



International Conference on
Precision Medicine

From Discovery to Public Health

July 19 & 20, 2018

DELEGATES' HANDBOOK

**International Conference on Precision Medicine
From Discovery to Public Health
July 19 & 20, 2018
Crown Plaza Bangkok Thailand**

Host:

Chulalongkorn University
King Chulalongkorn Memorial Hospital
The Royal Society of Thailand
National Research Council of Thailand
Thailand Research Fund
Ministry of Public Health

Sponsors:

Chulalongkorn University
King Chulalongkorn Memorial Hospital
National Research Council of Thailand
The Royal Society of Thailand
Thai Research Fund

Organizers:

Professor Vorasuk Shotelersuk, MD
Professor Emeritus Somchai Bovornkitti, MD
Professor Anond Bunyaratvej, MD
Associate Professor Supatporn Tepmongkol, MD
Associate Professor Pawinee Rerknimitr, MD

Editorial Team:

Honorable advisor:
Professor Emeritus Somchai Bovornkitti, MD, DScMed
Editor:
Associate Professor Pawinee Rerknimitr, MD

Prologue

The Health Forum is an activity of The Academy of Science of The Royal Society of Thailand, first launched in 2013. The Forum's primary goal is to bring together scientific minds dedicated to addressing both the issues and challenge in medicine at the national, regional, and international levels.

As Chairman of the Forum since its inception, one of my principle assignments has been to organize its annual conference, and I am proud that I have succeeded in completing that task. It may be recalled that the first two conferences drew attention to the controversies surrounding industrial use of asbestos in Thailand.

Then, following the launch of the ASEAN Economic Community (AEC) in 2015, I was inspired to highlight the value to medicine and science brought about by the AEC. The Health Forum then shifted the focus of the following two conferences, namely: The First ASEAN Art Therapy Conference, 2015, held in Bangkok, Thailand; and the Conference on the Medical Status of ASEAN Countries, 2016, held in Chiang Mai Province, Thailand.

For 2017, the fifth meeting was organized in close cooperation with Burapha University, the Beijing Institute of Genomics of the Chinese Academy of Science, the Thailand Research Fund, and The National Research Council of Thailand. It was focused on the current state of precision medicine in the Sino-ASEAN context.

For 2018's activity, it is most fortunate that my personal goal of holding "The International Conference on Precision Medicine" will become a reality. It is being co-organized by Chulalongkorn University's Faculty of Medicine, The National Research Council of Thailand, and the Ministry of Public Health of Thailand. This event will surely enable participants from countries around the world to share information on similar interests and forge new friendships among themselves as well as get together with old colleagues who have known each other previously.

It is the Health Forum's hope, as well as my personal goal, that each participant not only derives value and inspiration from The International Conference on Precision Medicine but departs from the conference with a renewed appreciation for the global influence on precision medicine's continued development.

As is standard for scientific meetings, the organizers plan to publish the scientific proceedings soon after the conclusion of the

Conference. I therefore request all participants to kindly submit the manuscripts of their talks within three months after the Conference.

In the end, I am honored by your presence and inspired by your words.

With Sincerest Gratitude,

Somchai Bovornkitti, MD, DScMed

Chairman of the Health Forum, The Royal Society of Thailand

Message from Nibondh Saibejra, FRST

Academy of Science

Vice President, The Royal Society of Thailand

On behalf of the Royal Society of Thailand, I am very pleased and much honored to welcome all of you to Thailand to attend the International Conference on Precision Medicine: From Discovery to Public Health at Crowne Plaza Bangkok on July 19-20, 2018

You are famous participants locally and from many countries including Asian countries, United States, United Kingdom, China, Japan and Hong Kong.

In this modern world of high technology, precision medicine has been in practice for many years. New knowledge and techniques have been discovered worldwide. Therefore, the international conference on the subject is needed regularly. On behalf of the host country we thank you very much for visiting Thailand. We are very happy to give a warm welcome to all of you again. Please enjoy your life while staying in our country and returning home safely.

Thank you

Message from Kiat Ruxrungtham, MD

Vice President for Research and Innovation
Chulalongkorn University

Precision Medicine is a rapid growing field that helps in both early diagnosis and accurate personalized treatment. It is an inter-disciplinary field combining state-of-the-art knowledge and sciences from various fields. Thailand's research is heading toward this direction and Chulalongkorn University fully support this.

On behalf of Chulalongkorn University, it is our great pleasure to co-host this prestigious event, International Conference on Precision Medicine. I would like to express my sincere thank to all of our co-hosts, The Royal Society of Thailand, National Research Council of Thailand, The Thailand Research Fund, Ministry of Public Health and King Chulalongkorn Memorial Hospital, for all your support and collaboration to make this meeting become reality. I really appreciate all of our esteemed guest speakers from overseas and from Thailand to accept our invitation to share your research and knowledge. By this mean, we can altogether rapidly advance our knowledge. I would like to also thank all the participants who came from all over the world for your interest in this event and for sharing your knowledge with others.

On behalf of Chulalongkorn University, I would like to welcome all of you and hope you have a fruitful experience in this meeting.

Message from Suttipong Wacharasindhu, MD

Director of King Chulalongkorn Memorial Hospital,
The Thai Red Cross Society
Dean of Faculty of Medicine of Chulalongkorn University

On behalf of King Chulalongkorn Memorial Hospital, the Thai Red Cross Society, it is my great pleasure to welcome all attendees to the International Conference on Precision Medicine: From Discovery to Public Health, which is held on 19th – 20th July 2018, in Bangkok, Thailand.

The advancement of precision medicine has led to an important step in health care system. King Chulalongkorn Memorial Hospital is giving strong emphasis on the development of precision medicine in Thailand. These include the settlement of pharmacogenetics, genomic and tailored therapeutic cancer centers for Thai patients. In addition, we realize that it is important to distribute the knowledge and enhance the collaboration among experts in the field. Therefore, we, together with Faculty of Medicine, Chulalongkorn University, Royal Society of Thailand, National Research Council of Thailand, Thailand Research Fund, and the Ministry of Public Health of Thailand have come together to organize this special meeting.

I would like to express my sincere gratitude to all delegates and honorable speakers for their full cooperation and contribution to the International Conference on Precision Medicine. The meeting officially open. I wish you all a very fruitful and productive meeting.

Message from Sirirurg Songsivilai, MD

Secretary of the National Research Council of Thailand

On behalf of the National Research Council of Thailand (NRCT), the main government organization for national research and innovation policy and implementation according to the 20-Year National Strategy and the 20-Year Research and Innovation Strategy, NRCT is happy to cohost this International Conference of Precision Medicine: From Discovery to Public Health. Over our mission is focused on enhancing competitiveness and strengthening our economy, society, health and environment. Research has an important role in creating and applying knowledge for effectively developing the country. NRCT has initiated new research funding system under the Grand Challenges Thailand Program to support large-scale projects that have clear and challenging goals, and the outcome will enhance key areas of national development. The Precision Medicine in Cancer project one of our Grand Challenges Thailand Program.

The advances in genomics and omics will further our understanding of various diseases and provide new hopes for curing important diseases. The development of treatments based on precision medicine may enable selection for each patient treatment bases on individual genetic data. It is also expected that better understanding of biomolecular target will also allow highly specific diagnosis, as well as more effective and safer treatment. NRCT hopes that precision medicine will be effectively and appropriately applied for the betterment of our people. Our congratulations on the success of organizing this Conference.

Message from

Suthipun Jitpimolmard, MD, FRCP

Director of the Thailand Research Fund

On behalf of the Thailand Research Fund, It is my honor to welcome all of you to the International Conference on Precision Medicine: From Discovery to Public Health, held on 19th – 20th July 2018, in Bangkok, Thailand. We are honored by your presence and hope to make the followings two days as inspiring as they are informative.

This conference is made possible by the collaboration of the following distinguish hosts; Faculty of Medicine, Chulalongkorn University, King Chulalongkorn Memorial Hospital, Royal Society of Thailand, National Research Council of Thailand, Thailand Research Fund, and the Ministry of Public Health of Thailand.

Precision medicine is a tailored approach to health care that accounts for the individual variability in the genes, environment and lifestyle of each person. These have led to significant strides in promoting disease prevention and offering highly effective targeted treatments. I truly believe that this conference will be successful in disseminating the information and advance understanding of this outstanding issues.

I am proud to declare that the International Conference on Precision Medicine: From Discovery to Public Health officially open. I wish all attendees and presenters prosperity in both knowledge and health. Furthermore, I wish you a pleasant stay in Bangkok.

Message from Vorasuk Shotelersuk, MD

President of the Organizing Committee
Director, the Excellence Center for Medical Genomics
Faculty of Medicine, Chulalongkorn University

On behalf of the organizing committee, it is my great pleasure and honor to welcome you to the International Conference on Precision Medicine: From Discovery to Public Health, held on 19th – 20th July 2018, in Bangkok, the capital of Thailand. First of all, I would like to express my sincere appreciation to the Faculty of Medicine, Chulalongkorn University, King Chulalongkorn Memorial Hospital, Royal Society of Thailand, National Research Council of Thailand, TCELS, Thailand Research Fund, and the Ministry of Public Health of Thailand for co-hosting this Conference. I am particularly grateful to Professor Somchai Bovornkitti who is the one initiating this Conference. I am also thankful to Illumina, Pacific Biosciences, Beijing Genomics Institute, Macrogen (South Korea), Sanofi Genzyme, and BNK Bioscience for sponsoring this Conference.

We are extremely fortunate to have a large number of prominent scientists and researchers who will deliver exciting stories and results in the field of “Precision Medicine”. The Conference will host 28 presentations with speakers from 19 different institutes of United Kingdom, Japan, China, Hong Kong, Singapore, and Thailand.

I hope it will be an interesting and stimulating meeting for all the participants, both scientifically and socially. It will be a fantastic experience to have a diverse view on precision medicine and its impact. In addition, the free time social events are designed to create an opportunity for you to meet and discuss with your colleagues, make new friends and come up with new collaborations.

I would like to thank the members of the Organizing Committee, distinguished speakers, sponsors, and participants for making this Conference possible and successful. I hope you enjoy it and have a nice time in Bangkok.

Representative Host



Mr. Nibondh Saibejra
Royal Society of Thailand



Prof. Somchai Bovornkitti
The Royal Society of Thailand



Prof. Kiat Ruxrungtham
Chulalongkorn University



Prof. Suttipong Wacharasindhu
King Chulalongkorn Memorial Hospital
The Thai Red Cross Society



Prof. Sirirug Songsivilai
The National Research Council of Thailand



Prof. Suthipun Jitpimolmard
The Thailand Research Fund



Prof. Vorasuk Shotelersuk
President of the Organizing Committee

Speakers



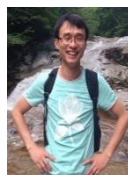
Prof. Philip Beales



Prof. Tohru Nakanishi



Prof. Zhang Zhang



Prof. Yu Xue



Prof. Vorasuk Shotelersuk



Prof. Ang Beng Ti



Prof. Kang Ning



Assoc. Prof. Vorapun Senanarong



Prof. Wei-hua Chen



Dr. Sissades Tongsim



Assoc. Prof. Wirote Tuntiwechapikul



Dr. Chiara Bacchelli



Asst. Prof. Ruibang Luo



Asst. Prof. Ge Gao



Prof. Shuhua Xu



Asst. Prof. Carol Tang Soo Leng



Surakameth Mahasirimongkol



Prof. Kai Ye



Prof. Guoliang Li



Prof. Manop Pithukpakom



Prof. Qiangfeng Cliff Zhang



Assoc. Prof. Suphat Subongkot



Prof. Emeritus Somchai Bovornkitti

Chair of Session and Master of Ceremony



Prof. Anond Bunyaratvej



Assoc. Prof. Supatporn Tepmongkol



Prof. Kanya Suphapeetiporn



Dr. Prasit Phowthongkum



Assoc. Prof. Thanrira Pomtaveetus

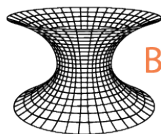


Assoc. Prof. Pawinee Rerknimitr



Dr. Yuda Chongpison

Sponsors



**BNK Bioscience
Limited**



**AUTHORIZED
CHANNEL PARTNER**



SANOFI GENZYME 



Bio-Active Co., Ltd.
บริษัท ไบโอแอคทีฟ จำกัด



RI Technologies

Enabling Next-Generation Science

Thursday July 19th, 2018

08.00 – 08.30 **Registration**

MC: Associate Professor Thantrira Pornaveetus, DDS,
PhD

08.30 – 09.00 **Welcome speech**

Professor Kiat Ruxrungtham, MD

Vice President, Chulalongkorn University

Professor Suttipong Wacharasindhu, MD

Director of King Chulalongkorn Memorial Hospital,

The Thai Red Cross Society

Dean, Faculty of Medicine, Chulalongkorn University

Professor Nipon Saipetch

The Royal Society of Thailand

Professor Suthipun Jitpimolmard, MD

President, Thailand Research Fund

09.00 – 09.15 **Opening Speech**

Professor Surapol Issaragrisil, MD

The Royal Society of Thailand

Professor Sirirug Songsivilai, MD

Secretary of the National Research Council of Thailand

Professor Vorasuk Shotelersuk, MD

Chair of Organizing Committee

Chair: Professor Anond Bunyaratvej, MD

The Royal Society of Thailand

09.15 – 09.45 **Personalised Medicine Opportunities, Challenges and Solutions: the UCL Perspective**

Professor Philip Beales, MD

UCL, Great Ormond Street Institute of Child Health,

London, United Kingdom

09.45 – 10.15 **Development of Tetraspanin CD81 as a Clinical Target of Rheumatoid Arthritis and Breast Cancer**

Professor Tohru Nakanishi, PhD

Shujitsu University Graduate School of Pharmacy, Japan

10.15 – 10.30 **Refreshment and Booth**

Chair: Professor Kanya Suphapeetiporn, MD, PhD

10.30 – 11.00 **Database Resources of the BIG Data Center in 2018**

Professor Zhang Zhang, PhD

Executive Director of BIG Data Center

Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS), China

11.00 – 11.30 **Identification of functional PTM events in neuronal autophagy**

Professor Yu Xue, PhD

the Department of Bioinformatics & Systems Biology,
College of Life Science and Technology of Huazhong
University of Science and Technology, China

11.30 – 12.00 **Precision Medicine for Rare Diseases**

Professor Vorasuk Shotelersuk, MD

Director of the Center of Excellence for Medical Genetics,
Faculty of Medicine, Chulalongkorn University, Thailand

12.00 – 12.10 **Small break**

12.10 – 13.10 **Luncheon Symposium: Short read VS Long read NGS technologies**

1.Clinical Capability of PacBio SMRT Sequencing

Li Xi

Senior Manager, Clinical Marketing, Pacific Biosciences
(PAC BIO), Inc.

**2.From Research to Precision Medicine – illumine
Leading the Path**

Thomas Patrick Klemm

Sr. Specialist, Human Genotyping Asia Pacific & Japan
Illumina

- 13.10 – 13.20 **Small break**
Chair: Associate Professor Supatporn Tepmongkol, MD
- 13.20 – 13.50 **Bridging glioma biology and advanced imaging for precision medicine**
 Professor Ang Beng Ti, MD
 Senior Consultant and Head, Department of Neurosurgery, Singapore General Hospital, Singapore
- 13.50 – 14.20 **Linking Alterations of the Gut Virome to the development of Hypertension**
 Professor Kang Ning, PhD
 Microbial Bioinformatics Group, Director of the Department of Bioinformatics and Systems Biology, School of Life Science and Technology, Huazhong University of Science and Technology, China
- 14.20 – 14.50 **Artificial Intelligence in Neurodegenerative Diseases**
 Associate Professor Vorapun Senanarong, MD, DTM&H, FRCP (London)
 Division of Neurology, Department of Medicine Siriraj Hospital, Mahidol University, Thailand
- 14.50 – 15.05 **Break**
Chair: Dr. Prasit Phowthongkum, MD
- 15.05 – 15.35 **Screening for cancer therapeutic targets through differentially essential genes**
 Professor Wei-hua Chen, MD
 Key Laboratory of Molecular Biophysics of the Ministry of Education, Hubei Key Laboratory of Bioinformatics and Molecular-imaging, Department of Bioinformatics and Systems Biology, College of Life Science and Technology, Huazhong University of Science and Technology, Hubei, China
- 15.35 – 16.05 **Bioinformatics: a keystone to drive -omics aspect in Thailand precision medicine**
 Dr. Sissades Tongsimma, PhD

National Science and Technology Development Agency
(NSTDA) Ministry of Science and Technology (MOST),
Thailand

16.05 – 16.35 **Ginger (*Zingiber officinale*) extract as telomerase suppressor**

Associate Professor Wirote Tuntiwechapikul, PhD
Department of Biochemistry, Faculty of Medicine
Chiang Mai University, Thailand

Friday July 20th, 2018

08.00 – 08.30 **Register**

MC: Dr. Yuda Chongpison, PhD
Chair: Associate Professor Thantrira Porntaveetus, DDS,
PhD

08.30 – 09.00 **Mining whole genomes for PGx variants: to respond or not to respond?**

Dr. Chiara Bacchelli, PhD
UCL, Great Ormond Street Institute of Child Health
London, United Kingdom

09.00 – 09.30 **Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing**

Assistant Professor Ruibang Luo, PhD
Department of Computer Science, The University of Hong Kong

09.30 – 10.00 **Characterizing the “Dark Matters” in Human Transcriptome.**

Assistant Professor Ge Gao, PhD
Center for Bioinformatics
Beijing Advanced Innovation Center for Genomics (ICG),
China

10.00 – 10.15 **Refreshment and booth**

Chair: Professor Kanya Suphapeetiporn, MD, PhD

- 10.15 – 10.45 **PGG.Population: A database for understanding the genomic diversity and genetic ancestry of human populations**

Professor Shuhua Xu, PhD

CAS-MPG Partner Institute for Computational Biology,
China

- 10.45 – 11.15 **Artificial Intelligence: Understanding the Development of Chemoresistance in Glioma Patients, a Case Study (STAT3)**

Assistant Professor Carol Tang Soo Leng, PhD

National Neuroscience Institute, Singapore

- 11.15 – 11.45 **Precision Medicine in Public Health**

Surakameth Mahasirimongkol MD, MSc, PhD

Ministry of Public Health (MOPH), Thailand

- 11.45 – 13.15 **Luncheon Symposium: Service Providers**

1.BGISEQ Based Tech Services Highlight & Featured Applications

Yonggang (Jason) Zhao

Int'l Tech Services Business Unit Director (BGI),
Shenzhen,China

2.Macrogen

Soul, South Korea

Chair: Dr. Prasit Phowthongkum, MD

- 13.15 – 13.45 **Morphling: An ultra-fast model-free framework for structural variant discovery**

Professor Kai Ye, PhD

Department of Automation Science and Technology
Xi'an Jiaotong University (XJTU), China

13.45 – 14.15 **Digestion-Ligation-Only Hi-C, a Simple, Cost-effective, and Highly Efficient Method for Chromosome Conformation Capture**

Professor Guoliang Li, PhD

College of Informatics, Huazhong Agricultural University, China

14.15 – 14.45 **Precision Medicine in Thai Cancer**

Professor Manop Pithukpakorn, MD

Siriraj Hospital, Mahidol University

14.45 – 15.00 **Break**

Chair: Associate Professor Pawinee Rerknimitr, MD

15.00 – 15.30 **Systematic identification of functionally conserved lncRNAs across vertebrates**

Professor Qiangfeng Cliff Zhang, PhD

Beijing Advanced Innovation Center for Structural Biology, Center for Synthetic and Systems Biology, Tsinghua-Peking Joint Center for Life Sciences, School of Life Sciences, Tsinghua University, Beijing, China

15.30 – 16.00 **Evolution of Cancer Treatment in Precision Medicine Era**

Associate Professor Suphat Subongkot, Pharm.D.

Khon Kaen University, Thailand

16.00 – 16.30 **Will Precision Medicine Ever Be A Possibility in the Control of Tuberculosis?**

Professor Emeritus Somchai Bovornkitti, MD, DScMed

The Royal Society of Thailand

16.30 – 16.45 **Closing Remarks**

Professor Anond Bunyaratvej, MD

The Royal Society of Thailand

Personalised Medicine Opportunities, Challenges and Solutions: the UCL Perspective

Phillip Beales

Great Ormond Street Institute of Child Health (ICH),
University College London (UCL), London, United Kingdom

Precision medicine promises to transform healthcare worldwide with medical decisions, treatments, practices, or products being tailored to the individual patient. Diagnostic testing is often employed for selecting appropriate and optimal therapies based on the context of a patient's genetic information or other molecular or cellular analysis. In 2010, at Great Ormond Street Hospital we established GOSgene, a centre to assist in diagnosing patients with rare undiagnosed inherited disease using next generation sequencing. GOSgene has identified mutations in over 110 genes and made more than 50 novel disease gene associations. In 2012, the UK government initiated the 100,000 Genomes project led by Genomics England for rare diseases and cancer. The project delivers objectives through the 13 Genomic Medicine Centres throughout England and involved over 1500 clinicians, 4500 researchers who assist in diagnosis and analysis of whole genomes throughout the country. I will discuss how these and other initiatives are contributing to the implementation of personalised medicine in the National Health Service.

Development of Tetraspanin CD81 as a Clinical Target of Rheumatoid Arthritis and Breast Cancer

Tohru Nakanishi

Department of Molecular Diagnosis, Shujitsu University School of Pharmacy, Okayama, Japan

Tetraspanin belongs to a family of cell-surface protein which has four transmembrane domains and two outer-membrane loops. Under the DNA chip analysis, we showed that there were several genes highly expressed in rheumatoid arthritis (RA) synoviocytes comparing with their expression in OA or normal synoviocytes. Among these genes, tetraspanin CD81 involved in the progression of RA through the stimulation of synoviolin expression. Both synoviolin and tetraspanin CD81 highly distributed in RA tissues. The therapeutic effect of small interfering RNA targeting tetraspanin CD81 was examined by in vivo electroporation method. Treatment with siRNA significantly ameliorated paw swelling of collagen-induced arthritic (CIA) rats. In histological examination, hypertrophy of synovium, bone erosion, and degeneration of articular cartilage were milder in rats treated with siRNA than in the control group and the non-specific siRNA group. Expression of synoviolin, a rheumatoid regulator, was also suppressed by siRNA. These results showed that siRNA would become effective tools for treatment of RA. Recently, we found high amount of CD81 was expressed in some types of breast cancer cells. We are now analysing the genetical background of these cancer cells.

Database Resources of the BIG Data Center in 2018

Zhang Zhang

BIG Data Center and CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, University of Chinese Academy of Sciences, Beijing, China.

The BIG Data Center at Beijing Institute of Genomics (BIG) of the Chinese Academy of Sciences provides freely open access to a suite of database resources in support of worldwide research activities in both academia and industry. With the vast amounts of omics data generated at ever-greater scales and rates, the BIG Data Center is continually expanding, updating and enriching its core database resources through big-data integration and value-added curation, including BioCode (a repository archiving bioinformatics tool codes), BioProject (a biological project library), BioSample (a biological sample library), Genome Sequence Archive (GSA, a data repository for archiving raw sequence reads), Genome Warehouse (GWH, a centralized resource housing genome-scale data), Genome Variation Map (GVM, a public repository of genome variations), Gene Expression Nebulas (GEN, a database of gene expression profiles based on RNA-Seq data), Methylation Bank (MethBank, an integrated databank of DNA methylomes), and Science Wikis (a series of biological knowledge wikis for community annotations). In addition, three featured web services are provided, viz., BIG Search (search as a service; a scalable inter-domain text search engine), BIG SSO (single sign-on as a service; a user access control system to gain access to multiple independent systems with a single ID and password) and Gsub (submission as a service; a unified submission service for all relevant resources). All of these resources are publicly accessible through the home page of the BIG Data Center at <http://bigd.big.ac.cn>.

Identification of functional PTM events in neuronal autophagy

Yu Xue

Key Laboratory of Molecular Biophysics of Ministry of Education, College of Life Science and Technology and the Collaborative Innovation Center for Biomedical Engineering, Huazhong University of Science and Technology, Wuhan, Hubei 430074, China.

Autophagy is a highly conserved process for degrading cytoplasmic contents, determines cell survival or death, and regulates the cellular homeostasis. Besides core ATG proteins, numerous regulators together with various post-translational modifications (PTMs) are also involved in autophagy. Recent studies demonstrated that the dysregulation of macroautophagy/autophagy is involved in human diseases such as cancers and neurodegenerative disorders. Thus, autophagy has become a promising therapeutic target for biomedical design. Here, we developed a database of The Autophagy, Necrosis, Apoptosis OrchestratorS (THANATOS, <http://thanatos.biocuckoo.org>), containing 191,543 proteins potentially associated with autophagy and cell death pathways in 164 eukaryotes. We performed an evolutionary analysis of core ATG genes and observed that ATGs required for the autophagosome formation are highly conserved across eukaryotes. Further analyses revealed that known cancer genes and drug targets were over-represented in human autophagy proteins, which were significantly associated in a number of signaling pathways and human diseases. By re-constructing a human kinase-substrate phosphorylation network for core ATG proteins, our results confirmed that phosphorylation play a critical role in regulating autophagy. Using this data resource, we performed a quantitative phosphoproteomic profiling to delineate the phosphorylation signalling networks regulated by 2 natural neuroprotective autophagy enhancers, corynoxine (Cory) and corynoxine B (Cory B). We developed a novel algorithm of in silico Kinome Activity Profiling (iKAP) to predict that Cory or Cory B potentially regulates different kinases. We discovered 2 kinases, MAP2K2/MEK2 (mitogen-activated protein kinase kinase 2) and PLK1 (polo-like kinase 1), to be potentially upregulated by Cory, whereas the siRNA-mediated knockdown of Map2k2 and Plk1 significantly inhibited Cory-induced autophagy. Furthermore, Cory promoted the clearance of Alzheimer disease-

associated APP (amyloid beta [A4] precursor protein) and Parkinson disease-associated synuclein alpha (SNCA/ α -synuclein) by enhancing autophagy, and these effects were dramatically diminished by the inhibition of the kinase activities of MAP2K2 and PLK1. Taken together, our study not only provided bioinformatics resources and approaches for analyzing PTMs in autophagy, but also identified the important role of MAP2K2 and PLK1 in neuronal autophagy.

Precision Medicine for Rare Diseases

Vorasuk Shotelersuk

Director of the Center of Excellence for Medical Genetics, Faculty of Medicine, Chulalongkorn University, Thailand

Currently, one of the most tangible benefits of clinical exome or genome sequencing is for care of rare diseases. With more than 7,000 different disorders, rare diseases are collectively not rare. In addition, studying rare diseases could lead to better understanding of common diseases.

My presentation will include 1) Discoveries of new human disease genes in our lab (genes for an intellectual disability, an autoimmune disease, a dilated cardiomyopathy, and a hypertrophic cardiomyopathy); 2) Unveiling pathogenesis of Mendelian disorders, in which genes were identified in our lab; and 3) Genome editing and in vitro universal platelet generation. In addition, I will share our real experience of applications of clinical exome and genome sequencing in clinical practice, including rapid exome sequencing to help diagnose and improve care of patients. Essentially, I will cover issues from bench work to medical practice.

Bridging glioma biology and advanced imaging for precision medicine

Ang Beng Ti

Senior Consultant and Head, Department of Neurosurgery, Singapore General Hospital, Associate Professor, Duke-NUS Graduate Medical School

In this era of precision medicine, a challenge is to link cancer biology to advanced imaging modalities so as to augment diagnosis, facilitate decision-making in therapeutics and follow-up in a non-invasive fashion. Glioblastoma multiforme (GBM) is the most common and aggressive primary malignant brain tumor in adults. Epidermal growth factor receptor (EGFR) amplification and a constitutively active mutant, EGFRvIII, is seen in 40% of these tumors, representing an attractive target for therapeutic intervention. Studies have shown that both EGFR and Fatty Acid Binding Protein 7 (FABP7) promote the proliferation and invasiveness of GBM-propagating cells (GPCs), and positively correlate with tumor grade and poor survival outcome. Utilization of an intracellular non-toxic imaging probe, CDr3, that binds to FABP7 could serve as a non-invasive real-time monitoring molecular marker. The ability to tap into potential biomarkers that represent the molecular state of tumor and assess disease progression when repeated surgery is not permissible is key to advancing real-time monitoring of disease progression in the clinic.

In this study, we showed that CDr3 staining positively correlates with FABP7 expression in our patient-derived GPCs. It also discriminates the stem-like, tumor-propagating cells from their terminally differentiated state. Our preliminary data indicates that FABP7 is significantly enriched in patient cohorts with EGFR amplification and/or gain-of-function mutations. Using an orthotopic patient-derived xenograft mouse model, intravenously injected CDr3 specifically stained the tumor, demonstrating its blood-brain barrier penetration capability. Moreover, GPCs treated with Gefitinib, an EGFR inhibitor in phase II clinical trial for GBM, showed a reduction in FABP7 protein expression. Flow cytometric analysis indicated a similar dose-dependent decrease in CDr3 staining intensity. Our data provides evidence that CDr3 represents a potential tool to monitor disease progression in patients subjected to anti-EGFR inhibition therapy. The

ability of CDr3 to mark EGFR-amplified gliomas suggests that it could be incorporated as an additional sequence to current MR imaging techniques.

Linking Alterations of the Gut Virome to the development of Hypertension

Kang Ning

Principal Investigator of Microbial Bioinformatics Group, Director of Department of Bioinformatics and Systems Biology, School of Life Science and Technology, Huazhong University of Science and Technology.

Hypertension is a global public health problem and affect about one third of the worldwide population, and it has already found that gut microbiome has an important link with the development of hypertension. Though previous researches have focused on the links of gut bacteria with hypertension, little has been known about the relation of viral alterations and the development of hypertension, largely due to the lack of computational tools for such investigation. Here we have proposed a framework for mining of gut virome data and linking viral alterations with the development of hypertension. We characterized the viral composition based on 196 hypertension related samples and classified these faecal samples into two viral-types. Additionally, our framework has selected 32 viruses as the biomarkers for identifying samples of these groups and we found that viruses could have superior resolution and discrimination power than bacteria for differentiation of healthy samples as well as hypertension samples from different stages. Moreover, as to the co-occurrence networks linking virus and bacteria, we found increasingly pervasive virus-bacteria attachments in the development of hypertension. Overall, our results have shown strong indications of the link between alteration of gut virome and the development of hypertension and might provide microbial solutions towards early diagnoses of hypertension.

Artificial Intelligence in Neurodegenerative Diseases

Vorapun Senanarong

Head of Division of Neurology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, THAILAND

Introduction: Digital health, advanced technologies such as genomics, biotechnology, or artificial intelligence (AI) are gradually leading to make patients the point-of-care and to create big data for advanced analytics. Materials & Methods: Pubmed searched with keywords: artificial intelligence, deep learning, support vector machine, Alzheimer, Parkinson. Results: Deep learning, a subset of machine learning, utilizes a high level of artificial neural networks to carry out machine learning. In health care, this can result in ability to classify or diagnose certain diseases, predictive of disease progression by algorithm derived from big data learned, and reinforcement of robotic performance base on specific problematic patterns. Alzheimer disease (AD) has linked to structural changes in the gray matter, responsible for processing information and cognitive functional ability, change in the white matter, responsible for the brain connectivity network. Significant loss of fiber tracts in the brain results in functional alternations, namely memory loss or executive dysfunction. Deep learning AI aids AD or Parkinson disease (PD) classification by utilizing data such as anatomical brain imaging, volumetric brain imaging data, functional brain imaging, biomarker data, subject characteristics or subject comorbid diseases. Support Vector Machine (SVM) modelling also produce comparable or improved predictive abilities in comparison to the conventional method of Logistic Regression. EEG data, PETs data, brain volume data, genetic and clinical data can be applied on SVM analysis with excellent predictive ability. Conclusion: Currently, machine learning can help prediction of disease and disease progression in neurodegenerative illness. The future of utilizing big data and AI should help select precise subjects with neurodegenerative diseases to choose proper treatment.

Screening for cancer therapeutic targets through differentially essential genes

Wei-Hua Chen

Key Laboratory of Molecular Biophysics of the Ministry of Education, Hubei Key Laboratory of Bioinformatics and Molecular-imaging, Department of Bioinformatics and Systems Biology, College of Life Science and Technology, Huazhong University of Science and Technology, 430074 Wuhan, Hubei, China

Ideal therapeutic targets for cancer treatment featuring both high sensitivity and specificity are extremely difficult to come by: it is often required that the functions and/or the 3D structures of the target genes should be known and of high-quality. Essential genes are those genes of an organism that are critical for its survival; essential genes are of particular importance because of their theoretical and practical applications such as studying the robustness of a biological system. Being essential is not an intrinsic feature of a gene; rather, it is highly dependent on a variety of factors including the function and expression pattern of the gene, the genetic background of the host, the environment, the experimental methods and other settings. Genes with variable essentiality statuses under different circumstances are referred to “conditionally essential genes (CEGs)” or “differentially essential genes (DEGs)”. CEG is a biologically meaningful and very important concept; for example, genes that are essential in a cancer cell line but are non-essential in human tissues can reveal the oncogenic drivers, paralogous gene expression pattern, and chromosomal structure of the corresponding cancer type, and are ideal targets for new drug development and treatment by existing drugs or even CRISPR-based genome-editing techniques. Here we present OGEE, an online gene essentiality database, in which we included results of 250 essentiality experiments from cancer cell lines, corresponding to nine different human cancers. We re-organized the results so that users can easily explore the shared and differentially essential genes within and between cancer types. These genes can be important targets for cancer therapy and/or new drug development. In addition, we proposed an integrated approach for further screening the identified gene targets.

Bioinformatics: a keystone to drive -omics aspect in Thailand precision medicine

Sissades Tongsima

National Science and Technology Development Agency (NSTDA)
Ministry of Science and Technology (MOST), Thailand

The completion of human genome reference sequence stirs up hope to utilize information from our DNAs to cure/prevent diseases. With the advent of high throughput sequencing technologies, sequencing cost keeps dropping, yet with high reliability as well as quality of base calling. With such a promising outlook, the concept of precision medicine (PM) was coined to describe a new paradigm in treating patients at a high precision level by utilizing DNA knowledge that makes all of us different. Although, DNA data can be generated so easily and quickly, processing them is a daunting task. The implementation of PM, hence, demands computational support not only in the aspect of low level high performance computing infrastructure but also related computational workflows/software tools that are tailored for PM for the people living in each country or to the level of unique (sub)populations with similar genetic profiles representing a country. PM initiative in Thailand is conceptually implemented under a collaborative project, named Genomics Thailand, whose members are from both academia and government sectors. In terms of applications, Genomics Thailand hopefully aims to come up with interventions from four main genetic-related burdens, namely rare and undiagnosed diseases, cancer, pharmacogenomics and noncommunicable diseases. To support the underlying PM practices, bioinformatics must be utilized to accurately identify with high confidence genetic factors that are related to such interventions. This talk covers the implementation of computational infrastructure, construction of population-level genomic variation databases as well as software tools to drive PM in Thailand.

Ginger (*Zingiber officinale*) extract as telomerase suppressor

Wirote Tuntiwechapikul

Department of Biochemistry, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

Most cancer cells achieve proliferative immortality by reactivating telomerase, mostly by upregulating the normally silent human TERT (hTERT) gene. Without telomerase, cancer cells would render themselves to replicative senescence in the same manner as normal somatic cells, which is the consequence of telomere shortening due to the end replication problem. Based on our studies, we found that crude *Zingiber officinale* extract (ZOE) suppressed the expression of the hTERT gene, leading to the reduction of hTERT protein and hence telomerase activity in A549 lung cancer cells. The long-term treatment with subcytotoxic doses of ZOE in A549 cancer cells induced telomere shortening without affecting the population doublings. The telomere shortening consequently induced cellular senescence in these cells, which was shown by the increase in the senescence associated β galactosidase positive cells and the reduction in clonogenicity. Identification of the active compounds in ZOE using assay-guided fractionation and GC/MS analysis found that the major compounds in all active subfractions contained paradols and shogaols of different chain lengths. The results from pure 6-paradol and 6-shogaol confirmed that these two compounds could suppress hTERT expression, as well as telomerase activity in A549 cells. Evaluation of safety profile of ZOE in rats found that ZOE was not toxic, had no clastogenicity effect, but had an anticlastogenic effect against DEN-induced liver micronucleus formation in rats. These findings suggest that ginger extract could potentially be useful as dietary cancer treatment and prevention.

“Mining whole genomes for PGx variants: to respond or not to respond?”

Chiara Bacchelli

Senior Lecturer in Personalised Medicine and Genomics, Head of Experimental and Personalised Medicine Section Institute of Child Health, University College London, United Kingdom

Different individuals vary substantially in their responses to medications, with many experiencing adverse drug reactions. Inter-individual genetic variations are responsible for these differences in drug response, giving rise to the field of pharmacogenetics (PGx). Pharmacogenetics uses polymorphisms in genes encoding drug-metabolising enzymes, transporters and drug targets, to interpret variable drug efficacies and toxicities among a population. Exploiting these genetic data will improve diagnostic and disease-predicting abilities and help identify new ‘personalised’ medicines specifically tailored to patients’ unique genetic predisposition. Many pharmacogenetic biomarkers have been identified and are currently being used to reduce trial-and-error prescribing and direct the selection of optimal therapies. The expansion in the understanding of how patients’ genetics influence drug response, coupled to technological advances making genome-sequencing cheaper, will result in personalised medicine becoming more common, hopefully resulting in safer and more effective drug therapy. However, there are still challenges and barriers that need to be addressed before pharmacogenetics is fully implemented in the clinical setting.

Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing

Ruibang Luo

Department of Computer Science, The University of Hong Kong

Identifying the variants of DNA sequences sensitively and accurately is an important but challenging task in the field of genomics. This task is particularly difficult when dealing with Single Molecule Sequencing, the error rate of which is still tens to hundreds of times higher than Next Generation Sequencing. With the increasing prevalence of Single Molecule Sequencing, an efficient variant caller will not only expedite basic research but also enable various downstream applications. To meet this demand, we developed Clairvoyante, a multi-task five-layer convolutional deep neural network model for predicting Variant Type, Zygosity, Alternative Allele and Indel Length. On NA12878, Clairvoyante achieved 99.73%, 97.68% and 95.36% accuracy on known variants, and achieved 98.19%, 91.71%, 72.71% F1 score on the whole genome, in Illumina, PacBio, and Oxford Nanopore data, respectively. Training Clairvoyante with a sample and call variant on another shows that Clairvoyante is sample agnostic and general for variant calling. A slim version of Clairvoyante with reduced model parameters produced a much lower F1, confirming the full model's power in disentangling subtle details in read alignment. Clairvoyante is the first method for Single Molecule Sequencing to finish a whole genome variant calling in two hours on a 28 CPU-core machine, with top-tier accuracy and sensitivity. A toolset was developed to train, utilize and visualize the Clairvoyante model easily, and is publicly available on GitHub at <https://github.com/aquaskyline/Clairvoyante>

Characterizing the “Dark Matters” in Human Transcriptome.

Ge Gao

Center for Bioinformatics, Beijing Advanced Innovation Center for Genomics (ICG), School of Life Sciences, Peking University, Beijing, China

Long noncoding RNAs (lncRNAs) are emerging as key regulators for multiple essential biological processes involving physiological and pathological processes including cancer. Despite large numbers of lncRNAs reported in various databases, less than one fifth of the lncRNA gene models are consistent across major databases suggesting the current lncRNA catalog are likely incomplete. Combining cutting-edge statistical learning model with the abundant omics data, we systematically survey the human lncRNAs landscape based on Peta-scale raw data. Along with multiple novel lncRNAs discovered, we also present a complete toolchain covering from expression profiling to function annotation of human lncRNAs for the community.

PGG.Population: A database for understanding the genomic diversity and genetic ancestry of human populations

Shuhua Xu

Max Planck Independent Research Group on Population Genomics,
Chinese Academy of Sciences and Max Planck Society (CAS-MPG)
Partner Institute for Computational Biology (PICB), Chinese Academy of
Sciences, Shanghai, China.

There are a growing number of studies focusing on delineating genetic variations that are associated with complex human traits and diseases due to recent advances in next-generation sequencing technologies. However, identifying and prioritizing disease-associated causal variants relies on understanding the distribution of genetic variations within and among populations. The PGG.Population database documents 7,122 genomes representing 358 global populations from 107 countries and provides essential information for researchers to understand human genomic diversity and genetic ancestry. These data and information can facilitate in the design of research studies and in the interpretation of results of both evolutionary and medical studies involving human populations. The database is carefully maintained and constantly updated when new data are available. We included miscellaneous functions and a user-friendly graphical interface for visualization of genomic diversity, population relationships (genetic affinity), ancestral makeup, footprints of natural selection, and population history etc. Moreover, PGG.Population provides a useful feature for users to analyze data and visualize results in a dynamic style via online illustration. The long-term ambition of the PGG.Population, together with the joint efforts from other researchers who contribute their data to our database, is to create a comprehensive depository of geographic and ethnic variation of human genome, as well as a platform bringing influence on future practitioners of medicine and clinical investigators.

Artificial Intelligence: Understanding the Development of Chemoresistance in Glioma Patients, a Case Study (STAT3)

Carol Tang

Department of Research, National Neuroscience Institute, Duke-National University of Singapore Medical School, Division of Cellular and Molecular Research, Humphrey Oei Institute of Cancer Research, National Cancer Centre Singapore

In the revised World Health Organization classification scheme, molecular characterization supersedes histology to characterize glioma tumors. Our NNI Brain Tumor Resource serves as a platform to spearhead precision medicine goals with its unique molecular data acquired from patient-derived material. Our group recently established a STAT3 functionally-tuned gene signature. We showed that the STAT3-signature had prognostic relevance and patients with active STAT3-signature pattern were enriched for mesenchymal and classical phenotypes, typically associated with poor survival outcome. Using cellular and animal models, we demonstrated that STAT3-high GBM tumors showed favorable response to AZD1480 (Astra Zeneca small molecule) while STAT3-low tumors developed resistance. Since kinases represent dominant therapeutic targets in major pharmaceutical pipelines, we established the approach of using biological evidence to substantiate our computational predictions, by measuring phosphorylation levels of 144 kinases in STAT3-signature-stratified GBM cells using the PamChip technology. We developed a novel computational pipeline on kinome assay data by integrating phospho-chemical interactions with functional genomics data through kinase-substrate databases. Our approach identified IGF-1R as a top-ranking tyrosine kinase uniquely elevated in STAT3-low tumors upon treatment with AZD1480. Our efforts demonstrate the strength of our NNI Brain Tumor Resource at addressing precision medicine goals.

Precision Medicine in Public Health

Surakameth Mahasirimongkol

Medical Life Sciences Institute

Ministry of Public Health (MOPH), Thailand

Precision medicine is an approach for medical practice that utilize the precise information for decision making in medicine. Higher precision can be achieved with human genomics information, environmental information and the lifestyles information. This approach promises an earlier detection of diseases by targeted screening program, better treatment responses by targeted treatment and aversion of adverse drug events by pharmacogenomics. To achieve these goals, each nation should establish the comprehensive plans for the development of the informatics infrastructure, information generating capacity and the comprehensive human resource development.

The near-term goals for the precision medicine initiative is to implement the well accepted targeted screening program that are economically feasible. The program that save the national health budget should be prioritized for implementation. The expedite guideline development for medical practice, pharmacy practice and laboratory testing should be established in the nation, this will enable the real benefit to the patients who have indications for novel technology. Once the guideline established, the nation should streamline the evaluation processes for establish of the nation-wide program. Not all technology will be accepted into the nation-wide program, which required the thorough evaluation and feasibility study.

The Genomics Thailand initiative was established on 16th March 2018, this included 11 founding organizations collaborating closely to enable this vision “Better Health, Benefit Society, With Precision medicine”. The initiative will last until 2023, at the end of the first four years, a comprehensive human resource development was accepted by all organizations. We envisioned the better healthcare deliver to our population based on this plan, it shall have immediate benefit to cancer, neonates and infant patients and prevention of adverse drug reactions.

Morphling: An ultra-fast model-free framework for structural variant discovery

Kai Ye

Electronic and Information Engineering School, Xi'an Jiaotong University, China

Recent developments of sequencing technology provide us an unprecedented opportunity to investigate our genetic background (Goodwin, et al., 2016). And the key to achieve better understanding lies in the comprehensive discovery of structural variants (SVs) from DNA sequence data. SVs such as deletions, insertions and duplications, are major part of genetic differences between individuals. Though SVs are considered less common than smaller-scale forms of genetic variations such as SNPs or INDELs, they are important implication in numerous diseases such as cancer (Carvalho and Lupski, 2016). Researchers have recognized that alignments around SVs are complex which will lead to a combination of multiple abnormal signals, including read-depth alteration, breakpoint spanning reads (clipped reads), discordant paired-end alignment, split alignment and etc. SVs detection methods such as CNVnator (Abyzov, et al., 2011), BreakDancer (Chen, et al., 2009) and Pindel (Ye, et al., 2009), have been developed based on these signals individually. Recently, several integrated SVs discovery methods such as Delly (Rausch, et al., 2012) and Lumpy (Layer, et al., 2014) have been developed based on multi-signals.

Though multiple signal integration methods achieve better results compare to single signal based method, the general idea of these methods is still based on established SVs models thus make them difficult to discover complex and novel SVs. To be specific, these methods have to model what a certain SV looks like and write specific code for the discovery of different types of SVs. As a result, existing tools will miss or predict incorrectly at some complex regions on the genome because of the incomplete model, such as repeat region where complex abnormal alignments are embedded. But SVs hidden in these repetitive regions are quite frequent and important for us to understand our genetic background and the mechanism of some diseases (Dzamba, et al., 2017). Moreover, a recent publication from 1000 Genome Project (Sudmant, et al., 2015) provides the first glimpse complex structural variants. Unfortunately, the

current short read sequence data and existing model based methods make it hard to detect those variants. In fact, researchers have to manually inspect breakpoints based on realignment or long reads both for SVs in the repeat region and complex SVs. Obviously, SVs in the complex region and complex SVs are hard to model ahead, but the most critical issue is that we even don't have enough such SV instances to construct a rather comprehensive model. Therefore, a model-free method or even an artificial intelligence method is in demand to overcome these difficulties and make SVs calling easy to use and generalize.

In this paper, we present a versatile model-free SVs discovery framework by mining local frequent sequential orders of different abnormal signals. The proposed framework does not rely on any models, but directly mine abnormal instances from the raw alignment data and identify breakpoint regions. Essentially, Morphling converts the alignment data into a novel database through different mutational signal channels. And this database allows the model-free framework to discover SVs based on sequential pattern mining. As far as we know, this is the first work talking about a model-free framework for SVs discovery. We start with introducing sequential pattern mining algorithm and the procedure of discovering SVs from alignment data. Meanwhile, we test the proposed method with simulated paired-end reads on Venter's SVs and human genome data NA12878 from two different sources to show Morphling is able to robustly detect reported, novel and complex SVs.

Digestion-Ligation-Only Hi-C, a Simple, Cost-effective, and Highly Efficient Method for Chromosome Conformation Capture

Guoliang Li

National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China.

Chromosome conformation capture technologies open an avenue to investigate the three-dimensional (3D) structures of genomes. However, high noise, high cost, and lack of straightforward noise evaluation in current methods impede the advancement of 3D genomic research. Here, we developed a simple Digestion-Ligation-Only Hi-C (DLO Hi-C) technology to explore the 3D landscape of the genome. This method requires only two rounds of digestion and ligation without biotin-labeling and pull-down for reducing the cost. The noise DNA was efficiently removed in a cost-effective step by purifying specific linker-ligated DNA fragments. Notably, random ligation could be quickly evaluated in an early quality-control step before sequencing. Moreover, we performed an in situ version of DLO Hi-C method based on 4-cutter restriction enzyme. We applied DLO Hi-C to delineate the genomic architecture of THP-1 and K562 cells and uncovered chromosome translocations. This technology may facilitate the investigation of genomic organization, gene regulation, and (meta-) genome assembly.

Precision Medicine in Thai Cancer

Manop Pithukpakorn

Head of Medical Genetics Division, the Department of Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand, an Assistant Dean for Research of the Faculty of Medicine and the leader of health cluster in the Research University Network (RUN)

Precision medicine is an emerging paradigm for disease diagnosis, treatment and prevention that takes individual genetic and molecular variability, environmental and lifestyle difference of each person into account. Contrary to “one-size-fits-all” approach, precision medicine will allow doctors and researchers to predict more accurately which treatment and prevention strategies for a particular disease will work in which patients.

Cancer is the best example to demonstrate the benefit of precision medicine. It has been universally accepted that cancer is a genetic disorder that results in abnormal cell growth and the invasiveness and spreading potential to other parts of the body. Better understanding in cancer genetics leads to new types of cancer diagnostic tests and several novel drugs which are designed to target specific genetic abnormalities in cancer.

The unprecedented throughput, speed and cost of next generation sequencing (NGS) enables researchers to investigate genetic contribution of cancer and implement this technology to the real world medical practice. We currently see widespread use of NGS to discover genetic alterations in each patient, to identify potential treatment target, and to predict response of medical treatment. In clinical practice, oncologists could select the best and most appropriate treatment for each patient, based on the patient's genetic data. Precision medicine widely become a standard approach in cancer diagnosis and treatment. Patients with lung or breast cancers with specific genetic alterations could get significant benefit from novel targeted therapies that specifically act on certain molecular pathway. Precision medicine also predict what medication would not work and that treatment could be avoided. This novel approach would improve cancer treatment efficacy, patient outcome, quality of life, reduce healthcare cost and overall social and economic burden.

Many studies have shown that genetic diversity plays role in phenotypic differences among various ethnic groups with the same diseases. Some cancer types are significantly more prevalent in Asian than in Western

population. Same cancers display difference in subtypes among countries. Many similar cancers from various ethnic groups also have different treatment outcome and prognosis. To be able to determine the role of genetic diversity in Thai cancer patients, as well as development and implementation of cancer precision medicine in Thailand, a multi-institute research collaboration was established under the 'Research University Network' (RUN). The research network aims to study genetic alterations in Thai cancer patients, develop a study platform for cancer biology and cancer treatment, apply clinical genetic testing for Thai cancer patients and develop precision medicine guidelines for cancer diagnosis and treatment. Since the inception, the network has established a collection of clinical data and bio-specimens from more than 1,500 cancer patients. The genome landscape study of Thai cancer patients showed distinct pattern of genetic alterations from Western patients. The research team has also developed the first-ever three-dimensional model of cancer cell culture and high-throughput cancer drug testing platform in Thailand.

In conclusion, Thai cancer precision medicine research has shown the difference between Thai and Western cancer, which could potentially result in different treatment options and prognosis. The research has also led to several Thailand's first successes including integrated genetic diagnostic laboratory for cancer diagnosis, patient-derived three-dimensional cancer cell cultures (cancer avatar), cancer drug testing system, cancer cell culture in zebrafish. The research can be translated to a comprehensive cancer diagnosis and treatment of cancer. In addition, Thai cancer patients could also benefit from widespread use of genetic testing and precision medicine approach for cancer care, which could result in an increased treatment effectiveness and improved quality of life.

Systematic identification of functionally conserved lncRNAs across vertebrates

Qiangfeng Cliff Zhang

Beijing Advanced Innovation Center for Structural Biology, Center for Synthetic and Systems Biology, Tsinghua-Peking Joint Center for Life Sciences, School of Life Sciences, Tsinghua University, Beijing, China.

Long noncoding RNAs (lncRNAs) as major regulators are implicated in diverse cellular processes and diseases. Recent advances in transcriptome sequencing have enabled extensive genomic annotation of lncRNA transcripts across many species. However, there has been a continuing debate over lncRNA evolution and function in part because of no available approaches, both in silico and in tube, to identify functionally homologous lncRNAs.

Here, we develop 1) iLncSMART (identification of lncRNA homologues based on Synteny and Motif Across RNA Transcriptome), a tool to identify homologous lncRNAs combining on synteny and motif analysis, and 2) homoCRISPRescue (homology validation by high-throughput CRISPR rescue), a high-throughput procedure to validate functional homologues by CRISPR rescue. In this study, we identified potentially homologous counterparts for about 36% of human lncRNA genes (GENCODE v24) in non-primate vertebrates, and the predicted homology were confirmed by replacement of distantly diverged homologues. Further interaction assays supported the function conservation in molecular mechanisms. In summary, the approach is able to identify functionally conserved lncRNAs across species on a transcriptome-wide scale for the first time. By our novel integrated method, a more comprehensive analysis for lncRNA transcriptome across deeper vertebrate lineages will further provide more detailed insights in lncRNA evolution and function.

Evolution of Cancer Treatment in Precision Medicine Era

Suphat Subongkot

clinical oncology specialist and associate professor at Faculty of Pharmaceutical Sciences, Khon Kaen University (KKU), Thailand

Precision medicine is an approach to patient care that allows us to select treatments based on a genetic manifestation of their illness. Advances in science and technology have facilitated to accelerate the accumulation of the new research in precision medicine area. In oncology setting, patients diagnosed with cancer usually receive the similar treatment with respect to the type and stage of the cancer. Nonetheless, outcome of the treatment would be varied. Following years of research, it becomes clearer that tumors have genetic alterations that cause cancer to progress. The mutagenic changes may be different despite the same type of tumors. In addition, the same genetic modification may also be occurred in different types of cancer. The knowledge of precision medicine will help tailoring treatment approach in each cancer patients according to their genetic variations. Genetic tests will be using to select treatment which is most likely to get response and, preventing the patient from receiving unnecessary treatments. There are several treatments known as targeted therapies that have been proven effective against cancers with specific genetic changes and are approved by the FDA. Many of these drugs will be addressed in this presentation.

Will Precision Medicine Ever Be A Possibility in the Control of Tuberculosis?

Somchai Bovornkitti, MD, DScMed

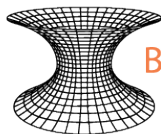
Chairman of the Health Forum, The Royal Society of Thailand

During the historic period not long ago global epidemic of tuberculosis the so-called “white plague” were put under control by means of energetic medical practice, i.e. providing BCG vaccination in newborn and early diagnosis and proper treatment of infected persons. Unfortunately, recently new episodes of reemerging tuberculosis are noted and cases of chemotherapeutic resistance prevail. The reasons of such incidents have been sorted and speculated as the followings:

- (1) Epidemics of drug-resistance causative agents.
- (2) Withering of enthusiasm in the control of disease, such as the lagging public health activity in the provision of BCG vaccination for newborns, and in energetic therapeutic practice leaving cases of drug resistance and treatment failure to become sources of infection.
- (3) Having not really eradicating the infection compared to other Infection such as leprosy and small pox.

Now as for public health activity, apart from revision the practices in general, and/or seeking new inventions, are ideology. Thanks for the advance in molecular or genomic medicine which open new fronts for the so-called “precision medicine” for dealing with a variety of diseases, including microbial infections, i.e. tuberculosis. In the context of tuberculosis, knowing that innate and likely also acquired resistance and susceptibility exist in certain diseases, In this regard, the mutated portions or any malicious genes present in DNA helix of any persons may possible be removed by molecular inventions, for instance by the CRISPR/Cas system. The practice can be instituted prenatally or subsequently at the time necessitated.

Sponsors



BNK Bioscience
Limited

