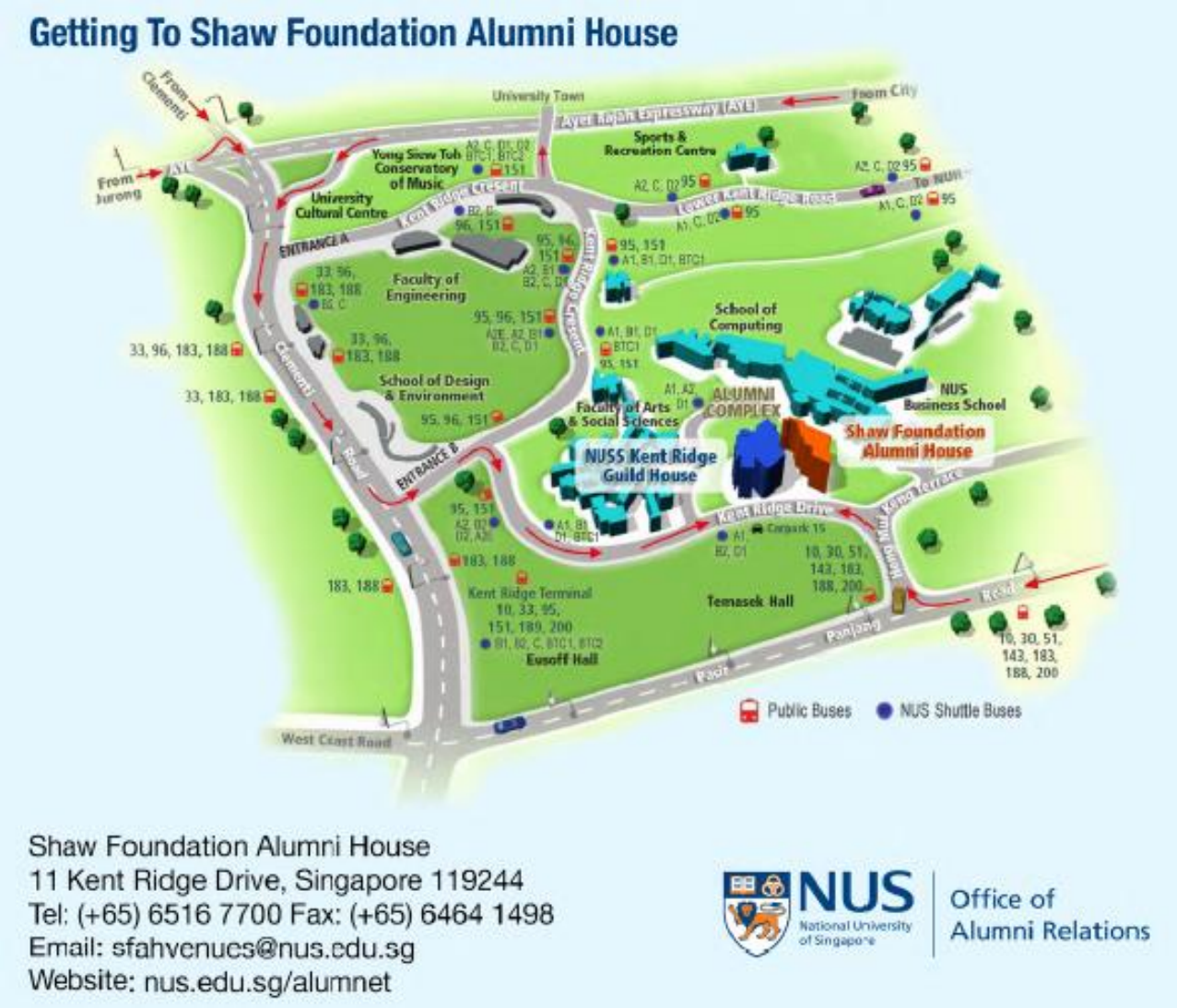
NUS National University of Singapore

AMGEN

IA-MEETINGS

On-site Venue

This year, the symposium will have its on-site event at the Shaw Foundation Alumni House, National University of Singapore.



On-site Wifi

To access the on-site Wifi, please follow the steps below:

1. Connect to "NUS_Guest" wireless network
2. Select "Event Login" at the login page
3. Enter the Wi-Fi PIN: **UIR6C7**

Virtual platform

Delegates not able to attend the on-site event will be joining through the virtual platform – Airmeets. Personal links to the platform will be sent via email to registered delegates and will be used for both symposium days. Please do not share this link.

Welcome Speech

Yu Hao

Professor

Head of Department,

Department of Biological Sciences,

National University of Singapore

Opening Address

Gregory A. Llacer

Director,

Global Program Office,

Amgen Scholars

Closing Address

Henry Mok

Associate Professor

Deputy Head of Department,

Department of Biological Sciences,

National University of Singapore

Keynote

Keynote Lecture 1

Victoria Elegant

Professor

Vice President, Amgen JAPAC Medical Affairs

Global Lead, Access to Medicines

TRANSFORMING BIOTECHNOLOGY INTO THERAPIES MAKING A DIFFERENCE TO PATIENTS' LIVES

Biography

Professor Victoria Elegant is based in Hong Kong for Amgen and is Vice-President, JAPAC Regional Medical Head, and Site Head, China Research Site, Shanghai. Prior to Amgen, Prof Elegant was the Vice-President, Regulatory and Medical Affairs, APAC, based in Shanghai for 10 years for Baxter, and Vice President, Medical Affairs, Asia for Baxalta.

Professor Elegant is a Fellow of the Faculty of Pharmaceutical Medicine UK (FPM), member of the FPM International Committee, and is an Adjunct Professor, Faculty of Medicine and member of the Board of Studies for the Masters in Pharmaceutical Medicine at the University of New South Wales, Sydney, Australia.

Professor Elegant has published and spoken extensively on regulatory affairs, medical affairs and clinical development in the Asia Pacific region and is President of the Asia Pacific chapter of the Medical Affairs Professional Society (MAPS). She is on the biotech advisory board to the Hong Kong Stock Exchange.

Professor Elegant holds a medical degree from the University of London and is passionate about improving standards of care and outcomes for patients in Asia. She is also involved in initiatives to support women in leadership.

Keynote

Keynote Lecture 2

Wallace I. Torres

Vice President,

Amgen Singapore Manufacturing

DAWN OF BIOTECHNOLOGY, INNOVATION REALIZED

Biography

Wallace I. Torres is Vice President of Amgen Singapore Manufacturing, home to Amgen's first Next-Generation Biomanufacturing and Chemical Synthesis commercial manufacturing plants in Asia. Based in Singapore, Wallace leads the site operations to position Amgen as one of the world's leading biotechnology companies and in ensuring a reliable supply of high-quality drug substances to improve patients' lives.

A veteran in the biotech industry, Wallace joined Amgen in 2013 and has excelled in a variety of leadership roles throughout his tenure. In his most recent role as Vice President, Drug Products in Puerto Rico, Wallace led the Drug Product organizations to optimize its operational performance and throughput. As Executive Director, Quality Site Lead for its Singapore operations, Wallace played an instrumental role in steering the site to deliver biotech therapies of increasing sophistication with the Single Use Systems (SUS) plant. Preceding these roles, Wallace was Executive Director, Quality Systems and Director, Quality Assurance Drug Product in Puerto Rico.

Prior to Amgen, Wallace was with Hoffmann La Roche for 25 years where he held several leadership positions across the Quality Control/Quality Assurance (QC/QA), Manufacturing, Strategy, and Supply Chain organizations in Switzerland, USA, Mexico, and Brazil. These responsibilities include serving as Site Head of Manufacturing plants, Global Head of Risk Management, Global Quality Manager and QA/QC Head at Contract Manufacturing facilities.

An active diversity, inclusion and belonging (DI&B) advocate, Wallace is passionate on causes to progress gender equity, in improving female representation at leadership roles and in advancing scientific causes, particularly for girls and young women in STEM (science, technology, engineering, and mathematics) to nurture the next generation of innovators.

Wallace holds a Bachelor's degree in biology from the University of Puerto Rico, a Master in management from the University of Phoenix, a Master in Advance Management Practices from the University of South Australia, and a PhD in International Business Management from the Swiss Business School.

Guest Lectures

Lecture 1

Masatoshi Hagiwara

Professor

Graduate School of Medicine,

Kyoto University

Biography

Professor Masatoshi Hagiwara was born in Mie prefecture, Japan and entered Mie University School of Medicine in 1978. After returning from the Salk Institute in 1993, Prof Hagiwara started his laboratory in the Nagoya University School of Medicine as an Assistant Professor. He moved to Tokyo in 1997 as a Professor of the Medical Research Institute of Tokyo Medical and Dental University and decided to try deciphering the splicing code to cure some genetic diseases caused by aberrant splicing. Prof Hagiwara moved to Kyoto University in 2010 as Professor of the Department of Anatomy and Developmental Biology in the Graduate School of Medicine. His long-lasting dream is to save people suffering from incurable diseases with his own “magic bullets”.

SPLICING THERAPY FOR INHERITED DISEASES

Abstract

Deep-intronic splicing mutations often cause inclusion of a pseudo exon, which in turn produces a premature stop codon leading to genetical inactivation. Number of disease-associated pseudo exonic mutations has dramatically increased because of recent advances in whole genome sequencing and transcriptome analysis. In contrast, mechanisms involved in pseudo exon recognition remain poorly explored. Understanding the mechanism of a disease-related splicing is crucial for finding an effective therapeutic strategy, as characterization of SMN2 exon 7 splicing led to development of Nusinersen for spinal muscular atrophy. In our hands, as previously demonstrated, splice-targeting therapeutics were achieved using small molecule compounds for genetic diseases such as Duchenne muscular dystrophy, NEMO deficiency syndrome, and familial dysautonomia, by targeting splicing regulators. Therefore, by analyzing genetic information with AI, we established a novel therapeutic strategy for pseudo exonic diseases.

Guest Lectures

Lecture 2

Eunyoung Chae

Assistant Professor

Department of Biological Sciences,

National University of Singapore

Biography

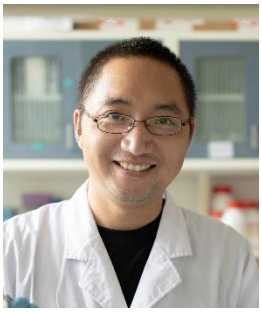
Eunyoung Chae is a plant geneticist and assistant professor in the Department of Biological Sciences, National University of Singapore. Her research area includes plant immunity, natural variation, trait evolution, and hybrid performances. The Chae lab focuses to investigate non-additive genetic interactions between plant immune components, and to develop a predictable model linking immune system diversity and growth traits, particularly in hybrid plants.

NATURAL VARIATION IN THE PLANT IMMUNE SYSTEM AND ITS CONTRIBUTION TO HYBRID PERFORMANCES

Abstract

Individuals of a species respond differently to environmental perturbations, and the genetic makeup is largely responsible for the variation in responses. With the advent of new sequencing tools that made tremendous genomic information available in a given species, we now have an unprecedented opportunity to investigate phenotypic variation in adaptive traits governed by genotype by environment (G x E) and G x G interactions. Numerous genome-sequencing projects revealed that genetic variability in plant immune components is exceptional, reflecting complex defense strategies that plants employ. The extreme variation sometimes makes a fatal outcome. Hybrid necrosis is the best-known example of genetic incompatibility in plants, in which autoimmune responses are triggered by deleterious interactions of independently evolved immune alleles. We exploited genetic and genomic tools available in the model plant species Arabidopsis thaliana to systematically investigate intraspecific hybrid necrosis. The species-wide work identified hot spots for genetic incompatibilities in the genome, often in regions densely populated by Nucleotide-binding Leucine-rich (NLR) immune receptor genes with extreme polymorphisms. A particularly dangerous locus is a highly variable cluster of NLR genes, DANGEROUS MIX2 (DM2), which causes multiple, independent incompatibilities with genes that encode a range of biochemical functions, including other NLRs. Our findings suggest that deleterious interactions of immune components that are presumably at the front lines of host-pathogen co-evolution would limit the combinations of favorable disease resistance alleles accessible to plant genomes. This systems genetics work provides a unique platform to further investigate molecular mechanisms of immune receptor activation and to dissect tradeoffs between immunity and growth in plants. In my talk, I will address topics on how genetics of speciation and genetic incompatibility contribute to mechanistic understanding of adaptation, how natural variation can be exploited to understand trait evolution, and how current knowledge gained from a model system shall be translated to improve breeding practices.

Guest Lectures



Lecture 3

Xiangyu Liu

Assistant Professor

Tsinghua University

Biography

Dr. Xiangyu Liu obtained his BS and PhD at Peking University in 2004 and 2011, respectively. From 2008 to 2010, he studied as an exchange PhD student at Aarhus University, Denmark, with the support from Chinese Scholarship Council. Dr. Liu conducted his first postdoctoral research at School of Life Sciences, Peking University from 2011 to 2013, and his second postdoctoral research at School of Medicine, Tsinghua University from 2013 to 2017. Then he worked as assistant researcher at School of Medicine, Tsinghua University. In August 2019, Dr. Liu joined School of Pharmaceutical Sciences as an assistant professor and a principal investigator, his research interest focuses on structural biology of G protein coupled receptors and structure guided drug development.

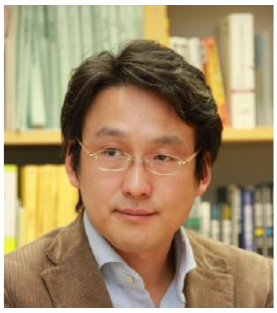
GPCR STRUCTURAL BIOLOGY AND DRUG INNOVATION

Abstract

G protein coupled receptors (GPCRs) account for about 1/3 of the targets of the FDA approved drugs. However, many pharmaceutically important GPCRs have different subtypes in human and as a result, drugs targeting on these GPCRs often meet problems with subtype selectivity. In this presentation, I will first introduce our work on revealing how noradrenaline achieves 10 fold selectivity towards the human β1 adrenergic receptor (β1AR) over the β2AR, despite the binding pockets of noradrenaline are identical in these two receptors. I will then introduce how we developed highly selective agonists for the β2AR based on the small differences between the orthosteric pockets of β1AR and β2AR. Furthermore, I will introduce how we developed a novel method to screen for GPCRs drugs based on the structural information of GPCR-G protein complexes and how we use the new method to screen for compounds that have potential to treat obesity and diabetes.

Guest Lectures

Lecture 4



Hiroki R. Ueda

Professor

Graduate School of Medicine,

The University of Tokyo

Biography

Professor Hiroki R. Ueda graduated from the Faculty of Medicine, the University of Tokyo in 2000, and obtained his Ph.D. in 2004 from the same university. He was appointed as a team leader in RIKEN in 2003. He became a full professor in Graduate School of Medicine, the University of Tokyo in 2013. In 2016, he found the first sleep-promoting kinases, CaMKIIalpha and CaMKIIbeta and proposed phosphorylation hypothesis of sleep that phosphorylation-dependent regulation of Ca2+-dependent hyperpolarization pathway underlies the regulation of sleep homeostasis in mammals. In 2018, he also found the first essential genes of REM sleep, muscarinic receptors M1 and M3. To accelerate these studies, he also invented whole-brain and whole-body clearing and imaging methods called CUBIC as well as the next-generation mammalian genetics such as Triple-CRISPR and ES-mice methods for one-step production and analysis of KO and KI mice without crossing.

TOWARDS SYSTEMS BIOLOGY OF HUMAN SLEEP/WAKE CYCLES: PHOSPHORYLATION HYPOTHESIS OF SLEEP

Abstract

The detailed molecular and cellular mechanisms underlying NREM sleep (slow-wave sleep) and REM sleep (paradoxical sleep) in mammals are still elusive. To address these challenges, we first constructed a mathematical model, Averaged Neuron Model (AN Model), which recapitulates the electrophysiological characteristics of the slow-wave sleep. Comprehensive bifurcation analysis predicted that a Ca2+-dependent hyperpolarization pathway may play a role in slow-wave sleep. To experimentally validate this prediction, we generate and analyze 26 KO mice, and found that impaired Ca2+-dependent K+ channels (Kcnn2 and Kcnn3), voltage-gated Ca2+ channels (Cacna1g and Cacna1h), or Ca2+/calmodulin-dependent kinases (Camk2a and Camk2b) decrease sleep duration, while impaired plasma membrane Ca2+ ATPase (Atp2b3) increases sleep duration. Genetical (Nr3a) and pharmacological intervention (PCP, MK-801 for Nr1/Nr2b) and whole-brain imaging validated that impaired NMDA receptors reduce sleep duration and directly increase the excitability of cells. Based on these results, we propose phoshporylation hypothesis of sleep that phosphorylation-dependent regulation of Ca2+-dependent hyperpolarization pathway underlies the regulation of sleep duration in mammals. We also recently developed a simplified mathematical model, Simplified Averaged Neuron Model (SAN Model), which uncover the important role of K+ leak channels in NREM sleep. In this talk, I will also describe how we identify essential genes (Chrm1 and Chrm3) in REM sleep regulation and propose a plausible molecular definition of a paradoxical state of REM sleep.

Program

DAY 1 (Thursday 4 August 2022)		
Time (SGT)	**Activity**	**Venue**
9.00 - 9.30am	**Registration** (30min)	Foyer
Session 1: Welcome speech		
9.30 - 9.35am	**Welcome speech** (5min) **Yu Hao** *(Head of Department, Department of Biological Sciences, National University of Singapore)*	Auditorium – in-person
9:35 - 9.45am	**Opening Address** (10min) **Gregory A. Llacer** *(Director, Amgen Scholars -- Global Program Office)*	Auditorium – live streamed
Session 2: Keynote		
9.45 - 10.30am	**Keynote Lecture 1** (45min) Title: Transforming Biotechnology into therapies Making A difference to Patients' Lives **Victoria Elegant** *(Professor, Vice-President JAPAC Region Head, Medical, Amgen)*	Auditorium – live streamed
10.30 - 11.00am	**Tea Break** (30min)	Foyer
Session 3: Kyoto University		
11.00 - 11.30am	**Lecture 1** (30min) Title: Splicing therapy for inherited diseases **Masatoshi Hagiwara** *(Professor, Graduate School of Medicine, Kyoto University)*	Auditorium – live streamed from Kyoto University
11.30am – 12.15pm	**Oral Presentations (Kyoto University)** (45min) Talk 1: Michelle Lu Talk 2: Devashish Girish Bhave Talk 3: Keely Bee Likosky	Auditorium – live streamed from Kyoto University
12.15pm – 1.15pm	**Lunch** (1hr)	Foyer

Session 4: National University of Singapore		
1.15 – 1.45pm	**Lecture 2** (30min) Title: Natural Variation in the Plant Immune System and its Contribution to Hybrid Performances **Eunyoung Chae** *(Assistant Professor, Department of Biological Sciences, National University of Singapore)*	Auditorium – in-person
1:45 – 2.30pm	**Oral Presentations (National University of Singapore)** (45mins) Talk 4: Adrija Adhikary Talk 5: Samantha Jinglin Yang Talk 6: Reneez Aiyana Felix	Auditorium – in-person
2.30 – 4.00pm	**Tea Break, Poster presentation 1** (1.5hr) Physical (Poster Number 1- 11) E-posters (Odd numbered Poster IDs)	Foyer for NUS Scholar presenting in-person
Session 5: Tsinghua University		
4.00 – 4.30pm	**Lecture 3** (30min) Title: GPCR structural biology and drug innovation **Xiangyu Liu** *(Assistant Professor, Tsinghua University)*	Auditorium – live streamed from Tsinghua University
4.30 – 5:15pm	**Oral Presentations (Tsinghua University)** (45min) Talk 7: Zefan Li Talk 8: Martin Echavarria Galindo Talk 9: Ruijie Tan	Auditorium – live streamed from Tsinghua University

Program

SCAN ME

For Day 2 Session 1 (Morning Programs) only:

Please scan the QR code or access the morning events via this Webex Link

Click this link to know your allocated group number to join in the WE2 dialogue with Amgen executives

DAY 2 (Friday 5 August 2022)

Time (SGT)	Activity	Venue
Session 6: Keynote 2 and Amgen Foundation		
9.00 – 9.45am	**Keynote Lecture 2** (45min) Title: Dawn of Biotechnology, Innovation Realized **Wallace Torres** *(Vice-President, Amgen Singapore Manufacturing)*	Auditorium – in-person
9:45 – 9:50am	**Welcome Address** (5 mins) **Denise Tan** *(Executive Director, Amgen Singapore Manufacturing, Biologics)*	Auditorium – streamed live from Amgen Singapore
9:50 –10:55am	**Plant and Lab Tours** (60 mins) - NextGen Biomanufacturing Plant (30 mins) - Process Development Lab (30 mins) - Q&A (5 mins)	Auditorium – streamed live from Amgen Singapore
10:55 – 11:10am	**Quick Announcements** (5 mins) **Tea Break** (15min)	*Note: NUS Scholars to proceed directly to their designated onsite breakout rooms after tea break*
11:10 – 12:00pm	**Virtual Dialogue with Amgen Executives** (50mins) - **Breakout** of 9 groups of 12 students (refer Appendix to check your respective breakout group allocation)	(Hybrid) NUS Scholars to proceed to breakout rooms (Lemongrass Rm or Clove Rm) Rest of Scholars to connect virtually from their laptops on Amgen's virtual platform
12:00 – 1:00pm	Lunch	Foyer

Session 7: The University of Tokyo		
1:00 – 1:30pm	**Lecture 4** (30 min) Title: Towards Systems Biology of Human Sleep/Wake Cycles: Phosphorylation Hypothesis of Sleep **Hiroki R. Ueda** *(Professor, Graduate School of Medicine, The University of Tokyo)*	Auditorium – streamed live from Tokyo
1:30 – 2:15pm	**Oral Presentations (The University of Tokyo)** (45min) Talk 10: Gretchen Margot Fujimura Talk 11: Saki Ichikawa Talk 12: Ruisi Fu	Auditorium – streamed live from University of Tokyo
2:15 – 3:45pm	**Tea Break, Poster presentation 2** (1.5hr) Physical (Poster Number 12 – 22) E-posters (Even numbered Poster IDs)	Foyer for NUS Scholar in-person presentation
Session 8: Closing		
3:45 – 3:50pm	**Closing speech** (5min) **Henry Mok** *(Deputy Head of Department, Department of Biological Sciences, National University of Singapore)*	Auditorium – in-person

Oral Presentations

Each oral presenter will have 12 minutes of speaking time followed by 3 minutes of Q&A.

Oral presenters should join their virtual sessions 15 mins before the start of their session.

Talk 1

EVALUATION OF METAL-ORGANIC FRAMEWORK MEMBRANES FOR WATER POLLUTANT TESTING

Michelle Lu, Amgen Scholar, Kyoto University

Pharmaceuticals and personal care products (PPCPs) are found in wastewater, but effective methods for removing and/or testing for them are lacking. Those that do exist often require large volumes of toxic solvents, which generate even more contamination. This has created a need for a solution that will effectively and sustainably test and treat wastewater for PPCPs.

Recently, mixed matrix membranes (MMMs), composed of metal-organic frameworks (MOFs), have gained attention for their high porosity, which lend them to applications such as water remediation and testing. Two barriers to implementation of MMMs for this purpose exist. Firstly, MMMs are unpredictable in their homogeneity, making precision in pollutant testing difficult. Secondly, MOF membranes must be optimized across a variety of variables to be most effective.

We aim to address both issues. Hierarchical hybrid membranes (HHMs) are a novel type of MOF membrane that achieve superior homogeneity to MMMs. Our goal is to 1) optimize these HHMs for the target analytes of choice, and 2) validate their efficacy in extraction of target analytes. To this end, we took three steps; first, we synthesized MOFs across a variety of properties. Second, we synthesized a comprehensive array of MOF membranes that represent a spectrum of synthesis types, functionalities, and pore size. Finally, we tested the extraction capacity and recovery of these membranes against a solution of 13 target PPCPs.

Our results give the following three conclusions. MOF membranes significantly outperform a pristine polymer membrane in extraction, demonstrating their efficacy. Secondly, tuning of the membrane by pore size or functional group allows for selectively targeting specific analytes. Lastly, MMMs outperform HHMs in recovery, but they perform comparably in extraction. These conclusions indicate that MMMs are more suitable to an analyte testing application, but HHMs should be explored in wastewater remediation.

Talk 2

SYNTHESIS OF [Mo_3S_4Pd] CLUSTERS AND APPLICATION TO CATALYTIC CO_2 REDUCTION

Devashish Girish Bhave, Amgen Scholar, Kyoto University

Global warming has become an increasingly alarming concern over the past few years. One of the greenhouse gases that has caused a global uproar is CO2. In an effort to convert it into the chemically more useful reduction products, we strive to find an efficient catalyst that can facilitate the difficult reaction.

Having taken inspiration from bio-enzymes, we mimic it's cofactors into synthetic cubic clusters that have a much longer lifetime under ambient temperature and pressure conditions. To further ensure a longer lifetime, I have used Pd, a heavy metal, as the catalytic centre to prevent ion escape.

Having successfully synthesised the cluster, I have used Cyclic Voltammetry to characterize it's redox abilities and applied the catalyst to CO2 reduction. The cluster has been found to successfully catalyse the reduction reaction as CO has been detected in the reduction products. Reaction conditions including the solvent, the proton source and the gas atmosphere have been optimized.

These conclusions indicated that the cluster is suitable to catalytic CO2 reduction and should be used as a basis for scaling up the process.

Talk 3

IMPROVED RNA GUIDE FOR CRISPR/Cas9-MEDIATED VISUALIZATION OF SINGLE SISTER CHROMATID FUSION

Keely Bee Likosky, Amgen Scholar, Kyoto University

Human cells contain cellular information in chromosomes, protected on the ends by DNA repeats and proteins called telomeres. When telomeres shorten, they lose function and cause chromosome fusion, which may lead to tumorigenesis. Chromosome fusions take multiple different conformations, including end-to-end chromosome-type fusion, ring chromosome-type fusion, and sister chromatid fusion between replicated sister chromatids. Conventional methods to induce chromosome fusions fail to regulate the types and numbers of fusion, which make it difficult to understand the exact fate of each distinct type of fusion.

Dr. Makoto Hayashi created the Fusion Visualization reporter system, FuVis, which induces and visualizes single sister chromatid fusion (SCF). It functions by using a guide RNA “pin” that binds to target reporter DNA sequences integrated near the telomere. Then, the pin allows a CRISPR/Cas9 “cutting” system to make cuts in the reporter DNA at the pinned location. The cut can randomly cause either a single SCF or deletion of the reporter sequence. Cells with single SCF glow yellow and cells with deletion without SCF glow blue.

However, the efficiency of SCF in the current system is relatively low, making it challenging to apply the system to downstream experiments. This study aims to improve the RNA pin’s efficiency to increase a single SCF event. Based on work done by Dang et al. Genome Biology (2015), two changes were made to the pin sequence; a 5 base pair stem-loop increase and a single point mutation, which increase the stability and the abundance of the RNA pin, respectively. These changes were introduced by molecular cloning using plasmid, which was then delivered to FuVis cells by a virus-mediated method. Outcomes were visualized and quantified by a flow cytometer that can distinguish the color of individual cells.

Through analysis, it was found that both improved sequences increased the number of single SCF events, confirming improved efficiency.

Talk 4

FUNCTION OF CXCR3 DURING OSTEOCLAST FORMATION IN MEDAKA OSTEOPOROSIS MODEL

Adrija Adhikary, Amgen Scholar, National University of Singapore

Bone remodelling is a dynamic process involving the combined activity of osteoblasts and osteoclasts working together to maintain the structural integrity of the bone. This study concentrates on the formation of osteoclasts from their progenitor monocyte/macrophage cells in transgenic medaka (Oryzias latipes). During Rankl overexpression, the osteoblast progenitor cell increased the expression of Cxcl9l to attract the Cxcr3.-positive macrophages from the AGM towards the vertebral column before differentiating into ectopic osteoclasts. Subsequently, the human CXCR3A gene, the homologue of the Cxcr3.2, was attempted to be cloned in Cxcr3.2 mutant medaka lines to see if the function of the macrophage was rescued at sufficient statistical significance. Further work and directions are also glanced at.

Talk 5

SYNERGISTIC INTERACTIONS OF NANONET-FORMING PEPTIDES TO COMBAT RESISTANCE

Samantha Jinglin Yang, Amgen Scholar, National University of Singapore

Multidrug resistant Gram-negative pathogens present an increasingly critical healthcare threat. While the intracellular therapeutic targets of multiple antibiotic classes are well conserved between Gram-positive and Gram-negative bacteria, the outer membrane of the latter is highly efficient at denying entry to xenobiotics, thus impeding drug discovery efforts. Our group previously designed a library of synthetic beta-hairpin antimicrobial peptides (AMPs). Some of the potent candidates displayed the unique ability to form on-demand bacteria-trapping nanonets. We hypothesized that mechanical damage to the outer membranes from entrapment by the nanonets would facilitate the entry of putative Gram-positive-selective antibiotics, thus expanding their activity spectrum against Gram-negative pathogens. We successfully demonstrated synergistic interactions between our peptides and a panel of clinically relevant antibiotic classes, with clear distinction in the synergy profile between non-fibrillating and fibrillating peptides. The inclusion of fibrillating peptides at sub-inhibitory concentrations strongly delayed resistance development against the antibiotic, whereas non-fibrillating peptides did not. Findings of strain-specific synergy profiles led us to postulate that intracellular mechanisms were involved. Overall, this work demonstrated the potential of nanonet-forming AMPs as an adjuvant for unlocking antibiotic activity against multidrug resistant Gram-negative bacteria.

Talk 6

CHARACTERIZATION OF PINX1 FUNCTION IN REGULATING MICROTUBULE DYNAMICS

Reneez Aiyana Gaspar Felix, Amgen Scholar, National University of Singapore

PIN2/TRF1-interacting telomerase inhibitor 1 (PinX1) is considered a novel gene, playing a vital role in maintaining telomere length and chromosome stability. Given this role, PinX1 has been demonstrated to be involved in tumour genesis and progression in most malignancies. However, the complete structure of PinX1 has not been well-characterized, specifically its microtubule-binding domain. Consequently, there is a lack of study on how this domain links to the function of PinX1 on governing chromosome segregation and genomic stability. Hence, this study aimed to investigate the function of PinX1 in regulating microtubule dynamics. GFP-PinX1 and FLAG-PinX1 plasmids were constructed and used to transfect HEK 293T and HeLa cells. After validating the correct protein expression of PinX1, imaging was conducted to identify the localization of PinX1. It was seen that PinX1 localizes in the nucleus during interphase and at the mitotic spindles during metaphase. It was also found that PinX1 overexpression elongates the spindle pole distance in mitotic cells. Given these findings, PinX1 functions as a microtubule-associated protein in mitotic cells.

Talk 7

CONDENSATES IN RESPONSE TO DNA DOUBLE STRAND BREAK

Zefan Li, Amgen Scholar, Tsinghua University

Biomolecular condensates are membraneless structures in cells formed by liquid-liquid phase separation (LLPS). Thanks to some desirable features, condensates are very common in life organization. DNA double strand break (DSB) is an extremely dangerous type of DNA damage that poses a big threat to genomic stability and must be settled properly in time. A variety of factors have been reported to participate in the process of DSB repair through LLPS. Here we propose the redistribution of condensates in response to DSB. To find out the factors that form condensates and redistribute upon DNA repair, first we picked out some candidates from a previous study that reported a number of DSB-associated genes via CRISPRi. Next, we overexpress them in cells to examine their ability to form condensates. Then we use CRISPR/Cas9-mediated knockin to label endogenous proteins to further observe their phase separation under physiological conditions. Finally, we observe whether they can redistribute to the damage site of laser-induced DSB. By exploring the roles of condensates in DSB repair, our research can not only provide a new perspective on life organization, but also offer inspiration for cancer treatment.

Talk 8

DIRECTED EVOLUTION OF K-Ras c-Raf PROTEIN-PROTEIN INTERACTION

Martin Echavarria Galindo, Amgen Scholar, Tsinghua University

The KRAS/ K-RAS oncogene is one of the most well-known human oncogenes due to its function as a “molecular switch” for multiple signal transduction pathways, and its gain-of-function mutations are present in over 10-30% of cancers. Since K-Ras inhibitors have potential as potent cancer treatments, the main goal of this study was to use directed evolution to develop a competitive inhibitor to active K-Ras from the c-Raf RBD.

This study first sought to build an effective system to characterize the strength of protein-protein interactions through the yeast two hybrid system, which was first tested using the dimerization domain of a leucine zipper structure under an IPTG-mediated protein expression system. The two-hybrid assay was then used to test the interaction of different c-Raf RBDs with K-Ras. This screening identified c-Raf RBD V1 and V12 as optimal drug candidates due to their strong binding to K-Ras, and these two will be used for future directed evolution experiments to improve their specificity and binding to K-Ras.

Talk 9

ASSESSMENT OF THE DELAY IN NOVEL ANTICANCER DRUGS BETWEEN CHINA AND THE UNITED STATES: A COMPARATIVE STUDY OF DRUGS APPROVED BETWEEN 2010-2021

Ruijie Tan, Amgen Scholar, Tsinghua University

Access to novel anticancer drugs has been a critical health issue in China for many years. We retrospectively collected novel anticancer drugs first approved in the United States between 2010-2021 to assess the evolving landscape of the drug lag in China by taking Japan and the European Union as comparisons. Our study shows that the median drug lag length in China and Japan was significantly reduced, although a minor rise was noted in the European Union. The median review lag of China in 2016-2021 was comparable to Japan, but dramatically lower than the European Union. Nevertheless, China had a significantly longer median submission lag than Japan and the European Union. The drug delay between China and the United States has shrunk dramatically, yet it still exists. China could adopt steps, including boosting the implementation of multi-regional clinical trials, to further reduce submission lag.

Talk 10

ANALYSIS OF AXONAL TRANSPORT OF MITOCHONDRIA

Gretchen Margot Fujimura, Amgen Scholar, University of Tokyo

Mitochondria are essential for the survival of any living cell. They produce ATP, or energy, which is paramount for many cellular processes such as DNA replication, protein synthesis, or respiration. Due to their important nature it is obvious that the locations in which they inhabit within cells are also vital to study and understand. This research focuses on the transport of mitochondria around a neuron, specifically the speed and direction of movement. Neurons are used as their unique shape makes them highly polarized, and their narrow axon can clearly show lateral movement. There are only two types of motor proteins that transport cargo around the cell, dynein (which moves towards the - end of microtubules, or retrogradely) and kinesin (which moves towards the + end of microtubules, or antegradely). This research looks at the interaction of kinesin with mitochondria, as well as a specific motor adaptor proteins called TRAK1 and TRAK2, which associate with both kinesin and mitochondria.

A large part of my research experience has been learning various techniques not only in the wet lab but also for computer based data analysis. Coming into the program I already had knowledge of basic wet lab techniques, but here I was able to learn specialized skills such as plasmid construction, PCR, and fluorescent microscopy. I also learned how to use specific programs to track mitochondrial movements and analyze the data collected. Overall this experience has been highly influential in my path towards becoming a scientist.

Talk 11

ELUCIDATION OF ABERRANT SPLICING MECHANISM OF SLC12A2 PRE-MRNA CAUSED BY MUTATIONS FOUND IN CONGENITAL DEAFNESS

Saki Ichikawa, Amgen Scholar, University of Tokyo

Congenital deafness is a disease that occurs at a high frequency. Since sensory system disorders greatly reduce the quality of life, there is a strong need to elucidate the causes and develop treatments. Our collaborators identified the SLC12A2 mutations with congenital deafness patients and revealed that those mutations cause skipping of exon21. SLC12A2 is a Na+, K+, and 2 Cl- cotransporter and is involved in the homeostasis of the endolymph, which contains high levels of K+. Those mutations cause hearing loss in human patients, but transgenic mice which have the same point mutation (=tm1 mouse) do not show hearing loss. We examined the causes of the difference in the effect of the point mutation on hearing across animal species.

For this purpose, we prepared a series of splicing reporters with either human or mouse SLC12A2 gene, which carry the CD-causing mutation. The main difference between human and mouse is the first nucleotide of exon21. The human exon21 has T as the first nucleotide, while mouse exon contains A. Those reporters were transfected into HEK293T cells, and their splicing patterns were analyzed by RT-PCR.

When the wild type reporter carrying mouse SLC12A2 gene portion was introduced into HEK293T cells, the mRNA product including exon21 was detected. Surprisingly, the mouse splicing reporter harboring tm1 mutation also produced exon21-included product. In contrast, the human-type reporter produced exon21-included product mainly, and exon21-skipped product was also slightly detected. Interestingly, the splicing reporter carrying human exon21 and tm1 mutation entirely produced exon21-skipped product.

These results indicate that the first nucleotide of exon21 plays an important role for exon21 recognition during splicing. In addition our results may explain why the mutation causing congenital deafness do not cause hearing loss in tm1 mice.

Talk 12

INVESTIGATION OF THE ASSOCIATION BETWEEN DAYTIME ACTIVITY LEVEL AND NIGHTTIME SLEEP USING ACCEL ALGORITHM

Ruisi Fu, Amgen Scholar, University of Tokyo

Sleep determines the physical and mental well-being of individuals across ages. While patients with various diseases, including cancer or neurological abnormalities, experience sleep disorders as symptoms, chronic sleep deprivation and other abnormal sleeping patterns directly and indirectly cause many diseases. Aiming to explore ways to improve sleep quality, this study investigates physical activity — one of the most important factors of sleep quality considered by the general public — and testifies the relationship between daytime activity level and nighttime sleep with real-world data. By using ACCEL (Ode et al., 2022), a state-of-the-art sleep-wake classification algorithm based on wristband-type accelerometers, the study monitors the activity of 20 subjects (mean age = 27.35, SD age = 7.71) for 2 weeks. After generating 4 sleep indexes (total sleep time, wake time after sleep onset, sleep window duration, and sleep efficiency) and analyzing their respective correlations with the duration of moderate to vigorous physical activity (MVPA) of the subjects, the result demonstrates a significant negative association between total sleep time and MVPA duration ($r = -0.57$, $p = 0.04$). Based on such a counterintuitive result, additional mediation analysis is performed to assess the impact of daytime nap duration on the association and proves that the relationship between MVPA duration and total sleep time is mediated by daytime nap duration ($z = -2.12$, $p = 0.03$ by Sobel test). The study suggests that the association between sleep and exercise may be more complicated than people's general impression. A more holistic investigation that covers the depth of sleep, sleep latency, and other indexes that characterize sleep quality may be necessary to fully understand the association.

E-Poster Presentations

Poster presenters from NUS will have to present their physical on-site posters.

The presentation schedule for NUS scholars would be as follows:

	Day 1 (4 Aug 2022)	Day 2 (5 Aug 2022)
Poster ID: **01 – 11**	On-site	Virtual
Poster ID: **12 – 22**	Virtual	On-site

All other poster presenters (Poster ID: 23 - 55) will follow the schedule:

Day 1 (4 Aug 2022)	Odd numbered poster ID
Day 2 (5 Aug 2022)	Even numbered poster ID

National University of Singapore

ID	Title	Presenter
01	Function Of Cxcr3 During Osteoclast Formation in Medaka Osteoporosis Model	Adrija Adhikary
02	Investigating candidate neuroprotective compounds with Drosophila model of synucleinopathy	Maitreyee Bhalme
03	Strategies for high-throughput screens for CRISPR-Cas9 mutants in Arabidopsis	Amrita Mahesh
04	Mechanical Control of Follicle Development By Theca Cells	Sanjana Balaji
05	EVs from Adipose cells can ameliorate senescence in senescent liver cells	Prince Jhandai
06	The Role of Hiltonol in Modulating NK Cell Activity	Siddham Jasoria
07	Role of odorant coreceptor in *Bicyclus anynana*	Aslan Cook
08	Probing the Intranuclear Environment with FCS using mEmerald as a Tag	Jasmine Kiley
09	Synergistic Interactions of Nanonet-Forming Peptides to Combat Resistance	Samantha Jinglin Yang
10	Relationship between Lysosome Acidity, Translation and mTORC1 in C2C12 Myoblasts	Anna Kozlov
11	Behavioral Effects of Odorant Injection on Larvae and Eggs of *Bicyclus anynana*	Fuminori Tanizawa
12	Nanoparticle-enhanced Protein Crystallization Quantitative Investigation of Silica-Nanoparticle Heterogeneous Nucleation.	Sarah Shirley
13	Investigating potential role of MOAP-1 in regulating hepatic lipid metabolism and senescence	Nguyen Le Uyen Nhi
14	Characterization of PinX1 function in regulating microtubule dynamics	Reneez Aiyana Felix
15	Bioactive Peptide and Protein Profiling of Plant-based (Soy) Meats to Understand Changes in Nutritional Value due to Food Processing and Interactions in Complex Food Matrices	Ryan Fan

16	Cryo-electron Microscopy Imaging of Apoferritin	Tammy Toh
17	Applying CRISPR/Cas9 Technology to Manipulate Immune Components in *A. thaliana*	Nafeesah Ibrahim
18	Production of modified virus-like particle as cancer vaccines	Jiahui Zheng
19	Capsular Polsyaccharide Synthesis in Streptococcus pneumoniae	Metta Sodian
20	Applying CRISPR/Cas9 Technology to Manipulate Immune Components in A. thaliana	Richelle Bertly Josefano
21	Intestinal Inflammation and Fibrosis Associated with Hepatocellular Carcinoma via the Gut-liver Axis Using the Zebrafish Model	Saruveish Mogan
22	Craniofacial Development in Zebrafish	Salmin R. Abd. Barri

The University of Tokyo

ID	Title	Presenter
23	Analysis of Axonal Transport of Mitochondria	Gretchen Fujimura
24	Elucidation of aberrant splicing mechanism of SLC12A2 pre-mRNA caused by mutations found in congenital deafness	Saki Ichikawa
25	Investigation of the association between daytime activity level and nighttime sleep using ACCEL algorithm	Ruisi Fu
26	Light therapy using optical microneedles	Enjy Katary
27	Porous Microneedles and Fabrication Methods	Altair Kossymbayev

Kyoto University

ID	Title	Presenter
28	Improved RNA Guide for CRISPR/Cas9-mediated Visualization of Single Sister Chromatid Fusion	Keely Bee Likosky
29	Development of Biomembrane Hybrid Silica Nanoparticles	George Shigematsu
30	Decorated MoS_2 Nanosheets on Bi_4NbO_8Cl for Enhancing Photocatalytic Hydrogen Evolution	Peerada Akaravinek
31	Study of Solvent Effect of Water in Triethylborane-induced Atom-transfer Radical Cyclization of Z-(Allylcarbonyl)Methyl Radical Using the RISM-SCF cSED Method	Aman Soni
32	Detection of SARS CoV-2 D614 and G614 Single-point Mutations via Micro Temperature Gradient Gel Electrophoresis	Leila Jamal
33	Characterisation of Microalgae Isolated from Lake Biwa, Japan	Bridget Lunn
34	Effective Photocatalytic Removal of Organic Pollutants in Wastewater using Molecular Imprinted TiO_2	Supaporn Klabklaydee
35	Transportation Transitions & Health Impacts in Australia	Aline Maybank
36	Genetic Analysis of Cell Competition in Drosophila	Karen Kai-Lin Hwang
37	*In vitro* Growth Cone Turning Assay for Screening of Candidate Synthetic GPR55 Inhibitors	Elise Rawlinson
38	Tale of Sleeping Cells and Their Environment	Urbi Paul

39	Investigation of XRCC4/C-terminus Phosphorylation Role on Xkr4 Scrambling Activity	Gregory Aaron
40	Detecting Structural Variants from Short Read Whole Genome Sequencing Data in (and Around) the pph-4.1 Gene Locus in *Caenorhabditis elegans*	Saptashwa Maity
41	Stress Granule Formation in Response to Different Stresses	Claire Liu
42	Elucidation of the Effect of Mechanical Force on Epithelial Cell Dynamics	Benjamin Johns
43	Graph Convolutional Networks and Parameterized Quantum Circuits for Predicting HIV Inhibition	Pranshav Gajjar
44	Synthesis of $[Mo_3S_4Pd]$ Clusters and Application to Catalytic CO_2 Reduction	Devashish Bhave
45	Liver Spheroid on a Chip: Usage of Microfluidic Devices to Mature Spheroids	Elif Yigit
46	Optimization of BSH-Biodegradable Periodic Mesoporous Organosilica (BSH-BPMO) Synthesis for Boron Nuclear Capture Therapy (BNCT)	Joey Chieng
47	Repurposing DNS-based Synthetic Tools for Cellular Rejuvenation	En Tong Lim
48	Phenylethynyl-linked Thiophene-fused 1,4-Diazapentalene ($plTAP_2$), a Nitrogen-doped 4nπ Antiaromatic Dimer	Helena Wen
49	Evaluation of Metal-Organic Framework Membranes for Water Pollutant Testing	Michelle Lu

Tsinghua University

ID	Title	Presenter
50	Assessment of the Delay in Novel Anticancer Drugs between China and the United States: A Comparative Study of Drugs Approved between 2010-2021	Ruijie TAN
51	Directed Evolution of K-Ras c-Raf Protein-Protein Interaction	Martin Echavarria Galindo
52	Reprogramming of Human Foreskin Fibroblast (HFF-1)	Shaofeng Xu
53	Discovery and Verification of Potential Gene Target to Reguate DC	Qing Zhang
54	Phosphoantigens are Molecular Glues that help Butyrophilin 3A1/2A1 Association Leading to Vγ9Vδ2 T Cell Activation	Jane Yun Gao
55	Condensates in Response to DNA Double Strand Break	Zefan Li