Program Book

Boston Taiwanese Biotechnology Association

BOSTON TAIWANESE BIOTECH SYMPOSIUM

BTBATW.ORG/2016

Welcome Message

On behalf of Boston Taiwanese Biotechnology Association (BTBA), we would like to welcome you to the 2016 Annual BTBA Symposium! Now in its fourth year, this has become the flagship event that young Taiwanese bio-scientists across the US look forward to attending, where we share experience in research, career, and networking.

This marks an eventful year for BTBA. First, we incorporated in Massachusetts and established 501(c)(3) non-profit organization status with the IRS. Second, we expanded our network of collaborators. In December 2015, National Taiwan University (NTU) Center for Biotechnology hosted the first Joint NTU-BTBA Mini-Symposium for Biotechnology, and several representatives from NTU are here today as speakers at this symposium. Our friends at Texas Taiwanese Biotechnology Association (TTBA) hosted a great symposium last November and will host their second one this November 12-13 in Dallas. In San Diego our friends formed SoCal Taiwanese Biotech Association and are planning a symposium on April 8-9, 2017. Finally, across the Atlantic, a group has formed in the United Kingdom (英國生醫界台灣人學術社群). As we strengthen our interactions with Taiwan and expand our networks in the US and Europe, we continue to build a lively community locally in Boston. In addition to regular academic seminar series and career workshops, our first mentoring program with Monte Jade New England (MJNE) was highly regarded by participants and will soon start another round.

The symposium activities also expanded beyond classical keynotes and panels to include more workshops. We hope everyone will find it fruitful in these activities designed into tracks:

- Academic: academic panel (US, Taiwan), oral and poster presentations, academic workshops (practical skills)
- Industry: industry panel (US), industry workshop (biotech job functions), resume workshop, Taiwan industry talks
- Entrepreneur: investor panel, entrepreneurial presentation, startup panel

One highlight is the inaugural Entrepreneurial Presentation. Nine selected teams will pitch their biomedical business proposal to a panel of seasoned investors.

We hope you will enjoy the symposium and look forward to seeing you!

Sincerely,

Ying-Ja Chen & Chih-Chieh Wang

Co-Chairs, Boston Taiwanese Biotechnology Association

Table of Contents

List of Organizers and Sponsors

Organizers

Boston Taiwanese Biotechnology Association

Sponsors

Ministry of Science and Technology, Taiwan, R.O.C. (中華民國科技部)

Science and Technology Division, Taipei Economic and Cultural Representative Office in the U.S. (駐美國台北經濟文化代表處科技組)

Taiwanese-American Foundation of Boston (波士頓台美基金會)

Education Division, Taipei Economic and Cultural Office in Boston (駐波士頓台北經濟文化辦事處教育組)

Taiwanese Association of America, Boston Chapter (波士頓台灣同鄉會)

PosterSmith.com

Mentors of the Mentoring Program

Carolyn Hsu, Sr. Project Manager, AbbVie Bioresearch Center

Andrew Ho, Executive Director, Clinical Development, SK Life Science

Ying Sun, Professor, University of Rhode Island

Mei-Hsiu Ling, Sr. Director, Biometrics, Vertex

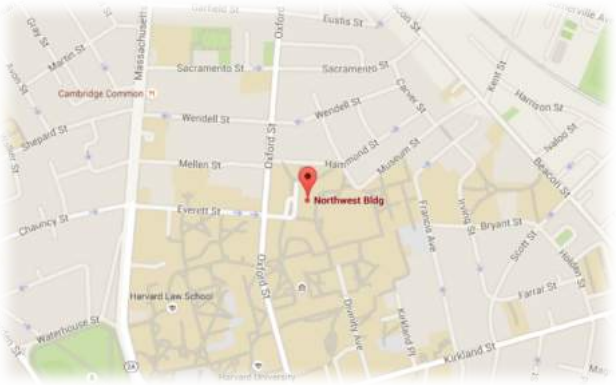
Friends & Supporters

Carolyn Hsu, Hui-Hsin Chang, Robert Wang, Ram Viswanatha, Thomas HoJenny Chen, Ho-Chou Tu, and Jennifer Wells-Qu.

Direction

Northwest Building, Harvard University

52 Oxford St., Cambridge, MA, 02138



By Public Transportation:

Take the MBTA (subway) RED Line to Harvard Square. Local bus #1 #66 #68 #69 #71 #72 #73 #74 #75 #77 #78 #86 #96 can also bring you to Harvard Square.

By Car:

From the Massachusetts Turnpike:
Take Exit 18 (Allston or Brighton/Cambridge). At 2nd traffic light, turn left onto Storrow Drive (Soldiers Field Road). Exit at Harvard Square. Turn right to cross the bridge and you will be on JFK Street headed into Harvard Square.

From the South (I-93 North):
Head north on Route 93, take the Mass Pike.

From the North (I-93 South)
Head south on Route 93 exit onto Storrow Drive west. Take Harvard Square/Cambridge exit. Turn right to cross the bridge and you will be on JFK Street headed into Harvard Square.

From Logan Airport:
As you leave the airport, follow signs to Rt. 90, Mass Turnpike West.

Parking:

On-street parking is scarce in Cambridge, but there are several public parking lots and garages around the square.

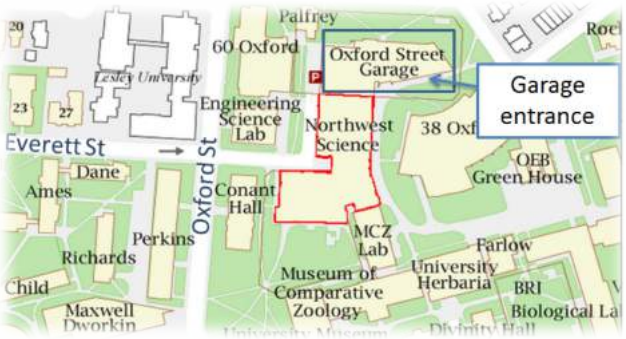
If it's a rental car…
We recommend you to check public parking in the Harvard Square:
http://www.transportation.harvard.edu/parking/visitors/public-parking-square

If you have your own car…
We recommend you to use Harvard Campus Services online purchase system to purchase parking permit: https://www2.uos.harvard.edu/cgi-bin/permit/purchase.pl

Direction

Please note that parking permit can only be purchased from two weeks to one day in advance, but **NOT** on the day of the event.

To use the online purchase system, please have your vehicle license plate number ready at hand and then follow the instructions below:



1. The first-time user needs to register. To complete the registration (as "visitor"), use "**Visitor to Campus**" as your department and department code **7700**.
2. You will receive a confirmation e-mail from Harvard University Daily Visitor Parking Permits Online Purchase System. Click the provided link to confirm registration.
3. You can now log in as a visitor with username and password you just created.
4. You will be asked to provide department information and department code again, which will be the same as in 1. This information has to be provided every time after you log in.
5. After entering into the system, **select a parking lot to begin** at the bottom of the webpage. We recommend our attendee to park at **52 Oxford St. Garage** (see the map below for its location.)
6. Weekend parking hours are 7am – 11:30pm. Please state yourself as "**Event Participant**" as your affiliation and specify yourself as "**HTSA event participant**" in "Adding Parking Permits" form.
7. Choose the intended date(s) to park on campus.
8. Provide your vehicle's **plate number** and **issued state**.
9. Hit "Add Parking Permit" button when completed.
10. Confirm/Modify your purchase and then hit "Checkout"
11. Agree with the disclaimer before proceed.
12. After you hit "complete order," you will be re-directed to PayPal.com to pay for the permit. **Please note that if errors occur during re-directing, try to use a different browser (different browsers may work on different computers.)** After logging into the system with a different browser, you should be able to find your unfinished order in "My basket" tab.
13. Use either PayPal account or debit/credit card to finish purchase.
14. Remember to print the permit and bring it with you on the day coming to the symposium. Put the permit on your dashboard before you leave.
15. Enjoy the symposium!

Agenda

Day 1 (Saturday, 07/16/2016)

	Room B101	Room B103
08:30-09:00	Registration and Poster Setup	
09:00-09:10	Opening Remarks	
09:10-10:10	Keynote Jane H. Hsiao, PhD, MBA	
10:10-10:40	Coffee Break	
10:40-11:50	Oral Presentations 1	US Industry Panel
11:30-12:00	Entry into Industry (Introduction)	
12:00-13:30	Lunch and Entry into industry (Networking)	
13:30-14:40	US Academic Panel	Investor Panel
14:40-15:10	Coffee Break	Entrepreneurial Presentation
15:10-16:30	Oral Presentations 2	
16:30-17:00	Coffee Break	
17:00-18:00	Industry Workshop: Career Opportunities in Drug Development	Entrepreneur & Startup Panel
18:00-20:30	Poster Session & Reception Dinner	

Agenda

Day 2 (07/17/2016)

	Room B101	Room B103
09:00-10:00	Keynote **Pan-Chyr Yang, MD, PhD**	
10:00-10:30	**Coffee Break**	
10:30-11:40	**Taiwan Academic Panel**	**Industry Resume Workshop** **Lauren Celano**
11:40-12:50	**Academic Workshop**	**Taiwan Industry Talks** **Karen Wen** **Mark Liu, PhD**
12:50-13:00	**Closing Remarks**	

Keynote Speaker

Jane H. Hsiao Ph.D., MBA, 許照惠 博士

Co-founder, OPKO Health Inc

Dr. Jane H. Hsiao, Ph.D., MBA. Dr. Hsiao is co-founder of OPKO Health, Inc. and has served as Vice Chairman and Chief Technical Officer since May 2007. She was a co-founder of IVAX Corporation in 1986 served as its Vice Chairman and Chief Technical Officer from July 1996 to January 2006, when Teva acquired IVAX. Dr. Hsiao has been a Director of Cocrystal Pharma, Inc. since January 2, 2014 and TransEnterix since August 2014. Dr. Hsiao is on the board of several public companies since 2007.

Dr. Hsiao received a B.S. degree in Pharmacy from the National Taiwan University and a Ph.D. degree in Medicinal Chemistry from the University of Illinois, Chicago in 1973. She also holds an M.B.A. degree. Dr. Hsiao's background in pharmaceutical chemistry and strong technical expertise, as well as her senior management experience, allow her to play an integral role in overseeing OPKO's product development and regulatory affairs and in navigating the regulatory pathways for OPKO's products and product candidates. In addition, as a result of her role as director and/or chairman of other companies in the biotechnology and life sciences space, she also has a keen understanding and appreciation of the many regulatory, product development and manufacturing compliance issues confronting the pharmaceutical and biotechnology industries.

Keynote Speaker

Pan-Chyr Yang M.D., Ph.D., 楊泮池 校長

President, National Taiwan University

Prof. Yang, MD, PhD, is a Professor of the Department of Internal Medicine and the current President of National Taiwan University. His major research interests are pulmonary and critical care medicine, lung cancer genomics, translational research and microarray gene expression technology. He is awarded as a member of Academia Sinica in 2006 because of his contributions in promoting the translational research in lung cancer.

Dr. Yang is a pioneer and leader in pulmonary ultrasound diagnostics and therapeutics that have revolutionized the management of pulmonary diseases. His research group developed the method for detection and quantification circulating cancer cells in peripheral blood and to better predict the prognosis and response to treatment for lung cancer patients. His research group has discovered novel genes and pathways that associated with lung cancer pathogenesis and progression. They identified specific gene expression and microRNA signatures that can assist to predict the treatment outcome and may be beneficial for personalized therapy of lung cancer patients.

Dr. Yang is the program director of the National Research Program for Biopharmaceuticals. He leads the translational biomedical research team to develop a fully integrated biopharmaceutical pipeline and set up comprehensive translational research platform as well as the biotech incubation centers, with the aim to strengthen biotech industry value chain and accelerate commercialization of biomedical research in Taiwan.

US Industry Panelist

Andrew Ho M.D., 何伯容 醫師

Executive Director, Clinical Development, SK Life Science

Andrew was born in Taiwan and moved to the U.S. with his parents when he was 11 years-old. After graduating from UCSD School of Medicine and completing training in psychiatry, he was faculty at UCLA for more than 10 years. In 2007, Andrew joined his best friend at Merck and started to learn drug development. Since that time, Andrew has led Phase I, II, and III teams at Merck, Amgen, Takeda, and Forum Pharma. He is currently the second MD and the only psychiatrist responsible for the psychiatric portfolio at SK.

Frank Lee Ph.D., 李文機 博士

Principal, FWL Consulting Services

Dr. Lee is a pharmacokinetics and drug metabolism expert with 38 years of pharmaceutical industry experience. He is the co-founder of BRIM Biotechnology, Inc. and Chinese Entrepreneur Association, a non-profit organization. He has been working as an individual consultant since his retirement in July 2012 from Millennium Pharmaceuticals, the Takeda Oncology Company as Vice President, NCDS in charge of DMPK. During his 38 years tenure in pharmaceutical industry Dr. Lee has made contributions to the development of several brand-name drugs such as Naprosyn®, Anaprox®, Ticlid®, Torado®, Avodart®, Flonase®, Imitrex®, Zofran®, Sustiva®, Velcade® Entyvio® and Ixazomib®. Dr. Lee obtained his BS degree in chemistry from Chung Yuan Christian University in Taiwan in 1968, MS degree in organic chemistry from the California State University at Sacramento in 1974, and PhD degree in Pharmaceutical Chemistry from the University of California at San Francisco in 1987.

US Industry Panelist

Joyce C. Chiu, CPIP, 裘錦澐

Formerly Associate Director, Program Management Lead, Shire Pharmaceuticals

Joyce Chiu, BS Chemical Engineering, Cornell University and MBA, Babson College, has worked in specialty chemicals serving the semi-conductor industry and in life sciences, with roles in process development, process engineering, quality management, new product development, and project and program management. She has led large complex global development teams across three continents, delivered innovative products that received U.S. patents and industry trade award with breakthrough performance. In her leadership roles, Joyce has coached and mentored subject matter experts and served as key liaison with stakeholders up to the C level and client contacts. Active in professional societies, Joyce has organized speaker programs, leadership and career development workshops and spoken at events. She mentors young professionals and students in the pursuit of their career goals. Joyce is pursuing new opportunities in senior program and portfolio management in life science or high tech industry.

Mei-Hsiu Ling Ph.D., 凌美秀 博士

Senior Director, Vertex Pharmaceuticals

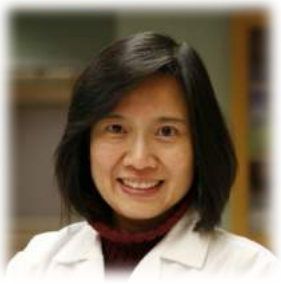
Dr. Mei-Hsiu Ling received a B.S in Math from National Tsing Hua University and a Ph.D. In Statistics from U.C. Berkeley. She then started working in the pharmaceutical industry. Prior to Vertex, she worked at Schering-Plough and Novartis. She has been involved in late phase drug development, including antibiotics, antiviral (HCV, HIV), anti-fungal, and respiratory (Asthma, COPD, Cystic Fibrosis). At Vertex, she is the Cystic Fibrosis statistics franchise head responsible for all statistical support for Cystic Fibrosis drug development. She is also the acting department head for the statistical programming group. She currently serves as the president of Monte Jade New England.

US Industry Panelist

Lih-Ling Lin Ph.D., 林俐伶 博士
Senior Director, Inflammation and Immunology
Research Unit, Pfizer

Lih-Ling Lin graduated from National Taiwan University with an undergraduate degree in Pharmacy and Master degree in Biochemistry. She then went to University of Arizona for her graduate work. After receiving her PhD degree in Biochemistry, Lih-Ling Lin joined Wyeth (Genetics Institute) and contributed to the discovery of several PLC and cPLA2 family members. She then led a discovery team targeting the signal transduction pathways in innate immunity involved in the production of inflammatory mediators and cytokines (e.g. TNF). These projects include development of kinase inhibitors and Biologics targeting innate receptors. This effort has led to the discovery of clinical candidates in treating autoimmune and inflammatory diseases such as rheumatoid arthritis and Inflammatory Bowel disease. Lih-Ling currently is leading the Exploratory Innate Immunity group dedicated in the emerging science for the drug discovery effort in the Inflammation and Immunology Research Unit. Lih-Ling is an author of over 70 scientific papers and patents.

US Academic Panelist



Dr. Yu-Hua Tseng, 曾玉華 博士

Associate Professor, Harvard Medical School

Yu-Hua Tseng, PhD, is an Associate Professor of Medicine at Harvard Medical School, an Investigator at the Joslin Diabetes Center, and a Principal Faculty of Harvard Stem Cell Institute. She received B.S. in Medical Technology and M.S. in Microbiology and Immunology from National Taiwan University (M.S. thesis advisor: Dr. Lih-Hwa Hwang). She then came to the United State and received Ph.D. in Developmental Biology and Cellular and Molecular Biology from the University of Wisconsin-Madison under the supervision of Dr. Linda Schuler. She completed postdoctoral training in the laboratory of Dr. C. Ronald Kahn at Joslin Diabetes Center, Harvard Medical School. The research in Dr. Tseng's laboratory has been focusing on unraveling the role of developmental signals in brown versus white adipose cell fate, the identification and characterization of progenitor/stem cells that give rise to different adipose depots, and the integration of genetic and humeral factors on thermoregulation and whole body energy homeostasis. Work from Dr. Tseng's lab has helped establish the role of developmental signals in brown fat biology, and increase our understanding on the physiological role of brown and beige fat in rodents and humans. Dr. Tseng was an Eleanor and Miles Shore Scholar in Medicine at Harvard Medical School, and received the Hazel K. Stiebeling Lectureship from Florida State University and Visiting Professorship from National Defense Medical Center, Taipei, Taiwan. She serves, or has served on, the grant review panels for the National Institutes of Health, the American Diabetes Association, the Department of Defense, the U.S. Army Medical Research and Material Command, and the European Research Council.

US Academic Panelist

Dr. Charles P. Lin

Associate Professor, Harvard Medical School / Massachusetts General Hospital

Dr. Lin is an Associate Professor at Harvard Medical School and lead the Advanced Microscopy Group at the Center for Systems Biology and at the Wellman Center for Photomedicine, Massachusetts General Hospital. Here, my laboratory and I are developing cutting-edge optical imaging techniques for in vivo cell tracking and molecular imaging studies. Our primary research focus is the development of minimally invasive optical techniques for in vivo imaging of stem cells and hematologic malignancies. There are several custom-built confocal and two-photon hybrid microscopes within my laboratory, each tailored for a specific live animal imaging application. Several of these systems have an additional "treatment" beam that can be used to localize light delivery to precise locations in tissue. These systems have unique open architectures to allow modification and rapid adaptation to new technology. My laboratory has also developed an in vivo flow cytometer for real-time detection and quantification of fluorescent cells in the circulation, eliminating the need for drawing blood samples. At present, we are actively engaged in several multidisciplinary collaborative studies with experts across the fields of stem cell biology, immunology, and cancer biology.

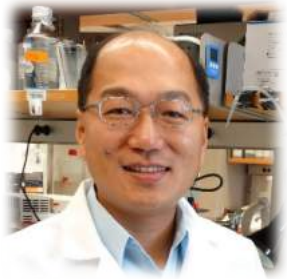
US Academic Panelist

Dr. Jing-Ruey Joanna Yeh, 葉景睿 博士

Assistant Professor, Harvard Medical School / Massachusetts General Hospital

Joanna Yeh received her PhD from Yale University working with Dr. Craig Crews on deciphering the mechanisms of anti-angiogenic compounds and on genetic targeting in mice. She then moved to the Cardiovascular Research Center at MGH and worked with Dr. Randall Peterson on developing zebrafish leukemia models and on in vivo chemical screening. Dr. Yeh received the Claflin Distinguished Scholar award in 2008, and is currently a principal investigator at the Cardiovascular Research Center at MGH. Her lab is interested in developing zebrafish models of human diseases to interrogate the disease mechanisms and to identify potential therapeutics against these diseases. Joanna Yeh's research team has also been at the forefront of advancing technologies for zebrafish genome engineering using various customizable site-specific nuclease platforms including CRISPR/Cas9. Additional research focuses are directed to study cancer metabolism and identify novel therapeutic approaches.

US Academic Panelist



Dr. Tzong-Shi Lu, 呂宗熙 博士

Instructor in Medicine, Harvard Medical School

Associate Biologist, Renal Division, Brigham and Women's Hospital

I am currently Instructor in Medicine at Harvard Medical School and Associate Biologist at the Renal Division of the Brigham and Women's Hospital. My current research focus is in the area of genetic profiling in kidney disease, specifically in the mechanisms of cystogenesis in Polycystic kidney disease (PKD) and genes involved in the prevention and treatment of accelerated Cardiovascular disease that affect patients with Chronic Kidney Disease (CKD).

During my Ph.D. training I studied the role of Heat Shock Proteins (HSPs) in the prevention of vascular permeability changes, tight junction disruption and mitochondrial dysfunction. In 2005-2007, I completed my research fellowship at Beth Israel Deaconess Medical Center (BIDMC). My research at BIDMC led to the identification of a potential role for CB1 as a therapeutic target for HIV management through blood-brain-barrier regulation. In 2008, I continued my training at the Renal Division, Brigham and Women's Hospital (BWH) in studying accelerated vascular disease in CKD. Our research revealed for the first time that vascular Klotho deficiency potentiates the development of human arterial calcification and mediates resistance to FGF-23 which led to a publication in Circulation in 2012 that was ranked the top 1% most highly cited articles in Clinical Medicine since 2014 to present. In addition, our findings on HSP72 and its role in inhibiting the development of vascular calcification (VC) was published in the Journal Cardiovascular Research. In 2013, my research career took a new focus in the molecular mechanisms of HSPs-cell-junctional proteins association, and its role in cyst formation in PKD which has become a core area of my research now as junior faculty member at BWH. At 2015, part of my new research project at PKD has been published in Physiological Genomics and led to two other manuscripts in review. Recently, I was awarded "New Investigator Award" from American Physiology Society at annual Experimental Biology 2016 meeting.

In the short term, my research goal is to investigate the genetic profiling and molecular mechanisms in the development of VC caused by CKD and cyst formation at PKD. My intermediate goal is to study the biological functions of HSPs induction medicines, and their potential to modulate vascular dysfunction in Metabolic Syndrome and cystogenesis at PKD. My long-term goal is to investigate whether HSPs are potential new diagnostic markers and therapeutic targets to prevent accelerated Cardiovascular disease and Kidney diseases.

US Academic Panelist

Dr. Jean J. Huang

Associate Professor of Biology, Olin College

Dr. Jean Huang joins Olin from the University of Washington, Seattle, where she was a postdoctoral scholar in the Department of Microbiology. She received a Ph.D. in biology from the California Institute of Technology, and a B.A. in Biology from Wellesley College. Dr. Huang has also studied the microbial world at the Marine Biological laboratory in Woods Hole, MA, first as a student and then as a teaching assistant for the Microbial Diversity Summer Course. Dr. Huang is recipient of a teaching award from Caltech, and she was a US EPA STAR predoctoral fellow. She has also been a faculty collaborator for the DOE-JGI Undergraduate Genome Annotation Program and a participant of the NSF/ASM Biology Scholars Program. Dr. Huang is enthusiastic about studying the diversity and physiology of photosynthetic bacteria and about applying bacterial metabolic capabilities towards solving environmental challenges.

Investor Panelist

Greg Sieczkiewicz, J.D., Ph. D.

Managing Director & Chief IP Counsel, MPM

Greg Sieczkiewicz, J.D., Ph.D., joined MPM in 2015. Greg serves as Chief IP Counsel at several MPM portfolio companies. Prior to joining MPM, Greg was the architect of IP strategy of over a dozen venture-backed life sciences companies across the spectrum—from nucleic acid therapeutics, oral biologics, the microbiome, oncology, to protein engineering. Starting in 2009, Greg was Vice President, IP at Flagship Ventures. Earlier in his career, Greg practiced patent counseling and enforcement at national law firms Mintz Levin, Proskauer Rose and Foley Hoag. Greg completed his post-doctoral fellowship at the National Cancer Institute. He graduated from the College of the Holy Cross with an A.B. in Biology, received his Ph.D. in Cell, Molecular and Developmental Biology from Tufts University School of Medicine and graduated magna cum laude from the evening program of Suffolk University Law School. Greg is a member of the bar of the Commonwealth of Massachusetts and is admitted to practice before the United States Patent and Trademark Office. Greg is the current President of the Boston Patent Law Association.

Investor Panelist

Michael Mee Ph.D.

Associate, Flagship VentureLabs

Michael joined Flagship in 2015 after completing the VentureLabs® Fellows program. At Flagship, Michael works with VentureLabs partners as part of a venture-creation team, conducting explorations into innovative ideas and promising technologies. He develops the science, intellectual property, and business strategy that form the foundation of breakthrough startups. Before joining Flagship, he completed his doctorate in biomedical engineering at Boston University. As part of his doctorate, Michael worked in the lab of Professor George Church at Harvard Medical School, where he used genome editing technologies to engineer microbial ecosystems and their metabolic exchange networks. His work resulted in multiple academic publications, including an article in the journal Nature.

While in graduate school Michael co-founded a company to modulate the livestock microbiome to improve feed conversion, an effort that was incubated at Harvard iLabs. He was also deeply involved in the Boston scientific community as an organizer of the Boston Bacterial Meeting. His graduate work was supported by a scholarship from the Natural Sciences and Engineering Research Council of Canada and the Canadian Institutes of Health Research.

Michael graduated from McGill University in 2009 with a bachelor's degree in engineering. In the Department of Bioresource Engineering, he applied engineering principles to research on microbial fuel cells, with a goal of enhancing the sustainability of global natural resources. While at McGill, Michael competed internationally on the Canadian National Team in Ice Dancing.

Investor Panelist

Luis Barros
Leading Business Ventures (LBV)

Luis Barros has over 25 years of private and public sector experience as an investor, entrepreneur, and advisor in the science and technology industries-- having held roles in University, Government and Corporate Venturing. He currently manages a boutique consultancy, Leading Business Ventures (LBV), with clients in USA, Europe, Latin America and Africa. Current and past affiliations and collaborations include serving as in concurrent roles as Advisor & Venture Partner of Portugal Ventures an $800M Venture Fund and appointment as Co-Director of Innovation at MIT's School of Engineering's Portugal Program (MPP); Senior Advisor at Mexico's Beamonte Investments' Venture Academy; Co-Founder and Course Director at Kendall Teams, an Int'l market exploration program (formerly started in 2011 as MIT's entrepreneurship training 'eTeams') which has served 14 European countries; Principal Advisor to US and State Government's SBIR, including the NIH; and Advisor and Head of Business Development and Alliances at Eisai, plc's Oncology initiative, H3 Biomedicine.

Mr. Barros, was formerly the Senior Vice-President of Investments at Massachusetts' $1B Life Sciences Center; Executive Vice-President at IC Sciences (holding co. of the co-founding family of Boston Scientific) and Principal at Eli Lilly Ventures; He advised and worked at several venture-backed startups, including 2 that were respectively by publicly-traded co's. Mr. Barros has degrees from MIT Sloan (MBA) and UMASS Amherst (BBA), and is a graduate Harvard Business School's Executive Program on Board Leadership.

Investor Panelist

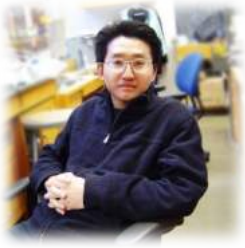
I-Hung Shih Ph.D., 施宜紅 博士

Associate Director for Life Sciences Investment, Temasek

I-Hung Shih is Associate Director for Life Sciences investment at Temasek, an investment company headquartered in Singapore with global presence. Her investment is focused on innovative growth biopharma companies in both public and private sectors in US. Previously, I-Hung was a member of Credit Suisse Biotech Investment Banking team advising biopharma companies on mergers and acquisitions, as well as public capital financing. Prior to that, I-hung served various capacities at Gilead Sciences, from drug discovery, business development and commercial strategy. She was Research Fellow at Whitehead Institute for Biomedical Research in Cambridge, Massachusetts, and Visiting Fellow at National Institute of Health in Bethesda, Maryland.

I-Hung holds a B.S. in Chemistry from National Taiwan University in Taipei, Taiwan, a Ph.D. in Biochemistry from Duke University in Durham, Carolina, and a MBA from The Wharton School of the University of Pennsylvania, Philadelphia, Pennsylvania.

Taiwan Academic Panelist



Chao-Min Cheng Ph.D., 鄭兆珉 博士

Associate Professor, Institute of Nano Engineering and Micro Systems & Department of Power Mechanical Engineering, NTHU

Dr. Cheng received his B.S. degree in Mechanical Engineering from the National Chiao Tung University, Taiwan in 1999. He received his Ph.D. training in Biomedical Engineering at Carnegie Mellon University in Pittsburgh, focused on understanding cell-based biopolymer structures through small-scale approaches, and got his Ph.D. in 2009. Then Dr. Cheng performed his post-doctoral research in Dept. of Chemistry & Chemical Biology at Harvard University until 2011. Cheng's group at NTHU focuses on developing cellulose-based diagnostic devices for public and food safety; studying cellular and molecular biomechanics and microfabrication, micropatterning through Bio-Inspiration Approaches.

Alan Yueh-Luen Lee Ph.D., 李岳倫 博士

Associate Investigator, National Institute of Cancer Research, National Health Research Institutes

Yueh-Leun Lee obtained his B.S. degree in Biology from Chinese Culture University in Taipei and later received his M.S. degree from Insitute of Botany, National Taiwan University in 1994. From 1999 to 2004, Yueh-Leun Lee did his graduate study at Institute of Biomedical Sciences at National Taiwan University. After obtaining his Ph.D degree, Dr. Lee joined Institute of Biotechnology at National Taipei University of Technology as an Adjunct assistant professor shortly then he went to the Scripps Research Institute for his post-doctoral research training in 2005. After doing research abroad, Dr. Lee joined Kaohsiung Medical University as an Assistant Professor in 2008. In 2010, Dr. Lee joined the National Institute of Cancer Research at National Health Research Institutes in Miaoli and is now an Associate Investigator. Dr. Lee's research focuses on the stress phenotypes of cancer in tumor microenvironment, includes survival response signaling and overcoming non-oncogene addition for anti-cancer therapy.

Taiwan Academic Panelist

Hsin-yu Lee Ph.D., 李心予 博士

Professor, Department of Life Science, NTU

Hsin-yu Lee received his PhD training in Biomedical Sciences at UCSF, after his postdoctoral training in the US. Dr. Lee joined Department of Life Sciences at National Taiwan University. Dr. Lee was promoted to full professor in 2009. Beside establishing an active lab and teaching in Department of Life Sciences, Dr. Lee also devoted his time as the director for Center for Biotechnology and director of office of International academic exchanges at NTU. Dr. Lee's lab is interested in endothelial cell physiology, lymph-angiogenesis, GPCR signaling, especially focuses on Lysophospholipid receptor functions in these processes.

Tang-Long Shen Ph.D., 沈湯龍 博士

Associate Professor, Department of Plant Pathology and Microbiology, NTU

Tang-Long Shen received his PhD in Molecular Medicine from Cornell University in 2003. He then went to American Heart Association for one year post-doctoral training before he joined Department of Plant Pathology and Microbiology at National Taiwan University, as an Assistant Professor, in 2004. Dr. Shen's group is interested in the signal transduction pathways, especially in integrin and growth factor signaling.

Taiwan Academic Panelist

Tsyr-Yan Yu Ph.D., 余慈顏 博士

Assistant Researcher, Institute of Atomic and Molecular Sciences, Academic Sinica

TY. Yu received his BS from National Taiwan University in 1998 and he obtained his PhD in Chemistry from Washington University in St. Louis in 2008. After a postdoc fellowship at Harvard Medical school, he joined Institute of Atomic and Molecular Sciences, Academia Sinica, as an assistant research fellow. He is currently engaged in three general fields of interests: the structures and functions of mitochondrial membrane proteins that are involved in apoptosis, the development of techniques for NMR spectroscopy and the application of optimal control theory in NMR spectroscopy.

Taiwan Industry Talk

Karen Wen, 溫國蘭 總經理

President, Mycenax Biotech Inc. (永昕生物醫藥)

Dr. Karen Wen currently serves as the President of Mycenax Biotech Inc and she is one of the founders of this company. She has 20 years of experience in the biopharmaceutical industry and is well versed in drug development. Prior to founding Mycenax, she worked at Development Center for Biotechnology in Taiwan as research fellow, project leader of biomedical plan and manager of research and development for biodevice pilot plant. Her work experience included cell line evaluation, manufacturing process development, clinical trial design, quality assurance and regulatory compliance. Throughout the ten years, she has successfully led her team to execute two biopharmaceutical programs from bench into clinical stage.

Mycenax, a member of Center Laboratories group which is one of the Taiwan leading biopharmaceutical conglomerate, is positioned as biopharmaceutical company specialized in high quality and competitive cost recombinant products. In 2020, Mycenax will have 2~4 biosimilars in autoimmune indications launched and two biosimilars in oncology indications are launched through our CDMO to CMO services (contract development and manufacturing services). Two bionovels will be in early clinical phase. In the meantime, Mycenax continues to provide CDMO services with CMC expertise and PIC/S GMP production.

Taiwan Industry Talk

Mark Liu Ph.D., 劉家宏 博士

Senior Director, Big Data Division, Meridigen Biotech co. (宣捷生技)

Dr. Liu specializes in automation of knowledge work, cloud-based services in biotech industry.

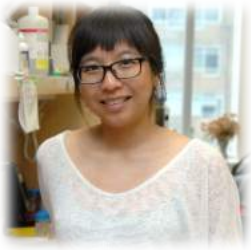
Meridigen Biotech co. was founded in 2011. With sustainability being the core value, we are a company based in Taiwan yet aim for world-class. Committed to mesenchymal stem cells (MSCs) research and drug development, we strive to manufacture MSCs drugs that live up to PIC/S GMP standards. Meridigen has the most experienced management team, world-class researchers and advanced techniques. We combine a comprehensive patent plan and exceptional business model that is expected to reduce the risk of drug development significantly.

The company has full access to the sources of stem cells. We take good care of the industrial chain all the way from R&D, manufacturing and sales. With integrity and persistence, Meridigen expects to better the quality of human life and bring visionary treatment to the World.

Career Opportunity in Drug Development

Are you considering going outside of academia but not sure what opportunities are out there? Are you thinking about transitioning into industry but don't know what areas or positions that may fit your interest and background? Come to this section and figure it out! This section is featured to introduce positions in several departments during drug development. Speakers with different expertise and backgrounds will share with you about their daily life at work and the qualifications required to land similar positions.

Drug Discovery



Ho-Chou Tu Ph.D., 杜荷洲 博士

Scientist, Alnylam Pharmaceuticals

Ho- Chou graduated from National Taiwan University, department of Zoology. She holds a PhD in Molecular and Cell Biology from Washington University in St. Louis, where she studied the mechanisms of apoptosis, autophagy and necrotic cell death in normal and cancer cells. Her post-doctoral training was done at Boston Children's Hospital where her research was on investigating the role of stem cell factors in tumorigenesis and tumor progression. Currently, Ho-Chou is a scientist in Alnylam Pharmaceuticals, a mid-size biotech company in Kendall Square. Alnylam is one of the leading companies focusing on RNAi therapeutics. Ho-Chou is in the research department, and her roles in the team include target identification, target validation, biomarker identification and establishing disease animal models.

Career Opportunity in Drug Development

Drug Discovery – in silico

Chia-Ling Huang Ph.D., 黃佳苓 博士

Investigator I, H3 Biomedicine

Chia-Ling Huang is currently an investigator of data science & IT at H3 biomedicine. Prior to joining H3 biomedicine in February, she was a translational informatics scientist at Sanofi Genzyme. Her research interests focus on network biology and functional genomics. She received her B.S. and M.S. degree from National Yang-Ming University in Taiwan. She did her graduate research at Boston University with Prof. Charles DeLisi and received her M.S. and Ph.D. degree in bioinformatics.

Analytical Department

Kuan-Wei (Wilson) Peng Ph.D., 彭冠為 博士

Bioanalytical Scientist, Berg Health

Kuan-Wei Peng is a bioanalytical scientist in Berg Health. He is working on protein biomarkers and therapeutic proteins to support pre-clinical and clinical studies. He obtained his Ph.D. in Dr. Judy L. Bolton's lab from University of Illinois at Chicago, where he studied carcinogenesis of the equine estrogen metabolites and estrogen receptor targeted chemotherapeutic agents in the field of drug metabolism and toxicology. He did postdoctoral research for anti-Tuberculosis in drug metabolism, and pharmacokinetic in Inst. for Tuberculosis Research, and then investigated ethnic variability in the expression of hepatic drug transporters in University of Kansas. He then did researches of potential protein biomarkers in Alzheimer disease and Lupus Nephritis in Genentech as senior scientific researcher (contractor).

Career Opportunity in Drug Development

DMPK: Drug Metabolism and Pharmacokinetic

Shu-Pei Wu Ph.D., 吳書沛 博士

Scientist II, Vertex Pharmaceuticals

I am currently working as a PK/PD pharmacokineticist in department of drug metabolism and pharmacokinetics at Vertex for 3 years. Prior to Vertex, I graduated from pharmaceutical sciences at University of Michigan - Ann Arbor focusing on the impact of PepT1 transporter in intestine. After graduation, I worked as a post-doctoral fellow in Department of Pharmacology and Systems Therapeutics at Mount Sinai School of Medicine. At Sinai, I was working on the impact of ABC efflux transporter at blood-brain barrier and hybrid PBPK/PD modeling.

Process Development and Manufacturing

Haofen (Eric) Peng Ph.D., 彭浩帆博士

Senior Engineer, Biogen

Haofan Peng (Eric) is a senior engineer in the Manufacturing sciences group at Biogen. He was in cell culture development, technical development, prior to current position. In Biogen, he is the team manager in biologics process development including protein and antibody targeting at Multiple Sclerosis, Hemophilia, and Alzheimer. His main role is to support large scale manufacture in clinical and commercial campaign (2000L to 15,000L) as well as next generation world-class facility design focusing on continuous perfusion process. He also leads multiple cross functional projects including cell line evaluation, medium optimization, process development, filtration integration and instrument automation. Aside from lab he also works closely with GMP manufacture facility in RTP (NC) and Hillerod (Denmark). He published several papers in raw material screening and analytical assay development where he collaborates with groups in analytical development, quality control, regulatory, supply chain, procurement and multiple external biotech companies/vendors. Eric obtained his chemical engineering BS degree at National Taiwan University and PhD from the SUNY Buffalo in chemical and biological engineering where he focused on regenerative medicine and preclinical animal model.

Career Opportunity in Drug Development

Toxicology

Hungyun (Hank) Lin Ph.D., 林弘昀 博士

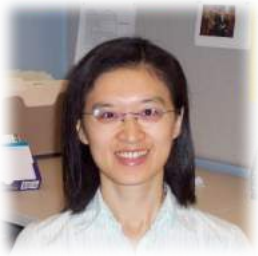
Principal Scientist, Pfizer

Hank is currently a Principal Scientist of Pfizer DSRD in Cambridge, MA. As a Drug Safety Subject Matter Expert, DSTL (Drug Safety Team Lead), he represents drug safety within project teams in multiple therapeutic areas and functions; and provides nonclinical safety strategy in support of both efficacy and toxicity studies in drug development and safety. Hank received his M.S. in Toxicology from National Taiwan University in Taiwan (1999) and his Ph.D. in Pathology and Laboratory Medicine from University of Rochester Medical School in Rochester, NY (2007) where he initiated his professional interests in metabolic syndrome and reproductive endocrinology. Currently he is in the D'Amore-McKim School of Business at Northeastern University to obtain the Master in Business Administration.

Prior to joining Pfizer DSRD, Hank was a Scientist at Vaxin (now Altimmune) in Gaithersburg, MD (2007-2009); and an Associate Scientist at the Taiwan Biotech Co. in Taiwan (1999-2001). During 2009-2010, he was a Postdoctoral Investigator in Molecular, Investigative, and Reproductive Toxicology, Safety Assessment at AstraZeneca in Wilmington, DE; providing expertise and technical insight for developing strategic initiatives of integrated biomarkers assessing mechanistic insight of target organ toxicities. Hank is a board certified toxicologist, a member of the Society of Toxicology (SOT), American Chemical Society (ACS), and ENDO. Hank has published more than 17 manuscripts in basic and applied pathology, molecular toxicology, and endocrinology.

Career Opportunity in Drug Development

Clinical Trials



Yu-Hui Chen M.S., MPH, 陳俞憓

Statistician III, Dana-Farber Cancer Institute

Yu-Hui Chen is Statistician III at Dana-Farber Cancer Institute (DFCI). She is engaged in various clinical trials, especially prostate cancer and radiation oncology trials from Phase I to Phase III. Her work is focused on study design, protocol development, trial monitoring and data analysis. She also serves as a reviewer at the institutional review board (IRB) at DFCI.

Yu-Hui graduated from National Taiwan University with a B.S. in Zoology and a M.S. in Health Policy and Management. She then went to Columbia University and received an MPH in Biostatistics.

Resume Workshop

Lauren Celano
Founder and CEO, Propel Careers

Lauren Celano is the co-founder and CEO of Propel Careers, a life science search and career development firm focused on connecting talented individuals with entrepreneurial life sciences companies. Propel works with current leaders and actively cultivates future leaders through full time placement, internships, mentoring, career coaching, and networking. Propel Careers is engaged across all areas of life sciences, including therapeutics, medical devices, healthcare IT, diagnostics, consulting, venture capital, and investment banking. Prior to Propel Careers, Lauren was a senior account manager for SNBL USA where she worked with emerging biotech companies in Europe, Asia, and the US to help characterize and advance their drug molecules. Prior to SNBL USA, she held business development positions with Aptuit and Quintiles, where she focused on IND enabling studies to advance therapeutics from discovery into the clinic. Earlier in her career, Lauren held positions as a marketing manager and account manager at Absorption Systems, where she was responsible for managing life sciences companies in the northeastern United States. She has a B.S. in Biochemistry and Molecular Biology from Gettysburg College and an MBA with a focus in the health sector and entrepreneurship from Boston University. Lauren is on the Board of MassBioEd, the Advisory Board of the Boston University School of Public Health Pharmaceuticals Program, and the Advisory board for Endicott College Boston. She also serves on the Gettysburg College Entrepreneurial Fellowship Advisory Council and the programming committee of the Capital Network.

Academic Workshop

The academic workshops aim to help equip symposium participants with practical skills for an academic career. The topics cover four essential aspects in the day-to-day task in academic, including grant application, job application, interview, and scientific writing. Each session will last for 30 minutes, and the participants can choose 2 sessions to attend.

There will be 4 parallel sessions:

1. Introduction to funding systems in Taiwan and tips for grant application. 李岳倫 (Faculty at 國衛院)
2. Essential skills in Interview, Job talk and Chalk talk. 余慈顏 (Faculty at 中研院)
3. Essential skills in scientific writing and publishing 郭昇翰 Dr. Sheng-Han Kuo (Faculty at Columbia University)
4. How to find position opening and prepare for application packages 李湘盈 Dr. Sherry Lee (Post doc at MIT)

Entry into the industry

Ming-Wei Chen
Principal Scientist, Novartis

Ming-Wei has a PhD in Biochemistry and Molecular Biology, and 2-year experience on non-viral gene editing.

Amy Shyu
Scientific Associate II, Novartis

Amy has a MS in Biotechnology and 2-year experience on immune-oncology, cellular therapy.

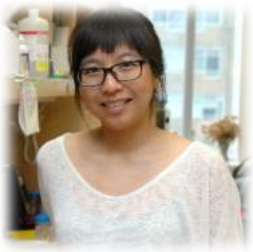
Wei-Lung Hsu
Business Analyst and Programmer, Novartis

Wei-Lung has a PhD in Biochemistry and Molecular Biology, and 2.5-year experience on bioinformatics and computational biology.

Entry into the industry

Rake Wu
Investigator II, Novartis

Rake has a PhD in Chemistry and 1-year experience on medicinal chemistry and synthetic chemistry.



Ho-Chou Tu
Scientist, Alnylam

Ho-Chou has a PhD in Molecular and Cell Biology, and 1-year experience on disease modeling, RNAi therapeutics, and cancer.

April Kuo
Scientist, Acceleron

April has a PhD in Biomedical Sciences and 1-year experience on research and development.

Entry into the industry

Kuo-Chan Hung
Postdoc, New England Biolabs

Kuo-Chan has a PhD in Genetic, Molecular & Cellular Biology, and 3.5-year experience on protein engineering, direct evolution, and high-throughput screening.

Kai-Yun (Kay) Chung
Account Manager, GenScript USA Inc

Kay has a Master in Biotechnology and 3-year experience on business development and project management.

Hao-Wei Su
Research Scientist, Fitbit

Hao-Wei has a PhD in Electric Engineering and Computer Science, and 1-year experience in the company and 6-year experience in the medical device area.

Entry into the industry

Po-Jung Tseng
Senior Scientific Associate, Vertex Pharmaceuticals

Po-Jung has a Master in Chemical Engineering and 2 years of experience (4 months in the company) on pharmaceutical continuous manufacturing.

Kuan-Wei Chen
Operations Associate, Moderna Therapeutics

Kuan-Wei has a Master in Biotechnology and half year experience on automation, mRNA science.

Yi-Ju Lin
Financial Analyst, Partners Healthcare

Yi-Ju has a Master in Health Care Policy and Management, and 1-year experience on contract finance.

Entry into the industry

Joyce Chen
Biostatistician, Paraxel

Joyce has a Master in Biostatistics and 1-year experience on statistical analysis.

Kuan-Wei (Wilson) Peng
Bioanalytical Scientist, Berg Health

Wilson has a PhD in Medicinal Chemistry and 2-year experience on bioanalysis in drug metabolism, protein biomarkers, and therapeutical proteins.

Kelly Ho
Process Engineer I, Genzyme

Kelly has a Master of Engineering in Biological and Environmental, and 1-year experience on downstream purification.

Entry into the industry

Daniel Wu
Technologist III, Sanofi Genzyme

Daniel has a Master in Cellular and Molecular Biology, and 1-year experience on cellular and molecular biology.

Wei-Chiang Chen
Scientist, ImmunoGen Inc

Wei-Chiang has a PhD in Chemical and Biomolecular Engineering, and 2-year experience on high throughput assays, analytical chemistry, cell line development.

Entrepreneur Presentation Index

Entrepreneur Presentation Finalists

Asclepiumm Taiwan Co., Ltd

Asclepiumm Taiwan Co., Ltd is a startup biotech company for (1) bio-therapeutic drugs and (2) peptide drugs development.

(1) The Company has developed an innovative Antibody Switch-on Cytotoxicity (ASC) platform for bio-drug delivery. This platform utilizes the nature of antibody-antigen interaction and the tumor microenvironment to switch-on and deliver cytotoxic peptides specifically to cancer cells. The ASC platform provides a breakthrough strategy for bio-therapeutic delivery via efficiently carrying the effector peptides into cells in a non-endocytic pathway. Thus, the effector peptides are not degraded by lysosomes within the cells. Such advantage allows the ASC platform to be used to generate many innovative therapeutic bio-drugs for unmet medical needs.

Currently, the company is developing ASC-S9, an ASC platform designed bio-drug with effector peptides blocking Hsp90, to treat various cancers including lung, breast, prostate, liver, esophageal and pancreatic cancers.

(2) The Company is also conducting a series of peptide drugs for eye diseases. The Dsg2 peptide drugs are not only novel pathway blockers of angiogenesis to reduce MMP9 activities, but may also be developed as topical use drugs for eye diseases including retinopathy of prematurity (ROP), diabetic macular edema (DME), and wet age-related macular degeneration (AMD).

Kynplex

Kynplex tackles the problem of inefficient communication in science by connecting innovators from science labs, companies, and funding agencies on a single platform. Our vision for Kynplex is to forge global infrastructure for scientific communication, enabling international and cross-disciplinary collaborations so that more research ideas can become life-saving applications.

Entrepreneur Presentation Finalists

Vibronix

Vibronix develops advanced imaging and sensor technologies for disease diagnosis and treatment. We currently focus on photoacoustic imaging system for intraoperative margin assessment. At present, 70% of the breast cancer patients undergo the lumpectomy, which is partial breast removal instead of whole breast removal. However, there is always a question that if all the tumors are removed. In fact, owning to the uncertainty, over 25% of the patients have to go back and experience a second or even third surgical operation to remove all tumors. That is painful, costly, and distressful. We are developing a technology called MarginPAT that can distinguish the cancer and normal tissue based on a multimodal imaging system. We examine the excised tissue, and this procedure only takes less than 10 min. Our recent preclinical study in 40 tissues shows a 93% sensitivity and 90% specificity. This means that our technology can help the doctor to completely remove all the tumor within one operation. Compared with our competitors, we take less time and generate more accurate results. We are currently looking for a 1 million investment to reach design freeze and get 510(k) approval.

U-ARK™ America, Inc.

U-ARK America is a U.S. based software company which strive on connecting the modern technology to long-term and post-acute care industry. We provide solutions include both software and hardware components to improve quality and affordability of senior care.

The original U-ARK Tech is first founded 2012 in Taipei Taiwan with a group of passionate talents from National Taiwan University. In 2014, U-ARK reached 10% of the market share in Taiwan's long-term care industry. The same year we started the U.S. localization procedure in Boston, Massachusetts where U-ARK America was founded. After a year of localization and developing, U-ARK America incorporated as U-ARK America, Inc. to start the new venture in the U.S.

Entrepreneur Presentation Finalists

Roundabout Therapeutics

Multi-drug resistant infections in both the hospital and community settings have reached crisis proportions. Nearly 2 million patients will contract one of these infections each year, resulting in high morbidity, extended hospital stays, and patient deaths. MDR infections kill more people per year in the US than breast cancer and prostate cancer combined. New compounds with novel antibiotic mechanisms are desperately needed to combat this growing problem.

Through careful study of the basic processes in resistant bacteria, Roundabout has discovered a conserved metabolic pathway that contributes to bacterial pathogenicity. Targeting this pathway affects virulence factors involved in bacterial pathogenicity. Years of research in the academic setting has created the technical foundations for Roundabout. The team has designed a novel screen and identified two compounds that demonstrate activity against Pseudomonas aeruginosa infection. These are both known compounds that have not previously been used as anti-infectives and Roundabout is evaluating them as re-purposing candidates.

With chemical molecules, screening platform and accumulated know-hows, Roundabout aim to develop a first-in-class anti-infective agent and bring it to IND or Phase I trials in the next few years.

BioMab BioMab, Inc.

BioMab, Inc. discovers and develops cutting edge immuno-based diagnostics and therapeutics to enable healthcare professionals provide patients with personalized care. The company was founded through close collaboration with a leading research group specializing in the field of antibody technologies and targeted therapy at Academia Sinica. BioMab aims to become a world leader and innovator in immuno-based diagnostic solutions and targeted therapeutics for patients worldwide. The company's products have gained recognitions from leading research institutes and has partnered with top 10 global pharmaceuticals, clinics and biotech companies worldwide.

Entrepreneur Presentation Finalists

XtalPi

XtalPi is a cloud-based technology company that solves drug polymorphism by providing accurate computational crystal structure prediction for small-molecule drugs.

As an industry pioneer, XtalPi applies its expertise in drug virtual development to create game-changing solutions for polymorph screening with unbeatable speed and accuracy. With a mission to make safe and effective treatments available to patients worldwide faster, XtalPi is dedicated to accelerate drug development for biopharmaceutical companies worldwide by translating leading-edge science and computational technology into R&D efficiency. Its technology holds the promise of revolutionizing the industry standard for drug development risk management, crystal form patent strategy, and lifecycle management.

Founded in 2014 by a group of quantum physicists on MIT campus, XtalPi has since grown into an elite team of 30 people with diverse backgrounds. It has received much recognition for its groundbreaking technology, innovative solution, and its potential for wide application across the pharmaceutical industry.

VACEPYLORI

Founded by Dr. Chung-Wei Lee, the well-known Helicobacter pylori researcher, VACEPYLORI is pioneering in immune-modulating, preventive and therapeutic vaccines to target H. pylori. As a carcinogenic bacterium, H. pylori infects more than half the population worldwide. Among the infected patients, >80% have gastritis, 15% develop peptic ulcer and atrophic gastritis, and about 1% eventually progress to gastric cancer. Facing an increasing drug resistant rate to standard antimicrobial treatments, H. pylori vaccines remain the primary preventive modality.

VACEPYLORI vaccine platform is proven to induce desirable host immunities in mice. Product pipelines are focusing on both prevention of H. pylori infection and treatment of peptic ulcer and gastric cancer associated with chronic H. pylori infection. Pre-clinical developments are undergoing in rodent models of chronic H. pylori infection and H. pylori-associated gastric cancer.

VACEPYLORI is collaborating with academic institutes in Taiwan for pre-clinical development and seeking industrial partners for clinical trials.

Entrepreneur Presentation Finalists

Qidza

CDC reports that 1 out 6 children have developmental problems, costing healthcare $30+ billion annually. Yet 52% of pediatricians don't have time or expertise to screen for developmental issues (American Academy of Pediatrics, 2011). To close the screening gap and offer parents peace of mind, Qidza is a population health mobile platform that enables parents work seamlessly with their physicians to track their children's developmental milestones and improve their health and well-being.

Abstract Index

#	Presenter	Title
1'-1	Hui-Lung Sun, Ohio state University	ERK activation globally downregulates miRNAs through phosphorylating exportin-5
1'-2	Ching-Lan Lu, Weill Cornell Medical College	Enhanced clearance of HIV-1 infected cells by broadly neutralizing antibodies against HIV-1 in vivo
1'-3	Yen-Hua Chen, Columbia University in the City of New York	Asymmetric rejuvenation of mitochondria guides the differentiation for effector and memory cells
1'-4	Linya Wang, USC postdoc	HCV induces the expression of Rubicon and UVRAG to temporally regulate the maturation of autophagosomes and viral replication
2'-1	Chih-Chieh Wang, "Department of Neurobiology, Harvard Medical School"	Calcium-Dependent Protein Kinase C is not Required for Post-Tetanic Potentiation at the Hippocampal CA3 to CA1 Synapse
2'-2	Yu-Mei Huang, Baylor College of Medicine	Alpha II-spectrin-dependent cytoskeletons are essential for axon function, domain assembly and integrity
2'-3	Chien-Ling Lin, Brown University	The Second Life of Intron
2'-4	Jian-geng Chiou, "University Program of Genetics and Genomics, Duke University"	Dynamic modeling reveals a saturation rule that governs the switch between uni- and multi-polar growth
2'-5	William C.W. Chen, Massachusetts Institute of Technology	Decellularized Zebrafish Heart Extracellular Matrix Promotes Myocardial Regeneration in Adult Mammals
2'-6	Ting-Yi Wang, Texas A&M University	Peptide translocation through the plasma membrane of human cells: a process mediated by oxidative stress

#	Presenter	Title
P01	Shu-Yu Liao, MIT	Conformational Analysis of the Full-Length M2 Protein and the Drug Binding in Different Constructs of Influenza M2 Protein by Solid State NMR
P02	Chien-Kuang Cornelia Ding, Duke University	Cystine Deprivation Triggers Regulated Necrosis in VHL-Deficient Renal Cell Carcinomas
P03	Yen-Hua Chen, Columbia University in the City of New York	Asymmetric rejuvenation of mitochondria guides the differentiation for effector and memory cells
P04	Brian E Hsu, Goodman Cancer Research Center	Differential mobilization of circulating neutrophil subpopulations in breast cancer metastasis
P05	Cheng-Yi Chen, Stowers Institute for Medical Research	Mining developmental origins of germline stem cells in early eumetazoa
P06	Chia-Hao Chang, McGill University	Site-specific phosphorylation of paxillin drives autophagy-mediated focal adhesion turnover and cancer cell locomotion
P07	Wei-Cheng Lu, UT Austin	Engineered human L-Methioninase for therapeutic purposes.
P08	Yu-Ting Huang, "Department of Medicine, University of Fribourg, Switzerland"	The matricellular protein CYR61 promotes lung metastasis of breast cancer cells through facilitating transmigration and anoikis resistance during extravasation
P09	Josephine Fang, University of Southern California	Tissue- engineered 3D osteoclast activation model
P10	Ming-Shuo Chen, Rutgers University	Nectin-like 2 (Necl-2) cell adhesion molecule is a negative regulator of Schwann cell myelination
P11	Yu-Mei Huang, Baylor College of Medicine	Alpha II-spectrin-dependent cytoskeletons are essential for axon function, domain assembly and integrity
P12	Min-Yu Sun, Washington University	Endogenous 24S-hydroxycholesterol modulates NMDAR-mediated function in hippocampal slices
P13	Chia-Yu Chung, University of Pennsylvania	A transcriptional regulator as a modulator of TDP-43 and G4C2 hexanucleotide repeat toxicity in amyotrophic lateral sclerosis disease models
P14	Rebecca Wu, University of Pittsburgh	Refining the mathematical model of evoked dopamine responses in the rats dorsal striatum with fast scan cyclic voltammetry and electrical stimulation
P15	WEI-CHAO HUANG, The University of Utah	Differential Allele Expression Effects in the Brain Shape Genetic Architecture at the Cellular Level

#	Presenter	Title
P16	"Hsin-Yu, Lin", McGill University	Optimal Fungal Space Searching Algorithms
P17	Chien-Ling Lin, Brown University	The Second Life of Intron
P18	Jian-geng Chiou, "University Program of Genetics and Genomics, Duke University"	Dynamic modeling reveals a saturation rule that governs the switch between uni- and multi-polar growth
P19	Yen-Chun Lu, Cornell University	Developing complex hydrogel microcapsules for high throughput, confined tissue culture: small packages, big potential
P20	Hao-jui Hsu, University of Illinois at Chicago	Dendritic architecture enhances the structural stability of self-assembled dendron micelles in the presence of serum proteins
P21	Jason, Purdue univ	Vibrational Spectroscopic Imaging of Molecular Dynamics in Living Systems
P22	Ting-Yu Shih, "School of Engineering and Applied Sciences, Harvard University"	Injectable, Tough Alginate Cryogels as Cancer Vaccines
P23	Ting-Yi Wang, Texas A&M University	Peptide translocation through the plasma membrane of human cells: a process mediated by oxidative stress
P24	WANG, HUEI-BIN, Student	Blue light therapy improves circadian dysfunction in two mouse models of Huntingtons disease
P25	Chen Jia-En, National Defense Medical Center	Characteristics of particulate matters emissions from a 3D printer
P26	Po-Hao Chang, Asclepiumm Taiwan	Innovative Antibody Switch-on Cytotoxicity (ASC) platform for cancer treatment
P27	Geng-Yuan Chen, Pennsylvania State University	Mechanical assays uncover diverse Eg5 inhibitor mechanisms
P28	Shih-Dun Liu, University of Pittsburgh School of Medicine	Exploring Indicators of Child Resilience in Early Childhood with the Taiwan Birth Cohort Study
P29	Hai-Yin Wu, Harvard University	Biophysics of mitotic spindle positioning in C. elegans embryos
P30	Wei Ting Chen, Harvard University	Chiral Imaging using Planar Meta-lenses

Oral Presentation Abstract

1-1. ERK activation globally downregulates miRNAs through phosphorylating exportin-5

Hui-Lung Sun[1,2], Ri Cui[1], Yong Peng[3], Kun-yu Teng[4], Yung-Hsuan Hsiao[5], Kotaro Nakanishi[6], Matteo Fassan[1,7], Jih-Hwa Guh8, Kalpana Ghoshal[4], Mien-Chie Hung[9], Che-Ming Teng[2], Carlo M. Croce[1]

[1]Department of Molecular Virology, Immunology and Medical Genetics, Ohio State University
[2]Pharmacological Institute, College of Medicine, National Taiwan University

[3]State key laboratory of Biotherapy and Collaborative Innovation Center, Sichuan University
[4]Department of Pathology, Ohio State University

[5]Department of Human Nutrition, Ohio State University

[6]Department of Chemistry and Biochemistry, Ohio State University

[7]ARC-NET Research Centre, University and Hospital Trust of Verona

[8]School of Pharmacy, National Taiwan University

[9]Department of Molecular and Cellular Oncology, MD Anderson Cancer Center

MicroRNAs (miRNA) are mostly downregulated in cancer. Systemic evaluation of miRNA has revealed that many pre-miRNA were retained in the nucleus of cancer cells. However, the mechanism underlying this phenomena and the precise consequence for tumorigenesis remains obscure. Here we showed that ERK suppresses pre-miRNA export from nucleus through phosphorylation of exportin-5 (XPO5) at T345/S416/S497. After phosphorylation by ERK, conformation of XPO5 is changed by prolyl isomerase Pin1, resulting in reduction of pre-miRNA loading. ERK also phosphorylates NUP153 to further inhibit pre-miRNA-XPO5 complex export. Globally miRNA downregulation was observed in liver cancer when XPO5 was phosphorylated, including the highly expressed miRNA, miR-122. Depletion of miR-122 increase SEPT9 expression to scaffold MAP4 and MARK4. Phosphorylated MAP4 detach from tubulin to increase microtubule dynamics, thereby inducing taxol resistance and tumorigenesis. Analysis of clinical specimens further showed that XPO5 phosphorylation is associated with poor prognosis for liver cancer patients. Our study reveals a novel function of ERK in miRNA biogenesis and suggests that modulation of miRNA export has potential clinical implications.

1-2. Enhanced clearance of HIV-1–infected cells by broadly neutralizing antibodies against HIV-1 in vivo

Ching-Lan Lu,[1,2] Dariusz K. Murakowski,[3] Stylianos Bournazos,[4] Till Schoofs,[1] Debolina Sarkar,[3] Ariel Halper-Stromberg,[1] Joshua A. Horwitz,[1] Lilian Nogueira,[1] Jovana Golijanin,[1] Anna Gazumyan,[1] Jeffrey V. Ravetch,[4] Marina Caskey,[1] Arup K. Chakraborty,[3,5,6,7,8†] Michel C.Nussenzweig[1,9†]

[1] Laboratory of Molecular Immunology, The Rockefeller University

[2] Weill Cornell Medical College

[3] Department of Chemical Engineering, Massachusetts Institute of Technology

[4] Laboratory of Molecular Genetics and Immunology, The Rockefeller University

[5] Ragon Institute of MGH, MIT, and Harvard

[6] Department of Physics, Massachusetts Institute of Technology

[7] Department of Biological Engineering, Massachusetts Institute of Technology

[8] Institute for Medical Engineering and Science, Massachusetts Institute of Technology

[9] Howard Hughes Medical Institute.

[†] Corresponding author

Although combination antiretroviral therapy (cART) suppresses HIV-1 viremia to undetectable levels in a majority of infected patients, viral rebound occurs 2~3 weeks following cART interruption. Recent studies show that broadly neutralizing antibodies (bNAbs) are not only effective as an immunoprophylaxis for HIV-1 acquisition, but can also suppress viral loads to undetectable levels in chronically infected humanized mice and macaques. Unlike ART, which prevents new infections by interfering with various elements required for HIV-1 replication, antibodies block infection, and accelerate the clearance of free virions from the blood of macaques. Antibodies also have the potential to kill infected cells in vivo and have been shown to do so in vitro by FcγR-mediated mechanisms. However, the majority of infected cells die rapidly by apoptosis or pyroptosis and whether bNAbs can accelerate their clearance in vivo has not been tested directly.

To determine whether bNAbs can utilize these cellular effector functions to mediate killing of infected cells in vivo, we used mathematical modeling to examine the kinetics of HIV-1 suppression in infected individuals who were enrolled in bNAb 3BNC117 phase I clinical trail. The analysis showed that neutralization of the virus alone doesn't explain the steep drop in the virus levels observed in patients, suggested that the effects of the antibody are not limited to free viral clearance and blocking new infection but also include acceleration of infected cell clearance. Consistent with these observations, we find that broadly neutralizing antibodies can target CD4+ T cells infected with patient viruses and can decrease their in vivo half-lives by a

mechanism that requires Fcγ receptor engagement in a humanized mouse model. The results indicate that passive immunotherapy can accelerate elimination of HIV-1–infected cells.

1-3. Asymmetric rejuvenation of mitochondria guides the differentiation for effector and memory cells

Yen-Hua Chen[1]

[1]Department of Microbiology and Immunology, Columbia University

In an immune response, naive or memory lymphocytes give rise to terminally differentiated antibody-secreting plasma cells to provide function while also regenerating less differentiated memory lymphocytes. However, it remained unclear how production of differentiated lymphocytes is coupled to renewal of the progenitor cell. Here we provide evidence

that asymmetric inheritance of healthy or aged mitochondria contributes to the generation of functional distinct daughter cell. We proposed a model that differentiating into effector cells may represent an accelerated aging phenomenon. The daughter cells that accumulate more old mitochondria tend to become effector cells, whereas the memory population maintains stem cell-like differentiation potential and self-renewal ability by asymmetric rejuvenation of mitochondria.

We showed that the healthy status of mitochondria is a timer for effector cell differentiation. Modulation of mitochondria function by pharmacological and genetic targeting of Drp-1 protein, which participated in mitochondrial renewal, accelerated the switching of transcriptional program to effector cells. For B cells, Mdivi-1 (Drp-1inhibitor) treatment or retrovirally expressing dominant negative Drp-1 (Drp1 K38A) in B cells increased IRF4-mediated Pax5 repression and differentiation into plasma cells.

Moreover, we found the linkage between mitochondria function and repressing of Pax5 involved reactive oxygen species (ROS) production and AMPK mediated quality control mechanism. ROS scavenger treatment increased the memory-like population (Pax5hi, IRF4low) and suppressed the differentiation of effector subsets (Pax5low, IRF4hi) in Mdivi-1 or Drp-1 K38A treated B cells. In addition, the AMPK knock cells tend to differentiate into effector cells, and they were more sensitive to Mdivi-1 induced Pax5 down regulation.

The nature source of the mitochondria stress comes from accelerated aerobic glycolytic after lymphocytes been activated. Over-expression of hexokinase hexokinase 2, which is one of the rate limited enzymes in glycolysis, resulted in Pax5 down regulation. By contrast, inhibiting glycolysis by 2-DG (a nonmetabolizable glucose analog) is sufficient to cancel the effect of Mdivi-1 in Pax5 repression. In sum, enhancing glycolytic pathway boosts effector cell differentiation, whereas suppressing glycolytic pathway helps to retain the self-renewal activity of activate lymphocytes.

Collectively, these evidence reveals mitochondria not only involved reprogramming metabolic pathways but also switching of transcriptional program. Thus, the metabolic status is an integrated part of the signaling pathway guiding the differentiation of lymphocytes, rather than the result of switching transcription program.

1-4. HCV induces the expression of Rubicon and UVRAG to temporally regulate the maturation of autophagosomes and viral replication

Linya Wang, Yongjun Tian and Jing-hsiung James Ou*

Department of Molecular Microbiology and Immunology, University of Southern California, Keck School of Medicine, Los Angeles, CA 90033, USA.

Hepatitis C virus (HCV) induces autophagy to enhance its replication. However, how HCV regulates the autophagic pathway remains largely unclear. In this report, we demonstrated that HCV infection could induce the expression of Rubicon and UVRAG, which inhibited and stimulated the maturation of autophagosomes, respectively. The induction of Rubicon by HCV was prompt whereas the induction of UVRAG was delayed, resulting in the accumulation of autophagosomes in the early time points of viral infection. The role of Rubicon in inhibiting the maturation of autophagosomes in HCV-infected cells was confirmed by siRNA knockdown and the over-expression of Rubicon, which enhanced and suppressed the maturation of autophagosomes, respectively. Rubicon played a positive role in HCV replication, as the suppression of its expression reduced HCV replication and its over-expression enhanced HCV replication. In contrast, the over-expression of UVRAG facilitated the maturation of autophagosomes and suppressed HCV replication. The HCV subgenomic RNA replicon, which expressed only the nonstructural proteins, could also induce the expression of Rubicon and the accumulation of autophagosomes. Further analysis indicated that the HCV NS4B protein was sufficient to induce Rubicon and autophagosomes. Our results thus indicated that HCV, by differentially inducing the expression of Rubicon and UVRAG, temporally regulated the autophagic flux to enhance its replication.

2-1. Calcium-Dependent Protein Kinase C is not Required for Post-Tetanic Potentiation at the Hippocampal CA3 to CA1 Synapse

Chih-Chieh Wang[1], Christopher Weyrer[1,2], Mounica Paturu[1], Diasynou Fioravante[1,3], and Wade G. Regehr[1]

[1]Department of Neurobiology, Harvard Medical School, Boston MA 02115.

[2]Department of Physiology, Development & Neuroscience, University of Cambridge, Cambridge, CB2 3EG, United Kingdom

[3]Present address: Center for Neuroscience, University of California at Davis, Davis CA 95618.

Post-tetanic potentiation (PTP) is a widespread form of short-term synaptic plasticity in which a period of elevated presynaptic activation leads to synaptic enhancement that lasts tens of seconds to minutes. A leading hypothesis for the mechanism of PTP is that tetanic stimulation elevates presynaptic calcium that in turn activates calcium-dependent Protein Kinase C (PKC) isoforms to phosphorylate targets and enhance neurotransmitter release. Previous pharmacological studies have implicated this mechanism in PTP at hippocampal synapses, but the results are controversial. Here we combine genetic and pharmacological approaches to determine the role of classic PKC isoforms in PTP. We find that PTP is unchanged in PKC triple knockout (TKO) mice in which all calcium-dependent PKC isoforms have been eliminated (PKCα, PKCβ, and PKCγ). We confirm previous studies and find that in wildtype mice 10 μM of the PKC inhibitor GF109203 eliminates PTP and the PKC activator PDBu enhances neurotransmitter release and occludes PTP. However, we find that the same concentrations of GF109203 and PDBu have similar effects in TKO animals. We also show that 2 μM GF109203 does not abolish PTP even though it inhibits the PDBu-dependent phosphorylation of PKC substrates. We conclude that at the CA3 to CA1 synapse Ca2+-dependent PKC isoforms do not serve as calcium sensors to mediate PTP.

(This paper is accepted in Journal of Neuroscience, 2016, in press)

2-2. Alpha II-spectrin-dependent cytoskeletons are essential for axon function, domain assembly and integrity

Yu-Mei Huang[1], Chuansheng Zhang[1], Daniel Zollinger[3], Joshua Lalonde[2], Jeffrey Noebels[2], Matthew Rasband[1]

Department of Neuroscience[1] and Neurology[2]

Baylor College of Medicine, Houston, TX

[3]Department of Pediatrics, UCSF School of Medicine, San Francisco, CA

Spectrins are a family of cytoskeletal proteins that provide structural support of the cell membrane, link membrane -associated proteins to actin and serve as platforms for cell signaling. Spectrins consist of α and β subunits, forming heterotetramers to function as a complex. Among the spectrins, αII- spectrin is the only α- spectrin expressed in the nervous system. α II-spectrin is also implicated in a variety of neurological disorders. Recently, we found that αII-spectrin forms a periodic cytoskeleton and interacts with βIV-spectrin at axon initial segments (AIS) and nodes of Ranvier.

To investigate the functions of αII-spectrin-dependent cytoskeletons, we generated conditional knockout (cko) mice. Loss of αII-spectrin in the central nervous system (CNS) causes profound neurological phenotypes including seizures, aberrant cortical lamination, AIS fragmentation, massive neurodegeneration and perinatal lethality. To more specifically interrogate spectrin functions in axons, we generated peripheral sensory neuron specific αII-spectrin cko mice using advillin- cre. We found that large diameter axons preferentially degenerate. By immunostaining, the injury marker ATF3 is observed in dorsal root ganglia (DRG) neurons in cko mice beginning at P10 and increasing with age. Consistent with EM results, ATF3+ neurons are mostly large diameter neurons. The preferential degeneration of large diameter neurons caused ataxia due to deficits in proprioception, while nociception remains unaffected. Mutant mice have fewer nodes of Ranvier and sodium channel intensity at nodes is significantly decreased. Paranodal junctions are extensively disrupted. Axon degeneration and disrupted nodes of Ranvier caused decreased nerve conduction velocity in cko mice. Thus, neuronal αII-spectrin is crucial for proper axon function, node of Ranvier assembly and axon integrity.

2-3. The Second Life of Intron

Chien-Ling Lin[1], Allison J Taggart[1] and William G Fairbrother[1,2,3]

[1]Molecular Biology, Cell Biology and Biochemistry, Brown University, Providence

[2]Center for Computational Molecular Biology, Brown University, Providence

[3]Hassenfeld Child Health Innovation Institute of Brown University, Providence, RI.

In mammalian genomes, coding sequences (exons) are intervened by long non-coding sequences (introns) which compose ~90% of genes. Pre-mRNA splicing is a remarkable process to remove long introns and ligate exons. The intron is excised out from a gene in a lariat shape with a unique 2'-5'phosphodiester bond at the branchpoint. Degradation of the long intronic lariat is essential to recycle and release the nucleic acids, splicing machinery and RNA binding proteins. Debranching enzyme DBR1 specifically hydrolyzes the 2'-5' phosphodiester bond, exposing ends of the introns for further degradation. Because of the transient nature of the RNA lariat, the specificity of DBR1 is poorly studied.

By biochemical enrichment of DBR1-senstive lariats and computational selection of deep sequencing reads that traverse branchpoints, we demonstrate that in human cells, DBR1 catalytic activity prefers short introns over long introns, A-branchpoint over C-branchpoint. Moreover, the upstream and downstream sequences to the branchpoint also affect DBR1 recognition. These results suggest some introns are more dependent on DBR1 and others may require other nucleases for turnover. Interestingly, the best DBR1 catalytic substrate is the most robust branchpoint sequence for splicing, suggesting that DBR1-mediated intron turnover co-evolves with the branchpoint splicing activity. Introns that escape DBR1 digestion in the nucleus get transported to the cytoplasm. They are shorter, GC-rich and contain mostly C-branchpoints. AU-rich introns that escape the nucleic degradation are re-ligated into stable intronic circles by a post-splicing reaction. These stable circular introns may have cellular functions as molecular sponges or transcription factors. Finally, we demonstrate that the branchpoint position and debranching direct the maturation of intron-coded CD-box snoRNAs. Over all, we show that introns with different length, GC-content and branchpoints, turn over through differential pathways, and that the regulation of intronic lariat hydrolysis is not only critical for recycling nucleic acid and protein factors but also for regulating several cellular processes.

2-4. Decellularized Zebrafish Heart Extracellular Matrix Promotes Myocardial Regeneration in Adult Mammals

William C.W. Chen[1,5,#], Zhouguang Wang[1,#], Maria Azzurra Missinato[2], Dae Woo Park[3], Kang Kim[1,3,4], Yadong Wang[1,4]

[1]Department of Bioengineering,

[2]Department of Developmental Biology,

[3]Center for Ultrasound Molecular Imaging and Therapeutics,

[4]McGowan Institute for Regenerative Medicine, University of Pittsburgh

[5]Research Laboratory of Electronics and Department of Biological Engineering, Massachusetts Institute of Technology

[#]Equal Contributions

The adult human heart has very limited regenerative capacity after heart attack. However, evolutionarily primitive species generally have higher tissue regenerative capability than mammals. The tissue-specific extracellular matrix (ECM) in evolutionarily primitive species may induce regeneration post-injury and contribute to this difference. In marked contrast to the highly regenerative zebrafish heart, the injured adult mammalian heart typically elicits fibrotic, instead of regenerative, responses. Hence mammalian heart ECM may not be optimally inductive for myocardial regeneration. We hypothesize that administration of decellularized zebrafish heart ECM (zECM) made from normal or healing hearts promotes mammalian heart regeneration after myocardial infarction (MI). Using adult zebrafish and mouse as representative species of lower vertebrates and mammals, we show a single injection of zECM, particularly the healing one, enables mouse cardiac regeneration and functional recovery after acute MI. In particular, we observed proliferation of cardiomyocytes and multiple cardiac precursor cell (CPC) populations as well as reactivation of ErbB2 expression in cardiomyocytes in zECM-treated mouse hearts. Moreover, zECM exhibits pro-proliferative and chemotactic effects on human CPC populations in vitro. These regenerative responses correlate with the higher contractile function, less ventricular dilatation, and more elastic myocardium in zECM-treated hearts than control hearts treated with decellularized mouse heart ECM or saline. These benefits likely contribute to the structural preservation post-MI. We further demonstrated the critical role of ErbB2 in zECM-mediated benefits, likely via neuregulin-1 signaling, by chemical inhibition of ErbB2 activity. Overall this study pioneers the usage of decellularized ECM from evolutionarily primitive species in mammals and imposes a new approach for mammalian heart regeneration.

2-5. Dynamic modeling reveals a saturation rule that governs the switch between uni- and multi-polar growth

Jian-geng Chiou[1], Timothy C. Elston[2], Thomas P. Witchelski[3], David G. Schaeffer[3], Daniel J. Lew[1]

[1]Department of Pharmacology and Cancer Biology, Duke University

[2]Department of Pharmacology, University of North Carolina at Chapel Hill

[3]Department of Mathematics, Duke University

Precisely orchestrated polarization is crucial for the development of complex cell morphology. For example, neuron cells require polarized growth at multiple cortical domain to form dendrites, but robustly switch to uni-polar growth so that only one further elongates and eventually becomes the axon. Results from both experiments and dynamic modeling have shown that the polarization of Rho-GTPases directs polarized growth throughout Eukaryotes, but what determines the number of polarity domain remains elusive.

In previous studies, it has been shown that a two-component partial differential system that models Rho-GTPase dynamics captures the "competition" behavior between multiple transient polarity clusters, which guarantees uni-polarity. Intriguingly, we demonstrated that with appropriate change of parameters, this system switches to multi-polarity. Applying mathematical analyses, we introduced a "Saturation rule", which formulates the criteria of uni- and multi-polarity, and it can be applied generally to models of similar structures. In the intuitive sense, the saturation rule states that there exists an innate saturation point of Rho-GTPase concentration, and the number of polarity domain that will persist is determined by the number of Rho-GTPase clusters that approach the saturation point.

We then turned to the budding yeast, and showed with fluorescent microscopy that simulations of our model recapitulate the dynamics of polarity clusters in vivo. We further showed with cytokinesis defect mutants that the Rho-GTPase machinery of the budding yeast is competent to produce multiple buds. Lastly, we tested the saturation rule by genetically manipulating the Rho-GTPase machinery, and showed that the saturation point and the level of polarity proteins can be engineered to change the number of buds. Confirmed in the budding yeast, this research can be applied to different Rho-GTPase systems in various cell types, where the reason of saturation may differ depending on the specific molecular interactions, but the general rule holds universally.

2-6. Peptide translocation through the plasma membrane of human cells: a process mediated by oxidative stress

Ting-Yi Wang[1], Yusha Sun[1], Nandhini Muthukrishnan[1], Alfredo Erazo-Oliveras[1], Kristina Najjar[1], and Jean-Philippe Pellois[*, 1]

[1]Department of Biochemistry and Biophysics, Texas A&M University, College Station, TX

Cell-penetrating peptides (CPPs) are promising tools to deliver proteins and nucleic acids into live cells. However, the fundamental mechanisms by which CPPs translocate across cellular membrane remains uncharacterized. This in turn impedes their therapeutic applications and usage for cell biology studies. Here we report that the cell penetration activity of CPPs is dependent on the oxidative state of the membrane. We found that hypoxic culture and supplement of antioxidants abolish the cell delivery efficiency of peptides. Mild oxidation of live cells by oxidants significantly promotes the translocation of CPPs. We also revealed that the native anionic oxidized lipids mediate the efficient and direct transport of the peptide across the plasma membrane of human cells. Our results support a model that CPPs permeate through the lipid bilayer via forming inverted micelles with anionic lipids, which is present as a result of oxidative damage. Our data point to a highly complex and underappreciated interplay between CPPs and oxidized membrane species. This novel mechanism also provides a fundamental basis for rationale design of highly efficient cell-permeable compounds and robust drug delivery strategies.

Poster Presentation Abstract

P-1. Conformational Analysis of the Full-Length M2 Protein and the Drug Binding in Different Constructs of Influenza M2 Protein by Solid State NMR

Shu-Yu, Liao,[1] Keith Fritzsching,[2] and Mei Hong[1]

[1]Department of Chemistry, Massachusetts Institute of Technology, Cambridge, MA 02139 [2]Department of Chemistry, Brandeis University, Waltham, MA 02453

The 97-residue influenza A M2 protein forms a tetrameric proton channel that is essential for the virus life cycle and is the major target for the amantadine class of antiviral drugs. Extensive structural information has been obtained about the transmembrane (TM) domain and the adjacent amphipathic helix (AH) domain; however, little is known about the N-terminal ectodomain and the C-terminal cytoplasmic tail. The proton channel is activated by the low pH of the endosome, with His37 of the TM domain being responsible for acid activation and proton conduction. Several p Ka's of His37 have been determined in different constructs of M2. A recent study of M2(21-97), indicated that the pKa's of His37 are 7.1 and 5.4.

Using 2D 13C solid-state NMR spectroscopy (SSNMR), we have analyzed the secondary structure and dynamics of full-length M2 (M2FL). The conformation and dynamics of M2FL are sensitive on the membrane composition. The protein exhibits strong β-strand chemical shifts for the extra-membrane residues when bound to 1,2-dimyristoyl-sn-glycero-3-phosphocoline (DMPC) bilayers, but predominantly α-helical chemical shifts in cholesterol -rich lipid membranes. Chemical shift prediction for various structural models and comparison with the experimental spectrum indicate that DMPC-bound M2FL contains a β-strand segment, which is most likely located in the N-terminal ectodomain, and a significant coil content in the rest of the two extra-membrane domains. The fact that cholesterol increases the α-helical content of the extra-membrane domains may be relevant to M2 interaction with the matrix protein M1 during virus assembly and budding.

Residue Ser31 in the TM of the M2 protein is the primary binding site for the antiviral drug amantadine (Amt) and rimantadine (Rmt) . Previous studies show no chemical shift perturbation in the 15N-13C HETCOR spectra when Amt is titrated in the VM+-bound M2(21-61). On the contrary, M2(22-46) reconstituted in the VM+ membrane displays drug-induced chemical shift perturbation. We use SSNMR to show that the length of the construct and the membrane composition affect antiviral drug binding to the M2 channel. 2D 15N-13C HETCOR spectra of M2(21-97), that contains the entire cytoplasmic tail show chemical shift perturbation of residue Ser31 in both DMPC and VM+ membranes, indicating that the antiviral drug binds to the pore. The fact that Amt is not able to bind M2(21-61) is due to the extremely high membrane curvature created by the amphipathic helix alone. These results demonstrate the

ability of SSNMR to determine protein-drug interaction in the presence of different lipid membranes.

P-2. Cystine Deprivation Triggers Regulated Necrosis in VHL-Deficient Renal Cell Carcinomas

Xiaohu Tang[1,2], Jianli Wu[1,2], Chien-Kuang C. Ding[1,2], Min Lu[2,3], Melissa M. Keenan[1,2],Chao-Chieh Lin[1,2], Chih-An Lin[1,2], Charles C. Wang[1,2], Daniel George[3], David S. Hsu[2,3], and Jen-Tsan Chi[1,2]

[1]Department of Molecular Genetics and Microbiology, Duke University, Durham, North Carolina.

[2]Center for Genomic and Computational Biology Duke University, Durham, North Carolina.

[3]Department of Medicine, Duke University, Durham, North Carolina

Oncogenic transformation may alter tumor metabolism and render cancer cells addicted to extracellular nutrients. Deprivation of these nutrients may therefore represent a therapeutic opportunity; therefore, understanding the mechanism behinds the dependency is essential. Here we performed a nutrigenetic screen to determine the nutrient dependency of extracellular amino acid in clear cell renal cell carcinoma (ccRCC). Although most amino acid deprivation leads to growth inhibition, only cystine deprivation triggers rapid regulated necrosis. We applied genome-wide siRNA screens to identify genetic determinants, and integrated our screen findings with the transcriptional and metabolomic profiling of ccRCC to investigate the mechanism of cystine-deprived necrosis. We identified that: 1) VHL deficiency could potentiate ccRCC to cystine-deprived cell death by preexisting elevation of TNFα-RIPK1/RIPK3-MLKL level and reciprocal amplification of Src-p38 (MAPK14)-Noxa (PMAIP1) pathway. 2) The inhibition of pro-growth pathways such as mTORC1 signaling could lead to resistance to cystine-deprivation cell death. Together, our findings reveal our findings reveal that cancer cells could be "addicted" to specific nutrients, which might represent alternative targets in treating drug-resistant tumors

P-3. Asymmetric rejuvenation of mitochondria guides the differentiation for effector and memory cells

Yen-Hua Chen[1]

[1]Department of Microbiology and Immunology, Columbia University

In an immune response, naive or memory lymphocytes give rise to terminally differentiated antibody-secreting plasma cells to provide function while also regenerating less differentiated memory lymphocytes. However, it remained unclear how production of differentiated lymphocytes is coupled to renewal of the progenitor cell. Here we provide evidence

that asymmetric inheritance of healthy or aged mitochondria contributes to the generation of functional distinct daughter cell. We proposed a model that differentiating into effector cells may represent an accelerated aging phenomenon. The daughter cells that accumulate more old mitochondria tend to become effector cells, whereas the memory population maintains stem cell-like differentiation potential and self-renewal ability by asymmetric rejuvenation of mitochondria.

We showed that the healthy status of mitochondria is a timer for effector cell differentiation. Modulation of mitochondria function by pharmacological and genetic targeting of Drp-1 protein, which participated in mitochondrial renewal, accelerated the switching of transcriptional program to effector cells. For B cells, Mdivi-1 (Drp-1inhibitor) treatment or retrovirally expressing dominant negative Drp-1 (Drp1 K38A) in B cells increased IRF4-mediated Pax5 repression and differentiation into plasma cells.

Moreover, we found the linkage between mitochondria function and repressing of Pax5 involved reactive oxygen species (ROS) production and AMPK mediated quality control mechanism. ROS scavenger treatment increased the memory-like population (Pax5hi, IRF4low) and suppressed the differentiation of effector subsets (Pax5low, IRF4hi) in Mdivi-1 or Drp-1 K38A treated B cells. In addition, the AMPK knock cells tend to differentiate into effector cells, and they were more sensitive to Mdivi-1 induced Pax5 down regulation.

The nature source of the mitochondria stress comes from accelerated aerobic glycolytic after lymphocytes been activated. Over-expression of hexokinase hexokinase 2, which is one of the rate limited enzymes in glycolysis, resulted in Pax5 down regulation. By contrast, inhibiting glycolysis by 2-DG (a nonmetabolizable glucose analog) is sufficient to cancel the effect of Mdivi-1 in Pax5 repression. In sum, enhancing glycolytic pathway boosts effector cell differentiation, whereas suppressing glycolytic pathway helps to retain the self-renewal activity of activate lymphocytes.

Collectively, these evidence reveals mitochondria not only involved reprogramming metabolic pathways but also switching of transcriptional program. Thus, the metabolic status is an integrated part of the signaling pathway guiding the differentiation of lymphocytes, rather than the result of switching transcription program.

P-4. Differential mobilization of circulating neutrophil subpopulations in breast cancer metastasis

Brian Hsu[1, 2], Sébastien Tabariès[1,2], Matthew G Annis[1,2], and Peter M Siegel[1,2,3]

[1]Goodman Cancer Research Center, McGill University

[2]Department of Medicine, McGill University

[3]Department of Biochemistry, McGill University

Breast cancer is the most common cancer among Canadian women over the age of 20, representing 26% of all cancer cases in Canadian women. Metastatic breast cancer is the most advanced stage (stage IV) of the disease and it is largely incurable. Breast cancer cells display preferences for specific metastatic sites including the bone, lung, and liver. The liver represents a prominent site for breast cancer metastasis, with 50-70% of women with metastatic breast cancer developing hepatic metastases.

The steps involved in the metastatic cascade rely on reciprocal interactions between cancer cells and their microenvironment. Distinct immune infiltrates can either impair the metastatic process or conversely, assist in the seeding, colonization and growth of disseminated cancer cells. Within distal organs, immune cells and their mediators are known to facilitate metastasis formation. However, the contribution of tumor-induced systemic inflammation to metastasis and the mechanisms regulating systemic inflammation are not well characterized. Using lung and liver-metastatic variants of 4T1 breast cancer cells model, we have revealed that there are increased recruitment of myeloid-derived/granulocytic (Gr-1+) and neutrophils (NE+) in the lungs and livers of mice bearing lung and liver metastasis respectively. However, based on the Gr-1+ depletion studies, it was observed that infiltrating myeloid-derived/granulocytic cells, including neutrophils, were essential for the formation of liver metastases but not for lung metastases. Intriguingly, we have found that in peripheral blood, lung and liver metastases have the ability to mobilize differently the two distinct populations of high-density (HDNs) and low density neutrophils (LDNs) based on a density gradient centrifugation. In the peripheral blood of mice bearing liver metastases, there is a dramatic increase in the mobilization of LDNs compared to mice bearing lung metastases. Thus, we believe that liver metastatic breast cancer cells rely on interactions with neutrophils within the liver microenvironment for colonization and growth. Our results demonstrate the importance of investigating the role played by these two neutrophil subpopulations which may represent a new potential therapeutic strategy to inhibit metastatic diseases.

P-5. Mining developmental origins of germline stem cells in early eumetazoa

Cheng-Yi Chen*, Matthew C. Gibson

Stowers Institute for Medical Research, Kansas City, MO

Stem cells differentiate into different lineages during animal development. Among bilaterian model organisms, such as mouse, zebrafish, fly and nematode worms, specialized germline stem cells fates are distinguished during embryogenesis and maintained in adulthood. However, how primordial germ cells differentiate during development in the pre-bilaterian animals, like sponge and hydra, is still unknown. Because of hardly-accessible pre-bilaterian embryos, most previous studies focus on their multifunctional adult stem cells, which can give rise to soma and germ cells. To demonstrate pre-bilaterian germline development and the underlying mechanism, we introduce an emerging Cnidarian model, Nematostella vectensis, featuring with tractable developmental process and distinct adult gonad. In this project, we specifically aim to interrogate the functions of conserved germline genes and to search for novel germline regulators. First, vasa and nanos homologs were characterized in developing N. vectensis germline; however, whether they are necessary or sufficient in this process is yet confirmed. With the advent of well-developed CIRSPR/Cas9 genome editing tool in N. vectensis, we will manipulate germline genes by knocking them out. Second, because vasa and nanos homologs are not exclusive germline land marks, but also expressed in some N. vectensis somatic cells, other germline markers are required for tracking germline development. Therefore, we will compare gonad RNA expression profiles with different tissues to characterize specific germline genes. Then, we plan to confirm their specificity by in situ hybridization to test if they are expressed in certain germ cell differentiation stage or in the gonad "niche". Through these methods, N. vectensis germline research will provide insights into eumetazoan (i. e. Cnidarian and bilaterian) germline segregation evolution.

P-6. Site-specific phosphorylation of paxillin drives autophagy-mediated focal adhesion turnover and cancer cells

Chia-Hao Chang, Krikor Bijian, DingHong Qiu, Michael Samir Dahabieh, Wilson Miller and Moulay A. Alaoui-Jamali*

Cancer cell locomotion is a highly regulated process, where focal adhesion (FA) assemble/disassembly cycles are necessary for effective migration. Posttranslational mechanism(s) regulating the dynamics of this FA turnover at focal adhesion sites are not fully understood. In this study, we uncovered a novel direct function of autophagy in the regulation of FA disassembly in breast cancer cells. We established that inhibition of cellular autophagy, either by exposure to chloroquine (CQ) or suppression of autophagosome maturation by Rab7 downregulation, resulted in enhanced FA disassembly along with reduced cell migration. Under similar conditions, we demonstrated that one of the major components of FAs, namely paxillin, accumulated in autophagosomes. Moreover, down-regulation of upstream regulators of autophagy (Atg12) or the endocytic pathway (Rab5) further confirmed the contribution of the autophagic pathway in paxillin removal from FA sites, where phosphorylation of paxillin on tyrosine 118 was required for autophagic targeting and engulfing. Finally, we identified c-Cbl as the major cargo receptor required for paxillin targeting to the LC3 complex, independent of its E3 ubiquitin ligase activity. Together, these results provide new insights into the role of autophagy in the regulation of FA dynamics and cancer cell migration, while providing new therapeutic opportunities for targeting breast cancer progression.

P-7. Engineered human L-Methioninase for therapeutic purposes.

Wei-Cheng Lu[1,3], Wupeng Yan[2], Olga Paley[1], Kendra Garrison[1], Andrew Ellington[2], Yan Zhang[2], Everett Stone[1,3], and George Georgiou[*,1,3]

[1]Department of Chemical Engineering, University of Texas at Austin, Austin, TX

[2]Department of Biochemistry, University of Texas at Austin, Austin, TX

[3]Aeglea BioTherapeutics, Austin, TX

In cancer biology research, it has been found that cancer cells exhibit different metabolism compared to normal cells and it has been shown that some types of cancer cells, such as glioblastomas, medulloblastomas and neuroblastomas are much more sensitive than normal cells to methionine starvation. Past studies have shown that methionine-dependent tumor cells are not able to survive if the serum methionine is decreased to ≤ 5uM. Systemic depletion of serum methionine can be achieved by Pseudomonas putida methionine gamma-lyase (pMGL) but it has proven to be rapidly inactivated in vitro and be highly immunogenic in primate models. In order to apply systemic methionine depletion to human cancer therapy, we engineered human cystathionine γ-lyase to accept methionine as a substrate and have isolated several human Methioninase (hMETase) variants with high activity. Several active hMETase variants isolated from a phylogenetic analysis library and the best variant, hMETase V8.4 showed a 10-fold improved KM (12.2 vs. 1.8mM) and 10-fold better kcat/KM values (0.59 to 5.3 1/s.1/mM) in degrading methionine compared to our previous version of variant, hMETase V3.1. Furthermore, hMETase V8.4 showed greater stability in thermal melting analyses (melting temperature: 63.2 vs. 70.20C) and also in serum stability (half-life: 75 vs. >100 hours) compared to hMETase V3.1. In pharmacodynamic analyses, hMETase V8.4 efficiently lowered serum methionine concentration from 75 μM to ~15 μM in 48 hours without the requirement of a methionine restricted diet (one dose: 50 mg/ kg). In addition, we tested the efficacy of hMETase V8.4 on C57L/6 mice bearing A375 melanoma xenografts and it significantly improved the median survival from 35 – 43 days compared to the control group. The hMETase V8.4 efficiently lowered serum methionine concentration in pharmacodynamic analyses. Also, it significantly improved the survival time of C57L/6 mice bearing A375 melanoma xenografts. The hMETase V8.4 is a promising therapeutic enzyme candidate for systemic methionine depletion in cancer therapy.

P-8. The matricellular protein CYR61 promotes lung metastasis of breast cancer cells through facilitating transmigration and anoikis resistance during extravasation

Yu-Ting Huang[1,2], Qiang Lan[1,2] and Curzio Rüegg1'[2]

[1]Department of Medicine, Faculty of Science, University of Fribourg, Fribourg, Switzerland

[2]National Center for Competence in Research (NCCR), Molecular Oncology, Swiss Institute for Experimental Cancer Research (ISREC)-Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland

Cysteine-rich 61 (CYR61) belongs to the CCN (CYR61/CTGF/NOV) family of matricellular proteins, and regulates cell proliferation, migration, apoptosis through binding with different integrin receptors or heparin sulfate proteoglycans. Recently, the significant contribution of microenvironment matricellular proteins during cancer progression has been gradually unveiled. However, how these proteins involve in the multistep formation of life-threatening metastases still needs to be further elucidated.

In this study, we showed that, by knocking down CYR61, breast cancer cells growing in pre-irradiated mammary fat pads formed less lung metastasis. The promoting effect of CYR61 during natural course of cancer metastasis was further confirmed using the conventional orthotopic xenograft model without irradiation and the tail-vein xenograft model. At the time-point of 24 hours after tail-vein injection, there were already less cancer cells retained in the lung parenchyma of mice injected with CYR61-knocking down (KD) cells. In addition, delayed induction of CYR61 shRNA 24 hours after tail-vein injection compromised the decreasing effect of knocking down CYR61 on lung metastasis formation, indicating that CYR61 promotes metastasis formation mainly through facilitating extravasation instead of the following step of colonization in lung. Besides the well-known function of CYR61 on enhancing migratory ability, we showed here for the first time that CYR61 also supports cell survival under anoikis. By using chemical inhibitors and shRNA, we demonstrated that the CYR61-maintained anoikis resistance was independent of activation of ERK1/2 pathway, but partially mediated by the activation of AMPK pathway. Overall, our data provide the first evidence that CYR61 expression promotes lung metastasis formation of breast cancer cells through facilitating migration and supporting anoikis resistance during extravasation. These results indicate the potential of CYR61 to serve as a predictive marker for the risk of distant metastasis spreading and as a therapeutic target to develop in the future.

P-9. Tissue- engineered 3D osteoclast activation model

Josephine Y. Fang[1,2], Yi-Chen Wu[1], Shi-Jye Tan[1,3], Zhi Yang1 and Bo Han[1]

[1]Nimni-Cordoba Tissue Engineering and Drug Discovery Laboratory, Division of Plastic and Reconstructive Surgery, Departments of Surgery and, Keck School of Medicine, University of Southern California, Los Angeles, California

[2]Department of Craniofacial Biology, Herman Ostrow School of Dentistry, University of Southern California, Los Angeles, California

[3]Department of Biomedical Engineering, Viterbi School of Engineering, University of Southern California, Los Angeles, California

Bone regeneration and bone resorption processes are simultaneously occurring in the bone environment. With simulations of mechanical and chemical signals, the bone metabolism maintains homeostasis or deviate to diseases. Currently, osteoblast differentiation in vitro model are well- established to screen potential treatments or materials for bone regeneration. However, not all animal response the same with the same treatment and the selection of animal model would influence the result of implantation. Even in the clinical manifestation, the successful rate of same bone grafting also vary among patients. In addition to the quality of bone, this variation may result from the diversity of individual immune responses in the bone environment. The status of osteoclast activation and recession determine the fate of bone grafts or implants and also determine bone regeneration or resorption.

The results of mechanical stimuli on osteoclast activation are equivocal among different studies. Regarding the force application such as compression, shear force, or micro-motion from the bone graft particles, the impact of mechanical stimuli could either inhibit or aggravate osteoclast activation. In addition to the type of mechanical stimuli, we noticed that matrix-derived mechanical stimuli could induce murine myoblast, C2C12, to promote osteoblast differentiation synergistically and cancer cells were able to switch their competent and quiescence state with alteration of matrix. We hypothesized that the matrix- induced mechanical signal could lead pro-osteoclasts to perform proliferative or non- proliferative state and this on-going status may synergistically influence pro- osteoclasts with additional mechanical loading or chemical stimuli to decide activate or inactivate.

In the Col-Tgel 3D model, we observed the progression of Raw264.7 cell proliferation, migration, and activation without chemical signals under a specific Col-Tgel condition. The activated Raw264.7 cell displayed tartrate- resistant acid phosphatase activity with staining and p-nitrophenyl phosphate substrate conversion. For those conditions were not optimal for osteoclast activation, Raw264.7 cells tend to migrate out of gel and release protease to modify extracellular matrix (ECM). The treatment of lipopolysaccharide or BMP2 can alter the Raw264.7 cell state of activation. These phenomena implied that cells dynamically interact with ECM simultaneously with and without external signals. This model demonstrated that

extracellular matrix played as inertial driven force to impact the cell to response external signals.

P-10. Nectin-like 2 (Necl- 2) cell adhesion molecule is a negative regulator of Schwann cell myelination

Ming-Shuo Chen, Corey Heffernan, Richa Sharma and Patrice Maurel

Department of Biological Sciences

Rutgers, the State University of New Jersey Newark, NJ USA 07102

Axo-glial interactions are critical for Schwann cell genesis, myelination and domain organization of myelinated fibers. Axon-bound type III neuregulin-1 (Nrg-1) regulates Schwann cell proliferation, survival and myelination by activating the PI3K/Akt pathway through the ErbB2/ErbB3 tyrosine kinase receptors. Nectin-like proteins (Necls) are homo- and heterophilic cell adhesion molecules. Recent studies have shown that Schwann cell Necl-4 and its bona fide binding partner, axonal Necl-1 promote axon-glia interactions along the internode. Further studies, in vitro and in vivo, have shown that Necl-4 promotes Schwann cell myelination. Surprisingly however, in vitro data suggest that axonal Necl-1 negatively regulates myelination. This raises the question of how Necl-4 and Necl-1, which are strong heterophilic binding partners, have opposite effect. The response may lie in Necl-2, a lower affinity heterophilic binding partner for Necl-1 that is also expressed by Schwann cells. We could then envision the following hypothesis: a myelin-promoting Necl1/Necl4 interaction, and a myelin-inhibiting Necl-1/Necl-2 interaction. To start testing the idea that Schwann cell Necl-2 may therefore be inhibitory to myelination, we have used lentiviral-mediated knockdown or ectopic expression of Necl-2, associated with the well-established Schwann cell-DRG myelinating coculture system. We show that Necl-2 negatively regulates myelin formation by Schwann cells, without affecting the axon contact-mediated Schwann cell proliferation. In the context of axo-glial interaction, we observed a marked increase (Necl-2 KO Schwann cells), or decrease (Necl-2 over-expressing cells), in Akt activation in direct correlation with the observed myelination results. The effects were specific to Akt, with no observable changes in activation of ErbB2, ErbB3, Erk1/2, PTEN and PDK1. Interestingly Necl-2 over-expression or knockdown did not affect the activation of the ErbB/PI3K/Akt signaling cascade by soluble neuregulin. In Schwann cells, co-immunoprecipitation studies suggest that Necl2 does not form a complex with ErbB3, or ErbB2. Necl-2 also did not prevent the recruitment of ErbB2 by ErbB3 upon neuregulin stimulation. Taken together, these results suggest that Necl-2 may regulate Schwann cell myelination by affecting Akt activity in a mechanism independent of the Nrg-1/ErbB/PI3K signaling cascade. Our future studies will aim to identify the axonal signal provided to Necl-2 (possibly Necl-1 and/or Necl-2) as well as the molecular machinery linking Necl-2 to Akt.

P-11. Alpha II-spectrin-dependent cytoskeletons are essential for axon function, domain assembly and integrity

Yu-Mei Huang[1], Chuansheng Zhang[1], Daniel Zollinger[3], Joshua Lalonde[2], Jeffrey Noebels[2], Matthew Rasband[1]

[1]Department of Neuroscience and [2]Neurology, Baylor College of Medicine, Houston, TX

[3]Department of Pediatrics, UCSF School of Medicine, San Francisco, CA

Spectrins are a family of cytoskeletal proteins that provide structural support of the cell membrane, link membrane -associated proteins to actin and serve as platforms for cell signaling. Spectrins consist of α and β subunits, forming heterotetramers to function as a complex. Among the spectrins, αII- spectrin is the only α- spectrin expressed in the nervous system. α II-spectrin is also implicated in a variety of neurological disorders. Recently, we found that αII-spectrin forms a periodic cytoskeleton and interacts with βIV-spectrin at axon initial segments (AIS) and nodes of Ranvier.

To investigate the functions of αII-spectrin-dependent cytoskeletons, we generated conditional knockout (cko) mice. Loss of αII-spectrin in the central nervous system (CNS) causes profound neurological phenotypes including seizures, aberrant cortical lamination, AIS fragmentation, massive neurodegeneration and perinatal lethality. To more specifically interrogate spectrin functions in axons, we generated peripheral sensory neuron specific αII-spectrin cko mice using advillin- cre. We found that large diameter axons preferentially degenerate. By immunostaining, the injury marker ATF3 is observed in dorsal root ganglia (DRG) neurons in cko mice beginning at P10 and increasing with age. Consistent with EM results, ATF3+ neurons are mostly large diameter neurons. The preferential degeneration of large diameter neurons caused ataxia due to deficits in proprioception, while nociception remains unaffected. Mutant mice have fewer nodes of Ranvier and sodium channel intensity at nodes is significantly decreased. Paranodal junctions are extensively disrupted. Axon degeneration and disrupted nodes of Ranvier caused decreased nerve conduction velocity in cko mice. Thus, neuronal αII-spectrin is crucial for proper axon function, node of Ranvier assembly and axon integrity.

P-12. Endogenous 24S-hydroxycholesterol modulates NMDAR-mediated function in hippocampal slices

Min-Yu Sun[1], Yukitoshi Izumi[1, 3], Ann Benz1, Charles F. Zorumski[1, 2, 3], and Steven J. Mennerick[1, 2, 3]

[1]Department of Psychiatry, Washington University School of Medicine, St. Louis

[2]Department of Neuroscience, Washington University School of Medicine, St. Louis

[3]Taylor Family Institute for Innovative Psychiatric Research

N-methyl-D-aspartate receptors (NMDARs), a major subtype of glutamate receptors mediating excitatory transmission throughout the CNS, play critical roles in governing brain function and cognition. Because NMDAR dysfunction contributes to the etiology of neurological and psychiatric disorders including stroke and schizophrenia, NMDAR modulators are potential drug candidates. Our group recently demonstrated that the major brain cholesterol metabolite, 24S-hydroxycholesterol (24S-HC), positively modulates NMDARs when exogenously administered. Here, we studied whether endogenous 24S-HC regulates NMDAR activity in hippocampal slices. In CYP46A1-/- (knockout; KO) slices where endogenous 24S -HC is greatly reduced, NMDAR tone, measured as NMDAR to AMPAR EPSC ratio, was reduced. This difference translated into more NMDAR-driven spiking in wild-type (WT) slices compared with KO slices. Application of SGE-301, a 24S -HC analogue, had comparable potentiating effects on NMDAR EPSCs in both WT and KO slices, suggesting that endogenous 24S-HC does not saturate its NMDAR modulatory site in ex vivo slices. KO slices did not differ from WT slices in either spontaneous neurotransmission or in neuronal intrinsic excitability, and exhibited LTP indistinguishable from WT slices. However, KO slices exhibited higher resistance to persistent NMDAR-dependent depression of synaptic transmission induced by oxygen -glucose deprivation (OGD), an effect restored by SGE-301. Together, our results suggest that loss of positive NMDAR tone does not elicit compensatory changes in excitability or transmission, but it protects transmission against NMDAR-mediated dysfunction. We expect that manipulating this endogenous NMDAR modulator may offer new treatment strategies for neuropsychiatric dysfunction.

P-13. A transcriptional regulator as a modulator of TDP-43 and G4C2 hexanucleotide repeat toxicity in amyotrophic lateral sclerosis disease models

Chia-Yu Chung, Nancy Bonini

Department of Biology, University of Pennsylvania

The TAR DNA binding protein of 43 kDa (TDP-43) was identified as the major disease protein in ubiquitinated cytoplasmic inclusions in neurons of patients with amyotrophic lateral sclerosis (ALS) and frontotemporal lobar degeneration (FTLD) with ubiquitinated inclusions (FTLD-TDP). Through a screen in Drosophila to define modifiers of TDP-43 toxicity, the Bonini laboratory has identified modulators that mitigate TDP-43-associated neurodegeneration. Among them, I focus on a modifier, which regulates transcriptional pausing and has not previously been implicated in neurodegenerative disease. In addition to the toxicity of TDP-43, my preliminary findings suggest that the toxicity of G4C2 hexanucleotide repeat expansion, which is another important disease factor of ALS and FTLD, is also suppressed by downregulation of the transcriptional regulator.

P-14. Refining the mathematical model of evoked dopamine responses in the rats dorsal striatum with fast scan cyclic voltammetry and electrical stimulation.

Rebecca Wu

As one of the most important neurotransmitters in the central nervous system (CNS), dopamine (DA) contributes to many critical functions such as reward mechanisms, learning and motor control. Any kind of abnormality in the DA system could lead to disorders including schizophrenia, Parkinson's disease, addiction and Alzheimer's disease. By introducing artificial electrical stimulation in vivo at the rat's medial forebrain bundle (mfb), evoked DA signals can be measured at a carbon fiber microelectrode with fast scan cyclic voltammetry (FSCV) in the dorsal striatum. Previously, our lab discovered that DA kinetics are highly heterogeneous for measurements in the dorsal striatum. The responses were widely categorized into slow and fast sites. Hypothetically, the slow responses result from autoinhibition, which exists prior to the stimulus, presumably due to the occupation of pre-synaptic D2 autoreceptors by basal DA in the extracellular space.1 Fast responses have minimal autoinhibitory effect because the DA can be observed within 200 ms while it can require more than 2 s for the slow sites.

Previously, the Diffusion Gap (DG) model was the reigning explanation of the heterogeneous kinetics of DA. This model proposes that there is a physical gap between the DA terminal and the recording site2. However, there are several problems with this model. For example, if there is a response delay at the onset of the stimulus due to the gap, the fall of the response should have the same delay when the stimulus ends, however this is not always observed. In addition, raclopride, a D2 antagonist, can eliminate the delay in the onset of the DA signal observed in a slow site. This would not be possible if there is a physical gap between the recording site and the DA terminals.

To address this problem, a new model was introduced by our lab based on the concept of restricted diffusion (RD)3. It suggests that DA is first released to an inner compartment then transported to an outer compartment. DA is detected in the outer compartment by FSCV and then cleared by re-uptake. The delay between the stimulus and the electrode's response is represented by kT, which is a first-order term dominated by mass transport. The uptake from the outer compartment back to the vesicles is represented by a first-order term kU, and the release term is represented by Rp which represents amount of DA released per pulse. A fourth parameter kR was introduced as an exponential release modulator because the DA release is affected by autoinhibition4 (equation 1 & 2). The RD model is based on mathematical calculations to examine experimental data and investigate the dopaminergic system (figure 3). To further refine the RD model, a study was designed to explore different stimuli pulses which are super-physiological to force evoked release and examine how these responses are seen in the dorsal striatum after the rats are given raclopride. Modeling responses obtained with high-pulse stimuli, the RD model reveals new information about the kinetics of the slow kinetic domains3.

However, the RD model was not sufficient to describe the responses of longer stimulation length. Although post-raclopride responses can be depicted by the 4-parameter model, pre-drug, 600 pulses responses cannot be portrayed presumably due to two components of the dopamine release. While the mfb is being stimulated the entire time, the vesicles release DA for the duration, but the dopamine concentration increases to a certain degree then starts to decrease until the stimulus ends (unlike the 1 second and 3 seconds evoked responses).

To investigate whether introducing a fifth parameter, kR2, to the RD model is appropriate, rats were treated with raclopride to reduce the autoinhibition effect. 600 pulses at 60 Hz were applied, and pre-drug and post-drug responses were modeled (figure 4). Fits are very good, and all the parameters remained almost unchanged while the kR2 of the post-raclopride model increased for more than tenfold. This indicates that a fifth parameter is essential for describing longer stimulation responses, and the original RD model was not capable of creating such good fits without the kR2 term (equation 3).

As autoreceptors function in both fast and slow domains, it seems that the domains are different in autoinhibitory tone which derives from different basal DA concentration required to activate the D2 receptors. Due to this effect, future experiments will be focused on investigating the fast sites kinetics and whether the refined RD model can portray the responses. Moreover, lower frequency (i.e. 30 Hz, 15 Hz) stimulations will be applied to both slow sites and fast sites and the responses will be modeled. By studying the physiological sources of DA kinetics, we can investigate the responses similar of human neurons since the mammalian neuron fires at around 20 Hz5. Nomifensine (a DA uptake inhibitor) might need to be applied to the lower frequency responses in order to increase the signal amplitude since the signal to noise ratio decreases as the frequency decreases.

P-15. Differential Allele Expression Effects in the Brain Shape Genetic Architecture at the Cellular Level

Wei-Chao Huang[1], Elliott Ferris[1], Christopher Gregg[1]

[1]Department of Neurobiology & Anatomy, University of Utah School of Medicine, Salt Lake City, Utah

Several genomic studies revealed that loss-of-function heterozygous mutations, rather than recessive mutations, are involved in autism spectrum disorders as well as schizophrenia. We do not fully understand how heterozygous mutations contribute to complex disease. In a diploid genome, most genes have two copies and the healthy backup copy can reduce the impact of heterozygous mutations. However, if the mutated allele is the only allele expressed and the expression of the healthy allele is silenced, then a heterozygous mutation could have a stronger impact. Currently, the allele-specific effects best understood are genomic imprinting effects in which either the maternal or paternal allele is silenced for a small number of genes in the genome. Random monoallelic expression effects are also known to exist in the genome and impact genes on the X-chromosome in females, immune genes, and some autosomal genes. However, little is known about the prevalence of allele-specific effects in vivo for most genes in the genome.

We asked whether or not the maternal or paternal alleles are equally co-regulated for most genes in the genome. We developed a novel approach that analyzes maternal and paternal allele co-expression effects using RNASeq. Surprisingly, we discovered that thousands of genes in the genome differentially express their alleles. To determine the nature of genes with differential allele expression at the cellular level, we used a novel ultra-sensitive in-situ hybridization to detect allele-specific expression at the cellular level in tissue sections. The analysis revealed that genes with differential allele expression at the tissue level by RNASeq exhibit monoallelic expression in subpopulations of cells in vivo in the brain. Furthermore, we analyzed the cellular expression of the mutant lacZ allele versus the wildtype allele in vivo by using heterozygous mutant transgenic mice with a lacZ reporter gene inserted to disrupt the gene with differential allele expression to determine whether these novel effects impact the cellular expression of mutated and healthy alleles for inherited heterozygous mutations. We found some cells preferentially express the mutant allele, while other cells preferentially express the healthy allele. Overall, our new approach and discovery that many genes exhibit differential allele expression, and that these effects impact the cellular expression of heterozygous mutations, will improve our understanding of the genetic architecture of complex diseases.

P-16. Optimal Fungal Space Searching Algorithms

Hsin-Yu Lin[1], Dan V. Nicolau[2]

[1]Department of Mechanical Engineering, McGill University

[2]Department of Bioengineering, McGill University

Previous experiments have shown that fungi use an efficient natural algorithm for searching the space available for their growth in micro-confined networks, e.g., mazes. This natural 'master' algorithm comprises two 'slave' sub-algorithms, i.e., collision-induced branching and directional memory. Collision-induced branching is that the fungus grows without branching until it hit walls or corners. On the other hand, each branch of the fungus is able to 'remember' the initial direction of growth, which is called directional memory. While each hypha has to negotiate various geometries, whenever the branch has the opportunity to grow in the direction it had initially, it will follow this with a high probability. It has been shown that the co-existence of both sub-algorithms is more efficient than alternatives, with one, or the other, or both sub-algorithms turned off.

In this project, a novel algorithm was developed based on the fugal space searching algorithm mentioned above to solve mazes. The present contribution compares the performance of the fungal natural algorithm against several standard artificial homologues. It was found that the space-searching fungal algorithm consistently outperforms uninformed algorithms, such as Depth-First-Search (DFS). Furthermore, while the natural algorithm is inferior to informed ones, such as A*, this under-performance does not importantly increase with the increase of the size of the maze. These findings suggest that a systematic effort of harvesting the natural space searching algorithms used by microorganisms is warranted and possibly overdue. These natural algorithms, if efficient, can be reverse-engineered for graph and tree search strategies.

P-17. The Second Life of Intron

Chien-Ling Lin[1], Allison J Taggart1 and William G Fairbrother[1,2,3]

[1]Molecular Biology, Cell Biology and Biochemistry, Brown University, Providence

[2]Center for Computational Molecular Biology, Brown University, Providence

[3]Hassenfeld Child Health Innovation Institute of Brown University, Providence, RI.

In mammalian genomes, coding sequences (exons) are intervened by long non-coding sequences (introns) which compose ~90% of genes. Pre-mRNA splicing is a remarkable process to remove long introns and ligate exons. The intron is excised out from a gene in a lariat shape with a unique 2'-5'phosphodiester bond at the branchpoint. Degradation of the long intronic lariat is essential to recycle and release the nucleic acids, splicing machinery and RNA binding proteins. Debranching enzyme DBR1 specifically hydrolyzes the 2'-5' phosphodiester bond, exposing ends of the introns for further degradation. Because of the transient nature of the RNA lariat, the specificity of DBR1 is poorly studied.

By biochemical enrichment of DBR1-senstive lariats and computational selection of deep sequencing reads that traverse branchpoints, we demonstrate that in human cells, DBR1 catalytic activity prefers short introns over long introns, A-branchpoint over C-branchpoint. Moreover, the upstream and downstream sequences to the branchpoint also affect DBR1 recognition. These results suggest some introns are more dependent on DBR1 and others may require other nucleases for turnover. Interestingly, the best DBR1 catalytic substrate is the most robust branchpoint sequence for splicing, suggesting that DBR1-mediated intron turnover co-evolves with the branchpoint splicing activity. Introns that escape DBR1 digestion in the nucleus get transported to the cytoplasm. They are shorter, GC-rich and contain mostly C-branchpoints. AU-rich introns that escape the nucleic degradation are re-ligated into stable intronic circles by a post-splicing reaction. These stable circular introns may have cellular functions as molecular sponges or transcription factors. Finally, we demonstrate that the branchpoint position and debranching direct the maturation of intron-coded CD-box snoRNAs. Over all, we show that introns with different length, GC-content and branchpoints, turn over through differential pathways, and that the regulation of intronic lariat hydrolysis is not only critical for recycling nucleic acid and protein factors but also for regulating several cellular processes.

P-18. Dynamic modeling reveals a saturation rule that governs the switch between uni- and multi-polar growth

Jian-geng Chiou[1], Timothy C. Elston[2], Thomas P. Witchelski[3], David G. Schaeffer[3], Daniel J. Lew[1]

[1]Department of Pharmacology and Cancer Biology, Duke University

[2]Department of Pharmacology, University of North Carolina at Chapel Hill

[3]Department of Mathematics, Duke University

Precisely orchestrated polarization is crucial for the development of complex cell morphology. For example, neuron cells require polarized growth at multiple cortical domain to form dendrites, but robustly switch to uni-polar growth so that only one further elongates and eventually becomes the axon. Results from both experiments and dynamic modeling have shown that the polarization of Rho-GTPases directs polarized growth throughout Eukaryotes, but what determines the number of polarity domain remains elusive.

In previous studies, it has been shown that a two-component partial differential system that models Rho-GTPase dynamics captures the "competition" behavior between multiple transient polarity clusters, which guarantees uni-polarity. Intriguingly, we demonstrated that with appropriate change of parameters, this system switches to multi-polarity. Applying mathematical analyses, we introduced a "Saturation rule", which formulates the criteria of uni- and multi-polarity, and it can be applied generally to models of similar structures. In the intuitive sense, the saturation rule states that there exists an innate saturation point of Rho-GTPase concentration, and the number of polarity domain that will persist is determined by the number of Rho-GTPase clusters that approach the saturation point.

We then turned to the budding yeast, and showed with fluorescent microscopy that simulations of our model recapitulate the dynamics of polarity clusters in vivo. We further showed with cytokinesis defect mutants that the Rho-GTPase machinery of the budding yeast is competent to produce multiple buds. Lastly, we tested the saturation rule by genetically manipulating the Rho-GTPase machinery, and showed that the saturation point and the level of polarity proteins can be engineered to change the number of buds. Confirmed in the budding yeast, this research can be applied to different Rho-GTPase systems in various cell types, where the reason of saturation may differ depending on the specific molecular interactions, but the general rule holds universally.

P-19. Developing complex hydrogel microcapsules for high throughput, confined tissue culture: small packages, big potential

Yen-Chun Lu[*1], Wei Song[1], Duo An[1], Beum Jun Kim[1], Robert Schwartz[2], Mingming Wu[1], Minglin Ma[1]; Cornell University

[1]Department of Biological and Environmental Engineering

[2]Weill Medical College of Cornell University

[*]: Presenter, e-mail yl2347@cornell.edu

Cell encapsulation in hydrogel microparticles has been investigated for decades in various bioengineering applications including tissue engineering, and cell therapy. However, most of the time, the cells are encapsulated randomly in whatever material that forms the microparticles, most commonly alginate. The lack of control over the spatial organizations of the cells and the extracellular environment within the microparticles significantly limits for advanced applications. Here we report a novel, multi- fluidic cell microencapsulation approach where 1 or more types of cells are encapsulated in pre-assigned compartments in the microparticles with controlled extracellular matrix. These microparticles can be produced with controllable and nearly monondispersed sizes at rates of over 10,000 microparticles per min and therefore provide a promising platform for high throughput applications. We demonstrated the utilization of these extracellular matrix-supported microparticles for 3D culturing of cells that typically require specific microenvironment to survive such as human umbilical vein endothelial cells (HUVECs) and small intestine stem cells. By taking advantage of the confinement effect, we also showed robust and scalable productions of size- controlled multicellular microtissues. Lastly, to demonstrate the broad applications of these microparticles, we performed proof-of- concept studies on three different co-culture systems including cell segregations under 3D confined space, the supporting role of stromal cells in hepatocyte functions and the paracrine cell signaling in aggregation of endothelial cells, all in a high throughput manner.

P-20. Dendritic architecture enhances the structural stability of self-assembled dendron micelles in the presence of serum proteins

Hao-jui Hsu[1], Ryan M. Pearson[1], Petr Král[2], and Seungpyo Hong[1, 3]

[1]Department of Biopharmaceutical Sciences, University of Illinois at Chicago

[2]Department of Chemistry, University of Illinois at Chicago

[3]Department of Integrated OMICs for Biomedical Science and Underwood International College, Yonsei University, Seoul, Korea

Dendrimers and linear-block copolymer (LBC)-based micelles are two types of nanocarriers that have been largely studied. The multivalent interactions enabled by the hyperbranched dendrimers and the modularity, along with high drug loading capability, of the LBC-based micelles are key features of each platform. Our group previously developed PEGylated dendron-based copolymers (PDC), which incorporated these key characteristics into a single system. The PDCs self-assemble into dendron micelles (DMs) with high thermodynamic stability as measured by low critical micelle concentrations (in an order of 10-9 M), demonstrating their potential as efficient nanocarriers. In addition, because the dendritic PEG chains can form a dense inert layer on the surface of DMs, this hybrid design is expected to minimize non-specific interactions between the nanocarriers and biological components. These non-specific interactions are known to negatively affect the ability of nanocarriers to deliver their cargos. For instance, non-specific micelle-serum protein interactions can cause micelle disintegrations and subsequently a premature release of loaded drugs. In this study, we hypothesized that DMs are more stable than LBC-based micelles (LMs) in the presence of serum proteins because their dense PEG outer layers can lower micelle-serum protein interactions. To test our hypothesis, we compared the integrities of DMs and LMs in the presence of serum proteins using a FRET method. Our results showed that DMs have superior stability over their LM counterparts. The half-life of DMs was approximately 2 times longer than that of the LMs in a 50% fetal bovine serum solution. These results indicate that the dendritic PEG outer layers reduce the binding and/or penetration of serum proteins into the micelles. While additional studies are required to fully understand the effect of the dendritic PEG layers on micelle-serum protein interactions and corresponding biological consequences, our results support that DMs have great potential as a novel drug delivery platform.

P-21. Vibrational Spectroscopic Imaging of Molecular Dynamics in Living Systems

Chien-Sheng Liao[1], Ji-Xin Cheng[1,2]

[1]Weldon School of Biomedical Engineering, Purdue University

[2]Department of Chemistry, Purdue University

Cell metabolism involving uptake and conversion of small biomolecules is the foundation for cell survival and proliferation. Quantitation of metabolic conversions in live tissues and in real time is essential to determining how a cell responds to an intervention such as drug treatment or exposure to a risk factor. Nevertheless, most of our knowledge about cellular content is derived from in vitro analysis of isolated cells or measurement of tissue homogenates, either by biochemical assays, omics or sequencing technologies. This gap highlights a need of developing new techniques that are able to repetitively assess the same single cell in a vital organism.

Raman scattering based vibrational spectroscopy has been traditionally used for quantitative analysis of biomolecules and biochemical reactions in solutions by detecting the molecular vibrations induced by laser pulses. Raman spectral imaging of live cells has been limited by the very small cross section of Raman scattering. It still takes tens of minutes for the most advanced Raman spectroscopy to acquire an image. Recently coherent Raman microscopy focusing on a specific Raman band has improved imaging speed to real-time with no spectral information. Hyperspectral coherent Raman microscopy based on either fast laser wavelength tuning or pulse shaping technique has been demonstrated with an integration time of several milliseconds per pixel or minutes per image, which still does not allow for imaging of a highly dynamic living system.

Here we developed microsecond hyperspectral coherent Raman techniques that enable repetitive assessment of single cell metabolism in a vital organism. By multiplex excitation and parallel detection in space or in frequency domain, we demonstrated spectral acquisition of one coherent Raman spectrum within several microseconds. This speed is 100 times faster than the state-of-art technology. We demonstrated several applications, including compositional analysis on single cell level, study of lipid metabolism in C. elegans and histological assessment of cancerous tissues.

P-22. Injectable, Tough Alginate Cryogels as Cancer Vaccines

Ting-Yu Shih[1,2], Serena Blacklow[1], Weiwei Aileen Li[1,2], Sidi Bencherif[1,2], Sandeep Koshy[1,2,3], David J Mooney[1,2]

[1]School of Engineering and Applied Sciences, Harvard University;

[2]Wyss Institute for Biologically Inspired Engineering at Harvard University;

[3]Harvard-MIT Division of Health Sciences and Technology

Cancer vaccines have the potential to eliminate tumors and prevent recurrence. Recently, a covalently crosslinked methacrylated (MA)-alginate cryogel-based vaccine has been shown to successfully modulate host immune cells in situ and evoke potent antitumor responses. The cryogel allows minimally invasive delivery but is not mechanically robust and requires a large 16G needle for delivery. A network of covalently and ionically crosslinked polymers has previously demonstrated strikingly high toughness in bulk form. Therefore, we hypothesized that combining covalent and ionic crosslinking would result in a tough MA-alginate cryogel with improved injectability.

Cryogels were fabricated by covalently crosslinking MA-alginate by free radical polymerization at -20°C overnight. The cryogels were then soaked in a calcium chloride solution to introduce ionic crosslinking. The cryogels were injected through a 16G needle repeatedly until visible damage was observed. Increasing calcium concentration in the cryogel led to enhanced injectability up to 37 mM, beyond which injectability decreased. The optimized tough cryogels could be injected via an 18G needle while maintaining their gel structure; all of the covalently crosslinked only cryogels fractured when injected through this needle size. The tough cryogel provided sustained release of the dendritic cell (DC) chemoattractant GM-CSF and adjuvant CpG-ODN in vitro. Tough cryogels delivering GM-CSF recruited five times more DCs than blank gels by Day 7 in vivo. The tough cryogel vaccine with irradiated HER2+ breast cancer cells as antigen generated significantly higher anti-HER2 antibody titer than blank gels and provided complete protection against breast cancer in 60% of the mice for at least 7 weeks in a prophylactic vaccination study. These tough cryogels provide a promising minimally invasive delivery platform for cancer vaccinations.

P-23. Peptide translocation through the plasma membrane of human cells: a process mediated by oxidative stress

Ting-Yi Wang[1], Yusha Sun[1], Nandhini Muthukrishnan[1], Alfredo Erazo-Oliveras[1], Kristina Najjar[1], and Jean-Philippe Pellois[*, 1]

[1]Department of Biochemistry and Biophysics, Texas A&M University, College Station, TX

Cell-penetrating peptides (CPPs) are promising tools to deliver proteins and nucleic acids into live cells. However, the fundamental mechanisms by which CPPs translocate across cellular membrane remains uncharacterized. This in turn impedes their therapeutic applications and usage for cell biology studies. Here we report that the cell penetration activity of CPPs is dependent on the oxidative state of the membrane. We found that hypoxic culture and supplement of antioxidants abolish the cell delivery efficiency of peptides. Mild oxidation of live cells by oxidants significantly promotes the translocation of CPPs. We also revealed that the native anionic oxidized lipids mediate the efficient and direct transport of the peptide across the plasma membrane of human cells. Our results support a model that CPPs permeate through the lipid bilayer via forming inverted micelles with anionic lipids, which is present as a result of oxidative damage. Our data point to a highly complex and underappreciated interplay between CPPs and oxidized membrane species. This novel mechanism also provides a fundamental basis for rationale design of highly efficient cell-permeable compounds and robust drug delivery strategies.

P-24. Blue light therapy improves circadian dysfunction in two mouse models of Huntington's disease

Huei-Bin Wang, Dawn H Loh, Daniel Whittaker, Danny Truong, Christopher S Colwell

Laboratory of Circadian and Sleep Medicine, Semel Institute for Neuroscience and Human Behavior, Department of Psychiatry and Biobehavioral Sciences, University of California - Los Angeles, Los Angeles CA 90095-1759

Patients with Huntington's disease (HD) exhibit movement disorders, psychiatric disturbance and cognitive impairments as the disease progresses. Abnormal sleep/wake cycles are common among HD patients. In addition to the reports of delayed sleep onset and greater sleepiness during the waking phase, the changed circadian pattern of melatonin suggests dysfunction in the circadian timing system. Moreover, previous studies in mouse models of HD have demonstrated that the circadian rhythm system in HD is disrupted.

Importantly, circadian dysfunction manifests early in disease, even before the classic motor symptoms, in both patients and mouse models. Therefore, we hypothesize that circadian dysfunction may interact with the disease and exacerbate the HD symptoms. Moreover, early intervention may benefit patients and delay disease progression. One test of this hypothesis is to determine whether light therapy designed to strengthen this intrinsic timing system can delay the disease process in mouse models of HD. Light is a strong environmental regulator of circadian timing with blue wavelength light having the strongest impact. In addition, the blue-enriched light therapy has potential benefits over current light therapy, including shorter therapy sessions, more comfortable light intensity, and energy savings. Therefore, this study applied blue-enriched light during the first 6h of light phase during the pre-manifest stage of two HD mouse models: the BACHD (3mo) and Q175 heterozygous

(6mo) mouse models. After 3 months of treatment, both genotypes showed improvements in their locomotor activity rhythm and motor performance. Finally, the profound improvements of Q175 mice triggered us to further study the underlying signaling pathways and biological processes altered by blue light. Our results showed that the expression of a number of HD relevant markers were altered in the striatum and cortex of the treated mice. Our study suggested the possibility that novel environmental intervention can delay the progression of HD in pre-clinical models.

This work was supported by the CHDI Foundation.

P-25. Characteristics of particulate matters emissions from a 3D printer

Chen Jia En[1],Ching-Huang Lai[1], Yi-Fong Tsai[2]

[1]School of Public Health, National Defence Medical Center, Taipei, Taiwan, R.O.C.

[2]Joint Center for Instruments and Researches, College of Bioresources and Agriculture, National Taiwan University.

Nowadays, the development of 3D printing technique is changing the tradition manufacture system. Three-dimensional (3D) printers recently is widely used for rapid prototyping and small-scale fabricating in office and home. However, as the 3D printer commonly used indoors, hazardous particular matter (PM) emissions were not noticed by the users. To our knowledge, only few studies discuss the ultrafine particles (UPFs), volatile organic compounds (VOCs), and PM2.5 emissions simultaneously from 3D printers.

This study evaluated the emissions characteristics of hazardous material during fused deposition modeling (FDM) type of 3D printing. The commercially available 3D printer (UP plus 2), which is capable of testing ABS, PLA, HIPS plastic used in all experiments. Six different commonly used filaments with1.75 mm diameters (three ABS, two PLA and one HIPS cartridges.) were used as materials in the experiment and each test was repeated at least three times. All measurement and operation were conducted in the enclosed chamber system. The results displayed the particle concentration of 3D printing using ABS and HIPS materials were 10 times higher than that of PLA materials and the particle matter distributions were different from different filament companies. Furthermore, the particle sizes of the particulate matter emissions from the 3D printer were between 1μm and 2μm diameters. We suggest the 3D printer users should improve the ventilation and other engineering control for hazards during the operating process.

P-26. Innovative Antibody-onCytotoxicitySwtch (ASfor cancertreatment

Po-Hao Chang, Ya-Chuan Liu, Min-Che Chen

Asclepiumm Taiwan, Mackay Memorial Hospital Incubation Center, New Taipei City, Taiwan

Cancer is a disease with high mortality. Despite that numerous anti-cancer drugs have been used, the prognosis of late stage patients has not been significantly improved. Since the past decade, monoclonal antibody therapy targeting specific cell surface receptors of cancer cells has been developed. Such therapeutic strategy can increase the target specificity, reduce side effects and allow patients to have better quality of life. However, most of the antibody drugs were designed solely to interfere the ligand-receptor interaction, which is not sufficient for eliminating cancer cells and inhibiting tumor development.

We have developed an Antibody Switch-on Cytotoxicity (ASC) platform, an innovative bio-drug delivery system which provides a better strategy for targeted cancer therapy. We first generated an antibody against a cell surface marker. This antibody was modified by insertion of a linker-X and cytotoxic peptides. We then utilized the protease, secreted only from the cancer cells but not normal cells, to digest linker-X and release the cytotoxic peptides (such step is defined as linker-X switch-on). Once linker-X switch-on occurs, the peptides can penetrate into cancer cytoplasm and cause cytotoxicity. Such strategy utilizing the cancer specific microenvironment provides opportunities to reduce side-effects.

Currently, we have established two ASC-peptide drugs, ASC-KLA and ASC-S9, and tested their specificity and effectiveness using FACS, immunofluorescence, soft agar colony formation and xenograft tumorigenesis assays. Our results demonstrated that ASC-S9 could be a better candidate for inhibiting tumorigenesis.

P-27. Mechanical assays uncover diverse Eg5 inhibitor mechanisms

Geng-Yuan Chen, You-Jung Kang, William O. Hancock

Department of Bioengineering, Pennsylvania State University

The mitotic kinesin Eg5/KSP contributes to spindle formation, regulates neuronal growth, and enhances microtubule (MT) polymerization. Drugs such as monastrol and ispinesib, which act as ATP-uncompetitive inhibitors, generally modulate loop L5 or its proximal regions, stabilizing the nucleotide and trapping the motor in the weak-binding (ADP or ADP-Pi) state. Several ATP-competitive inhibitors that generate a strong-binding apo-state have also been reported. Here, we used mixed-motor gliding assays to reveal the influence of small molecule inhibitors on the mechanical performance of Eg5. Microtubules moved by populations of kinesin-1 and Eg5 motors move near the slow Eg5 gliding speed due to this motors' "braking" ability. In this assay, monastrol and ispinesib result in faster gliding speeds, consistent with Eg5 being in a weak-binding state, whereas the inhibitor BRD9876 slowed gliding in all cases, consistent with it being inhibited in a strong-binding state. In single-molecule experiments, the lack of motor diffusion in the presence of BRD9876 further supports this conclusion. Single-molecule and bulk biochemical assays reveal that BRD9876 serves as an ATP- and ADP-competitive inhibitor of Eg5, suggesting that BRD9876 interferes with the nucleotide-binding and creates an apo-state motor that binds strongly to the MT. The MT-uncompetitive behavior shows that drug binding requires the conformational change associated with MT binding by the motor. This drug-induced strong-binding state provides an alternate strategy of strong-binding state rather than a weak-binding state for inhibiting bipolar spindle formation. Additionally, this strong-binding motor may serve as an effective "brake" to slow down the neuronal growth, or serve as a stabilizer to reduce MT catastrophe.

P-28. Exploring Indicators of Child Resilience in Early Childhood with the Taiwan Birth Cohort Study

Shih-Dun Liu, MS[1, 2]; Shilpa Jani, MS[2]; Michael CY Chu, BS[2]; C Jason Wang, MD, PhD[2]

[1]University of Pittsburgh School of Medicine, Pittsburgh, PA

[2]Center for Policy, Outcomes and Prevention, Stanford University, Palo Alto, CA

The Known: Resilience, in a contemporary definition, refers to the capacity of a dynamic system to withstand or recover from significant challenges that threatens its stability, viability or development. As a subset of health potential, resilience can also be defined as an attribute that predicts such aforementioned capacity to adapt to achieving relatively normal health and developmental outcomes despite exposure to social adversity.

The Unknown: The definition of resilience has continually evolved as scientific knowledge expands, but still lacks consensus on an operational definition. Because of the evolving and complex definition, it remains unknown whether early attributes can reliability predict later resilience capacity. Moreover, literature on resilience has been predominantly confined to westernized countries. Since resilience depends, at least in part, on culture-specific definitions of successful outcomes and normal functioning, we offer a different perspective via a unique dataset as part of the Taiwan Birth Cohort Study (TBCS). TBCS is a large-scale longitudinal study currently conducted by the Taiwanese government, following more than 20,000 children a with nationally-representative sample in Taiwan. It provides a unique opportunity to assess resilience in the context of traditionally Eastern culture.

Resilience Capacity is a construct we termed that is measured with a composite scale using validated instruments. Relevant indicators from the same age range were added to the scale based on clinical relevance, fit to conceptual model, psychometric test and exploratory factor analysis. With resilience capacity, we created a composite scale for resilience capacity, and utilized it to identify indicators in early childhood that potentially influences resilience capacity (e.g. child's gender, poverty, urban vs. rural, mother from China or foreign country)

P-29. Biophysics of mitotic spindle positioning in *C. elegans* embryos

Hai-Yin Wu[1, 2], Che-Hang Yu[1, 3], Reza Farhadifar[1, 4], Daniel Needleman[1, 3, 4, *]

[1]FAS Center for Systems Biology, Harvard University

[2]Department of Physics, Harvard University

[3]School of Engineering and Applied Sciences, Harvard University

[4]Department of Molecular and Cellular Biology, Harvard University

The spindle is positioned asymmetrically during the first mitotic division in *C. elegans*. We are investigating how different forces coordinated to move the spindle, and if these forces are generated from interactions with the cytoplasm, the cortex, or a combination of both. For this purpose, we constructed a laser ablation system capable of cutting complex patterns with high spatial and temporal precision, and are applying it to quantitatively perturb spindle movements. We are also using fluorescent nanodiamonds to track cytoplasmic fluid flow as the spindle moves. Our results suggest that dynamic net pulling forces from the cortex drive key aspects of spindle motions, including the asymmetric positioning and the transverse oscillating behaviors. Further combining with mathematical simulation, we hope to provide a quantitative, integrated understanding of spindle positioning.

P-30. Chiral Imaging using Planar Meta-lenses

Wei Ting Chen[1], Mohammadreza Khorasaninejad[1], Robert C. Devlin[1], Jaewon. Oh[1,2], Alexander Y. Zhu[1], and Federico Capasso[1]

[1]Harvard John A. Paulson School of Engineering and Applied Sciences, Harvard University, Cambridge, MA 02138, USA.

[2]University of Waterloo, Waterloo, ON N2L 3G1, Canada.

Traditionally, a lens shapes the wavefront of light via propagation through a bulky medium; this results in a heavy and large system that is often unsuitable for bio-imaging purposes.. Despite of the existence of planar and compact Fresnel lenses, they lack the ability to distinguish between different polarization states of light, and additionally, have a very limited numerical aperture (NA). Here, we develop a new method of using TiO_2 nano-structures as building blocks to demonstrate planar lenses (called meta-lenses hereinafter). These meta- lenses are not only extremely compact (600 nm thick excluding their supporting substrates) but are also capable of splitting different states of circularly polarized light. In this way, the chiroptical properties of an object can be probed across the entire visible spectrum, using only the meta-lens and a camera, without any additional polarizers or waveplates. Two meta-lenses of different numerical apertures of 0.05 and 0.8 are demonstrated for high performance imaging. For the low numerical aperture meta-lens, we not only image, but also map the circular dichroism of the exoskeleton of a chiral beetle, Chrysina gloriosa, which is known to exhibit high absorption of right-circularly polarized light. For another meta-lens, we show it perform subwavelength resolution, and the resulting imaging quality is comparable to that obtained from using a commercial objective with the same NA. Our results conclusively show that meta-lenses can simultaneously extract spatial and polarization information, enabling a wide variety of imaging applications.

Organizing Committee

會長 Chair

- 陳映嘉 Ying-Ja Chen, Patent Agent, Axcella Health
- 王志傑 Chih-Chieh Wang, Postdoc, Harvard Medical School

學術組 Academic Track

- 謝富凱 Fu-Kai Hsieh, Postdoc, Mass. General Hospital/Harvard Medical School
- 周怡吟 Yi-Ying Chou, Postdoc, Harvard Medical School/Boston Children's Hospital
- 蔡宇承 Yu-Chen Tony Tsai, Postdoc, Harvard Medical School
- 張嘉容 Chia-Jung Chang, Graduate Student, MIT
- 劉大鳴 Ta-Ming Liu, Postdoc, Dana-Farber Cancer Institute
- 林聖軒 Postdoctoral scientist, Columbia University

業界組 Industry Track

- 洪國展 Kuo-Chan Hung, Postdoc, Harvard SEAS and Spherebio Inc.
- 楊鎮遠 Charlie Yang, Graduate Student, Boston University
- 徐艾梅 Amy Shyu, Scientific Associate II, Novartis
- 麥惠明 Huey-Ming Mak, Research Associate II, Synlogic
- 鄭永志 Yung-Chih Cheng, Postdoc, Boston Children's Hospital/Harvard Medical School
- 郭姿杏 Tzu-Hsing (April) Kuo, Scientist, Acceleron Pharma
- 彭浩帆 Haofan (Eric) Peng, Senior engineer, Biogen
- 李以如 I-Ju Lee, Postdoc, Dana-Farber Cancer Institute
- 錢正浩 Cheng-Hao Chien, Postdoc, Tufts University
- 陳偉強 Wei-Chiang Chen, Scientist, Immunogen Inc

Organizing Committee

創業組 Entrepreneur Track

- 張劭聿 Shaoyu Chang, Senior Research Manager & Asia BD Liaison, Life Science Nation
- 杜荷洲 Ho-Chou Tu, Scientist, Alnylam Pharmaceuticals
- 李璧君 Pi-Chun Li, Scientist, Dana-Farber Cancer Institute

網頁 Website

- 魏曉英 Hsiao-Ying Wey, Instructor, Mass. General Hospital/Harvard Medical School
- 李婉萍 Wan-Ping Lee, Senior Lead Scientist/Head of London R&D, Seven Bridges Genomics
- 林嬌鳳 Chiao-Feng Lin, Senior Bioinformatician, Research Associate, Partners HealthCare, Brigham and Women's Hospital, Harvard Medical School
- 魏嘉英 Margaret Wey, Research Pharmacist, Mass. General Hospital
- 彭冠為 Kuan-Wei (Wilson) Peng, Bioanalytical Scientist, Berg LLC
- 黃天韻 Tien-Yun Huang

宣傳 Promotion

- 張筱琦 Shiao-Chi Chang, Research Technician, Dana-Farber Cancer Institute
- 蔡百騏 Pai-Chi Tsai, Postdoc, Harvard University
- 陳冠煒 Kuan-Wei Chen, Operation Associate, Moderna Therapeutics
- 黃仲軒 Chung-Hsuan Huang, Research Associate, Harvard Medical School / Harvard Institute of Medicine
- 蔡賢奕 Hsien-Yi Tsai, Graduate Student, Rutgers University

Organizing Committee

專案 Regular Activities

- 張德寬 De-Kuan Chang, Scientist, Juno Therapeutics Inc. [Fundraising]
- 彭聲翔 Sheng-Shiang (Anson) Peng, Research Associate, Broad Institute [Career Workshops and Food]
- 陳昇宏 Sheng-hong Chen, Postdoc, Harvard Medical School [NTU Collaboration]
- 周慧婷 Hui-Ting Chou, Postdoc, Harvard Medical School [Clerk, 501(c)(3)]
- 黃士芳 Elise Huang, Bioprocess Engineer, Merrimack Pharmaceuticals [Souvenirs]
- 林昱秀 Ruth Lin [Housing matching]
- 李湘盈 Sherry Lee, Postdoc, Whitehead Institute for Biomedical Research [Treasurer]
- 吳佳璘 Chia-ling (Leslie) Wu, Postdoc, Boston University School of Medicine [Mentoring Program]

Attendee List

Name	Affiliation
ANTONIO, ARCINIEGAS	Postdoc
PO-HAO, CHAN	Manager
ANGELA, CHANG	Biostatistician
CHIA-HAO, CHANG	Graduate student
CHUN CHIA, CHANG	Medical student
CHUN-YA, CHANG	Jabseeker
HAN-WEN, CHANG	Postdoc
JANET, YA, CHANG	Graduate student
KAI-TI, CHANG	Postdoc
KAREN, CHANG	Graduate student
MARIE, CHANG	Pharmacist
PO-YIN, CHANG	Postdoc
SHIAO-CHI, CHANG	Research Technician
TING-CHIA, CHANG	Graduate student
WEI TING, CHANG	Research associate
YATING, CHANG	Postdoc
YU-LING, CHANG	Graduate student
YI-SHENG, CHAO	Postdoc
CHEN-HAO, CHEN	Graduate student
CHENG-YI, CHEN	Graduate student
CHI-LI, CHEN	C4 Therapeutics
CHIA-YEN, CHEN	Postdoc
CHIEN-JU, CHEN	Graduate student
CHIEN-MING, CHEN	Graduate student
CHIENWEN, CHEN	Postdoc
CHING-CHIH, CHEN	Graduate student

CHING-HUAN, CHEN	Graduate student
CHUN-WEI DAVID, CHEN	Instructor
GENG-YUAN, CHEN	Graduate student
HO-CHUNG, CHEN	Research Technician
HSIN-YI, CHEN	Postdoc
HSING-YU, CHEN	Postdoc
JENNY, CHEN	Shareholder
JENNY, CHEN	Shareholder
JOYCE, CHEN	Biostatistician
KAI-YU, CHEN	Staff Research Associate
KUANG EN, CHEN	Graduate student
KUANWEI, CHEN	Operation Associate
LEON, CHEN	Chief Executive Officer
LEON, CHEN	Chief Executive Officer
MIN-CHE, CHEN	Founder & CEO
MING-SHUO, CHEN	Graduate student
MINSHAN, CHEN	Graduate student
MOLLY, CHEN	Account Manager
MONG-JEN, CHEN	Postdoc
PO-TAO, CHEN	Research Specialist
SHENG-WEN, CHEN	Graduate student
SONYA HONG-LING, CHEN	Associate Scientist
TANYA, CHEN	Head of Business Development
TSE-WEI, CHEN	Engineer
WEI-CHIANG, CHEN	Scientist
WEI-HUNG, CHEN	Graduate student
YEN-HUA, CHEN	Graduate student
YI-CHUN, CHEN	Graduate student
YI-HSUAN, CHEN	Graduate student

YI-SHAN, CHEN	Associate Scientist II
YING-CHEN, CHEN	PM
YING-JA, CHEN	Patent AgentPatent Agent
YU-FAN, CHEN	Postdoc
MELODY, CHENG	Postdoc
SHAO CHUAN, CHENG	Graduate student
SHUN YUN, CHENG	Graduate student
YUNG-CHIH, CHENG	Postdoc
CHENG-HAO, CHIEN	Postdoc
MIAO-PING, CHIEN	Postdoc
YI-CHEN, CHIH	Pharmacist
JIAN-GENG, CHIOU	Graduate student
HSIU-CHIANG, CHIU	Full time missionary
YICHI, CHIU	Clinical Data Manager
HEE JUNE, CHOI	Postdoc
BIN-KUAN, CHOU	Postdoc
HUI-TING, CHOU	Postdoc
LEO, CHOU	Postdoc
SHAO-PEI, CHOU	Graduate student
YI-YING, CHOU	Postdoc
CANDICE PEI-HUA, CHU	Graduate student
PEI-LUN, CHU	Graduate student
TZU-YING, CHUANG	Graduate student
YA-SHAN, CHUANG	Graduate student
CHENGYU, CHUNG	Graduate student
CHIA-YU, CHUNG	Graduate student
CHIEN-KUANG, DING	Graduate student
JING YING, ENG	R&D Associate II
YAO-YUN, FAN	Senior Scientist

JOSEPHINE, FANG	Graduate student
JOSHUA, HO	Founder
CHIH-YUN, HSIA	Graduate student
CHING-HAN, HSIAO	SAS Programmer
JEAN, HSIAO	research scientist
YU-SHAN STEPHANIE, HSIAO	Research Scientist I
YUNG-TSE, HSIAO	Graduate student
CHIA-YUN, HSIEH	Graduate student
FU-KAI, HSIEH	Postdoc
KANG LIN, HSIEH	Graduate student
WEI-CHE, HSIEH	Graduate student
BRIAN, HSU	Graduate student
CHIA GEORGE, HSU	Postdoc
CHIA-LIN, HSU	Postdoc
HAO-JUI, HSU	Graduate student
HUNG-LUN, HSU	Graduate student
JIUN-MIN, HSU	Graduate student
PEI-WEN, HU	Research Technician
CATHY, HUANG	Postdoc
CHIUNG-WEI, HUANG	Graduate student
CHUNG-HSUAN, HUANG	Research Associate
HAO, HUANG	Graduate student
HUBERT, HUANG	Graduate student
KANG-CHIEH, HUANG	Graduate student
NAI-JIA, HUANG	Postdoc
RICHARD, HUANG	Graduate student
TING-NI, HUANG	Graduate student
WEI-CHAO, HUANG	Graduate student
YU-HUI, HUANG	Postdoc

YU-MEI, HUANG	Graduate student
YU-TING, HUANG	Postdoc
YUCHUNG, HUANG	Visiting scientist
YUNG-CHI, HUANG	Graduate student
KUO-CHAN, HUNG	Postdoc
LUNG-HSIN, HUNG	Microfluidics Engineer
PUTZER, HUNG	Graduate student
YIH-CHII, HWANG	Bioinformatician
YUNG, HWANG	Graduate student
LIM, IVY ZHU WEI	undergraduate student
CHEN, JIA-EN	Graduate student
YIDE, JIANG	Chief Strategy Officer
JESSICA, JIN	Research Assistant
MARK, KAO	Director
SU-MEI, KAO	President
HUNGTNAG, KO	Graduate student
CHI-CHON, KONG	Graduate student
I-HSIN, KUO	Clinical program coordinator
TZU-HSING (APRIL), KUO	Scientist
CHUNG-WEI, LEE	Sr. Scientist
HSU-YANG, LEE	Graduate student
I-JU, LEE	Postdoc
NICK, LEE	Consultant
PEI-JU, LEE	Graduate student
SHERRY, LEE	Postdoc
TIEN-JUI, LEE	Graduate student
YIWEI, LEE	Graduate student
YU-RU, LEE	Postdoc
YUAN-CHO, LEE	Postdoc

PI-CHUN, LI	Scientist
OLIVIA, LIANG	Solution Sales Manager
RICHARD, LIANG	Professor / Research Investigator
CHIEN-SHENG, LIAO	Graduate student
SHU-YU, LIAO	Graduate student
AGNES, LIN	Associate Scientist II
CHIA-CHING, LIN	Postdoc
CHIAO-FENG, LIN	Senior Bioinformatician, Research Associate
CHIEN-LING, LIN	Postdoc
CHIH-HSU, LIN	Graduate student
HSIN-YU, LIN	Graduate student
HSUAN-NI, LIN	Graduate student
KE-CHIH, LIN	Graduate student
PAO, LIN	Professor
RAY, LIN	Senior Scientist
RUTH, LIN	Others
YI-DONG, LIN	Postdoc
YI-FEN, LIN	Graduate student
ZE-YUN, LIN	Ex-demand planning manager in P&G
CHI-HSIU, LIU	Postdoc
JIAN-CHANG, LIU	Research Associate II
PO-TING, LIU	Graduate student
TA-MING, LIU	Postdoc
CHI-WEN, LO	Graduate student
JOYCE, LO	Scientist I
MENG-CHEN, LO	Postdoc
CHI, LU	Graduate student
CHING-LAN, LU	Graduate student
WEI-CHENG, LU	Postdoc

YEN-CHUN, LU	Graduate student
HUEY-MING, MAK	Research Associate II
DEBASHIS, MANDAL	Postdoc
JIANGHE, NIU	Clinic Research Coordinator
HSIN MEI, PAN	Med student
ANSON, PENG	Research Associate
HAOFAN, PENG	Senior engineer
KUAN-WEI (WILSON), PENG	Bioanalytical Scientist
ROBERT, ROSENBERG	president
ZIH-JIE, SHEN	Postdoc
TING-YU, SHIH	Graduate student
DAVID, SHIS	Postdoc
AMY, SHYU	Scientific Associate II
FENG-HSIU (MANDY), SU	Senior Biostatistician
HAO-WEI, SU	Research Scientist
JUN-HAN, SU	Graduate student
KUO-HUI, SU	Postdoc
HUI-LUNG, SUN	Postdoc
MIN-YU, SUN	Postdoc
JUI-CHENG, TAI	Postdoc
I-LI, TAN	Graduate student
YOU CHI, TANG	Graduate student
NAI-WEN, TIEN	Graduate student
HSIEN-YI, TSAI	Graduate student
JENNIFER, TSAI	Postdoc
PAI-CHI, TSAI	Postdoc
PEI-YUN, TSAI	Graduate student
SHANG-PU, TSAI	Postdoc
SHENG TZUNG, TSAI	Postdoc

YU-CHEN, TSAI	Postdoc
HSIEN-CHUNG, TSENG	Senior Research Scientist
KUANGCHING, TSENG	Product Development Scientist
WEI CHOU, TSENG	Postdoc
BENJAMIN PANG HSIEN, TU	Seminary Student
HO-CHOU, TU	Scientist
YANG, TZU WEI	Graduate student
CHEN-YU, WANG	Graduate student
CHIEN-CHUNG, WANG	Postdoc
CHIH-CHIEH, WANG	Postdoc
CHIH-HAO, WANG	Postdoc
HUEI-BIN, WANG	Lab Assistant
KATE, WANG	Laboratory Exchange Student
KUAN-YUAN, WANG	Attending Physician
LI-CHUN, WANG	Graduate student
LI-TING, WANG	Graduate student
LINYA, WANG	Postdoc
SHU-PING, WANG	Postdoc
TING-YI, WANG	Graduate student
YUJEN, WANG	Graduate student
DENNIS, WEI	Founding Scientist / Biology lead
PEI-CHI, WEI	Postdoc
STEVE, WEISNER	Director
JENNIFER, WELLS-QU	Director of Partnerships
SHUHAO, WEN	CEO
HSIAO-YING (MONICA), WEY	Professor / Instructor
MARGARET, WEY	Research Pharmacist
CHI-FANG, WU	Postdoc
CHUNG-YEH, WU	Investigator II

CYRIL, WU	Research Associate
HAI-YIN, WU	Graduate student
HSIN-TA, WU	Graduate studentPhD
I-HSIEN, WU	Lab Manager
KUNTA, WU	Postdoc
LESLIE, WU	Postdoc
MENG-JU, WU	Graduate student
MING-RU, WU	Postdoc
MINGYUEH, WU	Graduate student
REBECCA, WU	Graduate student
SHU-PEI, WU	Scientist
WEI-PU, WU	Research Technician
YI-CHEN, WU	Technician
GRACE, XIAO	Co-Founder of Kynplex
CHARLIE, YANG	Graduate student
CHIH-CHAO, YANG	Postdoc
CHIHSHENG, YANG	Postdoc
SHIH-TING, YANG	Associate Researcher
CHIEN-LIN, YEH	Graduate student
KE-JUI, YEN	Graduate student
SHIH-CHIEH, YEN	Student
SHUO-TING, YEN	Graduate student
CHE-HANG, YU	Graduate student
CC, YUAN	Scientist II
WEI-CHIEN, YUAN	Postdoc
GEORGE, ZHANG	President

TECRO Science and Technology Division

駐美國台北經濟文化代表處 科技組

Science & Technology Service & Communication

務實服務 科技交流

- 推動科技協議訂定、執行及交流合作
  To promote S&T cooperative agreements and collaboration
- 促進科技產業返國投資及技術轉移
  To promote S&T industrial investment & technology transfer
- 促進科技界人士互訪
  To enhance S&T personnel bilateral exchanges
- 延攬海外科技人才
  To recruit overseas experts
- 參與並協助海外科技社團舉辦之科技活動
  To support the activities of Chinese-American S&T community organizations
- 協助國內蒐集科技資訊
  To help collect S&T information
- 服務區域包括華盛頓特區、美東及美中地區共20州
  Service area including 20 states（ME, VT, NH, MA, CT, NY, RI, PA, NJ, DE, MD, VA, WV, IA, WI, MN, OH, MI, IL, IN) and Washington D.C.

➢ 國內人才海外培訓計畫：

- 千里馬計畫(Graduate Students Study Abroad Program)
  博士生至國外研究
- 龍門計畫(Dragon Gate Program)
  補助任務導向型團隊赴國外研習計畫
- 赴國外從事博士後研究計畫
  (Postdoctoral Research Abroad Program)

內容請詳https://www.most.gov.tw/sci/ch
科技部科教及國際合作司網頁內
「一般性及專案型國際交流方案補助」

➢ 海外人才延攬培訓計畫：

- 國家攬才網站
  Contact Taiwan
  www.contacttaiwan.tw
- 台灣暑期研究生計畫
  Summer Institute in Taiwan
  美國研究生暑假赴台研究
  www.nsf.gov/eapsi
- 候鳥計畫
  Taiwan Tech Trek
  台裔優秀青年暑期赴台研習
  www.most.gov.tw/ttt/

4201 Wisconsin Avenue, N.W., Washington, DC 20016, Tel: 202-895-1930, Fax: 202-895-1939
Website：http://dc.most.gov.tw, E-Mail: std@tecro.us

中華民國經濟部為協助國內企業延攬海外科技人才，特設立國家層級單一對外攬才網站「Contact Taiwan」，針對下列十大攬才重點領域提供人才與企業媒合機制，敬請多多利用。

十大攬才重點領域

一.生產力 4.0
二.高階製程設備
三.先進電子零件製造(含 IC 設計、半導體製造)
四.智慧系統整合應用(含大數據、物聯網及雲端)
五.5G 及前瞻通訊
六.生技新藥及醫療器材
七.再生能源
八.產品及使用者經驗設計
九.創新前瞻研究發展
十.國際金融服務

詳細資訊請登入
Contact TAIWAN
http://www.contacttaiwan.tw
(延攬海外人才單一對外攬才網站)

TECRO Science and Technology Division
駐美國台北經濟文化代表處 科技組

The Taiwanese American Foundation of Boston (TAF-Boston) is a non-profit organization, established in 2000 by a group of Taiwanese-Americans residing in or related to the New England area.

The purposes of the Foundation are (1) to advance the social, socio-economic, cultural, humanitarian, literary, environmental, educational, scientific, public-policy, and foreign-relations interests of Taiwan and thereby improve the quality of life for people of Taiwan and Taiwanese-Americans; and (2) to preserve and promote Taiwanese culture and traditions in a diverse American society.

Each year the Foundation provides funds to individuals or organizations in furtherance of the Foundation's purposes. One regular TAF-Boston program — University Fellowship Program — is intended for graduate students who are enrolled in an U.S. institution and whose study or research is sufficiently related to the advancement of (a) any social, cultural, socio-economic, literary, environmental, educational or scientific interest of Taiwan or (b) any issue of public policy or foreign relations impacting Taiwan, with the goal of producing a report (dissertation/thesis) of the grantee's study or research. The Foundation will grant up to $6,000 to each selected proposal.

Applications to the scholarship and fellowship programs will be accepted two times a year. The closing dates are February 1 and September 1. Interested candidates are welcome to visit the Foundation Website at www.taf-boston.org for details of the application requirements.

Best Wishes for the Success of 2016 BTBA Symposium!

Taiwanese Association of America (TAA)- Boston Chapter

波士頓台灣同鄉會

https://sites.google.com/site/taabostonorg/