香港中文大學理學院
FACULTY OF SCIENCE
THE CHINESE UNIVERSITY OF HONG KONG

2021-22
Science Faculty
Postgraduate
Research Day

14 DEC 2021
0915 – 1600 · LSK LT6

PROGRAMME

AM Session

Time	Session
09:15 - 09:30	**Opening Remarks by Dean & Souvenir Presentation** *Professor SONG Chunshan* Dean of Science
09:30 - 09:50	**Impacts of Changes in Land Use, Climate, and Anthropogenic Emissions on Global Air Quality by the Mid-21st Century Following the Shared Socioeconomic Pathways** *BHATTARAI Hemraj* Year 2 PhD Student in Earth and Atmospheric Science
09:50 - 10:10	**Enormous Water Input in the Southern Mariana Subduction Zone: Seismic Evidence Derived from Ocean Bottom Seismographic Experiments** *CHEN Han* Year 4 PhD Student in Earth and Atmospheric Science
10:10 - 10:30	**Testing Variance Change under Varying Mean Structure** *LEUNG Cheuk Wai Dominic* Year 2 MPhil Student in Risk Management Science
10:30 - 10:50	**scAMACE: Model-Based Approach to the Joint Analysis of Single-Cell Data on Chromatin Accessibility, Gene Expression and Methylation** *WANGWU Jiaxuan* Year 4 PhD Student in Statistics
10:50 - 11:00	**Break**
11:00 - 11:20	**New Analytical Lens Focusing on Interstellar Turbulence** *YEUNG Cheung Hei* Year 2 PhD Student in Physics
11:20 - 11:40	**Three-Loop Braiding Statistics for Fermionic Topological Phases** *ZHOU Jingren* Year 4 PhD Student in Physics
11:40 - 12:00	**Peterson Isomorphism and Seidel Representations** *CHOW Chi Hong* Year 4 PhD Student in Mathematics
12:00 - 12:20	**Beating the Saturation Phenomenon of Stochastic Gradient Descent** *ZHOU Zehui* Year 4 PhD Student in Mathematics

Science
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	PM Session
13:30 - 13:50	**Development of Advanced Photodynamic Molecular Beacons with Multiple Controls for Targeted Photodynamic Therapy** *TAM Ka Bo* Year 4 PhD Student in Chemistry
13:50 - 14:10	**Gold-in-copper at Low *CO Coverage Enables Efficient Electromethanation of CO_2** *XIE Yi* Year 3 PhD Student in Chemistry
14:10 - 14:20	**Break**
14:20 - 14:40	**Evolutionary Landscape of Non-canonical RNA G-Quadruplexes: Hidden Side of a Versatile Structural Element** *CHOW Yui Ching* Year 6 PhD Student in Cell and Molecular Biology
14:40 - 15:00	**Characterization of Extracellular Vesicles (EVs) and EXPO in Plant** *GAO Jiayang* Year 5 PhD Student in Cell and Molecular Biology
15:00 - 15:20	**Priming-Induced Alterations in Histone Modifications Modulate Transcriptional Responses in Soybean under Salt Stress** *YUNG Wai Shing* Year 6 PhD Student in Molecular Biotechnology
15:20 - 15:40	**The Neuronal Adaptor FE65 Potentiates ARF6-Mediated Neurite Outgrowth by the Activation of ARNO** *ZHAI Yuqi* Year 4 PhD Student in Cell and Molecular Biology
15:40	**Closing Remarks** *Professor SONG Chunshan* Dean of Science

Welcome Message from the Dean of Science
Professor Chunshan SONG

I would like to welcome all of you to the 2021-2022 Science Faculty Postgraduate Research Day. With the resumption of face-to-face academic activities on CUHK campus, we are very pleased to have you join the Second Postgraduate Research Day as our first physical meeting with research students.

Despite the challenges of the COVID-19 pandemic, we successfully held the first Postgraduate Research Day online in January 2021. Conducting original research is a critical part of postgraduate education in a world-class university. With the Faculty's mission of educating and inspiring the next generation of scientific innovators and leaders, we greatly value high quality research in postgraduate education as young researchers represent the future of scientific innovation and the world's sustainable development.

Apart from gaining in-depth expertise in their area of research under the supervision of our leading scholars, the critical thinking and creative thinking involved in first-class research will help to further advance the thinking skills and develop the intellectual capabilities of our postgraduate students. The research education also helps expand students' horizon on how impactful research contributes to the advance in science and technology and the development of the society.

Riding on the success of the first Postgraduate Research Day, we hope the physical event this time will offer an excellent opportunity for our postgraduates to gain exposure in a scientific meeting, to showcase their original research work and to network with our faculty and research staff members and fellow students.

At the Forum of Guangdong-Hong Kong-Macau Greater Bay Area (GBA) Conference on 28 October 2021, CUHK unveiled seven new strategic partnerships that are set to strengthen Hong Kong's presence in the region. The "14th Five-Year Plan" calls for the development of the GBA into an international centre of innovation and technology and a comprehensive national science hub.

The GBA Forum also saw the execution of a new framework agreement for the Strategic Cooperation between CUHK and the Greater Bay Area University for establishing a new joint institute on "Advanced Materials and Green Energy Research", led by CUHK Faculty of Science. So our Faculty of Science is actively involved in advancing the Greater bay Area. Apart from gaining in-depth expertise in cutting-edge research as Postgraduate students under the supervision of scientists in the Faculty, we hope many of you would take up the role of constructive player to build up the science, technology, and innovation in Greater Bay Area in the new future.

Today we are very pleased to have 14 excellent postgraduate researchers from different units to showcase their research this year. We hope the symposium will facilitate exchange of ideas and help expand students' horizons. We also hope this event will bring greater awareness for the importance of, and facilitates the learning of the soft skills of postgraduate students in technical presentation and oral communication.

I would like to finish my remarks by thanking all of the postgraduate speakers and all of the participants, as well as the organizing team members from our Science Faculty!

Please enjoy the presentations. Thank you.

Yours sincerely,

Chunshan SONG

Impacts of Changes in Land Use, Climate, and Anthropogenic Emissions on Global Air Quality by the Mid-21st Century Following the Shared Socioeconomic Pathways

BHATTARAI Hemraj
Year 2 PhD Student in Earth & Atmospheric Science
Supervisor: Professor TAI Pui Kuen Amos

Surface ozone (O_3) and $PM_{2.5}$ are the major air pollutants, which have adverse effects on human and vegetation health, environment, and the climate system. However, the influence of future land use and land cover change (LULCC), climate, and anthropogenic emissions on the concentration and composition of air pollutants are largely unknown. Thus, we performed a series of model experiments for 2010 to 2050 using the Community Earth System Model (CESM_2.1.3) to investigate the individual and combined effects associated with LULCC, climate and anthropogenic emissions on global O_3 and $PM_{2.5}$ over the mid-21st century following the Shared Socioeconomic Pathways (SSP3 and SSP5) projections. Our results reveal that climate and emission induced change largely determine the global O_3 and $PM_{2.5}$ concentration in all scenarios considered. Climate-induced isoprene emission increased globally by ~20% (~ 7 mg/m2/day) in 2050, which decreases summertime O_3 (~ 6 ppb) concentration over remote NOx limited regions (such as tropical rainforest over South America, mid-Africa), however, over the polluted regions in South-east China and North-east US, O_3 concentration increases (~ 10 ppb) with an increase in isoprene emission. Similarly, in both scenarios, future emissions of NOx largely increased in India and mid-Africa. This results in reduced O_3 over India possibly due to O_3 titration by NOx, whereas O_3 over mid-Africa increased indicating O_3 formation limited by NOx. Moreover, annual $PM_{2.5}$ concentration is influenced by the future change in emission, with a significant reduction over East China following the SSP5 scenario, with a particular reduction of black carbon (BC), SO_4^{2-} and organic matter, which are reduced by half of the base year (2010). In contrast, following the SSP3 scenario, $PM_{2.5}$ increases over India and China making air pollution worse than today. The impact of LULCC is relatively insensitive to emission and climate change on determining future air pollution. However, the effect of land-use changes alone could change summer O_3 (~2-5 ppb) in East China and mid-Africa. LULCC could be an important but overlooked driver of O_3 air quality in the future that substantially modulates the generally more dominant effect of climate change per se. This study illustrates the importance to consider changes in anthropogenic emission, climate and land use in future air pollution control planning and management.

Enormous Water Input in the Southern Mariana Subduction Zone: Seismic Evidence Derived from Ocean Bottom Seismographic Experiments

CHEN Han
Year 4 PhD Student in Earth & Atmospheric Science
Supervisor: Professor YANG Hongfeng

Estimating the amount of water transported into Earth's interior plays an important role in the global water cycle but is still poorly understood. The only mechanism that the water carried into the deep inter-earth is the subduction of the hydrated slabs in the subduction zones. The water content of subducted plate also significantly influences the geology process in the subduction zone, such as the mantle melting and forearc volcano activity. Thus, estimating the hydration degree of the subducting plate is a crucial scientific problem. The hydration of subducting plate in the outer rise region results in a reduction of seismic velocities. The distribution of outer-rise normal faults and the seismic velocities of incoming plates and forearc mantle, therefore, could be employed to study the hydration degree of the subducting plate. An OBS network was deployed in the southernmost Mariana, near the challenge deep from December 2016 to June 2017, covering both overriding and subducting plates, providing near-field seismicity data. In this study, a machine learning based earthquake detection method was applied and thousands of local earthquakes were detected, and the Rayleigh wave tomography was used to derive the SV-wave velocity structure near the trench. The located outer-rise earthquakes reveal a deep-cutting normal fault, extending to ~50 km in depth in the outer-rise region in southern Mariana. The deep normal fault and the low velocities (3.6–4.1 km/s) within the upper ~25 km of the mantle near the trench, indicate extensive mantle hydration of the incoming plate and enormous water input in southern Mariana.

Keywords: Ocean Bottom Seismometer, Mariana subduction zone, earthquake location, Rayleigh wave tomography, Machine learning

Testing Variance Change under Varying Mean Structure

LEUNG Cheuk Wai Dominic
Year 2 MPhil Student in Risk Management Science
Supervisor: Professor CHAN Kin Wai Keith

Variance change is an important signal that indicates structural instability or a behavioural change. Mean-constancy is typically assumed by the classical cumulative sum (CUSUM) approach in detecting a variance change, however, this assumption is violated in many real applications. Strong dependence among consecutive observations has also been shown to reduce the power of the CUSUM tests.

In this talk, we address the two aforementioned problems by optimally transforming the observations by a data-driven differencing procedure. The proposed method utilizes the originally harmful dependence structure to escalate the power. Besides, it automatically achieves mean invariance without the need of modelling the mean structure. Derivation and implementation of the optimal differencing procedure will be discussed. The power improvement of the proposal will be illustrated via asymptotic theory and Monte Carlo experiments. An application to the crypto market sentiment data is investigated.

scAMACE: Model-Based Approach to the Joint Analysis of Single-Cell Data on Chromatin Accessibility, Gene Expression and Methylation

WANGWU Jiaxuan
Year 4 PhD Student in Statistics
Supervisor: Professor LIN Zhixiang

The advancement in single-cell sequencing technologies enables measuring of different genomic contents at the single cell resolution. The growth of available single-cell datasets motivates integrative analysis of multiple single-cell genomic datasets. Integrative analysis of multimodal single-cell datasets (chromatin accessibility, gene expression and methylation) combines complementary information offered by single-omic datasets and can offer deeper insights on complex biological process.

In the single-cell data analysis, the cell types are usually unknown in prior, hence clustering methods that identify the unknown cell types are among the first few steps in the analysis of single-cell datasets, and they are important for downstream analysis built upon the identified cell types. However, existing clustering methods are not designed to integrate all three data types simultaneously. Moreover, most of them also do not quantify the uncertainty in the assignment of clusters, which may be suboptimal when there are cells at the intermediate stage of development.

In this work, we propose scAMACE (integrative Analysis of single-cell Methylation, chromatin ACcessibility and gene Expression) for the integrative clustering of single-cell data on chromatin accessibility, gene expression and methylation. scAMACE takes the biological and technical variabilities into consideration when integrating multiple data types. In addition, scAMACE can provide statistical inference on the cluster assignments. We demonstrate that by combining complementary biological information from multiple data types, better cell type separation can be achieved.

We thank Zexuan Sun for the implementation of Python package, and Jinwen Yang, Wenyu Zhang, Pengcheng Zeng for the helpful discussions.

New Analytical Lens Focusing on Interstellar Turbulence

YEUNG Cheung Hei
Year 2 PhD Student in Physics
Supervisor: Professor LI Huabai

Turbulence, the last frontier in classical physics, is ubiquitous in the Universe. Molecular clouds in the Milkyway is my lab for studying turbulence. I will first briefly introduce the role of turbulence in star-formation processes, followed by the conventional methods in analyzing the turbulence structure of molecular clouds using molecular line emissions. Predominantly, these methods study the averaged behavior of the gaseous turbulence along the entire line of sight. I will discuss the limitations of these methods and propose an improved strategy illustrated by magnetohydrodynamic simulations. I end my talk with the potential of the new method on actual data from the Milkyway.

Three-Loop Braiding Statistics for Fermionic Topological Phases

ZHOU Jingren
Year 4 PhD Student in Physics
Supervisor: Professor GU Zhengcheng

First, we introduce some of the terminologies. (1) What we mean by gapped system, is that there is a finite energy gap between the ground states and excited states. (2) And there is a special kind of gapped phase of matter that is long-range entangled, called topological order, which generally exhibits ground state degeneracies, nontrivial braiding statistics among the quasiparticle excitations, and gapless edge modes. (3) However, when the system possesses some global symmetries, even a trivial product state can be entangled, but short-range entangled. This kind of phase of matter is called symmetry protected topological (SPT) phases, which is not an intrinsically entangled system, as the short-range entanglement disappears when all symmetries are broken. (4) If symmetries come to a topologically ordered system, the number of possible phases of matter will be enriched by the symmetries, and they are symmetry-enriched topological (SET) phases.

Here we focus on the classification of fermionic SPT (FSPT) phases in 3D. And our method to classify 3D FSPT phases via three-loop braiding statistics. And there is a previous established method to classify 3D FSPT phases via finding the equivalence classes of fermionic symmetric local unitary (FSLU) transformations on fixed-point wavefunctions. We expect the classification results from the two methods totally matches.

There is an interesting fact that each anomaly-free SPT phase can be mapped to a corresponding topological order, by a technic called "gauging the symmetry". By fully gauging all symmetries, the global symmetries now become local gauge invariance. And we obtain a topological order without any symmetry, but with topological particle-like and loop-like excitations in 3D. The particle-like excitations carry symmetry charges, and the loop-like excitations carry symmetry-fluxes. The particle-loop braiding process can be understood in a way analogous to the Aharonov-Bohm effect. While since loop-like excitations are topological, i.e. the braiding statistics is invariant under smooth deformations of the loops, a particle-loop braiding can be equivalently transformed to a particle-loop braiding. However, if we insert a base-loop to the two braiding loops, which forms the so-called three-loop braiding process, a loop cannot be equivalently treated as a particle anymore. And the loops with a base loop inserted now become anyons, that may even exhibit non-Abelian braiding statistics. And we find that studying all three-loop braiding statistics gives a classification of all 3D FSPT phases with on-site unitary symmetries.

Peterson Isomorphism and Seidel Representations

CHOW Chi Hong
Year 4 PhD Student in Mathematics
Supervisor: Professor LEUNG Nai Chung Conan

In enumerative geometry, an unpublished result of Peterson states that the affine Schubert calculus associated to any complex semi-simple Lie group determines explicitly and completely the quantum Schubert calculus associated to the same group. The only known proof, due to Lam-Shimozono, is combinatorial. In this talk, I will present a new and geometric proof which realizes Peterson's map as a parametrized version of Seidel representations. The latter was first introduced by Savelyev in the symplectic context. The key is to observe that the moduli stacks for Savelyev's map are in fact the affine analogue of the moduli stacks of stable maps to flag varieties.

Beating the Saturation Phenomenon of Stochastic Gradient Descent

ZHOU Zehui
Year 4 PhD Student in Mathematics
Supervisor: Professor ZOU Jun

Stochastic gradient descent (SGD) is a promising method for solving large-scale inverse problems, due to its excellent scalability with respect to data size. The current mathematical theory in the lens of regularization theory predicts that SGD with a polynomially decaying stepsize schedule may suffer from an undesirable saturation phenomenon, i.e., the convergence rate does not further improve with the solution regularity index when it is beyond a certain range. In this talk, I will present our recent results on beating this saturation phenomenon:

(i) By using small initial stepsize. We derive a refined convergence rate analysis of SGD, which shows that saturation does not occur if the initial stepsize of the schedule is sufficiently small.

(ii) By using Stochastic variance reduced gradient (SVRG), a popular variance reduction technique for SGD. We prove that, for a suitable constant step size schedule, SVRG can achieve an optimal convergence rate in terms of the noise level (under suitable regularity condition), which means the saturation does not occur.

Development of Advanced Photodynamic Molecular Beacons with Multiple Controls for Targeted Photodynamic Therapy

TAM Ka Bo
Year 4 PhD Student in Chemistry
Supervisor: Professor NG Kee Pui Dennis
Co-supervisor: Professor CHEUNG Chi Keung Peter

Photodynamic therapy (PDT) is an established treatment modality for various superficial and localized cancers. The therapeutic outcome can be enhanced by conjugating the photosensitizers with tumor-targeting ligands and/or controlling their photoactivities via tumor-associated stimuli. Photodynamic molecular beacons (PMBs), which are quenched by various mechanisms in the native form, can be activated in terms of fluorescence emission and reactive oxygen species generation upon interactions with cancer-related stimuli. We report herein a series of advanced PMBs to demonstrate the combination of active targeting and stimuli-responsive properties for targeted PDT.
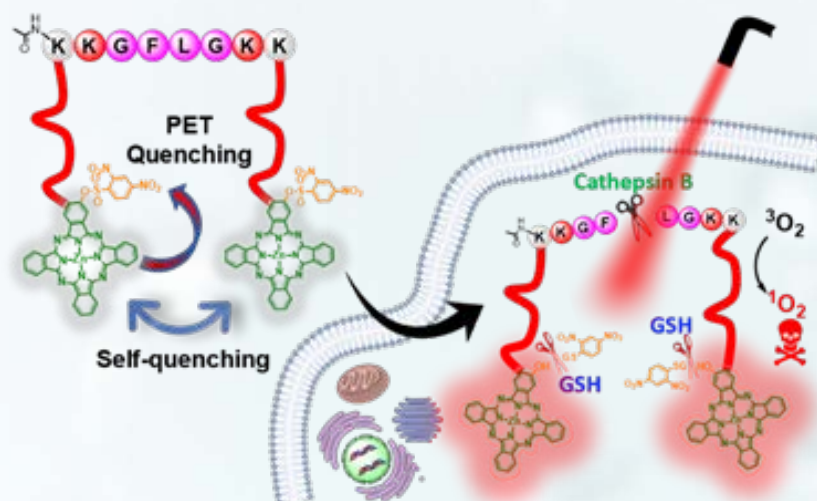
We will first report two dual activatable PMBs, which contains two or three glutathione (GSH)-cleavable 2,4-dinitrobenzenesulfonate-substituted zinc(II) phthalocyanine (ZnPc) units connected by one or two cathepsin B-cleavable GFLG peptide linker(s). The photosensitizing properties of these systems could only be fully activated in the presence of both GSH and cathepsin B, as demonstrated in phosphate-buffered saline and inside a range of cancer cells. The trimeric ZnPc-based PMB was further conjugated with a cyclic MYIEALDKYA peptide, which exhibited a strong and selective binding affinity toward the epidermal growth factor receptor overexpressed in cancer cells. Its photobiological properties will also be reported in the presentation. In addition, an advanced "double-locked" PMB was also developed, in which a boron dipyrromethene-based photosensitizer and a quencher were connected via a cyclic peptide consisting of a cathepsin B-cleavable GFLG peptide linker and a matrix metalloproteinase-2 (MMP-2)-cleavable PLGVR peptide linker. The synthesis of this PMB and its dual activation property by intracellular cathepsin B and MMP-2 will also be reported.

This work is in collaboration with Professor LO Pui-Chi of Department of Biomedical Sciences, City University of Hong Kong.

Gold-in-copper at Low *CO Coverage Enables Efficient Electromethanation of CO_2
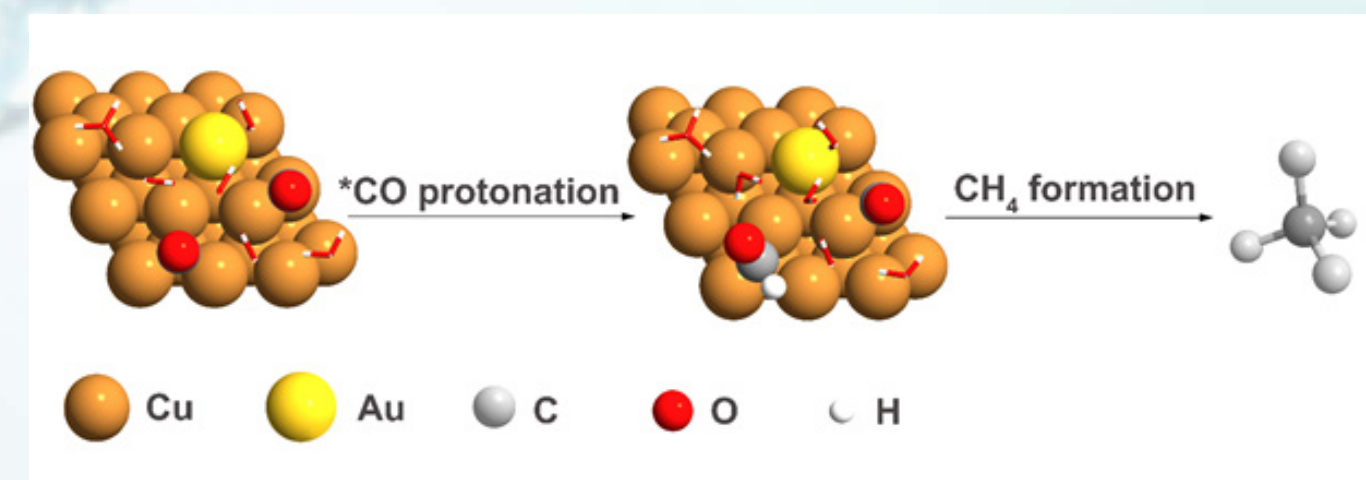
XIE Yi
Year 3 PhD Student in Chemistry
Supervisor: Professor WANG Ying
Co-supervisor: Professor YU Chai Mei Jimmy

With the increasing of global fossil energy-related CO_2 emissions and the following serious impact on the ecological environment, the issue of transformation of energy enterprises and the evolution of sustainable development is becoming attractive. The research of high-efficiency carbon dioxide capture, storage and conversion technologies, especially carbon dioxide reduction reaction (CO_2RR) driven by renewable electric energy, has received extensive attention. At present, CO_2RR studies have reported the conversion of CO_2 to C_1 (methane, methanol and CO) to C_3 (n-propanol) and other different products. Among them, **renewable methane has aroused people's interest due to the established natural gas infrastructure.** We present a strategy wherein we **introduce Au into Cu and regulate *CO availability on catalysts surface, enabling selectivity to methane at high production rates in CO_2RR.** We report a CO_2-to-methane conversion with a high methane faradaic efficiency of $(56\pm2)\%$ at a partial current density of (112 ± 4) mA cm^{-2} with a CO_2-N_2 co-feed. These findings suggest a strategy to promote the conversion of CO_2 to carbon-neutral methane with the advantages of high selectivity, high conversion rate and high cathode energy efficiency.

Evolutionary Landscape of Non-canonical RNA G-Quadruplexes: Hidden Side of a Versatile Structural Element

CHOW Yui Ching
Year 6 PhD Student in Cell and Molecular Biology
Supervisor: Professor CHAN Ting Fung

RNA G-quadruplexes (rG4s) are non-classical RNA secondary structures that have been first observed decades ago. Over the years, these four-stranded structural motifs have been demonstrated to have versatile regulatory roles in diverse biological processes, but challenges remain in profiling them comprehensively in across different biological systems.

rG4s structures can be further subclassified as "canonical" and "non-canonical" based on their underlying nucleotide sequences. Historically, our understanding of rG4 structures is highly shaped by work studying canonical rG4s, which are described by the structural motif $G_3N_{1-7}G_3N_{1-7}G_3N_{1-7}G_3$. In contrast, less is understood about non-canonical rG4s, which are described by relaxed motif definitions based on recent findings suggesting rG4s structure can tolerate minor structural imperfections at the cost of reduced thermostability. Despite the difference in sequences, both canonical and non-canonical rG4s are suggested to fold into equivalent G-quadruplex structures, and can perform the same set of biological functions indistinguishably. We hypothesized that a complete catalogue of all rG4 structures regardless of their sequence motifs would facilitate further elucidation of rG4 biology. With this motivation, we have recently developed an *rG4-seq* method and an *rG4-seeker* software for confident transcriptome-wide mapping of rG4 structures at single-nucleotide resolution. By applying the technique to human cell model, it was found that not only non-canonical rG4s contributed >75% of all rG4s in human transcriptome, but they could also tolerate more extensive structural imperfections than previously reported. Meanwhile, by applying the technique to the malaria parasite *Plasmodium falciparum*, we showed that rG4s can form and affect *in vivo* translation in its very highly A/T-biased transcriptome, where most rG4s detected were non-canonical.

Based on the rG4-seq results and incorporating comparative genomics techniques, we further explored the evolutionary landscape of rG4s. Findings suggested an overall increase in rG4 densities per transcriptome length along evolution, the prevalence of non-canonical motifs in eukaryotes transcriptomes especially among lower eukaryotes, and that canonical motifs would only appear in a later evolutionary timepoint. Moreover, it was observed that rG4s residing in protein-coding regions (CDS) and un-translated regions (UTR) likely underwent distinct modes of molecular evolution: CDS rG4s may be imprinted by protein sequence features and codon usage patterns, while *de novo* UTR rG4s could evolve from random sequences. In both processes, non-canonical motifs can possibly serve as evolutionary intermediate states, which facilitate the expansion of functional rG4 structures in eukaryotic transcriptomes.

Characterization of Extracellular Vesicles (EVs) and EXPO in Plant

GAO Jiayang
Year 5 PhD Student in Cell and Molecular Biology
Supervisor: Professor JIANG Liwen

Extracellular vesicles (EVs) are lipid bound vesicles secreted by cells into the extracellular space. In eukaryotic cells, EVs play important roles in mediating intercellular communication via delivering biomolecules to extracellular space. In mammalian cells, there are three kinds of EVs including 1) exosomes derived from multivesicular bodies (MVB)-plasma membrane (PM) fusion, 2) shedding microvesicles directly budding from the PM, and 3) apoptic bodies generated by cell death.

Distinct from mammalian cells, plant cells contain cell wall which may prevent the formation and function of EVs. Interestingly, recent studies have identified two types of plant EVs: (1) Exosome-like EVs isolated from apoplastic wash of the pathogen-challenged *Arabidopsis* leaves via ultra-centrifugation, and (2) the novel double membrane organelle termed EXPO (exocyst positive organelle) that mediates an unconventional protein secretion (UPS) pathway. However, the nature and identity of EVs in plants in vivo remain elusive.

Here we use a combination of 3D Electron Tomography (ET) and Correlated Light microscope and Electron Microscope (CLEM) approaches to study the types and structures of EVs in various cell types. Based on their sizes and internal contents, we have classified the identified EVs into three types: Type1 EVs (electron-transparent, 30-200nm in diameter), Type2 EVs (contain ribosomes, 200-500nm in diameter), and Type3 EVs (contain ribosomes and small vesicles, 500-2000nm in diameter) in root cells. Further CLEM and immunogold-TEM analysis have distinguished the Exo70E2-positive EXPO from other types of EVs in term of size, shape and cargo contents in the root apoplast. Functionally, a new cargo of EXPO has been identified likely to be involved in plant defense against pathogens. On-going studies include functional characterization of EVs in plants.

Priming-Induced Alterations in Histone Modifications Modulate Transcriptional Responses in Soybean under Salt Stress

YUNG Wai Shing
Year 6 PhD Student in Molecular Biotechnology
Supervisor: Professor LAM Hon Ming

Understanding how plants adapt to stress conditions is important for developing strategies for crop improvement. Plants that have experienced certain abiotic stress may gain tolerance to a similar stress in subsequent exposure. This phenomenon is known as priming. Modulation of transcriptional responses is one of the features underlying the priming mechanism. Emerging studies have reported that epigenetic marks such as histone modifications play a key role in transcriptional regulation in plant response to abiotic stress. However, their roles in abiotic stress priming in crops are still largely unknown. In this study, the priming phenomenon was observed in soybean (*Glycine max*) seedlings exposed to salt stress. Time-course transcriptomic profiles revealed distinctively different transcriptional responses in the primed seedlings from those in the non-primed seedlings under high salinity stress, indicating a stress response strategy of repressing unhelpful biotic stress responses and focusing on the promotion of those responses important for salt tolerance. To identify histone marks altered by the priming salinity treatment, a genome-wide profiling of Histone 3 Lysine 4 dimethylation (H3K4me2), Histone 3 Lysine 4 trimethylation (H3K4me3), and Histone 3 Lysine 9 acetylation (H3K9ac) was performed. Our integrative analyses revealed that priming induced drastic alterations in these histone marks, which coordinately modified stress response, ion homeostasis and cell wall modification. Furthermore, transcriptional network analyses unveiled epigenetically modified networks which mediate the strategic downregulation of defense responses. Altering the histone acetylation status using a chemical inhibitor of histone deacetylase could elicit the priming-like transcriptional responses in non-primed seedlings, confirming the importance of histone marks in forming the priming response.

The Neuronal Adaptor FE65 Potentiates ARF6-Mediated Neurite Outgrowth by the Activation of ARNO

ZHAI Yuqi
Year 4 PhD Student in Cell and Molecular Biology
Supervisor: Professor LAU Kwok Fai

FE65 is a brain-enriched adaptor protein that possess three protein-protein interaction domains: one WW domain and two phosphotyrosine binding domains (PTB1 and PTB2). Like other adaptor proteins, FE65 binds to different cellular proteins to form functional complexes. Our previous finding demonstrates for the first time that FE65 interacts with the small GTPase ADP-ribosylation factor 6 (ARF6) via its PTB1 domain. ARF6 is reported to regulate multiple cellular processes, including endocytic membrane trafficking and actin cytoskeleton remodeling. We demonstrate that the interaction between FE65 and ARF6 potentiates neurite outgrowth, a process that requires extensive cytoskeleton rearrangement. However, how does FE65 activate ARF6 remain elusive as it holds no GTPase activating function. As FE65 is a molecular adaptor, we hypothesize that it activates ARF6 utilizing a guanine nucleotide exchange factor (GEF) of ARF6. In fact, we identify an ARF6 GEF, namely ARNO (ARF Nucleotide-Binding Site Opener) as a new FE65 interactor. Their interaction is mediated by FE65 PTB2 and ARNO PH domains. As reported, ARNO enhanced ARF6 activation and ARF6-mediated neurite outgrowth. Intriguingly, the stimulatory effects were further potentiated by FE65 and such effect was attenuated by an FE65 mutant that does not interact with ARNO. Overexpression of FE65 enhanced the dimerization and the relief of the autoinhibitory conformation of ARNO. Therefore, we propose that FE65 potentiates ARF6-mediated neurite outgrowth by the activation of ARNO.