2020

Multiomics and Precision Medicine Joint Conference

多體學及精準醫學聯合會議

11/14 Sat
11/15 Sun

長庚大學

主辦單位：台灣蛋白體學會 / 長庚大學

協辦單位：台灣生物資訊與系統生物學會
台灣基因醫學暨生物標記學會
台灣演化暨計算生物學學會
台灣精準醫學學會
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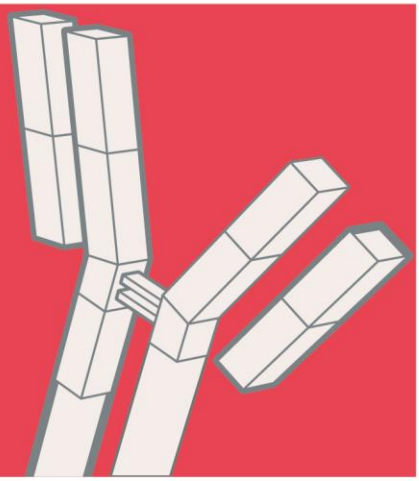

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目錄 Content

大會主席歡迎詞 Welcome Remarks

由於知識的累積與科技的進步，生物現象的片面了解已無法滿足研究者的期待。近年來興起的生物分子高通量分析技術（high-throughput technologies）已廣泛地應用於核酸、蛋白質、代謝物小分子等研究領域，發展出各種定性與定量的體學（omics）分析平台，包括：基因體、轉錄體、蛋白質體、代謝體等。經由高通量分析技術產出的巨量數據又須仰賴生物資訊的工具開發與數據分析，才能將數據（data）轉換為訊息（information），進而被有效整合與精確解讀。此一多體學整合研究策略徹底顛覆了以往的單一體學的研究思維，讓研究人員更有機會探勘出以往無法得知的新線索。而（多）體學的分析與整合又以人類疾病相關研究居多，這些體學數據除了提供更全面更完整的資訊增加研究者對疾病的了解，更是找出新的致病機轉、用藥指標、與診斷或監控疾病的生物標誌的重要工具。

基於推廣多體學研究的初衷，國內三個體學相關學會(台灣生物資訊暨系統生物學會、台灣蛋白體學會、與台灣基因醫學暨生物標記學會)，首度於 2019 年 12 月 7~8 日聯合舉辦「2019 多體學及精準醫學聯合會議」，為國內第一個多體學領域之聯合學術會議，成功的讓與會者快速獲知國內外多體學之最新進展與趨勢，獲得相當迴響與肯定。有了成功第一步的經驗，今年籌備委員會進一步邀請台灣演化與計算生物學會、台灣精準醫學學會、與台灣胞外體學會加入，共同籌辦「2020 多體學及精準醫學聯合會議」，讓會議的成員擴及基因體、蛋白體、代謝體、胞外體、生物資訊及後端的精準醫學臨床應用，更為完整豐富。希望結合六個學會的專業與力量，讓會議內容更多元精采，讓台灣的學子對新興的多體學與精準醫學領域有更多的了解，更促成不同領域之間的研究人員有更多交流與合作的機會。此次會議籌辦過程中遇到新冠病毒肆虐全球，因應此突發疫情，聯合會議隨即調整為現場直播的線上會議型式，但也提高了會議舉辦的複雜度與工作份量。在此要特別感謝所有來自各學會全力投入籌備會議的工作同仁、國內外受邀演講的專家學者及熱情贊助聯合會議的生技公司與廠商，並預祝聯合會議順利圓滿成功，參與會議的學員能透過線上直播及錄影重播觀看方式，完整掌握聯合會議所要傳遞的重要資訊，為多體學及精準醫學研究注入新的活水動力。

2020 多體學及精準醫學聯合會議 大會主席
台灣蛋白體學會 理事長

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注意事項 General Inforamtion

會場

長庚大學 第二醫學大樓 B1 第一~三會議廳 **(本次會議不開放觀眾進場)**

網路

會場提供免費 Wi-Fi

名稱：mopm2020；密碼：20201114

名稱：mopm2020_1；密碼：20201114

報到櫃台

11/14 (六) 8:30-17:30

11/15 (日) 8:30-13:50

會議廳內

配合現場直播，發問請至演講台前特定位置

禁止飲食、手機請開靜音、全程配戴口罩

線上直播

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會議首頁：https://bit.ly/2020mopm

會議議程：https://reurl.cc/4mjEZ2

會議結束後一週，每場演講均會剪輯為影片置於會議網站，請以**網站註冊之帳號密碼**登入觀看

晚宴

時間：11/14 (六) 17:00

地點：長庚高爾夫俱樂部 -- 桃園市龜山區舊路里長庚球場路 66 號

接駁車 16:30 自長庚大學台塑文物館旁發車 (p.205)，前往長庚高爾夫俱樂部

19:30 自長庚高爾夫俱樂部發車，先返回長庚大學，再停靠機捷 A8 站

- ❖ 校園禁止吸菸
- ❖ 請配合現場量體溫、噴酒精、全程配戴口罩等防疫措施

會議議程 Conference Program Day 1

Nov. 14th 2020 (Day one)	TPS & TSEV 第一會議廳	TSECB & TBSB 第二會議廳	TGMBS & TPMS Lectures in Chinese 第三會議廳 (中文演講)
08:40 - 09:10	來賓報到		
09:10 - 09:20	開幕式 (第一會議廳)		
09:20 - 10:10	特別演講 I (第一會議廳) 主持人：張玉生 特聘教授 (Dr. Yu-Sun Chang)　長庚大學 生物醫學研究所 講員：Dr. Henry Rodriguez Director of Office of Cancer Clinical Proteomics Research, NCI, NIH, USA 題目: Beyond Cancer Genomics: Toward Precision Medicine		
10:10 - 10:40	團體照 / 中場休息		
Section I	**Multiomics** 主持人：余兆松 主任 (Dr. Jau-Song Yu) 長庚大學 分子醫學研究中心	**Population Gemomics** 主持人：王弘毅 教授 (Dr. Hurng-Yi Wang) 國立台灣大學 臨床醫學研究所	**Cell & Immune Therapy** 主持人：蔡婉琪 副教授 (Dr.Wan-Chi Tsai) 高雄醫學大學 醫學檢驗生物技術學系
10:40 - 11:05	陳玉如 特聘研究員 (Dr. Yu-Ju Chen) 中央研究院化學研究所 Taiwan Cancer Proteogenomics Moonshot : Pathway to Next Generation Precision Medicine in Cancer	蔡懷寬 研究員 (Dr. Huai-Kuang Tsai) 中央研究院 資訊科學研究所 Deciphering the Multiple Facets of Gene Regulation via Multi-omics Data Integration and Analysis	林泰元 副教授 (Dr. Thai-Yen Ling) 國立臺灣大學　藥理學科所 細胞治療的藥理觀點 The Pharmacolog of Cellular Therapy
11:10 - 11:35	陳昌熙 教授 (Dr. Chang-Shi Chen) 國立成功大學 基礎醫學研究所 A Multiomic Analysis Reveals the Role of Fumarate in Regulating the Virulence of Enterohemorrhagic Escherichia Coli	吳育瑋 副教授 (Dr. Yu-Wei Wu) 臺北醫學大學 醫學資訊研究所 Predicting Antimicrobial Resistance Activities from the Bacterial Pan-genomes Using Machine Learning Algorithms	莊國祥 副教授 (Dr. Kuo-Hsiang Chuang) 臺北醫學大學 生藥學研究所 Novel Anti-cancer Armed T Cell Therapeutic Technology
11:40 - 12:05	高承源 副研究員 (Dr. Cheng-Yuan Kao) 國家衛生研究院 免疫中心 A Multi-omics Analysis Reveals Novel Insights of Gut Microbiota Shaping and Inflammation Control	王禹超 副教授 (Dr. Yu-Chao Wang) 國立陽明大學 生物醫學資訊研究所 Identification of Genomic Predictors for Treatment Response to Cancer Immunotherapy Using Omics Data Analysis	陳冀寬 執行長 (Dr. Chi-Kuan Chen) 光晟生技研發中心 Pitfalls in Autologous Cellular Immunotherapy
12:10 - 12:35	TPS 線上時間	TSECB 線上時間	TGMBS 線上時間
12:40 - 13:20	科技新知分享 台灣賽默飛世爾科技股份有限公司 Orbitrap Exploris™ Mass Spectrometry – The Preferred Platform for Proteomics	六學會理事長專訪 學會的回顧與展望	科睿唯安 Clarivate 使用AI工具加速研究創新
13:20 - 13:30			
13:30 - 14:20	特別演講 II (第一會議廳) 主持人：沈湯龍 教授 (Dr. Tang-Long Shen)　國立臺灣大學 植物病理與微生物學系 講員：Dr. Koji Ueda Project Leader, Cancer Precision Medicine Center, The Cancer Institute of JFCR, Japan 題目: Proteogenomic Approaches in Development of Cancer Liquid Biopsy and Precision Immunotherapy		
14:20 - 14:40	中場休息		
Section II	**New Technology** 主持人：陳逸然 副研究員 (Dr. Yet-Ran Chen) 中央研究院 農業生物科技研究中心	**Bioinformatics** 主持人：蔡少正 講座教授 (Dr. Shaw-Jenq Tsai) 國立成功大學 生理學科暨研究所	**Microbiota** 主持人：黃旼儀 教授 (Dr. Ming-Yii Huang) 高雄醫學大學 醫學系
14:40 - 15:05	賴品光 助理研究員 (Dr. Pin-Kuang Lai) 中央研究院 原子與分子科學研究所 Multi-resolution Imaging of Cancer-derived Extracellular Vesicles and Exomeres Identifies Distinct Biodistribution Profiles with Redirected Tropism	楊欣洲 研究員 (Dr. Hsin-Chou Yang) 中央研究院 統計科學研究所 Population Pharmacogenomics: Enrichment of Ancestry-informative Markers in Pharmacogenetic Loci	吳俊穎 教授/主任 (Dr. Chun-Ying Wu) 臺北榮民總醫院 醫學研究部轉譯研究科 Gut Microbiota, FMT and Human Diseases
15:10 - 15:35	許觀達 助理教授 (Dr. Guan-Da Syu) 國立成功大學 生物科技與產業科學系 Application of Functional Protein Microarray in Research and Drug Development	呂曉沛 助理教授 (Dr. Hsiao-Pei Lu) 國立成功大學 生物科技與產業科學系 The Application of Metagenomics, Metatranscriptomics, and Metabolomics on Ecological Issues	曾景鴻 總經理 (Dr. Ching-Hung Tseng) 微菌方舟生物科技股份有限公司 The Gut Microbiome in Human Health and Diseases, a Recent Perspective
15:40 - 16:05	簡昆鎰 副教授 (Dr. Kun-Yi Chien) 長庚大學 生化暨分子生物學科 A NanoLC-MS System for Single-cell Proteomic Analysis	江士昇 助理研究員 (Dr. Shih-Sheng Jiang) 國家衛生研究院 癌症研究所 Dissecting Tumor Microenvironment Using Gene Expression Profiling Data for Prognostic Biomarkers of OSCC	許庭源 醫師 (Dr. Ting-Yuan Hsu) 安禾診所 Integrative Treatments of Advanced Cancers by Combined Both Cytokine-induced Killer Cells and Personalized Probiotic Therapy
16:20 - 16:30	集合乘坐接駁車		
17:00 - 19:30	晚宴 長庚高爾夫俱樂部餐廳		

會議議程 Conference Program Day 2

Nov. 15th 2020 (Day two)	TPS & TSEV 第一會議廳	TSECB & TBSB 第二會議廳	TGMBS & TPMS Lectures in Chinese 第三會議廳 (中文演講)
08:40 - 09:10	來賓報到		
09:10 - 10:00	特別演講 III (第一會議廳) 主持人：丁照棣 教授 (Dr. Chau-Ti Ting)　國立臺灣大學 生態學與演化生物學研究所 講員：Dr. Sarah A. Tishkoff David and Lyn Silfen University Professor, Department of Genetics, Perelman School of Medicine and Department of Biology, School of Arts and Sciences, University of Pennsylvania 題目: Genomic Evolution and Adaptation in Africa: Implications for Health and Disease		
10:00 - 10:30	中場休息		
Section III	Extracellular Vesicles 主持人：蔡少正 講座教授 (Dr. Shaw-Jenq Tsai) 國立成功大學 生理學科暨研究所	Artificial Intelligence 主持人：孫孝芳 主任 (Dr. H. Sunny Sun) 國立成功大學 分子醫學研究所	Precision Medicine 主持人：周輝政 副院長 (Dr. Hei-Jen Jou) 臺安醫院
10:30 - 10:55	李華容 副研究員 (Dr. Hua-Jung Li) 國家衛生研究院 細胞及系統醫學研究所 Exosomes in Stem Cell Homeostasis, Cancer, and Regeneration Medicine	阮雪芬 特聘教授 (Dr. Hsueh-Fen Juan) 國立臺灣大學 生命科學系 AI for Drug Repositioning	王子豪教授紀念講座 Memorial Lecture for Prof. Tzu-Hao Wang 賴鴻政 副院長 (Dr. Hung-Cheng Lai) 衛生福利部雙和醫院 FemTech: Precision Women Health
11:00 - 11:25	王竹安 助理研究員 (Dr. Chu-An Wang) 國立成功大學 分子醫學研究所 The Function and Regulation of EV-VEGF-C in Pancreatic Cancer Early Metastasis	陳倩瑜 教授 (Dr. Chien-Yu Chen) 國立臺灣大學 生物機電工程學系 Whole Genome Sequencing Data Analysis Using Deep Learning	李妮鍾 醫師 (Dr. Ni-Chung Lee) 台大醫院 基因醫學部暨小兒部 兒童罕病的精準醫療－機會與挑戰 Precision Medicine for Critically Ill Children – Opportunities and Challenges
11:30 - 11:55	徐瑋萱 助理教授 (Dr. Wei-Hsuan Hsu) 國立成功大學 食品安全衛生暨風險管理研究所 Development and Application of Extracellular Vesicles Derived from Probiotics	張家銘 助理教授 (Dr. Jia-Ming Chang) 國立政治大學 資訊科學系 Computational Protein Function Prediction	張璧月 主任 (Dr. Pi-Yueh Chang) 林口長庚紀念醫院 檢驗醫學部 我會得癌症嗎? 遺傳性癌症基因檢測經驗分享 Am I Susceptible to Cancer?
12:00 - 12:25	TSEV 線上時間	TBSB 線上時間	TPMS 線上時間
12:30 - 13:10	科技新知分享 法德利科技股份有限公司 全球疫情帶來的醫藥產業新秩序 －數據為王、有「它」就強！	六學會理事長專訪 學會的回顧與展望	凱杰生物科技有限公司 QIAGEN實現NGS樣本定序到數據分析解決方案
13:10 - 13:30			
Section IV	Disease Biomarker & Mechanism 主持人：周涵怡 副教授 (Dr. Han-Yi E. Chou) 國立台灣大學 口腔生物科學研究所	Genomics of Pathogens 主持人：丁照棣 教授 (Dr. Chau-Ti Ting) 國立臺灣大學 生態學與演化生物學研究所	Target Therapy 主持人：盧章智 理事長 (Dr. Jang-Jih Lu) 台灣精準醫學學會
13:30 - 13:55	徐丞志 副教授 (Dr. Cheng-Chih Hsu) 國立臺灣大學 化學系 Ambient Mass Spectrometry and Machine Learning for Disease Diagnosis	王弘毅 教授 (Dr. Hurng-Yi Wang) 國立台灣大學 臨床醫學研究所 The Origin and Underlying Driving Forces of SARS-CoV-2 Outbreak	嚴成文 教授 (Dr. Chen-Wen Yen) 國立中山大學 機械與機電工程學系 睡眠醫學遇上機器學習 When Sleep Medicine Meets Machine Learning
14:00 - 14:25	郭文宏 醫師 (Dr. Wen-Hung Kuo) 台大醫院 一般外科 Clinical Application of Circulation Extracellular mi-RNA in Breast Cancer	林明德 副教授 (Dr. Ming-Der Lin) 慈濟大學 分子生物暨人類遺傳學系 The Genome of Prorhinotermes Flavus: A Termite Species with High Salinity Tolerance	楊晶安 主任 (Dr. Chin-An Yang) 中國醫藥大學附設醫院 竹北分院 精準用藥：從高維度次世代定序資訊分析談起 Drug Selection Using High-dimensional NGS Data Analysis
14:30 - 14:55	吳子珩 執行長 (Dr. Tzu-Heng Wu) PlasmonicTron Engineered Aptamer Based Plasmonic Sensing Toward Exosome Liquid Biopsy and Beyond	顧銓 助研究員 (Dr. Chuan Ku) 中央研究院 植物暨微生物學研究所 Genome Content Evolution in Giant Viruses of Eukaryotes	楊博鈞 副總經理 (Dr. Eric P. Yang) 奎克生技光電股份有限公司 The Various Diagnostic Technologies for Precision Target Therapy
15:10 - 15:30	閉幕式 (第一會議廳)		

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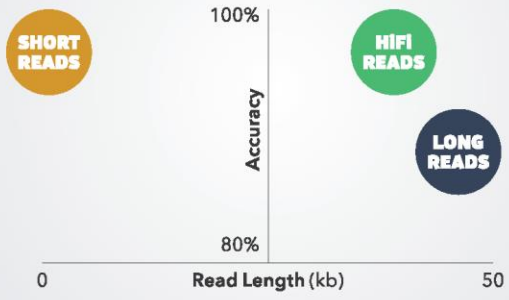

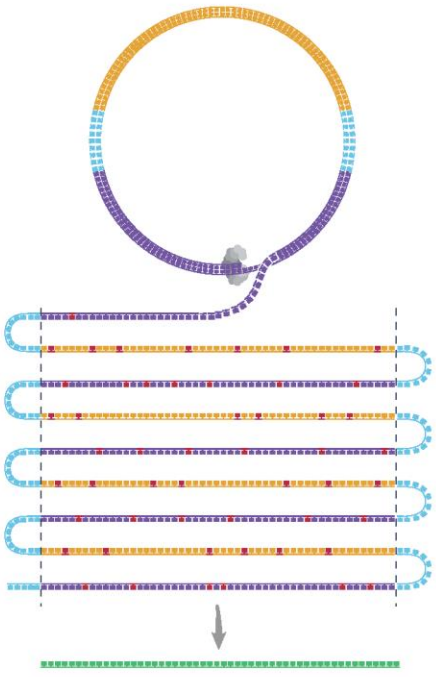

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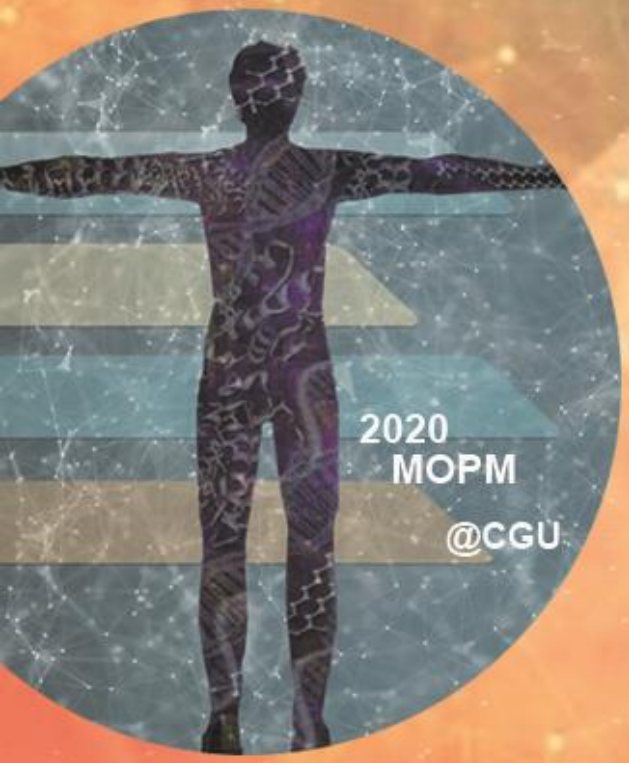

Yu-Sun Chang, Ph.D. (張玉生)

Current position and professional experiences

2020/2 ~ Present	**Visiting Professor**, Molecular Medicine Research Center, Chang Gung University
2014 ~ 2020	**Chair Professor**, Graduate Institute of Biomedical Sciences, Chang Gung University
2005 ~ 2016	**Director**, Molecular Medicine Research Center, Chang Gung University
1999 ~ 2001	**Professor and Director**, Graduate Institute of Basic Medical Sciences, Chang Gung University

Research interest

1. Epstein-Barr virus and nasopharyngeal carcinoma
2. Cancer biology
3. Molecular medicine (biomarkers/biosignatures)

Short research summary

Dr. Chang received her Ph.D. degree from the graduate program of Microbiology, University of California at Davis. She has started her career in Chang Gung University since 1986, started by setting up the Department of Microbiology. Her research interest has been focused on

(1) Nasopharyngeal carcinoma/Epstein-Barr virus

The long term and continued research interest of her team is to understand the role of Epstein-Barr virus (EBV) in the development of nasopharyngeal carcinoma (NPC), and to study candidate biomarkers for early detection, prognosis and therapy of NPC. Her team has contributed few pioneered research including a) discovery multiple NPC-associated loci within the HLA region at Chromosome 6p21.3 by genome-wide association study (GWAS); b) Discovery and verification of NPC biomarkers for translational study; c) Functional studies of EBV-encoded oncogene latent membrane protein 1 (LMP1); and d)Biological and clinical role of inflammasomes in NPC.

(2) Cancer Biomarkers and translational application

Dr. Chang has initiated the cancer biomarker studies since 2003 mainly through collaboration with clinical colleagues: a) Collaboration with colleagues or groups from Chang Gung Molecular Medicine Research Center/Chang Gung Memorial Hospital on cancer biomarkers-directed translational research; b) Collaboration with National Cancer Institute, NIH, USA and International Cancer Proteogenome Consortium (associated with the US Cancer Moonshot project) on oral squamous cell carcinoma.

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Henry Rodriguez, Ph.D., M.S., MBA

Current position and professional experiences

2006 ~ Present	**Director**, Office of Cancer Clinical Proteomics Research, National Cancer Institute, National Institutes of Health; Bethesda, Maryland
2008 ~ Present	**Director**, Antibody Characterization Program, National Cancer Institute, National Institutes of Health; Bethesda, Maryland
2009 ~ Present	**Senior Scientific Officer**, National Cancer Institute, National Institutes of Health
2016 ~ Present	**Visiting Scholar (Professor)**, Academia Sinica, Taipei, Taiwan

Research interest

1. Precision oncology
2. Cancer biology
3. Genomics and proteomics metrology
4. Technology development

Short research summary

Dr. Henry Rodriguez is the founding Director of the Office of Cancer Clinical Proteomics Research at the National Cancer Institute (NCI), National Institutes of Health (NIH), and a member of the NCI Senior Leadership where he assists in the development of strategies and priorities to achieve the mission and goals of the NCI. Previously, Dr. Rodriguez served as at the Acting Deputy Director of the Center for Strategic Scientific Initiatives at the NCI, and held multiple roles at the National Institute of Standards and Technology, including Director of a research group and Health Sciences Program/Policy Analyst in the Office of the Director that involved coordination with the Department of Commerce Office of Financial Management, Congress, and the Department of Health and Human Services Secretary's Advisory Committee on Genetic, Health and Society.

Dr. Rodriguez has over 25 years of management and research experience, with a focus on understanding mechanisms of cancer and age-related diseases, including development of molecular-based technologies in basic and clinical science. Dr. Rodriguez is a member of several organizations, and is a recipient of numerous honors. Dr. Rodriguez has authored more than 140 original research papers, including co-editing a best-selling book on oxidative stress and aging. Dr. Rodriguez received his B.S. in biology/chemistry and M.S. in biology/toxicology from Florida International University, Ph.D. in cell and molecular biology from Boston University, and M.B.A. in finance and management from Johns Hopkins University Carey Business School. Fellowships were conducted at the Scripps Research Institute and City of Hope Comprehensive Cancer Center.

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Beyond Cancer Genomics: Toward Precision Medicine

Henry Rodriguez
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Although recent genomic landscape studies have provided a comprehensive map of the genetic alterations associated with human cancers, the direct consequences of these alterations on the functional proteome are not well understood. So while genomic markers can be used to determine predisposition to tumor development, unfortunately, molecularly targeted treatment strategies are not widely available for most cancers. Integration of proteomic data with genomic data (proteogenomics) facilitates to advance our understanding of the causes of cancer and narrow target selection for potential therapeutic intervention by providing increased granularity regarding cancer-relevant pathways triggered by somatic DNA variants or DNA copy number alterations. In particular, the analysis of phosphorylation and other post-translational modifications by mass spectrometry-based proteomics provides pathway insights not obtainable from genomic analysis alone. As such, proteogenomics provides an opportunity to generate new insights by melding the complexity of cancer genomics with cancer proteomics to more completely understand how somatic genomes activate aberrant signal transduction events that drive cancer pathogenesis, with the potential to fast become an essential part of laboratory medicine. This seminar will discuss how genomics, transcriptomics, and proteomics are being combined in the quest to understand the etiology of cancer – in basic clinical sample studies and translational research (clinical trials).

Tang-Long Shen, Ph.D. (沈湯龍)

Current position and professional experiences

Director, Center of Industry-Academia Cooperation, National Taiwan University
Director, Center for Biotechnology, National Taiwan University
Professor, Department of Plant Pathology and Microbiology, National Taiwan University, Taipei, Taiwan
Professor, Program of Genomics and Systems Biology, National Taiwan University, Taipei, Taiwan
President, Taiwan Society for Extracellular Vesicles (TSEV)

Research interest

1. Signal transduction (migration/cell cycle)
2. Pre-metastatic niche/exosomes/organotropism
3. Neurodegenerative and aging
4. Microbial secondary metabolites
5. Molecular plant-microbe interactions

Awards and honors

1. The American Society for Cell Biology (ASCB) 2001 annual meeting Predoctoral Travel Awards. 2001
2. Liu Memorial Award in Cornell University for an excellent progress in graduate program and high potential for a successful academic career. 2002
3. American Heart Association Postdoctoral Fellowship, USA 2003-2005
4. Blind Prevention Foundation Scholar Travel Award, USA 2010
5. The 6th Breast Cancer Outstanding Research Award, Breast cancer prevention foundation, Taiwan

Short research summary

Prof. Tang-Long Shen received his BS and MS degrees from National Taiwan University in the Department of Plant Pathology in 1991 and 1994, respectively, and obtained his PhD from Cornell University in the Department of Molecular Medicine in 2002. After his postdoc training in American Heart Association, Prof. Shen joined the Department of Plant Pathology and Microbiology at the National Taiwan University since 2004. His research explores varied subjects, including microbes, plants to human, to understand the basic mechanisms of various pathologic complications as well as how to utilize the microbial metabolites or natural product for human health. By using molecular biology, biochemistry and cellular biology approaches as well as animal models, Prof. Shen deciphers the molecular mechanism of cancer progression, especially how cancer cells interact with tumor microenvironment in cell migration, the formation of pre-metastatic niches and metastatic organotropism. Several key targets, including integrins, receptor tyrosine kinases (e.g. EGFR), non-receptor tyrosine kinases (e.g. FAK, Src), adaptor proteins (e.g. Grb7, C35) and cytokines as well as extracellular vesicles (e.g. exosomes), are main focuses. Additionally, Shen lab is also seeking useful natural products and de novo protein components in human cells including critical secondary metabolites from traditional Chinese medicinal fungi, Cordyceps spp, Antrodia cinnamomea, and metallothioneins, to apply for anti-cancer, anti-aging or other therapeutics.

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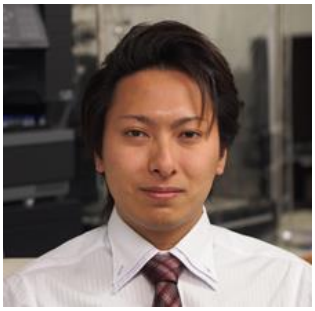
Koji Ueda, Ph.D. (植田幸嗣)



Current position and professional experiences

2015 ~ Present **Group Leader**,
Cancer Proteomics Group
Project Leader,
Project for Realization of Personalized Cancer Medicine
Cancer Precision Medicine Center,
Japanese Foundation for Cancer Research (JFCR)

Research interest

1. Proteogenomics
2. Cancer early detection
3. Cancer liquid biopsy
4. Cancer immunology

Short research summary

Dr. Koji Ueda is a Group Leader of Cancer Proteomics Group at Japanese Foundation for Cancer Research (JFCR). Dr. Ueda received his Ph.D degree from the University of Tokyo and has been involved in cancer genomics and proteomics researches for the past 15 years. His research interest focuses on the development of innovative proteomic technologies and application of them to establish novel cancer diagnosis. Especially, in recent years, he has worked on development of technologies for cancer liquid biopsy using extracellular vesicles. In Cancer Precision Medicine Center, JFCR, he also leads basic and translational research teams for cancer immunotherapy.

He has served as a council member of Japanese Cancer Association, a board member of Japanese Proteomics Society, and a board member of Japanese Society for Extracellular Vesicles.

Publications

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Proteogenomic Approaches in Development of Cancer Liquid Biopsy and Precision Immunotherapy

Koji Ueda
Japanese Foundation for Cancer Research, Japan

Recent development and clinical application of liquid biopsy technologies have moved cancer diagnosis into a new stage. Indeed, a variety of liquid biopsy tools (cfDNA, extracellular vesicles (EVs), CTC, etc.) have been established and tested. However, a modality utilizing mutated proteins has been rarely assessed yet, mainly due to difficulties in comprehensive and sensitive detection. Here we present our approach to develop a diagnostic model based on a mutated protein panel in circulating EVs.

To globally identify mutated EV proteins, we constructed a mutated proteome database for mass spectrometric analysis, in which publicly-available 1,066,470 cancer-associated mutations were listed as peptide sequences. We extracted EVs from viable tissue samples (normal mucosa, primary colon cancer, and liver metastasis, n = 17) and performed proteome analysis using Orbitrap Fusion Lumos-FAIMS Pro LC/MS and the in-house mutated proteome database. Whole exome sequence analysis was also performed for the identical set of tissue samples. As the second part, EV mutated protein panel diagnostics for colon cancer was established using the multiple reaction monitoring (MRM) method on LCMS-8060 and a set of isotope labeled mutated peptide standards.

The LC/MS analysis identified 5,543 EV proteins including, importantly, 207 mutated proteins (FDR < 0.01). From this analysis, in addition to 31 common mutations in primary colon cancer and liver metastasis, 32 primary cancer-specific mutations, 58 metastasis-specific mutations were identified. Based on this list, results of whole exome analysis, and allele frequency information in public database, our challenge to establish EV mutated protein panel diagnostics for colon cancer will be shared in this presentation, for which 96-well automated EV isolation robot and the high throughput mass spectrometric absolute quantification method are employed.

On the other hand, immunotherapy has really revolutionized the treatment of cancer. Human leukocyte antigen (HLA) binding peptide (HLAp) with somatic mutation, recognized as a neoantigen, is considered as a key initiation factor of these cancer-specific immunological reactions. However, the global analysis of neoantigens remains difficult due to a technical limitation that a large amount of sample (> 1 g of a tissue block) is needed for in-depth analysis (> 5,000 HLAp identification).

To overcome this technological task, we optimized experimental conditions for isolation of MHC complexes and employed a leading-edge LC/MS system equipped with the high-field asymmetric ion mobility spectrometry (FAIMS) ion source. By use of this method, 11 neoantigens out of 6,767 HLAps were identified from 1.5E7 cells of HCT116 cells. For neoantigen identification, tailored protein data base was established from whole exome sequencing data individually and searched for HLAp with mutation. Here we present pairwise HLAp maps acquired from colon cancer tissues and adjacent normal mucosa (n = 17), identifying 44,499 non-redundant HLAps including 2 neoantigens. These methodology and knowledgebase could contribute to establishment of future innovative cancer immunotherapy.

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垂直電泳槽 /電源供應器

轉漬

Yrdimes Semi-Dry Blotter
半乾轉漬器

E-Blotter system
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Chau-Ti Ting, Ph.D. (丁照棣)

Current position and professional experiences

2020 ~ Present	**Professor**, Department of Life Science, National Taiwan University, Taiwan
2006 ~ 2020	**Associate Professor,** Department of Life Science, National Taiwan University, Taiwan
2004 ~ 2006	**Associate Professor**, Department of Life Science, National Tsing Hua University, Taiwan
2000 ~ 2004	**Assistant Professor**, Department of Life Science, National Tsing Hua University, Taiwan

Research interest

1. Molecular evolution
2. Population genetics and genomics
3. Speciation
4. *Drosophila* genetics

Short research summary

Dr. Chau-Ti Ting is a Professor of Department of Life Science at the National Taiwan University, Taiwan. Dr. Ting received her Ph.D. degree from the National Taiwan University and has been involved in population genetics and genomics researches for more than 20 years. Dr. Ting's research interest focuses on the genetics changes during species formation and her team has applied advanced molecular genetic techniques to investigate the phenotypic consequences and fitness differences. Her work on population genomics has also revealed the evolutionary dynamics of segmental duplications and the evolutionary forces acting on these segmental duplications. In addition to her primary role in research and teaching, Dr. Ting is also the Director of Center for International Academic Exchanges in College of Life Science.

Publications

1. Burlyaeva M, Vishnyakova M, Gurkina M. Konstanin K, Lee CR, Ting CT, Schafleitner R, Nuzhdin S, Samsonova M, von Wettberg E. 2019 Collections of Mungbean [Vigna radiata) (L.) R. Wilczek] and urdbean [V. mungo (L.) Hepper] in Vavilov Institute (VIR): traits diversity and trends in the breeding process over the last 100 years. Genet Resour Crop Evol 66: 767–781. (doi.org/10.1007/s10722-019-00760-2).
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Sarah A. Tishkoff, Ph.D.

Current position and professional experiences

2012 ~ Present	**David and Lyn Silfen University Professor**, Department of Genetics, Perelman School of Medicine and Department of Biology, School of Arts and Sciences, University of Pennsylvania (Penn Integrates Knowledge Professor)
2008 ~ 2012	**David and Lyn Silfen University Associate Professor**, Department of Genetics, Perelman School of Medicine and Department of Biology, School of Arts and Sciences, University of Pennsylvania (Penn Integrates Knowledge Associate Professor)
2005 ~ 2007	**Associate Professor**, University of Maryland, Department of Biology
2000 ~ 2005	**Assistant Professor**, University of Maryland, Department of Biology

Research interest

1. African integrative evolutionary genomics
2. African genomic and phenotypic diversity project
3. The genetic basis of resistance to infectious disease
4. The genetic basis of adaptation in humans

Short research summary

Dr. Tishkoff studies genomic and phenotypic variation in ethnically diverse Africans. Her research combines field work, laboratory research, and computational methods to examine African population history and how genetic variation can affect a wide range of traits – for example, why humans have different susceptibility to disease, how they metabolize drugs, and how they adapt through evolution. Dr. Tishkoff is a member of the National Academy of Sciences and a recipient of an NIH Pioneer Award, a David and Lucile Packard Career Award, a Burroughs/Wellcome Fund Career Award, an ASHG Curt Stern award, and a Penn Integrates Knowledge (PIK) endowed chair. She is a member of the Scientific Advisory Panel for the Packard Fellowships for Science and Engineering and the Board of Global Health at the National Academy of Sciences and is on the editorial boards at PLOS Genetics, Genome Research Journal, G3 (Genes, Genomes, and Genetics), and Cell.

Publications

1. Hunt SC, Hansen MEB, Verhulst S, McQuillan MA, Beggs W, Lai TP, Mokone GG, Mpoloka SW, Meskel DW, Belay G, Nyambo TB, Abnet CC, Yeager M, Chanock SJ, Province MA, Williams SM, Aviv A, Tishkoff SA. Genetics and Geography of Leukocyte Telomere Length in Sub-Saharan Africans. Hum Mol Genet. 2020 Aug 21:ddaa187. 2020
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Genomic Evolution and Adaptation in Africa: Implications for Health and Disease

Sarah A. Tishkoff
University of Pennsylvania, USA

Africa is thought to be the ancestral homeland of all modern human populations. It is also a region of tremendous cultural, environmental and genetic diversity. Differences in diet, climate, and exposure to pathogens among ethnically and geographically diverse African populations have produced divergent selection pressures, resulting in local genetic adaptations, including some that play a role in disease susceptibility. A number of common complex diseases (including hypertension, diabetes, and chronic kidney disease) occur at higher frequency in people of African descent and are rapidly on the rise in urban regions of Africa. And yet, most human genomic studies have focused on non-African populations. The under-representation of ethnically diverse populations impedes our ability to fully understand the genetic and environmental factors influencing complex traits and may exacerbate health inequalities. A comprehensive knowledge of patterns of variation in African genomes is critical for a deeper understanding of human genomic diversity, the identification of functionally important genetic variation, the genetic basis of adaptation to diverse environments and diets, and the origins of modern humans. We use an integrative and functional genomics approach to characterize patterns of genomic variation, ancestry, and local adaptation across ethnically and geographically diverse African populations, leading to identification of novel genetic variants that play a role in immune response, metabolism, and skin pigmentation.

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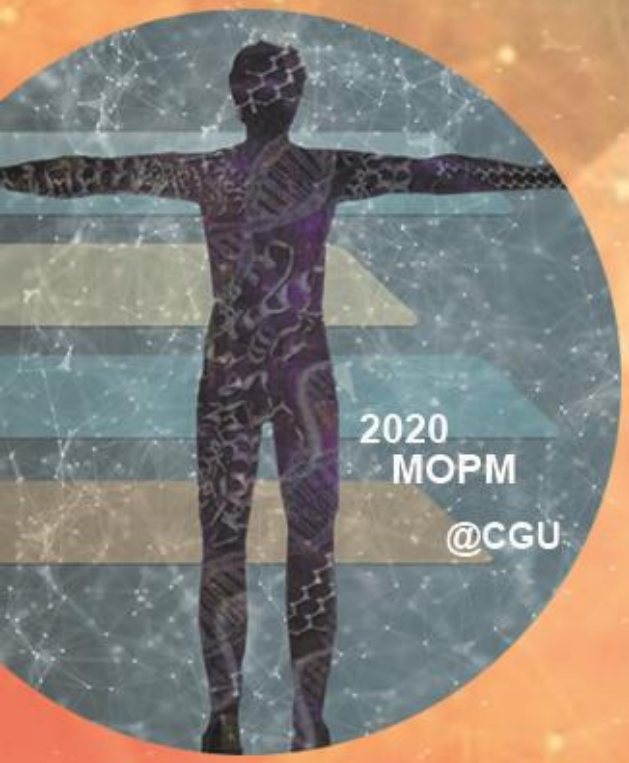

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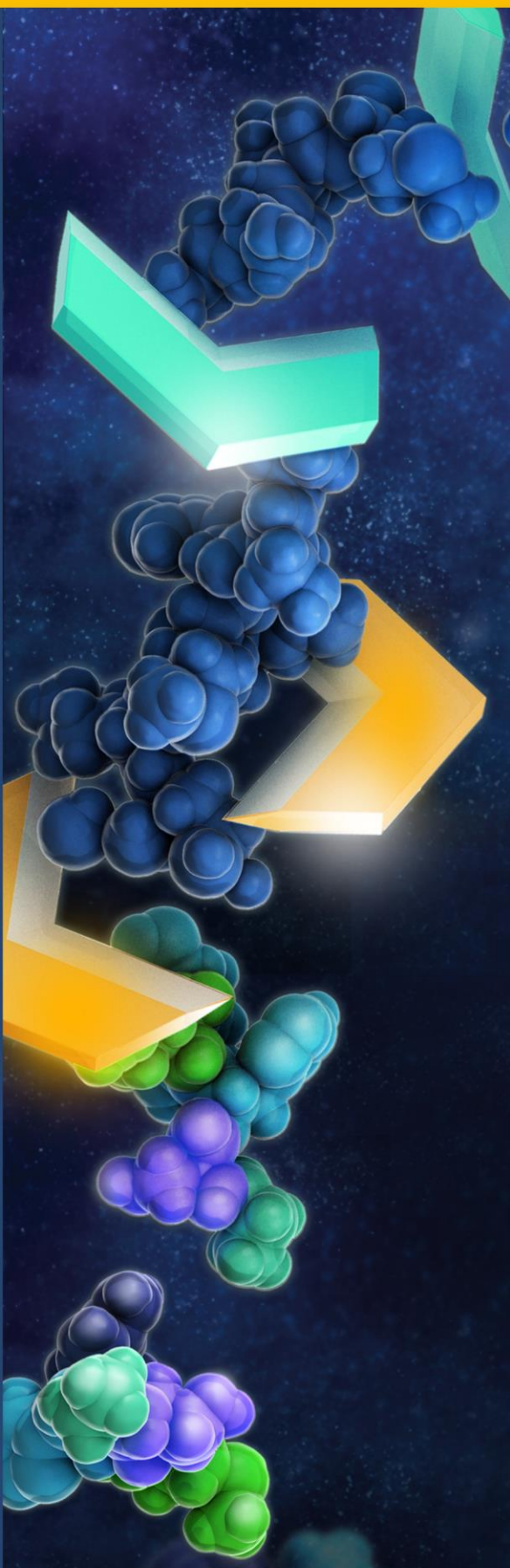

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- Trypsin Gold, Mass Spectrometry Grade
- Trypsin Platinum, Mass Spectrometry Grade
- Trypsin / Lys-C Mix, Mass Spec Grade
- Rapid Digestion–Trypsin and Rapid Digestion–Trypsin/Lys-C Kits
- Immobilized Trypsin
- AccuMAP™ Low pH Protein Digestion Kit

Alternative Protease

- Arg-C, Sequencing Grade
- Glu-C, Sequencing Grade
- Asp-N, Sequencing Grade
- rAsp-N, Mass Spec Grade
- Lys-N, Mass Spec Grade
- Lys-C, Mass Spec Grade
- rLys-C, Mass Spec Grade
- ProAlanase, Mass Spec Grade
- ProAlanase Plus, Mass Spec Grade
- Chymotrypsin, Sequencing Grade
- Thermolysin
- Pepsin
- Elastase

Glycosidase & IgG-Cleaving Protease

- PNGase F
- Endoglycosidase H
- IdeS Protease
- IdeZ Protease

GA201001

Jau-Song Yu, Ph.D. (余兆松)

Current position and professional experiences

2001/8 ~ Present	**Professor**, Department of Cell and Molecular Biology, College of Medicine, Chang Gung University, Tao-Yuan, Taiwan
2016/8 ~ Present	**Director**, Molecular Medicine Research Center, Chang Gung University, Tao-Yuan, Taiwan
2001/8 ~ 2016/7	**Director**, Core Instrument Center, Chang Gung University, Tao-Yuan, Taiwan

Research interest

1. Proteomics technology-development and application
2. Cancer biomarker and multiomics
3. Kinase-mediated signal transduction

Short research summary

Dr. Jau-Song Yu is a Professor of Department of Cell and Molecular Biology at Chang Gung University (CGU), Taiwan. Dr. Yu received his Ph.D. degree from the Department of Life Science, National Tsing-Hua University, Taiwan, R.O.C. and has been involved in proteomic researches for the past 20 years. Dr. Yu's research interest focuses on the development and application of Proteomics technologies to identify proteins deregulated in various diseases/cancer, which can be promising biomarkers with high potential for clinical use. In addition to his primary role in the University, Dr. Yu is also the Director of Molecular Medicine Research Center in CGU, in which he leads a team to develop clinically useful cancer biomarkers, investigate cancer multiomics, and provide services for multiomics analysis for basic and clinical researches.

Publications

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2. Lin YH*, Wu CC, Su WT, Tseng PC, Hsueh YY, Hsiao YC, Chang KP, Yu JS*, Chuang YR. (2020) Target peptide enrichment microfluidic chip for rapid detection of oral squamous cell carcinoma using stable isotope standards and capture by anti-peptide antibodies. Sensors and Actuators B: Chemical 322:128607
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14. Hsieh Y-J#, Chien K-Y#, Yang I-F, Lee I-N, Wu C-C, Huang T-Y, and Yu J-S* (2017) Oxidation of protein-bound methionine in Photofrin-photodynamic therapy-treated human tumor cells explored by methionine-containing peptide enrichment and quantitative proteomics approach. Scientific Reports 7(1):1370.
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Yu-Ju Chen, Ph.D. (陳玉如)

Current position and professional experiences

2013/7 ~ Present	**Director/ Distinguished Research Fellow**, Institute of Chemistry, Academia Sinica
2020/8 ~ 2022/12	**Associate Editor**, Analytical Chemistry
2020/1 ~ 2020/12	**President-Elect**, Human Proteome Organization
2021/1 ~ 2022/12	**President**, Human Proteome Organization
2017/1 ~ 2021/12	**Vice President**, Asia Oceana Human Proteome Organization
2012/1~2015/12	**President**, Taiwan Society for Mass Spectrometry
2008/1~2011/12	**President**, Taiwan Proteomics Society

Research interest

1. Biological mass spectrometry
2. Proteomic

Short research summary

Dr. Chen received Ph.D. at the Lowa State University (1997). After postdoctoral work at the Ames Laboratory (1997) and National Tsing Hua University, she joined the Institute of Chemistry, Academia Sinica, Taiwan, and was appointed as Director since 2013. She also holds adjunct professorship at National Taiwan University and National Ocean University. Though being trained as a physical chemist in photoionization mass spectrometry, she switched to the journey of proteomic research and became the pioneering scientist in establishing large-scale mass spectrometry-based proteomics in Taiwan. Dr. Chen's research focuses on developing novel nanomaterial, advanced mass spectrometry and bioinformatics tools towards comprehensive delineation of the membrane proteome and post-translation modificome. In particular, she is passionately interested in revealing the protein system network in cancer and stem cell biology. Her contribution to pioneer inter-disciplinary proteomics work has been recognized by domestic and international awards including Distinguished Young Chemists Award from Federation of Asian Chemical Societies and Outstanding Research Award from National Science Council, Taiwan. Dr. Chen is actively serving in the proteomics community by being President of HUPO, Vice President of AOHUPO, and Council Member of "International Mass Spectrometry Foundation". She has been the President of the Taiwan Proteomics Society and Taiwan Society for Mass Spectrometry. Dr. Chen is the Associate Editor of Analytical Chemistry, editorial board member of the Proteomics, European Journal of Mass Spectrometry, and Journal of Proteome Research.

Publications

1. "Proteogenomic Landscape of Early Stage Non-smoking Lung Adenocarcinoma in East Asia ", Yi-Ju Chen+, Theodoros I. Roumeliotis+, Ya-Hsuan Chang+, Ching-Tai Chen, Chia-Li Han*, Miao-Hsia Lin, Huei-Wen Chen, Gee-Chen Chang, Yih-Leong Chang, Chen-Tu Wu, Mong-Wei Lin, Min-Shu Hsieh, Yu-Tai Wang, Yet-Ran Chen, Inge Jonassen, Fatemeh Zamanzad Ghavidel, Ze-Shiang Lin, Kuen-Tyng Lin, Ching-Wen Chen, Pei-Yuan Sheu, Chen-Ting Hung, Ke-Chieh Huang, Hao-Chin Yang, Pei-Yi Lin, Ta-Chi Yen, Yi-Wei Lin, Jen-Hung Wang, Lovely Raghav, Chien-Yu Lin, Yan-Si Chen, Pei-Shan Wu, Chi-Ting Lai, Shao-Hsing Weng, Kang-Yi Su, Wei-Hung Chang, Pang-Yan Tsai, Ana I. Robles, Henry Rodriguez, Ting-Yi Sung*, Jin-Shing Chen*, Sung-Liang Yu*, Jyoti S. Choudhary* , Hsuan-Yu Chen*, Pan-Chyr Yang*, Yu-Ju Chen*, Cell 182, 226-244 (2020) IF:36.216

2. “Standardization and Harmonization of Distributed Multi-National Proteotype Analysis supporting Precision Medicine Studies “, Yue Xuan, Nicholas W. Bateman, Sebastien Gallien, Sandra Goetze, Yue Zhou, Pedro Navarro, Mo Hu, Niyati Parikh, Brian L. Hood, Kelly A. Conrads, Christina Loosse, Reta Birhanu Kitata, Sander R. Piersma, Davide Chiasserini, Hongwen Zhu, Guixue Hou, Muhammad Tahir, Andrew Macklin, Amanda Khoo, Xiuxuan Sun, Ben Crossett, Albert Sickmann, Yu-Ju Chen, Connie R. Jimenez, Hu Zhou, Siqi Liu, Martin R. Larsen, Thomas Kislinger, Zhinan Chen, Benjamin L. Parker, Stuart J. Cordwell, Bernd Wollscheid, Thomas P. Conrads, bioRxiv preprint doi: https://doi.org/10.1101/2020.03.12.988089 (2020)
3. “Proteomic Analysis Reveals Anti-Fibrotic Effects of Blue Light Photobiomodulation on Fibroblasts“, Lo-Yu Chang, Sabrina Mai-Yi Fan, Yen-Chen Liao, Wei-Hung Wang, Yu-Ju Chen and Sung-Jan Lin*, Lasers Surg Med, 52, 358-372 (2020), IF:3.262
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9. “Glycoproteomic Alterations in Drug-Resistant Nonsmall Cell Lung Cancer Cells Revealed by Lectin Magnetic Nanoprobe-Based Mass Spectrometry”, Juanilita T Waniwan, Yi-Ju Chen, Rey Capangpangan, Shao-Hsing Weng, Yu-Ju Chen*, J Proteome Res., 17 (11), 3761-3773, (2018), IF:3.950
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12. “Subcellular Proteome Landscape of Human Embryonic Stem Cells Revealed Missing Membrane Proteins”, Mehari Muuz Weldemariam, Chia-Li Han, Faezeh Shekari, Reta Birhanu Kitata, Ching- Yu Chuang, Wei-Ting Hsu, Hung-Chih Kuo, Wai-Kok Choong, Ting-Yi Sung, Fu-Chu

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15. “DNA Demethylation by DNMT3A and DNMT3B in vitro and of Methylated Episomal DNA in Transiently Transfected Cells”, Biswanath Chatterjee, Miao-Hsia Lin, Chun-Chang Chen, Kai-Lin Peng, Mu-Sheng Wu, Mei-Chun Tseng, Yu-Ju Chen, Che-Kun James Shen*, BBA-Gene Regul Mech, 1861(11), 1048-1061, (2018), IF:5.179
16. “Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function”, Young-Ki Paik, Lydie Lane, Takeshi Kawamura, Yu-Ju Chen, Je-Yoel Cho, Joshua LaBaer, Jong Shin Yoo, Gilberto Domont, Fernando Corrales, Gilbert S Omenn, Alexander Archakov, Sergio Encarnación-Guevara, Siqi Lui, Ghasem Hosseini Salekdeh, Jin-Young Cho, Chae-Yeon Kim, Christopher M Overall, J Proteome Res., 17(12), 4042-4050, (2018), IF:3. 950
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18. “Exploring the Expression Bar Code of SAA Variants for Gastric Cancer Detection”, Deng-Chyang Wu, Kai-Yi Wang, Sophie S.W. Wang, Ching-Min Huang, Yi-Wei Lee, Michael Isaac Chen, Szu-An Chuang, Shu-Hua Chen, Ying-Wei Lu, Chun-Cheng Lin, Ka-Wo Lee, Wen-Hung Hsu, Kun-Pin Wu, Yu-Ju Chen*, Proteomics, 17 (11), doi: 10.1002/pmic.201600356, (2017), IF:4.041 (Cover Story)
19. “One-Pot Two-Nanoprobe Assay Uncovers Targeted Glycoprotein Biosignature”, Mira Anne dela Rosa, Wei-Chun Chen, Yi-Ju Chen, Rofeamor Obena, Chih-Hsiang Chang, Rey Capangpangan, Tung-Hung Su, Chi-Ling Chen, Pei-Jer Chen, Yu-Ju Chen*, Anal. Chem. 89, 3973 – 3980, (2017), IF: 5.886
20. “Phosphoproteomics Reveals HMGA1, a CK2 Substrate, as a Drug-Resistant Target in Non-Small Cell Lung Cancer”, Yi-Ting Wang, Szu-Hua Pan, Chia-Feng Tsai, Ting-Chun Kuo, Hsin-Yung Yen, Wai-Kok Choong, Hsin-Yi Wu, Yuan-Ling Hsu, Tse-Ming Hong, Ting-Yi Sung, Pan-Chyr Yang, Yu-Ju Chen*, Sci Rep, 7 ,44021, (2017), IF:5.228
21. “Role of S-Palmitoylation by ZDHHC13 in Mitochondrial Dysfunction and Metabolic Disequilibrium”, Li-Fen Shen, Yi-Ju Chen, Kai-Ming Liu, Amir N. Saleem Haddad, I-Wen Song, Hsiao-Yuh Roan, Li-Ying Chen, Jeffrey J. Y. Yen, Yu-Ju Chen, Jer-Yuarn Wu, Yuan-Tsong Chen*, Sci. Rep. 7: 2182 (2017) , IF:4.259
22. “Identification of Siglec Ligands Using a Proximity Labeling Method”, Lanyi Chang, Yi-Ju Chen, Chan-Yo Fan, Chin-Ju Tang, Yi-Hsiu Chen, Penk-Yeir Low, Albert Ventura, Chun-Cheng Lin, Yu-Ju Chen , and Takashi Angata.*, J Proteome Res. 16(10):3929-3941, doi: 10.1021/acs.jproteome.7b00625, (2017) , IF:4.268
23. “Decoding the Effect of Isobaric Substitutions on Identifying Missing Proteins and Variant Peptides in Human Proteome”, Wai Kok Choong, T. Mamie Lih, Yu-Ju Chen, Ting-Yi Sung *, J Proteome Res., doi: 10.1021/acs.jproteome.7b00342, (2017) , IF:4.268
24. "iTop-Q: An Intelligent Tool for Top-down Proteomics Quantitation Us-ing DYAMOND Algorithm", Hui-Yin Chang, Ching-Tai Chen, Chu-Ling Ko, Yi-Ju Chen, Yu-Ju Chen, Wen-Lian Hsu, Chiun-Gung Juo, Ting-Yi Sung, Anal. Chem., 89 (24), 13128–13136 (2017), IF:6.32

25. "ROS-Independent ER Stress-Mediated Nrf2 Activation Promotes Warburg Effect to Maintain Stemness-Associated Properties of Cancer-Initiating Cells", Jeng-Fan Lo, Ching-Wen Chang, Yu-Syuan Chen, Yeou-Guang Tsay, Chia-Li Han, Yu-Ju Chen, Cheng-Chieh Yang, Kai-Feng Hung, C.H. Lin, Tsung-Yen Huang, Shou-Yen Kao, and Te-Chang Lee*, Cell Death Dis, (2017), IF:5.965
26. "Data for Whole and Mitochondrial Proteome of Human Embryonic Stem Cells", Faezeh Shekari, Hossein Nezari, Yu-Ju Chen, Hossein Baharvand*, Ghasem Hosseini Salekdeh*, J Proteomics, 162 (6), 108-118, (2017), IF: 3.914
27. "FAM198B is Associated with Prolonged Survival and Inhibits Metastasis in Lung Adenocarcinoma via Blockage of ERK-Mediated MMP-1 Expression", Chia-Ying Hsu, Gee-Chen Chang, Yi-Ju Chen, Yi-Chiung Hsu, Yi-jing Hsiao, Kang-Yi Su, Hsuan-Yu Chen, Chien-Yu Lin, Jin-Shing Chen, Yu-Ju Chen, Qi-Sheng Hong, Wen-Hui Ku, Chih Ying Wu, Bing-Ching Ho, Ching-Cheng Chiang, Pan-Chyr Yang, and Sung-Liang Yu, Clin Cancer Res, (2017) , IF:9.619
28. "Temporal Regulation of Lsp1 O-GlcNAcylation and Phosphorylation During Apoptosis of Activated B Cells", Jung-Lin Wu, Hsin-Yi Wu, Dong-Yan Tsai, Ming-Feng Chiang, Yi-Ju Chen, Shijay Gao, Chun-Cheng Lin, Chun-Hung Lin, Kay-Hooi Khoo, Yu-Ju Chen*, Kuo-I Lin*, Nat. Commun., 7:12526, (2016), IF:11.47
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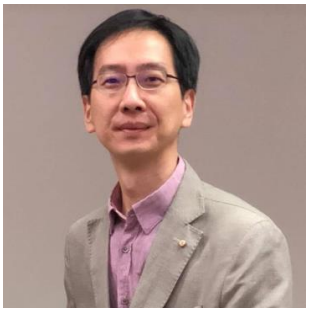
30. "Functionalized HgTe Nanoparticles Promote Laser-Induced Solid Phase Ionization/Dissociation for Comprehensive Glycan Sequencing", Indah Primadona, Yin-Hung Lai, Rey Y. Capangpangan, Rofeamor P. Obena, Mei-Chun Tseng, Ming-Feng Huang, Huan-Tsung Chang, Shiou-Ting Li, Chung-Yi Wu, Wei-Ting Chien, Chun-Cheng Lin, Yi-Sheng Wang*, Yu-Ju Chen* , Analyst, 141, 6093-6103, (2016), IF: 4.107
31. "Atomic force Microscopy Characterization of Kinasemediated Phosphorylation of a Peptide Monolayer", Roman Zhuravel, EinavAmit, Shir Elbaz, Dvir Rotem, Yu-Ju Chen, Assaf Friedler, ShlomoYitzchaik*, Danny Porath*, Sci. Rep., 6: 36793, (2016), IF: 5.228
32. "Chemical Inhibition of Human Thymidylate Kinase and Structural Insights into the Phosphate Binding Loop and Ligand-Induced Degradation", Yi-Hsuan Chen, Hua-Yi Hsu, Ming-Tyng Yeh, Chen-Cheng Chen, Chang-Yu Huang, Ying-Hsuan Chung, Zee-Fen Chang, Wei-Chen Kuo, Nei-Li Chan, Jui-Hsia Weng, Bon-chu Chung, Yu-Ju Chen, Cheng-Bang Jian, Ching-Chieh Shen,Hwan-Ching Tai, Sheh-Yi Sheu*, Jim-Min Fang*, , J. Med. Chem., 59 (21), 9906-9918, (2016), IF: 5.589
33. "Untargeted, Spectral Library-Free Analysis of Data Independent Acquisition Proteomics Data Generated Using Orbitrap Mass Spectrometers", Chih-Chiang Tsou, Chia-Feng Tsai, Guoci Teo, Yu-Ju Chen, Alexey I. Nesvizhskii*, Proteomics, 16, (15-16), 2257-2271, (2016), IF: 3.807
34. "Download: The Impact of Dupase on Ribonucleotide Reductase-Induced Genome Instability in Cancer Cells", Chih-Wei Chen, Ning Tsao, Lin-Yi Huang, Yun Yen, Xiyong Liu, Christine Lehman, Yuh-Hwa Wang, Mei-Chun Tseng, Yu-Ju Chen, Yi-Chi Ho, Chian-Feng Chen, Zee-Fen Chang*, Cell Rep., 16 (5), 1287-1299, (2016), IF: 7.87
35. "The Shp2-induced Epithelial Disorganization Defect is Reversed by HDAC6 Inhibition Independent of Cdc42", Sui-Chih Tien, Hsiao-Hui Lee, Ya-Chi Yang, Miao-Hsia Lin, Yu-Ju Chen, Zee-Fen Chang*, Nat. Commun., 7, 10420, (2016), IF:11.47
36. "A Photo-Cleavable Biotin Affinity Tag for the Facile Release of a Photo-Crosslinked Carbohydrate-Binding Protein", Tsung-Che Chang, Avijit K. Adak, Ting-Wei Lin, Pei-Jhen Li, Yi-Ju Chen, Chain-Hui Lai, Chien-Fu Liang, Yu-Ju Chen, Chun-Cheng Lin*, Bioorgan Med Chem. 24 (6), 1216–1224, (2016), IF:11.47

Taiwan Cancer Proteogenomics Moonshot: Pathway to Next Generation Precision Medicine in Cancer

Yu-Ju Chen
Institute of Chemistry, Academia Sinica, Taiwan

Advances in mass spectrometry-based proteomic technologies have opened the new avenue to identify and quantify thousands of proteins, post-translational modification (PTM) and their system network regulating various biological and physiological functions. Personalized proteomics starts to impact the development of personalized medicine by facilitating discovery of protein biomarkers, molecular signature of disease subtype and response to treatment of individual patients. Combing proteomics with the long standing success of genomics, proteogenomics was recently launched as an emerging tool for full delineation of genomic-to-proteomic network associated with disease. With the aim of accelerating the progress toward prevention, control and treatment for cancer, Taiwan joined the global effort of International Cancer Proteogenome Consortium (ICPC) under Cancer Moonshot initiated by US to apply proteogenomics as a precision approach to delineate the connection of genomic abnormalities and protein alteration in individual cancer patient's tissues. In this talk, I will present the first proteogenomics study on a prospectively collected cohort representing early stage lung adenocarcinomas in Taiwan. We delineated age-dependent mutational signatures as well as the proteogenomic hallmarks of tumor progression and propose a proteomics-informed classification to distinguish the diverse clinical trajectories of patients with EGFR mutation within early stages. Functional annotation of the molecular subtypes by protein network analysis highlights candidate biomarkers for patient stratification and therapeutic opportunity. Our integrative analysis reveals the molecular architecture of lung cancer in East Asia and enables the path for precision medicine.

Chang-Shi Chen, Ph.D. (陳昌熙)



Current position and professional experiences

2017 ~ Present	**Professor**, Biochemistry and Molecular Biology, National Cheng Kung University, Taiwan
2013 ~ 2017	**Associate Professor**, Biochemistry and Molecular Biology, National Cheng Kung University, Taiwan
2008 ~ 2013	**Assistant Professor**, Biochemistry and Molecular Biology, National Cheng Kung University, Taiwan
2006 ~ 2008	**Postdoctoral Scholar**, Cell and Developmental Biology, Division of Biological Sciences, University of California, San Diego

Research interest

1. Bacterial pore-forming toxins
2. Enterohemorrhagic *Escherichia coli*
3. Host-pathogen interactions
4. Caenorhabiditis elegans biology

Short research summary

Our laboratory studies the genetic bases of the intrinsic cell defense systems against pathogenic bacteria and their virulence factors. We apply chemical genomic, forward/reverse genetic, CRISPR/Cas9 genome editing, molecular and biochemical methodologies, and the model organism *Caenorhabditis elegans* to elucidate the conserved mechanisms in host-pathogen interactions. A rapidly growing number of human and animal microbial pathogens have been shown to infect and kill *C. elegans*. In many cases, microbial genes known to be essential for full virulence in mammalian models have been shown to be similarly required for maximum pathogenicity. Since the innate immune responses are highly conserved among different organisms throughout evolution, understanding the molecular basis of the intrinsic cell defense systems in *C. elegans* should shed light onto some aspects of immunity in human diseases.

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3. Wen-Chun Huang, Chung-Yen Lin, Masayuki Hashimoto, Jiunn-Jong Wu, Ming-Cheng Wang, Wei-Hung Lin, Chang-Shi Chen, and Ching-Hao Teng. The role of the bacterial protease Prc in the uropathogenesis of extraintestinal pathogenic Escherichia coli. J Biomed Sci. 2020 Jan 3;27(1):14.
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6. Ling-Hsien Tu, Ning-Hsuan Tseng, Ya-Ru Tsai, Yi-Wei Lo, Jien-Lin Charng, Hua-Ting Hsu, Yu-Sheng Chen, Rong-Jie Chen, Ying-Da Wu, Yi-Tsu Chan, Chang-Shi Chen, Jim-Min Fang, and Yun-Ru Chen. Rationally designed divalent caffeic amides inhibit amyloid-β fibrillization, induce fibril dissociation, and ameliorate cytotoxicity. Eur J Med Chem. 2018 Oct 5;158:393-404.
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bacteremic Aeromonas isolates: ex vivo, animal, and clinical evidences. PLoS One. 2014 Nov 6;9(11):e111213. *Corresponding authors.

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A Multiomic Analysis Reveals the Role of Fumarate in Regulating the Virulence of Enterohemorrhagic *Escherichia coli*

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Department of Biochemistry and Molecular Biology, College of Medicine,
National Cheng Kung University, Taiwan

The enteric pathogen enterohemorrhagic *Escherichia coli* (EHEC) is responsible for outbreaks of bloody diarrhea and hemolytic uremic syndrome (HUS) worldwide. Several molecular mechanisms have been described for the pathogenicity of EHEC; however, the role of bacterial metabolism in the virulence of EHEC during infection in vivo remains unclear. Here we show that aerobic metabolism plays an important role in the regulation of EHEC virulence in *Caenorhabditis elegans*. Our functional genomic analyses showed that disruption of the genes encoding the succinate dehydrogenase complex (Sdh) of EHEC, including the *sdhA* gene, attenuated its toxicity toward *C. elegans* animals. Sdh converts succinate to fumarate and links the tricarboxylic acid (TCA) cycle and the electron transport chain (ETC) simultaneously. Succinate accumulation and fumarate depletion in the EHEC *sdhA* mutant cells were also demonstrated to be concomitant by metabolomic analyses. Moreover, fumarate replenishment to the *sdhA* mutant significantly increased its virulence toward *C. elegans*. These results suggest that the TCA cycle, ETC, and alteration in metabolome all account for the attenuated toxicity of the sdhA mutant, and Sdh catabolite fumarate in particular plays a critical role in the regulation of EHEC virulence. In addition, we identified the tryptophanase (TnaA) as a downstream virulence determinant of SdhA using a label-free proteomic method. We demonstrated that expression of *tnaA* is regulated by fumarate in EHEC. Taken together, our multiomic analyses demonstrate that *sdhA* is required for the virulence of EHEC, and aerobic metabolism plays important roles in the pathogenicity of EHEC infection in C. elegans. Moreover, our study highlights the potential targeting of SdhA, if druggable, as alternative preventive or therapeutic strategies by which to combat EHEC infection.

Cheng-Yuan Kao, Ph.D. (高承源)

Current position and professional experiences

2017/9 ~ Present **Associate Investigator**, Immunology Research Center, National Health Research Institutes, Zhunan, Miaoli, Taiwan

2012/8 ~ 2017/8 **Assistant Investigator**, Immunology Research Center, National Health Research Institutes, Zhunan, Miaoli, Taiwan

Research interest

1. Microbiota
2. Systems biology
3. Gut barrier and mucosal immunity
4. Inflammatory diseases (obesity, metabolic disorder, colitis, etc.)

Short research summary

Dr. Cheng-Yuan Kao completed BS in National Cheng-Kung University and MS in National Yang-Ming University in Taiwan. He received PhD degree from University of California Davis in 2005 and then further worked as a postdoctoral researcher at University of California San Diego and project scientist in University of California Davis from 2005 to 2012. In 2012 he joined the Faculty at Immunology Research Center in National Health Research Institutes, and were promoted to Associate Investigator in 2017. Currently Dr. Kao's lab has been focusing on applying a multi-omics (transcriptomics, proteomics, metabolomics, culturomics and microbiome/metagenome) strategy and complementary in vitro and in vivo approaches to study the roles of microbiota in inflammaging and inflammatory diseases such as obesity/metabolic disorders and colitis.

Publications

1 Sarah Statt, Jhen-Wei Ruan, Chih-Ting Huang, Reen Wu and Cheng-Yuan Kao*. Lipidome and transcriptome profiling of pneumolysin intoxication identifies networks involved in statin-conferred protection of airway epithelial cells. Scientific Reports 2015 May 29;5:10624.

2 Chao-Yang Lai, Da-Wei Yeh, Chih-Hao Lu, Yi-Ling Liu, Li-Rung Huang, Cheng-Yuan Kao, Huan-Yuan Chen, Chi-Ying F. Huang, Chung-Hsing Chang, Yunping Luo, Rong Xiang and Tsung-Hsien Chuang. Identification of Thiostrepton as a novel inhibitor for psoriasis-like inflammation induced by TLR7-9. The Journal of Immunology 2015 Oct 15;195(8):3912-21.

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Autophagy 2017 Feb;13(2):371-385.

6 Wei-Chan Hsu, Ming-Yu Chen, Shu-Ching Hsu, Li-Rung Huang, Cheng-Yuan Kao, Wen-Hui Cheng, Chien-Hsiung Pan, Ming-Sian Wu, Guann-Yi Yu, Ming-Shiu Hung, Chuen-Miin Leu, Tse-Hua Tan, and Yu-Wen Su. DUSP6 mediates T cell receptor-engaged glycolysis and restrains TFH cell differentiation. Proceedings of the National Academy of Sciences of the United States of America. 2018 Aug 21;115(34):E8027-E8036.

7 Cherng-Shyang Chang, Jhen-Wei Ruan, and Cheng-Yuan Kao*. An overview of microbiome based strategies on anti-obesity. The Kaohsiung Journal of Medical Sciences 2019 Jan;35(1):7-16.

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10 Yi-Ting Tsai, Jhen-Wei Ruan, Cherng-Shyang Chang, Mei-Lan Ko, Hsiu-Chuan Chou, Chi-Chien Lin, Chiao-Mei Lin, Chih-Ting Huang, Yu-Shan Wei, En-Chi Liao, Hsin-Yi Chen, Cheng-Yuan Kao* and Hong-Lin Chan*. Antrodia cinnamomea confers obesity resistance and restores intestinal barrier integrity in leptin-deficient obese mice. Nutrients, 2020 Mar 10; 12(3), 726.

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A Multi-omics Analysis Reveals Novel Insights of Gut Microbiota Shaping and Inflammation Control

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National Health Research institutes, Taiwan

Gut microbiota has been recognized to play essential roles in host physiology and might be critically relevant to many human diseases particularly those associated with inflammation. Many studies have shown that dietary nutrients, pharmacologic treatments and many other environmental factors could modulate the gut microbial compositions. Moreover, some host genetic factors could be playing important roles on shaping the gut microbiota and the microbiome composition is indeed a state of equilibrium resulting from the dynamic crosstalks of intrinsic and external factors. In this talk, we report that a genetic knockout mouse strain could restrain inflammation in various inflammatory disease models. Further combining a multi-omics strategy and complementary in vitro mechanistic approaches, we illustrate how a host factor could shape the gut microbiota. Elucidating the host-microbiota interactions in the gut may not only provide the opportunities to improve host heath but may also be used for designing novel strategy for disease therapeutics.

Yet-Ran Chen, Ph.D. (陳逸然)

Current position and professional experiences

2015 ~ Present	**Principle Investigator**, Tenured Associate Research Fellow, Agricultural Biotechnology Research Center, Academia Sinica
2016 ~ Present	**Joint Associate Professor**, Department of Chemistry, National Chiayi University
2015 ~ Present	**Joint Associate Professor**, Institute of Biotechnology, National Taiwan University
2015 ~ Present	**Joint Associate Professor**, Biotechnology Center, National Chung Hsing University
2015 ~ Present	**Joint Associate Professor**, Institute of Bioscience and Biotechnology, National Taiwan Ocean University
2009 ~ Present	**Founder and Leader**, Academia Sinica Metabolomics Core Facility, Scientific Instrument Service Center, Academia Sinica

Research interest

1. High throughput mass spectrometry-based “omics” platform technologies
2. Early signaling events on the cell surface
3. Peptide hormone signaling involved in plant development and stress defenses
4. Plant damage associated molecular pattern (DAMP) triggered immunity
5. Interplay of biotic and abiotic stresses in plants

Short research summary

Dr. Yet-Ran Chen’s research group aims to overcome current technological limitations in the investigation of the dynamics of inter- and intra-cellular communication events regulated by plant peptides. Their studies started with the development of high-performance analytical technologies to identify novel plant peptide signals induced by stress. With highly integrated advanced analytical technologies as a research platform, they are now able to discover novel signaling peptides for the regulation of plant immune response. The technologies they have developed also helped to further elucidate the signaling mechanisms in proteins and metabolites more sensitively and reliably.

Currently, the use of agrochemicals to control pests and diseases is an efficient and common strategy to increase crop productivity. However, the usage of agrochemicals brings significant impacts on the environment, ecosystem, and human health, thus the need to curb the many negative effects of crop production on the environment is becoming increasingly clear. The development of alternative approaches to improve the crop immunity for better resistance of biotic threads is becoming more and more important now. By the development and application of new molecular profiling approach to identify plant immune peptide and study their regulating mechanisms. Dr. Chen’s group applied a novel peptidomics approach integrated the hypothetical database search to profile plant endogenous peptides and used this approach to discover defense signaling peptides in plants. A novel peptide (CAP-derived peptide1, CAPE1) derived from the PR-1 family was discovered to induce significant antipathogen and minor antiherbivore responses in tomato. The PR-1 is the most canonical protein biomarker for protein immunity but its role in the regulation of immunity was unknown for almost half a century. This discovery identified the role of PR-1 in immune signaling and suggests the potential application of plant endogenous peptides in efforts to defeat biological threats in crop production. As the PR-1 is conserved in not only plants but also animal kingdoms, the CAPEs may also involve in the regulation of innate immunity in diverse

species including humans.

Honors

2015 – Present	Council Member, Asia Oceania Agricultural Proteomics Organization.
2015 – Present	Executive Council Member / Chair of Finance Committee / Academic Committee, Taiwan Society for Mass Spectrometry
2015 – Present	Elected Council Member, Taiwan Society for Mass Spectrometry (3rd Highest Votes in 2015, Top Votes in 2018)
2014 – Present	Elected Council Member, Taiwan Society for Proteomics (2nd Highest Votes in 2017)
2012 – 2015	Chair of Finance Committee / Training Course Committee, Taiwan Society for Mass Spectrometry
2012 – 2015	Elected Council Member, Taiwan Society for Mass Spectrometry
2011 – 2014	Elected Council Member, Taiwan Society for Proteomics
2009 – 2012	Elected Council Member/Training Course Committee, Taiwan Society for Mass Spectrometry
2006 - 2009	Elected Council Member, Taiwan Society for Mass Spectrometry

Awards

2016	Junior Research Investigators Award, Academia Sinica.
2016	Significant Discovery of Academia Sinica in 2015.
2016	Career Development Award, Academia Sinica.
2015	Professor CY Lin Memorial Award for Innovative Research Program, The Chu-Yung Lin Memorial Foundation and Taiwan Society for Plant Biologists.
2015	The Shang-Fa Yang Young Scientist Award, The Shang-Fa Yang Memorial Foundation.
2015	Significant Discovery of Academia Sinica in 2014.
2013	TSMS Young Scholar Award, Taiwan Society for Mass Spectrometry.
2008	Biotechnology Creativity Award, Industrial Development Bureau, Ministry of Economic Affairs.

Publications

1. Y. L. Chen, K. T. Fan, S. C. Hung and Y. R. Chen* “The role of peptides cleaved from protein precursors in eliciting plant stress reactions” New Phytologist, 2020, 225(6), 2267. (SCI Category: Plant Science, IF(5-year, 2018):8.344) (On-line on 2019 Sep. and became top download paper of New Phytologist in 2018-2019)
2. Y. L. Chen, W. H. Chang, C. Y. Lee, Y. R. Chen* “An Improved Scoring Method for the Identification of Endogenous Peptides based on Mascot MS/MS Ion Search” Analyst, 2019, 144, 3045. (SCI Category: Analytical Chemistry, IF(2018):4.019)
3. K. T. Fan, K. H. Wang, W. H. Chang, J. C, Yang, C. F. Yeh, K. T. Cheng, S. C. Hung, Y. R. Chen* “Application of data-independent acquisition approach to study the proteome change from early to later phases of tomato pathogenesis responses.” Int. J. Mol. Sci., 2019, 20(4), E863. (SCI Category: Chemistry, Multidisciplinary, IF(5-years 2018):4.331)
4. H. J. Chen, Y. C. Shen, Y. J Shiao, K. T. Liou, P. H. Hsieh, C. Y. Lee, Y. R. Chen* and Y. L. Lin* “Multiplex Brain Proteomic Analysis Revealed the Difference in Molecular Therapeutic Effects of Tissue plasminogen activator and Buyang Huanwu Decoction on Cerebral Ischemic Stroke Mice” PLOS One, 2015, 10(10), e0140823. (SCI Category: Multidisciplinary Sciences, IF(5-year):3.702, Category Ranking (excluding review journals):9/57)
5. P. S. Chien, H. G. Nam and Y. R. Chen* “A salt-regulated peptide derived from CAP superfamily

protein negatively regulates salt stress tolerance in Arabidopsis" J. Exp. Bot., 2015, 66(17), 5301. (Invited Submission for Plant Peptide Special Issue) (SCI Category: Plant Science, IF(5-year):6.019, Category Ranking (excluding review journals):3/194)

Charles Pin-Kuang Lai, Ph.D. (賴品光)

Current position and professional experiences

2017 ~ Present **Assistant Research Fellow**, Institute of Atomic and Molecular Sciences, Academia Sinica

2018 ~ Present **Assistant Professor (adjunct),** Genome and Systems Biology Degree Program, Academia Sinica and National Taiwan University

2015 ~ 2017 **Assistant Professor**, Institute of Biomedical Engineering, National Tsing Hua University

2014 ~ 2015 **Instructor**, Program in Neuroscience, Harvard Medical School

Assistant in Neuroscience, Departments of Neurology, Massachusetts General Hospital

Research interest

1. Molecular bioimaging
2. Cell-cell and cell-ECM communications (e.g. extracellular vesicles, exosomes, gap junctions)
3. Gene therapy
4. Cancer cell biology

Short research summary

Dr. Lai received his PhD from the University of British Columbia, Canada, in 2010, where he focused on the role of gap junctions in brain cancer. He thereafter joined Dr. Xandra Breakefield's laboratory for his postdoctoral training and Instructor position in the Department of Neurology at Massachusetts General Hospital and Harvard Medical School. He served as an Assistant Professor of Biomedical Engineering at National Tsing Hua University from 2015 to 2017, and is currently an Assistant Research Fellow at the Institute of Atomic and Molecular Sciences in Academia Sinica, Taiwan. His current work focuses on developing molecular bioimaging methods and elucidating molecular mechanisms of nanosized extracellular vesicles and DNA double-strand break repairs.

Publications

1. Wu, A.Y., Sung, Y., Chen, Y., Chou, S.T., Guo, V., Chien, J.C., Ko, J.J., Yang, A.L., Huang, H., Chuang, J., Wu, S., Ho, M., Ericsson, M., Lin, W., Cheung, C.H.Y., Juan, H., Ueda, K., Chen, Y., Lai, C.P.* (2020). Multiresolution imaging using bioluminescence resonance energy transfer identifies distinct biodistribution profiles of extracellular vesicles and exomeres with redirected tropism. Advanced Science. In press.
2. Chien J.C., Pinkham, K., da Hora, C.C., Tabet E., Badr C.E.*, Lai, C.P.* Multiplexed bioluminescent reporter enables real-time tracking of DNA double strand break repair dynamics in vitro and in vivo. Nucleic Acids Research. In press. *Co-last authors.
3. Huang, Y., Fan, C., Hsu, N., Chiu, N., Wu, C., Chang, C., Wu, B., Hong, S., Chang, Y., Wu, A.Y., Guo, V., C, Y., Hsu, W., C, L., Lai, C.P., Yeh, C., Lin, Y. (2019). Sonogenetic modulation of cellular activities using an engineered auditory-sensing protein. Nano Letters. 20 (2): 1089-1100.
4. Sung, Y., Jin, P., Chu, L., Hsu, F., Wang, M., Chang, C., Chiou, S., Qiu, J.T., Gao, D., Lin, C., Chen, Y., Hsu, Y., Wang, J., Wang, F., Yu, P., Chiang, A., Wu, A.Y., Ko, J.J., Lai, C.P., Lu, T.*, Chen, Y.* (2019). Delivery of nitric oxide with a nanocarrier promotes tumor vessel normalization and

potentiates anti-cancer therapies. Nature Nanotechnology. 14 (12):1160-1169. *Co-last authors.
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6. Wu, Y.T., Ueda, K., Lai, C.P.* (2019). Review: Proteomic analysis of extracellular vesicles for cancer diagnostics. Proteomics. 19 (1-2): 1800162-12.
7. Chuo S.T., Chien, J.C., Lai, C.P.* (2018). Review: Imaging extracellular vesicles: current and emerging methods. Journal of Biomedical Science. 25 (1):91-100.
8. Reátegui, E.,* van der Vos, K.E.,* Lai, C.P.,* Zeinali, M., Atai, N.A., Aldikacti, B., Floyd Jr., F.P., Khankhel, A.H., Thapar, V., Hochberg, F.H., Sequist, L.V., Nahed, B.V., Carter, B.S., Toner, M., Balaj, L., Ting, D.T., Breakefield, X.O., Stott, S.L. (2018). Engineered nanointerfaces for microfluidic isolation and molecular profiling of tumor-specific extracellular vesicles. Nature Communications, 9 (1): 175-186. (IF: 12.121) *Co-first authors.
9. Sung, Y., Liu, Y., Chao, P., Chang, C., Jin, P., Lin, T., Lin, J., Cheng, H., Wang, J., Lai, C.P., Chen, L., Wu, A.Y., Ho, T., Chiang, T., Gao, D., Duda, D.G., Chen, Y. (2018). Combined delivery of sorafenib and a MEK inhibitor using CXCR4-targeted nanoparticles reduces hepatic fibrosis and prevents tumor development. Theranostics, 8 (4): 894-905.
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Multi-resolution Imaging of Cancer-derived Extracellular Vesicles and Exomeres Identifies Distinct Biodistribution Profiles with Redirected Tropism

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Extracellular particles (EPs) including extracellular vesicles (EVs) and exomeres play significant roles in diseases and therapeutic applications. However, their spatiotemporal dynamics *in vivo* have remained largely unresolved in detail due to the lack of a suitable method. Therefore, a bioluminescence resonance energy transfer (BRET)-based reporter, PalmGRET, is created to enable pan-EP labeling ranging from exomeres (<50 nm) to small (<200 nm) and medium and large (>200 nm) EVs. PalmGRET emits robust, sustained signals and allows the visualization, tracking, and quantification of the EPs from whole animal to nanoscopic resolutions under different imaging modalities, including bioluminescence, BRET, and fluorescence. Using PalmGRET, it is shown that EPs released by lung metastatic hepatocellular carcinoma (HCC) exhibit lung tropism with varying distributions to other major organs in immunocompetent mice. It is further demonstrated that gene knockdown of lung-tropic membrane proteins, solute carrier organic anion transporter family member 2A1, alanine aminopeptidase/Cd13, and chloride intracellular channel 1 decreases HCC-EP distribution to the lungs and yields distinct biodistribution profiles. It is anticipated that EP-specific imaging, quantitative assays, and detailed in vivo characterization are a starting point for more accurate and comprehensive in vivo models of EP biology and therapeutic design.

Guan-Da Syu, Ph.D. (許觀達)

Current position and professional experiences

2019/8 ~ Present	**Assistant Professor**, Department of Biotechnology and Bioindustry Sciences, National Cheng Kung University, Taiwan
2015 ~ 2019	**Postdoc**, Pharmacology and Molecular Sciences, Johns Hopkins School of Medicine, USA
2013 ~ 2015	**Postdoc**, Graduate Institute of Systems Biology and Bioinformatics, National Central University, Taiwan
2012 ~ 2013	**Postdoc**, Department of Physiology, National Cheng Kung University, Taiwan
2005 ~ 2012	**Ph.D.**, Graduate Institute of Basic Medical Science, National Cheng Kung University, Taiwan

Research interest

1. Protein microarray
2. Host and microbial interactions
3. High throughput technology
4. Exercise physiology, virology, and bioinformatics

Short research summary

G protein-coupled receptor (GPCR) is the most important family for signal transduction and drug development. However, the seven transmembrane domains increase the difficulty to purify and study GPCRs. Here, we developed virion-display (VirD) technology to express functional GPCR on the virus envelope and applied to all non-olfactory GPCRs. We used VirD technology to detect specificity of biologicals, measure binding affinity of small molecules, and identified receptors that important in bacterial invasion. We recently published our results in *Journal of the American Chemical Society* and *Nature Communications*.

Publications

- **Syu GD*** (*first and corresponding authors), Johansen E, Zhu H. Virion Display: A High-Throughput Method to Express Functional Membrane Proteins. Current Protocols. 2020; In press.
- **Syu GD*** (*first and corresponding authors), Dunn J, Zhu H. Developments and applications of functional protein microarrays. Mol Cell Proteomics. 2020; 19:916-927. (SCI; impact factor 5.2; ranking 9/79 = 11.4 % in biomedical research methods)
- S**yu GD**, Wang SC, Ma G, Liu S, Pearce D, Prakash A, Henson B, Weng LC, Ghosh D, Ramos P, Eichinger D, Pino I, Dong X, Xiao J, Wang S, Tao N, Kim KS, Desai P, Zhu H. Development and application of a high-content virion display human GPCR array. Nat Commun. 2019; 10:1997. (SCI; impact factor 12.4; ranking 3/64 = 4.7 % in multidisciplinary sciences)
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- Hsiao FS, Sutandy FR, **Syu GD**, Chen YW, Lin JM, Chen CS. Systematic protein interactome analysis of glycosaminoglycans revealed YcbS as a novel bacterial virulence factor. Sci Rep. 2016; 6:28425. (SCI; impact factor 4.1; ranking 12/64 = 18.8 % in multidiscipline sciences)
- Fan B, Sutandy FX, **Syu GD**, Middleton S, Yi G, Lu KY, Chen CS, Kao CC. Heterogeneous ribonucleoprotein K (hnRNP K) binds miR-122, a mature liver-specific microRNA required for hepatitis C virus replication. Mol Cell Proteomics. 2015; 14:2878-86. (SCI; impact factor 5.2; ranking 9/79 = 11.4 % in biomedical research methods)
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Patient and Tech transfer

- **Syu GD**. Application of coronavirus protein microarray in diagnosis. Nonexclusive tech transfers to CDI laboratories, U.S.A., 2020 (TC-109-052).

Application of Functional Protein Microarray in Research and Drug Development

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International Center for Wound Repair and Regeneration, National Cheng Kung University, Taiwan
Research Center of Excellence in Regenerative Medicine, National Cheng Kung University, Taiwan

Functional protein microarrays are crucial tools in the study of proteins in an unbiased and high-throughput manner. The adaptability of this technology has enabled its use in a wide variety of applications, including the study of proteome-wide molecular interactions, analysis of post-translational modifications, identification of novel drug targets, examination of pathogen-host interactions, profiling antibody specificity, and discovery of autoantibody biomarkers. Here, I want to share our recent progress of using coronavirus protein microarray in diagnosis and our new Virion Display (VirD) for expressing membrane proteins.

G protein coupled receptors (GPCRs) are the one of the most important membrane protein families that controls variety of cellular functions and often being designed as drug targets. To date, ~40% of the FDA-approved drugs target GPCRs. Despite the importance of the GPCRs, some ligands GPCRs are unknown and classified as orphan GPCRs. Since the lipid bilayer is required to maintain the conformation of GPCRs, purification attempts often disrupt the GPCR conformation. To overcome this hurdle, we developed VirD technology by replacing a viral envelope gene in herpes simplex virus-1 (HSV-1) with an ORF encoding a human transmembrane protein. The production of this recombinant virus from mammalian cells allowed the human receptor to be embedded in the viral envelope with correct conformation and function.

We used VirD technology and successfully expressed 315 human GPCRs on the virions and fabricated the world's largest functional membrane protein array for the biochemical interrogation. We demonstrated that the GPCR-VirD array is useful to profile specificity of mAbs, ligands, and even pathogen interactions. We believe that the VirD array is a robust platform to profile many different kinds of membrane protein interactions and will speed up the development of antibody and small molecule drugs.

Kun-Yi Chien, Ph.D. (簡昆鎰)

Current position and professional experiences

2013/8 ~ Present	**Associate Professor**, Department of Biochemistry and Molecular Biology, Chang Gung University
2003/10 ~ 2013/8	**Assistant Professor**, Department of Biochemistry and Molecular Biology, Chang Gung University
2002/3 ~ 2003/10	**Assistant Research Professor**, Chang Gung Memorial Hospital

Research interest

1. Proteomics
2. Separation science
3. Mass spectrometry
4. Biomarker discovery

Short research summary

Dr. Kun-Yi Chien is an Associate Professor of Department of Biochemistry and Molecular Biology at the Chang Gung University (CGU), Taiwan. Dr. Chien received his Ph.D degree from National Tsing-Hua University, Taiwan, and has been involved in proteomics research for the past ~20 years. Dr. Chien's research interest focuses on the development of separation techniques, especially multidimensional nanoLC systems, for proteome analysis. In addition to his primary role in the University, Dr. Chien is responsible for the maintenance of instruments and providing service in the proteomics core laboratory at CGU.

Publications

1 Fang YK, Chien KY, Huang KY, Cheng WH, Ku FM, Lin R, Chen TW, Huang PJ, Chiu CH, Tang P. 2016. Responding to a Zoonotic Emergency with Multi-omics Research: Pentatrichomonas hominis Hydrogenosomal Protein Characterization with Use of RNA Sequencing and Proteomics. OMICS. 20(11):662-669.

2 Kung YA, Hung CT, Chien KY, Shih SR. 2017. Control of the negative IRES trans-acting factor KHSRP by ubiquitination. Nucleic Acids Res. 45(1):271-287.

3 Lin YT, Chien KY, Wu CC, Chang WY, Chu LJ, Chen MC, Yeh CT, Yu JS. 2017. Super-SILAC mix coupled with SIM/AIMS assays for targeted verification of phosphopeptides discovered in a large-scale phosphoproteome analysis of hepatocellular carcinoma. J Proteomics. 157:40-51.

4 Bian XL, Chen HZ, Yang PB, Li YP, Zhang FN, Zhang JY, Wang WJ, Zhao WX, Zhang S, Chen QT, Zheng Y, Sun XY, Wang XM, Chien KY, Wu Q. 2017. Nur77 suppresses hepatocellular carcinoma via switching glucose metabolism toward gluconeogenesis through attenuating phosphoenolpyruvate carboxykinase sumoylation. Nat Commun. 8:14420.

5 Hsieh YJ, Chien KY, Yang IF, Lee IN, Wu CC, Huang TY, Yu JS. 2017. Oxidation of protein-bound methionine in Photofrin-photodynamic therapy-treated human tumor cells explored by methionine-containing peptide enrichment and quantitative proteomics approach. Sci Rep. 7(1):1370.

6 Hsiao YC, Chi LM, Chien KY, Chiang WF, Chen SF, Chuang YN, Lin SY, Wu CC, Chang YT, Chu LJ, Chen YT, Chia SL, Chien CY, Chang KP, Chang YS, Yu JS. 2017. Development of a Multiplexed Assay

for Oral Cancer Candidate Biomarkers Using Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry. Mol Cell Proteomics. 16(10):1829-1849.
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16 Chi LM, Hsiao YC, Chien KY, Chen SF, Chuang YN, Lin SY, Wang WS, Chang IY, Yang C, Chu LJ, Chiang WF, Chien CY, Chang YS, Chang KP, Yu JS. 2020. Assessment of candidate biomarkers in paired saliva and plasma samples from oral cancer patients by targeted mass spectrometry. J Proteomics. 211:103571.
17 Hsiao YC, Lin SY, Chien KY, Chen SF, Wu CC, Chang YT, Chi LM, Chu LJ, Chiang WF, Chien CY, Chang KP, Chang YS, Yu JS. 2020. An immuno-MALDI mass spectrometry assay for the oral cancer biomarker, matrix metalloproteinase-1, in dried saliva spot samples. Anal Chim Acta. 1100:118-130.
18 Cheng ML, Chien KY, Lai CH, Li GJ, Lin JF, Ho HY. 2020. Metabolic Reprogramming of Host Cells in Response to Enteroviral Infection. Cells. 9(2). pii: E473.
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20 Chakraborty A, Lin WC, Lin YT, Huang KJ, Wang PY, Chang IY, Wang HI, Ma KT, Wang CY, Huang XR, Lee YH, Chen BC, Hsieh YJ, Chien KY, Lin TY, Liu JL, Sung LY, Yu JS, Chang YS, Pai LM. 2020. SNAP29 mediates the assembly of histidine-induced CTP synthase filaments in proximity to the cytokeratin network. J Cell Sci. 133(9):jcs240200.

A nanoLC-MS System for Single-cell Proteomic Analysis

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Single-cell proteomics has emerged as a powerful approach for getting unique insights into biological processes which cannot be achieved by measuring mixtures of multiple cells owing to the cell heterogeneity. One of the challenges of analyzing a single cell is the difficulty of injecting the components of a single cell into the detection system completely. Sample lost due to the adsorption of proteins/peptides to the wall of processing containers is the major problem in analyzing such tiny amounts of samples. In this study, we make two improvements on a nanoLC system for single-cell proteome analysis. First, the extra column volume of the LC system is minimized by a special design of solvent flow path, starting from the gradient mixer. Second, an injection method which causes a lowest sample lost among tested conditions is obtained. We found that adsorption kinetics of peptides to the contact surface of injection vials is very fast, regardless of what types of vials are used. This phenomenon can be effectively prevented by introducing either detergents or acetonitrile into the samples. Finally, an online SCX-RP nanoLC system which allows dissolving samples in large volumes of acetonitrile-containing solvent for injection is established. The system is an automated, sensitive and scalable nanoLC system which is suitable for analyzing trace amounts of samples. By coupling with a highly sensitive mass spectrometer, ~1000 proteins can be identified from a single human cell. Furthermore, the system is also suitable for analyzing products which are obtained from some low-yield sample preparation processes such as pull-down assays of biotinylated peptides.

Shaw-Jenq Tsai, Ph.D. (蔡少正)

Current position and professional experiences

2019 ~ Present	**Chair Professor**, Department of Physiology, College of Medicine, National Cheng Kung University, Taiwan
2001 ~ Present	**Director**, Bioinformatic Center, National Cheng Kung University
2016 ~ 2020	**President**, The Chinese Physiological Society
2019 ~ Present	**President**, Asian Society of Endometriosis and Adenomyosis
2011 ~ Present	**Ambassador**, World Endometriosis Society

Research interest

1. Hypoxia-mediated epigenome regulation
2. Mechanisms of drug resistance in cancer
3. Endometriosis
4. Translational medicine

Short research summary

Professor Shaw-Jenq (Sean) Tsai received his PhD degree from the University of Wisconsin-Madison, USA in 1997. He then joined the Department of Physiology at the National Cheng Kung University, Taiwan, as an assistant professor in 1998. He was promoted to distinguished professor in 2008 in recognition of his great academic achievements. Professor Tsai also served as the Director-General of Department of Life Sciences, Ministry of Science and Technology, Taiwan during 2014-2017. Professor Tsai's research focuses on investigating molecular mechanisms underlying important human diseases, including cancer, polycystic ovarian syndrome, and endometriosis. He has published more than one hundred papers in prestigious journals such as Nature, Nature Communications, Journal of Clinical Investigation, Journal of Pathology, Cancer Research, Nucleic Acids Research, and Journal of Clinical Endocrinology & Metabolism. Those papers have been cited more than 5000 times with an H-index of 46. The outstanding research performance enables Professor Tsai to be awarded the "2014 Distinguished Scientist" by Society for Experimental Biology and Medicine and elected as a fellow in 2018. Professor Tsai serves as editorial board member of many journals including Journal of Endocrinology, Journal of Molecular Endocrinology, Reproductive Medicine & Biology, and is the Asian editor of Experimental Biology and Medicine.

Publications

1. WN Li, KY Hsiao, CA Wang, N Chang, PL Hsu, MH Wu*, SJ Tsai* Extracellular vesicle-associated VEGF-C as a novel target for endometriosis. **Proc Natl Acad Sci U S A**, 117 (41):25859-25868, Oct. 13, 2020.
2. PS Chen, WT Chu, PL Hsu, SC Lin, IC Peng, CY Wang, SJ Tsai* Pathophysiological implications of hypoxia in human diseases. **J Biomed Sci** 27: 63, 2020 May 11.
3. CA Wang, YH Chang, PC Hou, YJ Tai**,** WN Li, PL Hsu, **SR Wu,** CF Li, YS Shan, SJ Tsai* DUSP2 regulates extracellular vesicle-VEGF-C secretion and pancreatic cancer early dissemination. **J Extracell Vesicles** 9 (1): 1746529, 2020 April 4.
4. TM Chen, MC Lai, YH Li, YL Chan, CH Wu ,YM Wang, CW Chien, SY Huang, H. S Sun*, SJ Tsai* hnRNPM induces translation switch under hypoxia to promote colon cancer development. **EBioMedicine** 2019 Mar 6. pii: S2352-3964(19)30138-0. doi: 10.1016/j.ebiom.2019.02.059

5. PL Hsu, J Jou, SJ Tsai* TYRO3: a potential therapeutic target in cancer. **Exp Biol Med** 244: 83–9, 2019
6. SC Lin, HC Lee, CT Hsu, YH Huang, WN Li, PL Hsu, MH Wu*, SJ Tsai* Targeting anthrax toxin receptor 2 ameliorates endometriosis progression. **Theranostics**; 9(3): 620-632, 2019. doi: 10.7150/thno.30655
7. JL Fu, KY Hsiao, HC Lee, WN Li, N Chang, MH Wu*, SJ Tsai* Suppression of COUP-TFII upregulates angiogenin and promotes angiogenesis in endometriosis **Hum Reprod** 33 (8): 1517-27, 2018 Aug 1. doi: 10.1093/humrep/dey220.
8. KY Hsiao, HS Sun, SJ Tsai***** Circular RNA - New member of noncoding RNA with novel functions. **Exp Biol Med** (Maywood) 242(11):1136-1141.
9. SC Lin, HC Lee, PC Hou, JL Fu, MH Wu, SJ Tsai* Targeting hypoxia-mediated YAP1 nuclear translocation ameliorates pathogenesis of endometriosis without compromising maternal fertility. **J Pathol** 242: 476–487. doi: 10.1002/path.4922, 2017
10. PC Hou, YH Li, SC Lin, SC Lin, JC Lee, PW Lin, JP Liou, JY Chang, CC Kuo, YM Liu, HS Sun, SJ Tsai* Hypoxia-induced downregulation of DUSP-2 phosphatase drives colon cancer stemness. **Cancer Res**, 77 (16): 4305-4316. doi: 10.1158/0008-5472.CAN-16-2990, 2017
11. KY Hsiao, YC Lin, SK Gupta, N Chang, L Yen, H. S Sun*, SJ Tsai* Noncoding effects of circular RNA CCDC66 promote colon cancer growth and metastasis. **Cancer Res** 77:2339-2350. May 1, doi: 10.1158/0008-5472.CAN-16-1883, 2017 (Hot paper, high-cite paper)
12. SC Lin, KY Hsiao, N Chang, PC Hou, SJ Tsai* Loss of dual specificity phosphatase-2 promotes angiogenesis and metastasis via upregulation of interleukin-8 in colon cancer. **J Pathol** 241: 638–648, 2017
13. CW Chien, PC Ho, HC Wu, YL Chang, SC Lin, PW Lin, JC Lee, YJ Chang, HS Sun, SJ Tsai* Targeting TYRO3 inhibits epithelial-mesenchymal transition and increases drug sensitivity in colon cancer. **Oncogene** 35(45):5872-5881, 2016
14. KY Hsiao, MH Wu, N Chang, SH Yang, CW Wu, HS Sun, SJ Tsai* Coordination of AUF1 and miR-148a to destabilize DNA methyltransferase 1 mRNA under hypoxia in endometriosis. **Mol Hum Reprod** 21:894-904, 2015
15. CA Wang, SJ Tsai* 2015 The non-canonical role of vascular endothelial growth factor-C axis in cancer progression. **Exp Biol Med** (Maywood) 240(6):718-24, 2015
16. KY Hsiao, SC Lin, MH Wu*, SJ Tsai* Pathological functions of hypoxia in endometriosis. **Front Biol Sci** 7: 309-321, 2015
17. SC Lin, WL Liao, JC Lee, SJ Tsai* Hypoxia-regulated gene network in drug resistance and cancer progression. **Exp Biol Med** 239:779-792, 2014
18. SC Lin, YH Li, MH Wu, YF Chang, DK Lee, S Tsai, MJ Tsai, and SJ Tsai* Suppression of COUP-TFII by proinflammatory cytokines contributes to the pathogenesis of endometriosis. **J Clin Endocrinol Metab** 99(3): E427-37, 2014.
19. TM Chen, YH Shih, JT Tseng, MC Lai, Ch Wu, YH Li, SJ Tsai*, and HS Sun* Overexpression of FGF9 in colon cancer cells is mediated by hypoxia-induced translational activation. **Nucleic Acids Res** 42:2932-44, 2014
20. HM Chen, YH Lin, YM Cheng, LYC Wing, SJ Tsai* Overexpression of integrin-β1 promotes leiomyomal cell spreading and proliferation. **J Clin Endocrinol Metab** 98:E837-46, 2013.
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22. J Qin, SP Wu, F Dai, X Xie, CM Cheng, C J Creighton, A Frolov, Gustavo Ayala4, X Lin, XH Feng, MM Ittmann, SJ Tsai, MJ Tsai, S Y Tsai Inhibition of TGF-β-dependent growth barrier by COUP-TFII to promote prostate tumor growth and metastasis. **Nature** 493: 236-240, 2013

Hua-Jung Li, Ph.D. (李華容)

Current position and professional experiences

2019/7 ~ Present	**Associate Investigator**, Institute of Cellular and System Medicine, National Health Research Institutes, Zhunan, Taiwan
2012 ~ 2019	**Assistant Investigator**, Institute of Cellular and System Medicine, National Health Research Institutes, Zhunan, Taiwan
2009 ~ 2012	**Postdoctoral Fellow**, Whitehead Institute for Biomedical Research/MIT, Boston, MA, USA
2007 ~ 2009	**Postdoctoral Fellow**, University of California, Los Angeles (UCLA), CA, USA

Research interest

1. Extracellular vesicles
2. Stem cells
3. Regeneration medicine
4. Cancer

Short research summary

Dr. Hua-Jung Li received a PhD degree in Molecular and Medical Pharmacology from University of California, Los Angeles. During the period, Dr. Li studied targeting cancer therapy in Harvey Herschman lab. After receiving the PhD degree, Dr. Li was awarded by Susan G. Komen for the Cure. With the support by Susan G. Komen for the Cure, Dr. Li entered Robert Weinberg Lab at Whitehead Institute. In Weinberg lab, Dr. Li focused on cancer stem cell biology. She investigated the interactions of carcinoma cells and tumor stroma and found that the interaction controlled the tumor behavior via affecting cancer stem cell pools. Dr. Li joined National Health Research Institutes, Taiwan in 2013. Her lab currently works on dissecting the conversion of stem and non-stem cell states.

Publications

1 Chen SY, Lin MC, Tsai JS, He PL, Luo WT, Chiu IM, Herschman HR, and Li HJ* Exosomal 2',3'-CNP from mesenchymal stem cells promotes hippocampus CA1 neurogenesis/ neuritogenesis and contributes to rescue of cognition/learning deficiencies of damaged brain. Stem Cells Translational Medicine 2020;9:499–517 FEATURED ARTICLE

2 Chen SY, Lin MC, He PL, Tsai JS, Luo WT, Herschman HR, and Li HJ* EP4 antagonist-elicited extracellular vesicles from mesenchymal stem cells rescue cognition/learning deficiencies by restoring brain cellular functions. Stem Cells Translational Medicine. 2019;8(7):707-723 FEATURED ARTICLE

3 Lin MC, Chen SY, He PL, Herschman HR, and Li HJ* PGE2/EP4 antagonism enhances tumor chemosensitivity by inducing extracellular vesicle-mediated clearance of cancer stem cells. Int J Cancer. 2018;143(6):1440-1455 COVER STORY

4 Lin MC, Chen SY, Tsai HM, He PL, Lin YC, Herschman HR, and Li HJ* PGE2/EP4 signaling controls the transfer of the mammary stem cell state by lipid rafts in extracellular vesicles. Stem Cells 2017;35(2):425-444

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7 Li HJ, Everts M, Yamamoto M, Curiel DT, and Herschman HR*. Combined transductional untargeting/retargeting and transcriptional restriction enhance adenovirus gene targeting and therapy for hepatic colorectal cancer tumors. Cancer Research 2009;69(2):554-64.
8 Li HJ, Everts M, Pereboeva L, Komarova S, Idan A, Curiel DT and Herschman HR*. Adenovirus Tumor Targeting and Hepatic Untargeting by a Coxsackie/Adenovirus Receptor Ectodomain Anti-Carcinoembryonic Antigen Bispecific Adapter. Cancer Research 2007;67(11):5354-61

Exosomes in Stem Cell Homeostasis, Cancer, and Regeneration Medicine

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Extracellular vesicles (EVs) (i.e., exosomes) are responsible for intercellular communication by transferring membrane and cytosolic molecules between cells. Promoting EV release from basal mammary epithelial stem-like cells causes a transition of the cells to a non-stem, more epithelial phenotype. The basal mammary epithelial stem-like cells lose SC properties after releasing the EVs/exosomes. In contrast, uptake of the EVs drives conversion of mammary luminal cells to basal cell-like mammary epithelial stem cells able to form mammary glands. The stem cell EV-mediated stemness transfer provides a new direction for regeneration medicine. For example, adult brains have limited regenerative capacity. Consequently, both brain damage and neurodegenerative diseases often cause functional impairment for patients. Mesenchymal stem cells (MSCs), one type of adult stem cells, can be isolated from various adult tissues; MSCs “have been used in clinical trials to treat human diseases and the therapeutic potentials of the MSC-derived secretome and extracellular vesicles (EVs) have been under investigation. We found that EP4 antagonist-elicited MSC EVs/exosomes exhibit greatly enhanced therapeutic potential, in contrast to the comparatively low efficiency of EVs/exosomes derived from untreated MSCs, to rescue several CNS pathologies; (e.g., neuron degeneration and death, reactive astrogliosis, extensive inflammation, disrupted BBB), which are often associated with brain injury, stroke and many neurodegenerative diseases (e.g., AD and PD). Our study demonstrates EP4-antagonist elicited MSC EVs/exosomes as a regenerative medicine for CNS diseases.

A similar mechanism is observed in cancer. Similar to basal mammary epithelial stem-like cells, breast cancer cells expressing mesenchymal phenotypes are associated with cancer stem cell (CSC) properties and are often resistant to conventional chemotherapy. We can induce a conversion of mesnechymal breast cancer stem cells from a mesenchymal/CSC state to a more epithelial non-CSC state by promoting the release of EVs which remove CSC markers, mesenchymal markers, integrins, and drug efflux transporters from the CSCs. The induced EV release increases chemosensitivity of breast cancer cells, which suggests that, in combination with conventional chemotherapy, such an inhibitor might serve as an effective adjuvant for targeting cancer stem cells. This finding holds implications for the treatment of carcinomas in the oncology clinic.

Chu-An Wang, Ph.D. (王竹安)

Current position and professional experiences

2017 ~ Present **Assistant Investigator**,
Institute of Molecular Medicine, National Cheng Kung University, Taiwan

2014 ~ 2017 **Postdoctoral Fellow**,
Department of Basic Medical Science, National Cheng Kung University, Taiwan

2012 ~ 2014 **Postdoctoral Fellow**,
Department of Pharmacology, University of Colorado Denver, Anschutz Medical Campus, USA

2007 ~ 2012 **Ph.D.**, Molecular and Cancer Biology
University of Colorado Denver, Anschutz Medical Campus, USA

Research interest

1. Cancer biology
2. Extracellular vesicle
3. Angiogenesis/lymphangiogenesis

Short research summary

Dr. Wang is an Assistant Investigator at National Cheng Kung University (NCKU), Taiwan. Dr. Wang received her Ph.D. degree from the University of Colorado, Denver in the United State and has been involved in cancer research since her Ph.D. Dr. Wang's research interest focuses on molecular mechanisms of cancer metastasis and the function and regulation of extracellular vesicle in cancer progression.

Publications

1. Meng-Hsing Wu,* Chu-An Wang,* Chen-Chung Lin, Lei-Chin Chen, Wen-Chang Chang, and Shaw-Jenq Tsai. Distinct regulation of cyclooxygenase-2 by interleukin-1beta in normal and endometriotic stromal cells. J Clin Endocrinol Metab. 2005 Jan;90(1):286-95.
2. W. Chen,S.-J. Tsai, C.-A. Wang, J.-C. Tsai, C.C. Zouboulis. Human sebocytes express prostaglandin E2 receptors EP2 and EP4 but treatment with prostaglandin E2 does not affect testosterone production. Br J Dermatol. 2009 Sep;161(3):674-7.
3. Micalizzi DS, Wang CA, Farabaugh SM, Schiemann WP, Ford HL. Homeoprotein Six1 increases TGF-beta type I receptor and converts TGF-beta signaling from suppressive to supportive for tumor growth. Cancer Res. 2010 Dec 15;70(24):10371-80.
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5. Research was highlighted as a short article at: Metastasis: SIX1 of the best. Nat Rev Cancer. 2012 May 24;12(5):316.
6. Ritsuko Iwanaga, Chu-An Wang, Douglas S. Micalizzi, Chuck J. Harrell, Paul Jedlicka, Carol Sartorius, Peter Kabos, Andrew P Bradford, Heide L. Ford. Six1 enhances tumor initiating cell activity and predicts poor prognosis in luminal breast cancers. Breast Cancer Res. 2012 Jul 5;14(4):R100.
7. Wang CA, Harrell J, Iwanaga R, Jedlicka P, Ford HL. Vascular endothelial growth factor-C

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8. Wang CA, Drasin DJ, Pham C, Jedlicka P, Zaberezhnyy V, Guney M, Li H, Nemenoff R, Costello J, Tan AC, Ford HL. Homeoprotein Six2 Promotes Breast Cancer Metastasis via Transcriptional and Epigenetic Control of E-Cadherin Expression. Cancer Res. 2014 Dec 15;74(24):7357-70.
9. David J. Drasin , Anna L. Guarnieri , Deepika Neelakantan , Jihye Kim , Joshua H. Cabrera , Chu-An Wang , Vadym Zaberezhnyy , Pierluigi Gasparini , Luciano Cascione , Kay Huebner , Aik Choon Tan, Ford HL. TWIST1-induced microRNA-424 reversibly drives mesenchymal programming while inhibiting tumor initiation. Cancer Res. 2015 May 1;75(9):1908-21
10. Wang CA and Shaw-Jenq Tsai. The non-canonical role of vascular endothelial growth factor-C axis in cancer progression. Exp Biol Med (Maywood). 2015 Jun;240(6):718-24.
11. Towers CG, Guarnieri AL, Micalizzi DS, Harrell JC, Gillen AE, Kim J, Wang CA, Oliphant MU, Drasin DJ, Guney MA, Kabos P, Sartorius CA, Tan AC, Perou CM, Espinosa JM, Ford HL. The Six1 oncoprotein represses translation of p53 via concomitant regulation of RPL26 and microRNA-27a. Nat Commun. 2015 Dec 21;6:10077.
12. Chu-An Wang , Yi-Hern Chang , Pei-Chi Hou , Yu-Jing Tai , Wan-Ning Li, Pei-Ling Hsu, Shang-Rung Wu, Wen-Tai Chiu, Chien-Feng Li , Yan-Shen Shan , Shaw-Jenq Tsai. Targeting DUSP2-mediated extracellular vesicle-VEGF-C secretion ameliorates pancreatic cancer early dissemination. J Extracell Vesicles. 2020 Apr 4;9(1):1746529.
13. Wan-Ning Li, Kuei-Yang Hsiao,Chu-An Wang, Ning Chang, Pei-Ling Hsu, Chung-Hsien Sun, Shang-Rung Wu, Meng-Hsing Wu, Shaw-Jenq Tsai. Extracellular vesicle-associated VEGF-C promotes lymphangiogenesis and immune cells infiltration in endometriosis. PNAS. October 13, 2020 117 (41) 25859-25868.

The Function and Regulation of EV-VEGF-C in Pancreatic Cancer Early Metastasis

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Extracellular vesicles (EVs) are nanometer-sized, lipid bilayer-enclosed particles which carry bioactive material and mediate intercellular communication. Bioactive molecules on EVs surface may convey rapid and specific signaling in the recipient cells. We have identified that vascular endothelial growth factor-C (VEGF-C), the master lymphangiogenic growth factor, is associated with EVs produced by pancreatic cancer cells. EV-VEGF-C contributes to pancreatic cancer metastasis via promoting lymphangiogenesis and tumor cell invasion ability. We further identified that tumor suppressor dual specificity phosphatase-2 (DUSP2) controls VEGF-C at multiple levels including transcription, maturation, and extracellular vesicle (EV)-associated secretion. Our findings underscore the critical importance of DUSP2-VEGF-C axis in pancreatic cancer early metastasis.

Wei-Hsuan Hsu, Ph.D. (徐瑋萱)

Current position and professional experiences

2020 ~ Present	**The 2nd Council Member**, Taiwan Society for Extracellular Vesicles
2018/8 ~ Present	**Assistant Professor**, National Cheng Kung University Department of Food Safety / Hygiene and Risk Management
2015/6 ~ 2018/7	**Researcher**, Industrial Technology Research Institute Biomedical Technology and Device Research Labs
2014/9 ~2015/3	**Postdoctoral Researcher**, Purdue University Department of Medical Sciences
2013/9 ~2014/8	**Postdoctoral Researcher**, National Taiwan University Department of Biochemical Science and Technology

Research interest

1. Food microbiology
2. Food fermentation and biotechnology
3. Microorganisms and health

Short research summary

We study the communication of microorganisms and the bi-directional regulation between microbes and the host, especially gut. Specific probiotics are selected to regulate gut microbiota and to act as a target for disease therapeutics. We investigate the function of extracellular vesicles derived from probiotics and gut microbiota as well as their application on biomedicine and food science

Publications

1. Bao-Hong Lee, She-Ching Wu, Tang-Long Shen, Yi-Yun Hsu, Chia-Hsiu Chen, Wei-Hsuan Hsu*. 2020. The applications of Lactobacillus plantarum-derived extracellular vesicles as a novel natural antibacterial agent for improving quality and safety in tuna fish. Food Chem. 340, 128104.
2. Bao-Hong Lee, Wei-Hsuan Hsu, Cheng-Hui Lin. 2019. The anti-bacterial and anti-adherent effects of Pentraxin-3 on porcine kidney epithelial PK15 cells against Staphylococcus aureus infection. Int. J. Pept. Res. Ther. 25, 645-652.
3. Wei-Hsuan Hsu, Yu-Chun Lin, Bo-Rui Chen, She-Ching Wu*, Bao-Hong Lee*. 2018. The neuronal protection of a zinc-binding protein isolated from oyster. Food Chem. Toxicol. 114, 61-68.
4. Liang-Tzung Lin, Ying-Jang Lai, She-Ching Wu, Wei-Hsuan Hsu*, Chen-Jei Tai*. 2018. Optimal conditions for cordycepin production in surface liquid-cultured Cordyceps militaris treated with porcine liver extracts for suppression of oral cancer. J. Food Drug Anal. 26, 135-144.
5. Rui Zhang, Sherri Y. Huang, Kay Ka-Wai Li, Yen-Hsing Li, Wei-Hsuan Hsu, GuangJun Zhang, Chun-Ju Chang, Jer-Yen Yang*. 2017. Dual degradation signals destruct GLI1: AMPK inhibits GLI1 through β-TrCP-mediated proteasome degradation. Oncotarget 8, 49869-49881.
6. Chia-Woei Wang, Wei-Hsuan Hsu, Chen-Jei Tai*. 2017. Antimetastatic effects of cordycepin mediated by the inhibition of mitochondrial activity and estrogen-related receptor α in human ovarian carcinoma cells. Oncotarget 8, 3049-3058.

7. Yeu-Ching Shi, Kai-Sian Lin, Yi-Fen Jhai, Bao-Hong Lee, Yifan Han, Zhibin Cui, Wei-Hsuan Hsu*, She-Ching Wu*. 2016. Miracle fruit (Synsepalum dulcificum) exhibits as a novel anti-hyperuricaemia agent. Molecules 21, 140.
8. Wei-Hsuan Hsu, Bao-Hong Lee, Tzu-Ming Pan*. 2015. Leptin-induced mitochondrial fusion mediates hepatic lipid accumulation. Int. J. Obes. 39, 1750-1756.
9. Yifan Han, Zhibin Cui, Yen-Hsing Li, Wei-Hsuan Hsu*, Bao-Hong Lee*. 2015. In vitro and in vivo anticancer activity of pardaxin against proliferation and growth of oral squamous cell carcinoma. Mar. Drugs 14, 2.
10. Yu-Ying Chang, Wei-Hsuan Hsu, Tzu-Ming Pan*. 2015. Monascus secondary metabolites monascin and ankaflavin inhibit activation of RBL-2H3 cells. J. Agric. Food Chem. 63, 192-199.
11. Ya-Yun Tan#, Wei-Hsuan Hsu#, Tsung-Wei Shih, Chih-Hui Lin, Tzu-Ming Pan*. 2014. Proteomic insight into the effect of ethanol on citrinin biosynthesis pathway in Monascus purpureus NTU 568. Food Res. Int. 64, 733-742. (#Co-first author)
12. Wei-Hsuan Hsu, Bao-Hong Lee, Tzu-Ming Pan*. 2014. Monascin attenuates oxidative stress-mediated lung inflammation via peroxisome proliferator-activated receptor-gamma (PPAR-γ) and nuclear factor-erythroid 2 related factor 2 (Nrf-2) modulation. J. Agric. Food Chem. 62, 5337-5344.
13. Wei-Hsuan Hsu, Tzu-Ming Pan*. 2014. Treatment of metabolic syndrome with ankaflavin, a secondary metabolite isolated from the edible fungus Monascus spp. Appl. Microbiol. Biotechnol. 98, 4853-4863. (Review).
14. Wei-Hsuan Hsu, Tzu-Ming Pan*. 2014. A novel PPARgamma agonist monascin potentially applied in diabetes prevention. Food Funct. 5, 1334-1340. (Review).
15. Wei-Hsuan Hsu, Tin-Hong Chen, Bao-Hong Lee, Ya-Wen Hsu, *Tzu-Ming Pan. 2014. Monascin and ankaflavin act as natural AMPK activators with PPAR<alpha> agonist activity to down-regulate nonalcoholic steatohepatitis in high-fat diet-fed C57BL/6 mice. Food Chem. Toxicol. 64, 94-103.

Development and Application of Extracellular Vesicles Derived from Probiotics

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National Cheng Kung University, Taiwan

Extracellular vesicles (EVs) secretion is necessary and conserved situation that across all domains of life. Prokaryotes and eukaryotes release nano-sized and spherical extracellular vesicles (EVs) with lipid-bilayer that encased with proteins, DNA, different classes of RNAs, lipids, toxins, enzymes, and other cargo that they deliver to extracellular environment to communicate. Few studies have evaluated the function of EVs derived from bacteria and researched the role of EVs among microbes. It's reported that the EVs derived from protiotics such as *Lactobacillus* species and the next generation probiotics in the intestine such as *Akkermansia muciniphila* and *Bacteroides fragilis* can improve intestinal inflammation-related diseases and adjust immune function. We establish the isolation method of EVs derived from protiotics and characterize the EVs. The occurrence of leaky gut is associated with the enterobacteria, this study investigated whether EVs secreted by probiotics can inhibit the growth of enterobacteria, and further clarify their possible molecular mechanisms to understand the links and communication between bacteria. The results showed that the EVs derived from different probiotics should have specificity for the regulation of intestinal bacteria. It was concluded that the EVs derived from probiotics selectively enter bacteria and specifically affect the growth of enterobacteria. It is expected that the new reagents will be developed to treat intestinal related diseases.

HY. Elizabeth Chou, Ph.D. (周涵怡)

Current position and professional experiences

2015/8 ~ Present	**Associate Professor**, Graduate Institute of Oral Biology, National Taiwan University
2015/8 ~ Present	**Jointly Appointed Associate Research Fellow**, Center for Biotechnology, National Taiwan University
2007/8 ~ Present	**Associate Research Fellow**, Department of Dentistry, NTU Hospital

Research interest

1. Oral stem cell biology
2. Exosome biology
3. Biomedical engineering application

Short research summary

Dr. Han-Yi E. Chou serves as Associate Professor at the Graduate Institute of Oral Biology, School of Dentistry, National Taiwan University. She received her Ph.D. degree from the Institute of Molecular Medicine of the National Taiwan University, and completed her post-doctoral fellowship at the Department of Pathology of NTU Hospital. Dr. Chou is interested in the biological control for homeostasis upon environmental stress and, if this fails, how it conducts to pathological outcomes. Her team has been focusing on the molecular basis linking chronic stress responses to the promotion of stemness properties, with aim to translate the biological logistics underlying these findings into novel applications through engineering and tailored design of biomedical devices.

Publications

1. Healing kinetics of diabetic wounds controlled with charge-biased hydrogel dressings. Venault A, Bai YW, Dizon GZ, Chou HY, Chiang HC, Lo CT, Zheng J, Aimare P and Chang Y*. J Mater Chem B. 2019; 7: 7184
2. Self-powered ultrasensitive glucose detection based on graphene multi-heterojunctions. Chang C, Lin W, Liao Y, Chou HY* and Chen YF*. Lasers Electro-Optics. 2018; AM4P:4. (* Equal Corresponding Author)
3. TIF1β is phosphorylated at serine 473 in colorectal tumor cells through p38 mitogen-activated protein kinase as an oxidative defense mechanism. Shen TW, Chou HY and Kato M*. Biochem Biophys Res Comm. 2017; 292(3):310.
4. Chitosan-assisted differentiation of porcine adipose tissue-derived stem cells into glucose-responsive insulin-secreting clusters. Liu HY, Chen CC, Lin YY, Chen YJ, Liu BH, Wong SC, Wu CY, Chang YT, Chou HY* and Ding ST*. Plos One. 2017; Mar. (* Equal Corresponding Author)
5. A portable microfluidic device for the rapid diagnosis of cancer metastatic potential which is programmable for temperature and CO2. Yu IF, Yu YH, Chen LY, Fan SK, Chou HY* Yang JT*. Lab Chip. 2014; 14(18):3621. (* Equal Corresponding Author)
6. A biocompatible open-surface droplet manipulation platform for detection of multi-nucleotide polymorphism. Huang CJ, Fang WF, Ke MS, Chou HY*, Yang JT*. Lab Chip. 2014; 14(12):2057. (* Equal Corresponding Author)
7. Cancer-associated fibroblasts regulate the plasticity of lung cancer stemness via paracrine signalling. Chen WJ, Ho CC, Chang YL, Chen HY, Lin CA, Ling TY, Yu SL, Yuan SS, Chen YJ, Lin CY,

Pan SH, Chou HY, Chen YJ, Chang GC, Chu WC, Lee YM, Lee JY, Lee PJ, Li KC, Chen HW and Yang PC. Nat Commun. 2014; 5:3472.

8. Interaction between Salt-inducible Kinase 2 and Protein Phosphatase 2A regulates the activity of Calcium/Calmodulin-dependent Protein Kinase I and Protein Phosphatase Methylesterase-1. Lee CW, Yang FC, Chang HY, Tan BC, Chou HY and Lee SC. J Biol Chem. 2014; 289:21108.

Cheng-Chih Hsu, Ph.D. (徐丞志)

Current position and professional experiences

2015 ~ Present **Faculty member**, Department of Chemistry, National Taiwan University

2014 ~ 2015 **Postdoctoral research fellow**, Department of Chemistry, Stanford University

Research interest

1. Mass spectrometry imaging
2. Ambient ionization mass spectrometry
3. Clinical mass spectrometry
4. Human microbiota metabolomics

Honors and Awards

1. 2020 Young Scholar Research Award of Taiwan Society for Mass Spectrometry
2. 2019 MOST Young Scholar Fellowship – Columbus Program
3. Top 40 Under 40 Power List 2018 of the Analytical Scientist
4. Future Tech Breakthrough Award 2018 at MOST Future Tech Exhibition
5. 2016 Recruiting Outstanding Young Scholar Award, FAOS
6. 2015 Mass Spectrometry Imaging (MSI) Award

Publications

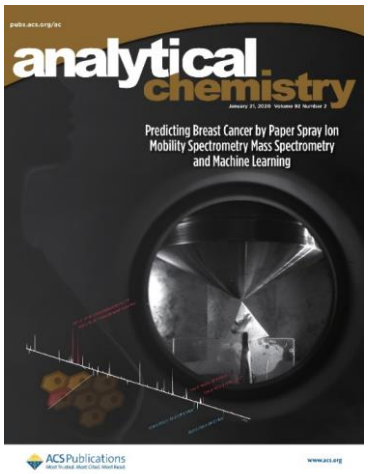
1. Y.-C. Huang, H.-H. Chung, E. P. Dutkiewicz, C.-L. Chen, H.-Y. Hsieh, B.-R. Chen, M.-Y. Wang,* C.-C. Hsu,* "Predicting Breast Cancer by Paper Spray Ion Mobility Spectrometry Mass Spectrometry and Machine Learning." Anal. Chem. 2020, 92, 1653-1657. (Front Cover)
2. T.-H. Kuo, E. P. Dutkiewicz, J. Pei,* C.-C. Hsu,* "Ambient Ionization Mass Spectrometry Today and Tomorrow: Embracing Challenges and Opportunities." Anal. Chem. 2020, 92, 2353-2363.
3. T.-H. Kuo, C.-T. Yang, H.-Y. Chang, Y.-P. Hsueh,* C.-C. Hsu,* "Nematode-Trapping Fungi Produce Diverse Metabolites during Predator–Prey Interaction." Metabolites. 2020, 10, 117.
4. P. Huang, C.-Y. Huang, T.-C. Lin, L.-E. Lin, E. Yang, C. Lee,* C.-C. Hsu,* P.-T. Chou,* "Towards the Rational Design of Universal Dual Polarity Matrix for MALDI Mass Spectrometry." Anal. Chem. 2020, 92, 7139-7145.
5. L.-E. Lin, C.-L. Chen, Y.-C. Huang, H.-H. Chung, Y.-J. Peng, S.-T. Ding, M.-Y. Wang, T.-L. Shen, C.-C. Hsu,* "Precision Biomarker Discovery Powered by Microscopy Image Fusion-assisted High Spatial Resolution Ambient Ionization Mass Spectrometry Imaging." Anal. Chim. Acta 2020, 1100, 75-87.
6. Y.-L. Gao, Y.-J. Wang, H.-H. Chung, K.-C. Chen, T.-L. Shen, C.-C. Hsu,* "Tandem mass spectral similarity networking as a dereplication strategy for metabolic products of medicinal herbs in cancer cells." Rapid Commun. Mass Spectrom. 2020, 34, e8549.
7. T.-H. Kuo, H.-H. Chung, H.-Y. Chang, C.-W. Lin, M.-Y. Wang, T.-L. Shen, C.-C. Hsu,* "Deep Lipidomics and Molecular Imaging of Unsaturated Lipid Isomers: A Universal Strategy Initiated by mCPBA Epoxidation." Anal. Chem. 2019, 91, 11905-11915.
8. T.-H. Kuo, H.-C. Huang, C.-C. Hsu,* "Mass Spectrometry Imaging Guided Molecular Networking to Expedite Discovery and Structural Analysis of Agarwood Natural Products." Anal. Chim. Acta 2019, 1080, 95-103.

9. Q. Lyu, T.-H. Kuo, C. Sun, K. Chen, C.-C. Hsu,* Xian Li* "Comprehensive Structural Characterization of Phenolics in Litchi Pulp Using Tandem Mass Spectral Molecular Networking", Food. Chem. 2019, 282, 9-17.
10. W.-K. Wu, C.-C. Chen, P.-Y. Liu, S. Panyod, B.-Y. Liao, P.-C. Chen, H.-L. Kao, H.-C. Kuo, C.-H. Kuo, H.T. Chiu, R.-A. Chen, H.-L. Chuang, Y.-T. Huang, H.-B. Zou, C.-C. Hsu, T.-Y. Chang, C.-L. Lin, C.-T. Ho, H.-T. Yu, L.-Y. Sheen*, M.-S. Wu* "Identification of TMAO-producer phenotype and host-diet-gut dysbiosis by carnitine challenge test in human and germ-free mice", Gut 2019, 68, 1439-1449.
11. K.-H. Huang, T.-H. Tu, S.-C. Wang, Y.-T. Chan,* C.-C. Hsu,* "Micelles Protect Intact Metallo-supramolecular Block Copolymer Complexes from Solution to Gas Phase during Electrospray Ionization", Anal. Chem. 2018, 90, 7691-7699.
12. Wang, F.; Yang, P.; Choi, J.; Antovski, P.; Zhu, Y.; Xu, X.; Kuo, T.-H. Lin, L.-E. Kim, D.N.H.; Huang, P.-C.; Xu, H.; Lee, C.-F. Wang, C.;* Hsu, C.-C.;* Chen, J.;* Weiss, P.;* Tseng, H.-R.* "Cross-Linked Fluorescent Supramolecular Nanoparticles for Intradermal Controlled Release of Antifungal Drug – A Therapeutic Approach for Onychomycosis", ACS Nano 2018, 12, 6851-6859.
13. L.-E. Lin, P.-R. Su, H.-Y. Wu, C.-C. Hsu,* "A Simple Sonication Improves Protein Signal in Matrix-assisted Laser Desorption Ionization Mass Spectrometry Imaging." J. Am. Soc. Mass Spectrom. 2018, 29,796-799.
14. Hsieh, H.-Y.; Li, L.-H.; Hsu, R.-Y.; Kao, W.-F.; Huang, T.-C.; Hsu, C.-C.* "Quantification of Endogenous Cholesterol in Human Serum on Paper Using Direct Analysis in Real Time Mass Spectrometry." Anal. Chem. 2017, 89, 6146-6152.
15. C.-C. Hsu, M. Baker, T. Gaasterland, M. Meehan, E. R. Macagno,* P. C. Dorrestein,* "Top-Down Atmospheric Ionization Mass Spectrometry Microscopy Combined With Proteogenomics." Anal. Chem. 2017, 89, 8251-8258.

Ambient Mass Spectrometry and Machine Learning in Disease Diagnosis

Cheng-Chih Hsu
Departmen of Chemistry, National Taiwan University, Taiwan

Mass spectrometry (MS) provides a wealth of chemical information. In our laboratory we combined MS-based metabolite and lipid profiling with machine learning to different clinical applications. First we use paper spray ionization (PSI) coupled with chip-based field asymmetry ion mobility spectrometry (FAIMS) to rapidly obtained the molecular features of breast core-needle biopsy. The predictive LASSO model gave a total accuracy close to 90% by training with about a hundred of patient breast samples. Later we utilized such strategy for real-time diagnosis of breast core-needle biopsy obtained from NTU Cancer Center. The tissue can be classified as benign or tumor within 10 minutes upon surgery. Secondly we utilized multimodal desorption electrospray ionization (DESI) mass spectrometry imaging (MSI)-microscopy image fusion to boost the spatial resolution of MSI. By such predictive molecular imaging we were able to find dozens of more potential lipid biomarkers that can be used to determine the tumor margins. We further utilized machine learning algorithms to explore if the dust chemical components from the environments can be used to give insights of the health status of household members. Lastly, we developed a molecular diagnostic veterinary platform using mobile mini-MS, in which the metabolite profiles of chicken stools were utilized to predict if the poultry were infected with parasites.

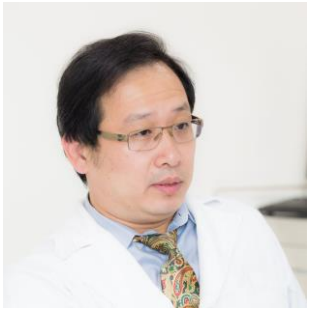


"Predicting Breast Cancer by Paper Spray Ion Mobility Spectrometry Mass Spectrometry and Machine Learning." ***Anal. Chem.*** **2020**, *92*, 1653-1657. (Featured as Front Cover)
https://pubs.acs.org/doi/10.1021/acs.analchem.9b03966

Wen-Hung Kuo, M.D., Ph.D. (郭文宏)

Current position and professional experiences

2014/8 ~ Present **Clinical associate professor**, College of Medicine, National Taiwan University
1998/8 ~ Present **Visiting staff,** Department of Surgery, National Taiwan University Hospital



Research interest

1. General surgery
2. Breast surgery
3. Sonography
4. Translational research

Short research summary

Wen-Hung Kuo, Council of the Breast Cancer Society of Taiwan, is a Clinical Associate Professor of Surgery at the National Taiwan University College of Medicine and visiting staff at department of surgery and breast care center of national Taiwan university hospital, Taipei, Taiwan. Dr Kuo got his MD and PhD from the National Taiwan University College of Medicine.

Dr. Kuo has dedicated his career to the diagnosis and treatment of breast cancer. His areas of research include: molecular profiling of breast cancer, computer-aid diagnosis of breast ultrasound, serum biomarker for early detection of breast cancer and genetic susceptibility in early onset breast cancer.

Publications

1. Chiu LY*, Kuo WH*, Chen CN, Chang KJ, Chen A. A 2-Phase Merge Filter Approach to Computer-Aided Detection of Breast Tumors on 3-Dimensional Ultrasound Imaging. J Ultrasound Med. 2020 Jun 21. doi: 10.1002/jum.15365. Online ahead of print. (*Co-first author)
2. Huang M, Li HY, Liao HW, Lin CH, Wang CY, Kuo WH*, Kuo CH*. Using post-column infused internal standard assisted quantitative metabolomics for establishing prediction models for breast cancer detection. Rapid Commun Mass Spectrom. 2020 Apr;34 Suppl 1:e8581. doi: 10.1002/rcm.8581. Epub 2020 Feb 5.PMID: 31693758(*corresponding author)
3. Tai YL, Chu PY, Lee BH, Chen KC, Yang CY, Kuo WH, Shen TL. Basics and applications of tumor-derived extracellular vesicles. J Biomed Sci. 2019 May 11;26(1):35.
4. Hsiao FH, Kuo WH, Jow GM, Wang MY, Chang KJ, Lai YM, Chen YT, Huang CS. The changes of quality of life and their correlations with psychosocial factors following surgery among women with breast cancer from the post-surgery to post-treatment survivorship. Breast. 2019 Apr;44:59-65.
5. Hsu SM, Kuo WH, Kuo FC, Liao YY. Breast tumor classification using different features of quantitative ultrasound parametric images. Int J Comput Assist Radiol Surg. 2019 Apr;14(4):623-633. doi: 10.1007/s11548-018-01908-8. Epub 2019 Jan 8.
6. Chan SH, Tsai KW, Chiu SY, Kuo WH, Chen HY, Jiang SS, Chang KJ, Hung WC, Wang LH. Identification of the Novel Role of CD24 as an Oncogenesis Regulator and Therapeutic Target for Triple-Negative Breast Cancer. Mol Cancer Ther. 2019 Jan;18(1):147-161.
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14. Wu LA, Kuo WH, Chen CY, Tsai YS, Wang J. The association of infrared imaging findings of the breast with prognosis in breast cancer patients: an observational cohort study. BMC Cancer. 2016 Jul 27;16:541.
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16. Wang J, Wang MY, Kuo WH, Chen KL, Shih TT. Proton MR Spectroscopy of Normal breasts: Association of Risk Factors for Breast Cancer with Water and Lipid Composition of the Breast. Magn Reson Imaging. 2016 May;34(4):524-8.
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18. Yao-Yin Chang* , Wen-Hung Kuo* , Jui-Hui Hung, Chien-Yueh Lee, Yung-Hua Lee, Ya-Chu Chang Wen-Chun Lin, Cheng-Ying Shen , Chiun-Sheng Huang , Fon-Jou Hsieh , Liang-Chuan Lai, Mong-Hsun Tsai , King-Jen Chang and Eric Y Chuang. Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. Molecular Cancer. 2015 Feb; 14:36. (*Co-first author)
19. Hsiao FH, Kuo WH, Jow GM, Chang KJ, Yang PS, Lam HB, Lee JJ, Huang CS, Liu YF, Lai YM. Habitual sleep-wake behaviors and lifestyle as predictors of diurnal cortisol patterns in young breast cancer survivors: A longitudinal study. Psychoneuroendocrinology. 2015 Mar; 53: 60-8.

Clinical Application of Circulation Extracellular mi-RNA in Breast Cancer

Wen-Hung Kuo
National Taiwan University Hospital, Taipei, Taiwan

The characteristic of cancer cells is continuously changing during cancer progression; however, there is often lacking clinical biomarkers for detection, monitoring and prediction of cancer development over time, which leads to higher mortality of cancer patients. Liquid biopsies (i.e. blood, urine, saliva etc.) with less invasive, low risk as well as time- and cost-effective features, compared to standard tissue biopsy, seem to match this clinical unmet need. Due to the emerging role critical for tumor formation and progression, in this current proposal, we attempt to use a large-scaled serum cohort from normal, benign (DCIS) as well as varied stages of ER+/PR+, HER2+, ER+/PR+/HER2+ and triple negative (TN) patients, to establish the signatures of circulation miRNAs in related to the early and malignant development of breast cancer. Our goal is to provide insightful information for cancer development and understanding of tumor-derived circulation extracellular miRNAs in cancer progression, subsequently these results can be translated to early detection and monitoring and even alternative therapeutic targets for breast cancer in complement with limited accessibility of standard tissue biospies.

By compares each clinical group of tumor development, we found that there are 13 miRNAs with significantly different expression between non-cancer group (healthy and benign) and cancer group. Based on these miRNAs, an elastic net regression model was built and could be used to identify a cancer patient from non-cancer group (healthy and benign tumor). The performance evaluated by validation shows the prediction accuracy as 98.13%. In addition, its positive predictive value was 96.08% and negative predictive value was 100%, showing the potential of early detection of breast cancer.

Furthermore, we have also tried to analysis by clustering the miRNAs into blocks and finding the correlation between miRNA blocks and cancer development, which could let us take a view from whole miRNA expression data. There are several types of expression patterns between different clinical groups and some of which imply the non-random changing as the development of breast cancer.

Tzu-Heng Wu, Ph.D. (吳子珩)

Current position and professional experiences

2020/1 ~ Present	**Chief Executive Officer**, PlasmonicTron, Taiwan
2018/7 ~ Present	**Co-founder**, PhaseLab Instrument, France
2019/12 ~ Presnet	**Invited Member**, Association of Chemical Sensor in Taiwan (ACST)
2017/6 ~ 2018/6	**Postdoctoral researcher**, Universite de Technologie de Troyes (2018-2019)

Research interest

1. Aptamer sensing strategy
2. Bioinformatics
3. Plasmonic sensors

Short research summary

Dr. Tzu-Heng Wu is currently the Chief Executive Officer of PlasmonicTron (Taiwan), and also the co-founder of PhaseLab Instrument (Paris, France). Dr. Wu received his double Ph.D degrees from both National Taiwan University and Université de Technologie de Troye (France). Dr. Wu's work focuses mainly on aptamer-based sensing strategy toward both proteins and nucleic acids. Combining empirical validation and in-silico design algorithm, the team of Dr. Wu is looking for highly functional sensing probes to carry out diagnostic under complex environments. Asides from Dr. Wu's primary duties in PlasmonicTron as CEO, he is also board member of PhaseLab Instrument (PLi). Dr. Wu sets strategy for PLi towards immunotherapy-based application, targeting EU market.

Publications

1 Wu, T. H., Chang, C. C., Yang, C. H., Lin, W. Y., Ee, T. J., & Lin, C. W. "Hybridization Chain Reactions Targeting the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)." International journal of molecular sciences,2020, 21(9), 3216.

2 Tzu-Heng WU, Chia-Cheng Chang, Julien Valiant, Aurélien BRUYANT and Chii-Wann LIN, "DNA biosensor combining single-wavelength colorimetry and a digital lock-in amplifier within a smartphone.", Lab-On-a-Chip,2016,23,4527

3 Aurélien Bruyant, Julien Vaillant, Tzu-Heng Wu, Yunlong Zhu, Yi Huang and Abeer Al Mohtar Interferometry Using Generalized Lock-in Amplifier (G-LIA): A Versatile Approach for Phase-Sensitive Sensing and Imaging" ("Optical Interferometry", Book chapter),

4 ,Intech,2016, ISBN 978-953-51-2956-1

5 Shih-Chung WEI, Pei-Tung YANG, Tzu-Heng WU, Yin-Lin LU, Frank GU, Kung-Bin Sung and Chii-Wann Lin."Characteristic investigation of scanning surface plasmon microscopy for nucleotide functionalized nano-array" Optical Express, 2015, 23, 20104

6 CC Chang, CY Chen, TL Chuang, TH Wu, SC Wei, H Liao, CW Lin "Aptamer-based colorimetric detection of proteins using a branched DNA cascade amplification strategy and unmodified gold nanoparticles" Biosensors and Bioelectronics 2016, 78, 200-205

7 Aurelien BRUYANT, Julien VAlAINT, Tzu-Heng WU, Chii-Wann LIN "Apparatus and method for compact interferometric sensor based on bi-reflective layer" ,PCT, 2016

8 CC Chang, CY Chen, X Zhao, TH Wu" SC Wei, CW Lin, "Label-free colorimetric aptasensor for IgE using DNA pseudoknot probe" Analyst 2014,139 (13), 3347-3351

Engineered Aptamer Based Plasmonic Sensing Toward Exosome Liquid Biopsy and Beyond

Tzu-Heng Wu
PlasmonicTron, Taiwan

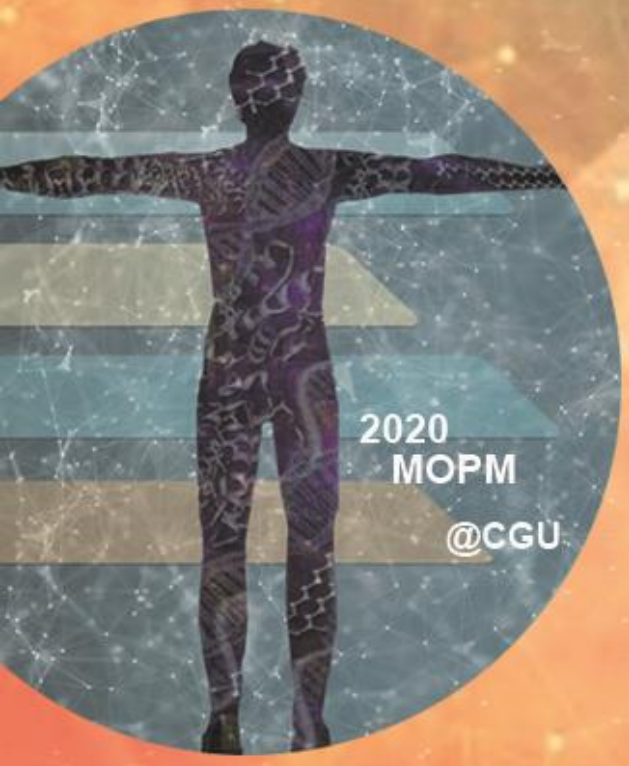
Exosome based liquid biopsy has great clinical potentials toward cancer metastasis diagnosis. Herein, we aim to discuss our recent advance on how aptamer, nucleic acid self-assembly and Surface Plasmon Resonance biosensor can be combined to build an excellent toolset toward exosome study. We will firstly discuss how aptamers can be engineered to have unique sensing properties towards exosomal surface protein, with a focus on surface integrin $\alpha_6\beta_4$. Exosomal surface Integrin has been proven by early stage work to be a vital indicator for organo-tropic metastasis. Through *in-silico* design and empirical validation via surface plasmon resonance biosensor, two novel integrin targeting aptamers are introduced herein, made from post-SELEX engineering. We will then explore how these engineered aptamers can be further leveraged with molecular self-assemblies to provide unprecedented molecular interaction capacities. As an example, bi-function integrin sensing probes are demonstrated, with a capacity to conduct chain reaction amplification upon capture of integrin. Finally, leveraging these unique exosome probes, highly sensitive detection can be undertaken using our automated Surface Plasmon Resonance system, simultaneously specifying the relevant physical parameters of the captured exosomes. With the above-mentioned results, we would like to finally explore the possibility to apply these technologies into a wider range of exosome applications.

受邀演講 Invited Speeches

台灣演化與計算生物學會 (TSECB)
Taiwan Society of Evolution and Computational Biology

台灣生物資訊與系統生物學會 (TBSB)
Taiwan Bioinformatics and Systems Biology Society

第二會議廳　　Lecture Hall II


2020
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Hurng-Yi Wang, Ph.D. (王弘毅)

Current position and professional experiences

2015/8 ~ Present	**Professor**, Graduate Institute of Clinical Medicine, National Taiwan University
2010 ~ 2015	**Associate Professor**, Graduate Institute of Clinical Medicine, National Taiwan University
2006 ~ 2010	**Assistant Professor**, Graduate Institute of Clinical Medicine, National Taiwan University

Research interest

1. Population genetics
2. Molecular genetics
3. Comparative genomics
4. Virology

Short research summary

Dr. Hurng-Yi Wang is a Professor of Graduate Institute of Clinical Medicine at the National Taiwan University (NTU), Taiwan. Dr. Wang received his Ph.D degree from the National Taiwan Normal University. The researches in Dr. Wang's lab are concentrated on molecular evolution and population genetics. Currently, there are two major domains in his lab. The first one is virus related research. He focuses on patterns of viral diversity change within host, rate of viral evolution, and interaction between pathogen and host. The second domain is to understand the mechanisms that drive population differentiation including nature as well as tumor cell populations.

Publications

1. Chaw SM, Tai JH, Chen SL, Hiseh CH, Chang SY, Yeh SH, Yang WS, Chen PJ, **Wang HY***. The origin and underlying driving forces of the SARS-CoV-2 outbreak. Journal of Biomedical Science. 2020 27(1):1-12 (IF=5.762; Medicine, Research, and Experimental 20/136=12%)
2. Hsieh CH, Huang, CG, Wu WJ, **Wang HY***. A rapid insect species identification system using mini-barcode pyrosequencing. Pest Management Science 2020 76 (4), 1222-1227 (IF: 3.750; Entomology 7/101=7%)
3. Chen PY, Chuang YC, Wu UI, Sun HY, Wang JT, Sheng WH, Lo HJ, **Wang HY**, Chun YC, Chang SC. Clonality of fluconazole-nonsusceptible Candida tropicalis in bloodstream infections, Taiwan, 2011–2017. Emerging Infectious Diseases, 2019 25(9): 1668. (IF:6.259, Infectious Disease 7/93=8%)
4. Chen YA, Lien JC, Tseng LF, Cheng CF, Lin WY, Wang HY, Tsai KH. Effects of indoor residual spraying and outdoor larval control on *Anopheles coluzzii* from São Tomé and Príncipe, two islands with pre-eliminated malaria. Malaria journal, 2019, 18(1): 405. (IF:2.631, Infectious Disease, 53/93=57%)
5. Zhang Y, Li Y, Shen X, Zhu T, Tao Y, Li T, Li X, Wang D, Ma Q, Hu Z, Liu J, Zheng C, Ruan J, Cai J, Wu CI, **Wang HY***, and Lu X*. "Rapid generation of copy number variation may lead to very high genetic load in cancer cell population." *Molecular Biology and Evolution*, 2019, 36 (3), 541-552. (IF: 11.062; Genetics and heredity 7/177=4%)
6. Wu LL, Peng WH, Wu H-L, Miaw SC, Yeh SH, Yang HC, Liao PH, Lin JS, Chen YR, Hong YT, Chen PJ, **Wang HY***, and Chen DS*. Ly6C+ Monocytes and Kupffer Cells Orchestrate Liver Immune Responses Against Hepatitis B Virus in Mice. *Hepatology*, 2019, 69 (6), 2364-2380. (IF: 14.679;

Gastroenterology and hepatology 6/88=7%)

7. Wen H, **Wang HY**, He H and Wu CI*. "On the low reproducibility of cancer studies." National Science *Review*, 2018, in press. (IF: 16.693; Multidisciplinary Sciences 3/71=4%)
8. **Wang HY**, Chen Y, Tong D, Ling S, Hu Z, Tao Y, Lu X and Wu CI*. "Is the evolution in tumors Darwinian or non-Darwinian?" National Science *Review.* 2018, 5: 15-17. (IF: 16.693; Multidisciplinary Sciences 3/71=4%)
9. Zhang Y, Shen X, Li Y, Zhu T, Tao Y, Li T, Wang D, Li X, Ma Q, Lu X*, **Wang HY***, Wu CI. Genetic load in cancer cell populations. Cancer Research, 2017, 77(13) Supplement: 514 (IF:9.727, Oncology, 19/244=8%)
10. Lin YY, Hsieh CH, Chen JH, Lu X, Kao JH, Chen PJ, Chen DS, **Wang HY***. "*De novo* assembly of highly polymorphic metagenomic data using in situ generated reference sequences and a novel BLAST-based assembly pipeline." *BMC Bioinformatics*. 2017, 18(1):223. (IF: 3.242; Mathematical and computational biology 9/59=15%)
11. **Wang HY***. Revealing the time-dependent evolution of the hepatitis B virus from a chain of sequentially infected chronic carriers. *Genes & Genetic Systems.* 90 (6), 359-359 (IF: 0.917; Genetics and Heridity 164/177=92%)
12. Wu CI*, **Wang HY**, Ling S, Lu X. "The Ecology and Evolution of Cancer: The Ultra-Microevolutionary Process." *Annual Review of Genetics*. 2016, 50:347-369. (IF: 11.146; Genetics and heredity 5/177=3%)
13. Chiou HY, Jeng CR, **Wang HY**, Inoue S, Chan FT, Liao JW, Chiou MT, Pang VF*. "Pathology and molecular detection of rabies virus in ferret badgers associated with a rabies outbreak in Taiwan." *Journal of Wildlife Diseases.* 2016, 52(1): 57-69. (IF: 1.187; Veterinary Sciences 66/142=46%)
14. Liu CJ*, Chen TC, Chen PJ, **Wang HY**, Tseng TC, Cheng HR, Liu CH, Chen DS and Kao JH*. "Micro-evolution of the hepatitis B virus genome in hepatitis B e-antigen-positive carriers: Comparison of genotypes B and C at various immune stages." *Journal of Gastroenterology and Hepatology.* 2015, 30(1): 172-7. (IF: 3.437; Gastroenterology & Hepatology 42/88=47 %)

Huai-Kuang Tsai, Ph.D. (蔡懷寬)

Current position and professional experiences

2015/11 ~ Present	**Research Fellow**, Institute of Information Science, Academia Sinica
2016/8 ~ Present	**Professor (Joint appointment)**, Genome and Systems Biology degree program, National Taiwan University
2016/8 ~ Present	**Professor (Joint appointment)**, Department of Biological Science and Technology, National Chiao-Tung University

Research interest

1. Bioinformatics and computational biology
2. Gene regulation
3. Machine learning
4. Comparative genomics

Short research summary

Dr. Huai-Kuang Tsai is a Research Fellow at Institute of Information Science, Academia Sinica. He received the B.S., the M.S., and the Ph.D. degrees in Computer Science and Information Engineering from the National Taiwan University, Taipei, Taiwan, in 1996, 1998, and 2003, respectively. Dr. Tsai's research interests include computational biology, bioinformatics, gene regulation, comparative genomics, and machine learning. His current research mainly focuses on understanding fundamental regulatory mechanisms in cells. He aims to understand the dynamic interactions between *cis*- and *trans*- regulatory elements, the impact of these interactions on gene expression and the evolutionary signatures of genes and genomes.

Publications

1. Chiang, S., Shinohara, H., Huang, J.H., **Tsai, H.K.***, and Okada, M.* (2020) Inferring the transcriptional regulatory mechanism of signal-dependent gene expression via an integrative computational approach, *FEBS Letters*, DOI: 10.1002/1873-3468.13757.
2. Chong, S.Y., Sutler, S., Lin, J.J., Tsai, C.H., **Tsai, H.K.**, Biggins, S., Tsukiyama, T., Lo, Y.C., and Kao, C.F. (2020) H3K4 methylation at active genes mitigates transcription-replication conflicts during replication stress, *Nature Communications*, 11(809).
3. Lin, C.Y., Chao, J.L., **Tsai, H.K.**, Chalker, D., and Yao, M.C. (2019) Setting Boundaries for Genome-wide Heterochromatic DNA Deletions Through Flanking Inverted Repeats in Tetrahymena thermophila, *Nucleic Acids Research*, 47(10), 5181-92.
4. Huang, J.H., Kwan, SY. Tsai, T.Y., and **Tsai, H.K.*** (2018) Expansion of transcription factor binding sites for introducing lineage-specific motifs in the promoter regions, *Frontiers in Genetics*, 9, 571.
5. Shiau, C.K., Huang, J.H. and **Tsai, H.K.*** (2018) CATANA: Comprehensive Alternative Transcript Atlas based oN Annotation, *Bioinformatics*, bty795.
6. Liu, W.H., Tsai, Z.T.Y., and **Tsai, H.K.*** (2017) Comparative genomic analyses highlight the contribution of pseudogenized protein-coding genes to human lincRNAs, *BMC Genomics*, 18, 786.

7. Ng, I.M., Huang, J.H., Tsai, S.C., and **Tsai, H.K.*** (2017) IsoPlot: a database for comparison of mRNA isoform variations in the fruit fly and mosquitoes, *Database*, 2017, bax069.
8. Cheng, J.H., Pan D., Tsai, Z.T.Y., and **Tsai, H.K.*** (2015) Genome-wide analysis of enhancer RNA in gene regulation across 12 mouse tissues, *Scientific Reports*, 5, 12648.
9. Tsai, Z.T.Y., Shiu, S.H.*, and **Tsai, H.K.*** (2015) Contribution of sequence motif, chromatin state, and DNA structure features to predictive models of transcription factor binding in yeast, *PLoS Computational Biology*, 11(8), e1004418.
10. Hung, C.L., Cheng, H.H., Hsieh, W.C., Tsai, Z.T.Y., **Tsai, H.K.**, Chu, C.H., Hsieh, W.P., Lai, C.H., and Wang, W.C.* (2015) The CrdRS two-component system in Helicobacter pylori responds to nitrosative stress, *Molecular Microbiology*, 97(6),1128-41.
11. Wang, T.Y. and **Tsai, H.K.*** (2014) MetaRank: Ranking Microbial Taxonomic Units or Functional Groups for Comparative Analysis of Metagenomes, *Encyclopedia of Metagenomics*, 1-7.Tsai, Z.T.Y., Chu, W.Y., Cheng, J.H., and **Tsai, H.K.*** (2014) Associations between intronic non-B DNA structures and exon skipping, *Nucleic Acids Research*, 42(2), 739-747.

Deciphering the Multiple Facets of Gene Regulation via Multi-omics Data Integration and Analysis

Huai-Kuang Tsai
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Gene regulation involves the mechanisms that act to induce or repress the expression of a gene. These include structural/chemical changes to the genetic material, binding of transcription factors (TF) to specific DNA elements to regulate transcription, or mechanisms that modulate translation of mRNA. Recently, the abundance and diversity of multiple “omes” provide an excellent opportunity for understanding the regulatory mechanisms. In this talk, I will introduce the way our lab decipher the gene regulatory programs via applying integrative approaches to multi-omics data. I will first try to answer how TF binding motifs became introduced into the cis-regulatory DNA regions of the genome over evolutionary time. Then, I will put focus on the relationship between TF binding to promoter and gene splicing patterns. In the last part, I will illustrate the way we combine bilinear regression and kinetic modeling to decipher the signal-dependent gene regulation. If there is still time left, I will introduce our newly developed tool for the identification of candidate regulators associated with biological traits.

Yu-Wei Wu, Ph.D. (吳育瑋)

Current position and professional experiences

2020/2 ~ Present	**Associate Professor**, Graduate Institute of Biomedical Informatics, Taipei Medical University
2016/10 ~ 2020/1	**Assistant Professor**, Graduate Institute of Biomedical Informatics, Taipei Medical University

Research interest

1. Metagenomics
2. Bioinformatics
3. Genomics
4. Machine learning

Short research summary

Dr. Yu-Wei Wu is an Associate Professor of the Graduate Institute of Biomedical Informatics at Taipei Medical University, Taiwan. Dr. Wu received his Ph.D. degree from School of Informatics and Computing at Indiana University. He then went to the Joint Bioenergy Institute at the Lawrence Berkeley National Laboratory to work as a postdoctoral research fellow before he came back to Taiwan. He has been working on resolving metagenomic problems using machine learning algorithms for more than 10 years. After joining Taipei Medical University he was also attempting to tackle the problem of predicting antimicrobial resistance activities for prokaryotic pathogens. His research interests include computational metagenomics, bioinformatics, machine learning, and anything related to prokaryotes.

Publications

1. Yi-Han Huang, Yu-Wei Wu, Jian-Ying Chuang, Yung-Chiao Chang, Hsiao-Fu Chang, Pao-Luh Tao, Horace H. Loh, Shiu-Hwa Yeh, “Morphine produces potent antinociception, sedation, and hypothermia in humanized mice expressing human mu-opioid receptor splice variants”, PAIN, 161(6):1177-1190, 2020.
2. Herdiantri Sufriyana, Yu-Wei Wu, and Emily Chia-Yu Su, “Artificial intelligence-assisted prediction of preeclampsia: Development and external validation of a nationwide health insurance dataset of the BPJS Kesehatan in Indonesia”, EBioMedicine, 54:102710, 2020.
3. Nai-Fang Chi, Tzu-Hao Chang, Chen-Yang Lee, Yu-Wei Wu, Ting-An Shen, Lung Chan, Yih-Ru Chen, Hung-Yi Chiou, Chung Y. Hsu, Chaur-Jong Hu, “Untargeted metabolomics predicts the functional outcome of ischemic stroke”, Journal of the Formosan Medical Association, in press, 2020.
4. Herdiantri Sufriyana, Yu-Wei Wu, and Emily Chia-Yu Su, “Prediction of Preeclampsia and Intrauterine Growth Restriction: Development of Machine Learning Models on a Prospective Cohort”, JMIR Medical Informatics, 8(5):e15411, 2020.
5. Te-Sheng Chang, Tzi-Yuan Wang, Tzu-Yu Hsueh, Yu-Wen Lee, Jiumn-Yih Wu, Chien-Min Chiang, Hsin-Mei Chuang, Wen-Xuan Cai, and Yu-Wei Wu*, "A Genome-Centric Approach Reveals a Novel Glycosyltransferase from the GA A07 Strain of Bacillus thuringiensis Responsible for Catalyzing 15-O-Glycosylation of Ganoderic Acid A", International Journal of Molecular Sciences, 20(20): 5192, 2019.
6. Te-Sheng Chang, Chien-Min Chiang, Yu-Han Kao, Jiumn-Yih Wu, Yu-Wei Wu, and Tzi-Yuan Wang,

"A New Triterpenoid Glucoside from a Novel Acidic Glycosylation of Ganoderic Acid A via Recombinant Glycosyltransferase of Bacillus subtilis", Molecules, 24(19): 3457, 2019.
7. Yu-Wei Wu*, Shih-Hung Yang, Myung Hwangbo, and Kung-Hui Chu, "Analysis of Zobellella denitrificans ZD1 draft genome: Genes and gene clusters responsible for high polyhydroxybutyrate (PHB) production from glycerol under saline conditions and its CRISPR-Cas system", PLoS ONE, 14(9): e0222143, 2019.
8. Ankita Kothari, Yu-Wei Wu, John-Marc Chandonia, Marimikel Charrier, Lara Rajeev, Andrea Rocha, Dominique Joyner, Terry Hazen, Steven Singer, and Aindrila Mukhopadhyay, "Large circular plasmids from groundwater plasmidomes span multiple incompatibility groups and are enriched in multi-metal resistance genes", mBio, 10(1):e02899-18, 2019.
9. Shan-Hua Yang; Kshitij Tandon; Chih-Ying Lu; Naohisa Wada; Chao-Jen Shih; Silver Sung-Yun Hsiao; Wann-Neng Jane; Tzan-Chain Lee; Chi-Ming Yang; Chi-Te Liu; Vianney Denis; Yu-Ting Wu; Li-Ting Wang; Lina Huang; Der-Chuen Lee; Yu-Wei Wu; Hideyuki Yamashiro; Sen-Lin Tang, "Metagenomic, phylogenetic and functional characterization of predominant endolithic green sulfur bacteria in the coral Isopora palifera", Microbiome, 7:3, 2019.
10. Shu-Miaw Chaw, Yu-Ching Liu, Yu-Wei Wu, Han-Yu Wang, Chan-Yi Lin, Chung-Shien Wu, Huei-Mien Ke, Lo-Yu Chang, Chih-Yao Hsu, Hui-Ting Yang, Edi Sudianto, Ming-Hung Hsu, Kun-Pin Wu, Ling-Ni Wang, James Leebens-Mack, and Isheng Tsai, "Stout camphor tree genome fills gaps in understanding of flowering plant genome evolution", Nature Plants, 5:63-73, 2019.
11. Sean Wei, Yu-Wei Wu, Tzong-Huei Lee, Yi-Shiang Huang, Cheng-Yu Yang, Yi-Lung Chen, and Yin-Ru Chiang, "Microbial functional responses to cholesterol catabolism in denitrifying sludge", mSystems, 3:e00113-18, 2018.
12. Xiaoyu Liang, Jason M. Whitham, Evert K. Holwerda, Xiongjun Shao, Liang Tian, Yu-Wei Wu, Vincent Lombard, Bernard Henrissat, Dawn M. Klingeman, Zamin K. Yang, Mircea Podar, Tom L. Richard, James G. Elkins, Steven D. Brown, and Lee R. Lynd, "Development and Characterization of Stable Anaerobic Thermophilic Methanogenic Microbiomes Fermenting Switchgrass at Decreasing Residence Times", Biotechnology for Biofuels, 11:243, 2018.
13. Yu-Wei Wu* and Yu-Chuan Jack Li, "Development and implementation of computational models provides solutions for biomedical community", Computer Methods and Programs in Biomedicine, 159: A1, 2018.
14. Jefferey Kimbrel, Nicholas Ballor, Yu-Wei Wu, Maude David, Terry C Hazen, Blake Simmons, Steven Singer, and Janet Jansson, "Microbial community structure and functional potential along a hypersaline gradient", Frontiers in Microbiology, 9:1492, 2018.
15. Hsuan-Lin Her and Yu-Wei Wu*, "A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the Escherichia coli strains", Bioinformatics, 34(13): i89-i95, 2018.
16. Harry R. Beller, Andria V. Rodrigues, Kamrun Zargar, Yu-Wei Wu, Avneesh K. Saini, Renee M. Saville, Jose H. Pereira, Paul D. Adams, Susannah G. Tringe, Christopher J. Petzold, and Jay D. Keasling, "Enzyme discovery for toluene synthesis in anoxic microbial communities", Nature Chemical Biology, 14: 451-457, 2018.
17. Yu-Wei Wu*, “ezTree: an automated pipeline for identifying phylogenetic marker genes and inferring evolutionary relationships among uncultivated prokaryotic draft genomes”, BMC Genomics, 19(Supp 1): 921, 2018.
18. Sebastian Kolinko, Yu-Wei Wu, Firehiwot Tachea, Evelyn Denzel, Jennifer Hiras, Raphael Gabriel, Nora Baecker, Leanne Jade Chan, Stephanie Eichorst, Dario Frey, Qiushi Chen, Parastoo Azadi, Paul Adams, Todd Pray, Deepti Tanjore, Christopher Petzold, John Gladden, Blake Simmons, and Steven Singer, “A Bacterial Pioneer Produces Cellulase Complexes that Persist through Community Succession”, Nature Microbiology, 3: 99-107, 2018.
19. Alexander Sczyrba, Peter Hofmann … Yu-Wei Wu … Alice C McHardy, “Critical Assessment of

Metagenome Interpretation—a benchmark of metagenomics software", Nature Methods, 14(11): 1063-1071, 2017.
20. Yu-Wei Wu, Yiru Shao, Kamil Khanipov, George Golovko, Maria Pimenova, Yuriy Fofanov, and Kung-Hui Chu, "Draft Genome Sequence of Zobellella denitrificans ZD1 (JCM 13380), a salt-tolerant denitrifying bacterium capable of producing poly(3-hydroxybutyrate)", Genome Announcements, 5(36): e00948-17, 2017.
21. Yu-Wei Wu, Brendan Higgins, Chaowei Yu, Amitha P. Reddy, Shannon Ceballos, Larry D. Joh, Blake A. Simmons, Steven W. Singer, and Jean S. VanderGheynst, "Ionic liquids impact the bioenergy feedstock degrading microbiome and transcription of enzymes relevant to polysaccharide hydrolysis", mSystems, 1(6): e00120-16, 2016.
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24. Jennifer Hiras, Yu-Wei Wu, Stephanie A Eichorst, Blake A Simmons, and Steven W Singer, "Refining the Phylum Chlorobi by Resolving the Phylogeny and Metabolic Potential of the Representative of a Deeply Branching, Uncultivated Lineage", ISME, 10:833-845, 2016. (co-First author)
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Predicting Antimicrobial Resistance Activities from the Bacterial Pan-genomes Using Machine Learning Algorithms

Yu-Wei Wu
Graduate Institute of Biomedical Informatics, Taipei Medical University, Taipei, Taiwan

Antimicrobial resistance (AMR) is becoming a huge problem for everyone. Bacterial pathogens usually gain resistance to certain antibiotic drugs by acquiring antimicrobial resistance genes or variants from other bacteria; hence it is important to understand what the AMR genes are and how to dig them out. In this talk I am going to introduce our approach to mine novel AMR genes from collections of bacterial genomes. We have previously shown in our 2018 Bioinformatics paper that using only a subset of known AMR genes can achieve better prediction accuracies for AMR activities of the *E. coli*. However known AMR genes only account for a tiny proportion of the entire gene collection, and there may be more genes potentially connected to antimicrobial resistance. As a result we continue pursuing the discovery of novel AMR genes in four common bacterial pathogens and show that 1) unprecedented AMR genes indeed serve as better predictors for AMR activities, and 2) most of the discovered AMR genes are hypothetical proteins (i.e. unknown function). To find their functions, we employ a network-based approach to determine the grouping or clustering effects of the genes and attempt to assign genes with unidentified functions to their neighbors with high confidence. We hope that such efforts can contribute to the expansion of the AMR gene repertoire and may serve as good predictors for AMR pathogens.

Yu-Chao Wang, Ph.D. (王禹超)

Current position and professional experiences

2019/8 ~ Present	**Associate Professor**, Institute of Biomedical Informatics, National Yang-Ming University
2013/8 ~ 2019/7	**Assistant Professor**, Institute of Biomedical Informatics, National Yang-Ming University

Research interest

1. Biomedical data analysis and AI in healthcare
2. Translational bioinformatics
3. Systems biology

Short research summary

Dr. Yu-Chao Wang is an Associate Professor of Biomedical Informatics at National Yang-Ming University (NYMU), Taiwan. Dr. Wang received his Ph.D. degree in electric engineering from National Tsing Hua University (NTHU), Taiwan, in 2010. His research interest focuses on multi-omics analysis for precision medicine. Specifically, omics data analysis and machine learning approaches are used to identify biomarkers for clinical applications and to unravel the underlying mechanisms of carcinogenesis.

Publications

1. Yeh YC, Lei HJ, Chen MH, Ho HL, Chiu LY, Li CP, **Wang YC***, “C-reactive protein (CRP) is a promising diagnostic immunohistochemical marker for intrahepatic cholangiocarcinoma and is associated with better prognosis” American Journal of Surgical Pathology, 41(12):1630-1641, 2017.
2. Lyu GY, Yeh YH, Yeh YC*, **Wang YC***, “Mutation load estimation model as a predictor of the response to cancer immunotherapy” npj Genomic Medicine, 3:12, 2018.
3. Yeh YC, Ho HL, Wu YC, Pan CC, **Wang YC***, Chou TY*, “AKT1 internal tandem duplications and point mutations are the genetic hallmarks of sclerosing pneumocytoma” Modern Pathology, 33(3):391-403, 2020.
4. Tan KT, Yeh CN, Chang YC, Cheng JH, Fang WL, Yeh YC, **Wang YC**, Hsu DS, Wu CE, Lai JI, Chang PM, Chen MH, Lu ML, Chen SJ, Chao Y, Hsiao M, Chen MH*, “PRKDC: new biomarker and drug target for checkpoint blockade immunotherapy” Journal for ImmunoTherapy of Cancer, 8:e000485, 2020.
5. Pan CC*, Yeh YC, **Wang YC**, Chang YH, “Differential expression analysis of clear cell renal cell carcinomas in The Cancer Genome Atlas distinguishes an aggressive subset enriched with chromosomes 7 and 12 gains” Histopathology, 76(7):950-958, 2020.
6. Pan YR†, Wu CE†, **Wang YC**†, Yeh YC, Lu ML, Hung YP, Chao Y, Yeh DW, Lin CH, Hsieh JC, Chen MH*, Yeh CN*, “Establishment of a novel gene panel as a biomarker of immune checkpoint inhibitor response” Clinical & Translational Immunology, 9:e1145, 2020. †co-first author
7. Wu CE, Yeh DW, Pan YR, Huang WK, Chen MH, Chang JW, Chen JS, **Wang YC***, Yeh CN*, “Chromosomal instability may not be a predictor for immune checkpoint inhibitors from a comprehensive bioinformatics analysis” Life (under revision).

Identification of Genomic Predictors for Treatment Response to Cancer Immunotherapy Using Omics Data Analysis

Yu-Chao Wang
Institute of Biomedical Informatics, National Yang-Ming University, Taiwan

Cancer is the leading cause of human deaths worldwide. Cancer therapeutics are intensively studied, and immune checkpoint inhibitors (ICIs) such as anti-PD-1, anti-PD-L1, and anti-CTLA-4 antibodies represent one of the novel promising therapeutic approaches. ICIs are now widely used in various cancers and have achieved impressive success in cancer treatment, resulting in a new era of anti-cancer therapy. However, treatment response is only observed in a subset of patients. Therefore, exploration of predictive biomarkers is critical to optimize the benefits of ICIs in patients.

Currently, several potential biomarkers have been identified, including tumor mutational burden (TMB), microsatellite instability (MSI) status, neoantigen burden, PD-L1 expression, $CD8^+$ T-cell density, and interferon-γ gene signature. Among these, TMB and MSI status have been identified as effective indicators of patients who might benefit from immunotherapy. However, MSI-high status is observed relatively infrequently, leading to limited use of MSI as a predictive biomarker in clinical practice. TMB is defined as the total number of mutations in the tumor. Whole exome sequencing (WES), which allows comprehensive measurement of TMB, is considered as the gold standard for TMB determination. However, high cost, long turnaround time, infrastructure requirements and bioinformatics demands have prevented WES from routine clinical practice. Therefore, we developed a computational framework to construct a TMB estimation model to accurately estimate TMB with the genetic information on a small number of genes. Even so, how to determine the TMB threshold to stratify TMB-high patients would be another problem. Since the TMB distribution varies for different cancer types, it may not be appropriate to use a fixed TMB threshold to identify TMB-high patients across different tumors. In view of this, another strategy is to develop a gene panel by selecting a small number of genes which mutation is associated with well-established predictive biomarkers. We established a DNA damage repair gene panel which alteration is associated with TMB and MSI in different cancers. The altered gene panel accounted for approximately 30% of various cancers and had a 60% predicted response rate in patients with a mutated gene panel undergoing treatment with ICIs. Hopefully, we can use omics data analysis to develop a reliable tool that can be used to predict the response to ICIs in cancer patients and guide the appropriate administration of ICIs in clinical practice.

Shaw-Jenq Tsai, Ph.D. (蔡少正)

Current position and professional experiences

2019 ~ Present	**Chair Professor**, Department of Physiology, College of Medicine, National Cheng Kung University, Taiwan
2001 ~ Present	**Director**, Bioinformatic Center, National Cheng Kung University
2016 ~ 2020	**President**, The Chinese Physiological Society
2019 ~ Present	President, Asian Society of Endometriosis and Adenomyosis
2011 ~ Present	**Ambassador**, World Endometriosis Society

Research interest

1. Hypoxia-mediated epigenome regulation
2. Mechanisms of drug resistance in cancer
3. Endometriosis
4. Translational medicine

Short research summary

Professor Shaw-Jenq (Sean) Tsai received his PhD degree from the University of Wisconsin-Madison, USA in 1997. He then joined the Department of Physiology at the National Cheng Kung University, Taiwan, as an assistant professor in 1998. He was promoted to distinguished professor in 2008 in recognition of his great academic achievements. Professor Tsai also served as the Director-General of Department of Life Sciences, Ministry of Science and Technology, Taiwan during 2014-2017. Professor Tsai's research focuses on investigating molecular mechanisms underlying important human diseases, including cancer, polycystic ovarian syndrome, and endometriosis. He has published more than one hundred papers in prestigious journals such as Nature, Nature Communications, Journal of Clinical Investigation, Journal of Pathology, Cancer Research, Nucleic Acids Research, and Journal of Clinical Endocrinology & Metabolism. Those papers have been cited more than 5000 times with an H-index of 46. The outstanding research performance enables Professor Tsai to be awarded the "2014 Distinguished Scientist" by Society for Experimental Biology and Medicine and elected as a fellow in 2018. Professor Tsai serves as editorial board member of many journals including Journal of Endocrinology, Journal of Molecular Endocrinology, Reproductive Medicine & Biology, and is the Asian editor of Experimental Biology and Medicine.

Publications

1. WN Li, KY Hsiao, CA Wang, N Chang, PL Hsu, MH Wu*, SJ Tsai* Extracellular vesicle-associated VEGF-C as a novel target for endometriosis. **Proc Natl Acad Sci U S A**, 117 (41):25859-25868, Oct. 13, 2020.
2. PS Chen, WT Chu, PL Hsu, SC Lin, IC Peng, CY Wang, SJ Tsai* Pathophysiological implications of hypoxia in human diseases. **J Biomed Sci** 27: 63, 2020 May 11.
3. CA Wang, YH Chang, PC Hou, YJ Tai**,** WN Li, PL Hsu, **SR Wu,** CF Li, YS Shan, SJ Tsai* DUSP2 regulates extracellular vesicle-VEGF-C secretion and pancreatic cancer early dissemination. **J Extracell Vesicles** 9 (1): 1746529, 2020 April 4.
4. TM Chen, MC Lai, YH Li, YL Chan, CH Wu ,YM Wang, CW Chien, SY Huang, H. S Sun*, SJ Tsai* hnRNPM induces translation switch under hypoxia to promote colon cancer development. **EBioMedicine** 2019 Mar 6. pii: S2352-3964(19)30138-0. doi: 10.1016/j.ebiom.2019.02.059

5. PL Hsu, J Jou, SJ Tsai* TYRO3: a potential therapeutic target in cancer. **Exp Biol Med** 244: 83–9, 2019
6. SC Lin, HC Lee, CT Hsu, YH Huang, WN Li, PL Hsu, MH Wu*, SJ Tsai* Targeting anthrax toxin receptor 2 ameliorates endometriosis progression. **Theranostics**; 9(3): 620-632, 2019. doi: 10.7150/thno.30655
7. JL Fu, KY Hsiao, HC Lee, WN Li, N Chang, MH Wu*, SJ Tsai* Suppression of COUP-TFII upregulates angiogenin and promotes angiogenesis in endometriosis **Hum Reprod** 33 (8): 1517-27, 2018 Aug 1. doi: 10.1093/humrep/dey220.
8. KY Hsiao, HS Sun, SJ Tsai***** Circular RNA - New member of noncoding RNA with novel functions. **Exp Biol Med** (Maywood) 242(11):1136-1141.
9. SC Lin, HC Lee, PC Hou, JL Fu, MH Wu, SJ Tsai* Targeting hypoxia-mediated YAP1 nuclear translocation ameliorates pathogenesis of endometriosis without compromising maternal fertility. **J Pathol** 242: 476–487. doi: 10.1002/path.4922, 2017
10. PC Hou, YH Li, SC Lin, SC Lin, JC Lee, PW Lin, JP Liou, JY Chang, CC Kuo, YM Liu, HS Sun, SJ Tsai* Hypoxia-induced downregulation of DUSP-2 phosphatase drives colon cancer stemness. **Cancer Res**, 77 (16): 4305-4316. doi: 10.1158/0008-5472.CAN-16-2990, 2017
11. KY Hsiao, YC Lin, SK Gupta, N Chang, L Yen, H. S Sun*, SJ Tsai* Noncoding effects of circular RNA CCDC66 promote colon cancer growth and metastasis. **Cancer Res** 77:2339-2350. May 1, doi: 10.1158/0008-5472.CAN-16-1883, 2017 (Hot paper, high-cite paper)
12. SC Lin, KY Hsiao, N Chang, PC Hou, SJ Tsai* Loss of dual specificity phosphatase-2 promotes angiogenesis and metastasis via upregulation of interleukin-8 in colon cancer. **J Pathol** 241: 638–648, 2017
13. CW Chien, PC Ho, HC Wu, YL Chang, SC Lin, PW Lin, JC Lee, YJ Chang, HS Sun, SJ Tsai* Targeting TYRO3 inhibits epithelial-mesenchymal transition and increases drug sensitivity in colon cancer. **Oncogene** 35(45):5872-5881, 2016
14. KY Hsiao, MH Wu, N Chang, SH Yang, CW Wu, HS Sun, SJ Tsai* Coordination of AUF1 and miR-148a to destabilize DNA methyltransferase 1 mRNA under hypoxia in endometriosis. **Mol Hum Reprod** 21:894-904, 2015
15. CA Wang, SJ Tsai* 2015 The non-canonical role of vascular endothelial growth factor-C axis in cancer progression. **Exp Biol Med** (Maywood) 240(6):718-24, 2015
16. KY Hsiao, SC Lin, MH Wu*, SJ Tsai* Pathological functions of hypoxia in endometriosis. **Front Biol Sci** 7: 309-321, 2015
17. SC Lin, WL Liao, JC Lee, SJ Tsai* Hypoxia-regulated gene network in drug resistance and cancer progression. **Exp Biol Med** 239:779-792, 2014
18. SC Lin, YH Li, MH Wu, YF Chang, DK Lee, S Tsai, MJ Tsai, and SJ Tsai* Suppression of COUP-TFII by proinflammatory cytokines contributes to the pathogenesis of endometriosis. **J Clin Endocrinol Metab** 99(3): E427-37, 2014.
19. TM Chen, YH Shih, JT Tseng, MC Lai, Ch Wu, YH Li, SJ Tsai*, and HS Sun* Overexpression of FGF9 in colon cancer cells is mediated by hypoxia-induced translational activation. **Nucleic Acids Res** 42:2932-44, 2014
20. HM Chen, YH Lin, YM Cheng, LYC Wing, SJ Tsai* Overexpression of integrin-β1 promotes leiomyomal cell spreading and proliferation. **J Clin Endocrinol Metab** 98:E837-46, 2013.
21. MH Wu, PC Chuang, YJ Lin, SJ Tsai* Suppression of annexin A2 by prostaglandin E_2 impairs phagocytic ability of peritoneal macrophage in women with endometriosis. **Hum Reprod** 28:1045-53, 2013 (recommended by Faculty 1000 of Medicine)
22. J Qin, SP Wu, F Dai, X Xie, CM Cheng, C J Creighton, A Frolov, Gustavo Ayala4, X Lin, XH Feng, MM Ittmann, SJ Tsai, MJ Tsai, S Y Tsai Inhibition of TGF-β-dependent growth barrier by COUP-TFII to promote prostate tumor growth and metastasis. **Nature** 493: 236-240, 2013

Hsin-Chou Yang, Ph.D. (楊欣洲)

Current position and professional experiences

2018/1 ~ Present	**Research Fellow**, Institute of Statistical Science, Academia Sinica
2008/2 ~ Present	**Core Faculty**, Bioinformatics Program, Taiwan International Graduate Program, Academia Sinica
2011/2 ~ Present	**Core Faculty**, Translational Medicine Program, Degree Program, Academia Sinica
2016/12 ~ Present	**Core Faculty**, Data Science Program, Degree Program, Academia Sinica & National Taiwan University
2017/12 ~ Present	**Joint Associate Professor**, Institute of Public Health, National Yang-Ming University
2018/8 ~ Present	**Joint Professor**, Department of Statistics, National Cheng Kung University
2019/7 ~ Present	**Coordinator**, Bioinformatics Program, Taiwan International Graduate Program, Academia Sinica

Research interest

1. Statistical genomics
2. Bioinformatics
3. Genetic epidemiology

Short research summary

Dr. Hsin-Chou Yang received his Ph.D. in Statistics from the National Tsing Hua University, Taiwan in 2002. Dr. Yang became a Postdoctoral Fellow at Institute of Biomedical Sciences, Academia Sinica from Oct. 2002 to Jun. 2006 and shifted his research from ecological statistics to statistical genetics and genetic epidemiology. In Jul. 2006, Dr. Yang joined Institute of Statistical Science, Academia Sinica as an Assistant Research Fellow and his research interest shifted to statistical genomics, genome medicine, and omics research. Dr. Yang was promoted to Association Research Fellow and Research Fellow at Mar. 2011 and Jan. 2018, respectively. Dr. Yang has devoted to developing novel statistical/bioinformatics methodologies and analysis tools for the omics (genomics, transcriptomics, epigenomics, and metabolomics) and pharmaco-omics data as well as to answering practical biomedical and biological issues via close collaborations with epidemiologists, clinicians, and geneticists. He won several titles including Career Development Award of Academia Sinica (2011), Elected member of Global Young Academy (2013), Junior Research Investigators Award, Academia Sinica (2013), Outstanding Young Alumni Award of National Cheng Kung University (2016), Future Technology Breakthrough Award of Ministry of Science and Technology (2018), Elected member of International Statistical Institute (2019), and Contribution Award of Chinese Institute of Probability and Statistics (2019). He has joint appointments in National Cheng Kung University and National Yang Ming University. He is the Associate Editor and Review Editor for three international journals and served as reviewers for more than 40 international journals and 140 papers. He is the Member of the Institution Review Board (IRB) in National Health Research Institute and Academia Sinica. He also serves as the Review Panel Member of Department of Nature Sciences and Sustainable Development, Ministry of Science and Technology and Panel Member of Mathematics Research Promotion Center, Ministry of Science and Technology.

Publications (Selective publications in the past 5 years, * Corresponding author)

1. **Yang, H.-C.**, Chu, S.-K., Kuo, H.-W., Wang, S.-C., Liu, S.-W., Ho, I.-K. and Liu, Y.-L.* (2016/03). Genome-wide pharmacogenomic study on methadone maintenance treatment identifies SNP rs17180299 and multiple haplotypes on *CYP2B6*, *SPON1*, and *GSG1L* associated with plasma concentrations of methadone *R*- and *S*-enantiomers in heroin-dependent patients. *PLoS Genetics* **12**, e1005910.
2. Huang, M.-C., Chuang, T.-P., Chen, C.-H., Wu, J.-Y., Chen, Y.-T., Li, L.-H.* and **Yang, H.-C.*** (2016/03). An integrated analysis tool for hybridization intensities and genotypes using new-generation population-optimized human arrays. *BMC Genomics* **17**, 266. (https://rdcu.be/6i0w)
3. Liang, Y.-J., Lin, Y.-T., Chen, C.-W., Lin, C.-W., Chao, K.-M., Pan, W.-H. and **Yang, H.-C.*** (2016/06). SMART: Statistical Metabolomics Analysis – an R tool. *Analytical Chemistry* **88**, 6334-6341.
4. **Yang, H.-C.*** and Lin, Y.-T. (2016/11). Homozygosity disequilibrium and its gene regulation. *BMC Proceedings* **10**, 159-163. (http://rdcu.be/mHtp)
5. **Yang, H.-C.**, Chen, I.-C., Tsay, Y.-C., Li, Z.-R., Chen, C.-H., Hwu, H.-G. and Chen, C.-H.* (2017/04). Using an event-history with risk-free model to study the genetics of alcoholism. *Scientific Reports* **7**, 1975. (http://rdcu.be/r18K)
6. Chu, S.-K. and **Yang, H.-C.*** (2017/09). Interethnic DNA methylation difference and its implications in pharmacoepigenetics. *Epigenomics* **9**, 1437-1454.
7. **Yang, H.-C.*** and Chen, C.-W. (2018/09). Homozygosity disequilibrium associated with treatment response and its methylation regulation. *BMC Proceedings* **12**, 45. (https://rdcu.be/6Z4m)

Chen, C.-W. and **Yang, H.-C.*** (2019/01). OPATs: Omnibus p-value association tests. *Briefings in Bioinformatics* **20**, 1-14.

Population Pharmacogenomics: Enrichment of Ancestry-Informative Markers in Pharmacogenetic Loci

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Institute of Statistical Science, Academia Sinica, Taiwan

Recent studies have pointed out the essential role of genetic ancestry in population pharmacogenetics. In this study, we analyzed the whole-genome sequencing data from The 1000 Genomes Project (Phase 3) and the pharmacogenetic information from Drug Bank, PharmGKB, PharmaADME, and Biotransformation. We found that ancestry-informative markers were enriched in pharmacogenetic loci (PGx), suggesting that trans-ancestry differentiation must be carefully considered in population pharmacogenetics studies. Ancestry-informative PGx were located in both protein-coding and non-protein-coding regions, illustrating that a whole-genome analysis is necessary for an unbiased examination over PGx. Finally, those ancestry-informative PGx that targeted multiple drugs were often a functional variant, which reflected their importance in biological functions and pathways. This study developed an efficient algorithm for an ultrahigh-dimensional principal component analysis, created genetic catalogues of ancestry-informative markers and genes, established a high-accuracy prediction panel of genetic ancestry, explored pharmacogenetic patterns, and constructed a genetic ancestry pharmacogenomic database “Genetic Ancestry PhD”.

Hsiao-Pei Lu, Ph.D. (呂曉沛)

Current position and professional experiences

2019/2 ~ Present **Assistant Professor**, Department of Biotechnology and Bioindustry Sciences, National Cheng Kung University

2012/8 ~ 2019/1 **Postdoctoral Fellow**, Institute of Oceanography, National Taiwan University

Research interest

1. Microbial ecology
2. Microbial evolution
3. Molecular genetics
4. Bioinformatics

Short research summary

Dr. Lu is now an Assistant Professor at the National Cheng Kung University (NCKU), Tainan, Taiwan. She received her M.S. and Ph.D. degrees from the National Taiwan University (NTU), Taipei, Taiwan. Dr. Lu is a molecular microbial ecologist with education and training in zoology and marine science. Dr. Lu's research interests are associated with microbial community ecology & microbial genome evolution. She applies meta-omics approaches (such as metagenomics, metatranscriptomics, and metabolomics) and bioinformatics tools (including phylogenetic and statistical analyses) to investigate microbe-involved systems. Her research aims are to develop new analytical methods and suitable theoretical concepts which can better interpret microbial biodiversity and biogeography.

Publications

1. **Hsiao-Pei Lu***, Yung-Hsien Shao, Jer-Horng Wu, and Chih-hao Hsieh. (2020). System performance corresponding to bacterial community succession after a disturbance in an autotrophic nitrogen removal bioreactor. ***mSystems*** 5: e00398-20.
2. Po-Yu Liu, An-Chi Cheng, Shiao-Wei Huang, **Hsiao-Pei Lu**, and Hon-Tsen Yu*. (2020). Body-size scaling is related to gut microbial diversity, metabolism and dietary niche of arboreal folivorous flying squirrels. ***Scientific Reports*** 10: 7809.
3. Wan-Hsuan Cheng, **Hsiao-Pei Lu**, Chung-Chi Chen, Sen Jan, and Chih-hao Hsieh*. (2020). Vertical beta-diversity of bacterial communities depending on water stratification. ***Frontiers in Microbiology*** 11: 449.
4. **Hsiao-Pei Lu**, Yi-Chun Yeh, Fuh-Kwo Shiah, Gwo-Ching Gong, and Chih-hao Hsieh*. (2019). Evolutionary constraints on species diversity in marine bacterioplankton communities. ***The ISME Journal*** 13: 1032–1041.
5. **Hsiao-Pei Lu**, Po-Yu Liu, Yu-bin Wang, Ji-Fan Hsieh, Han-Chen Ho, Shiao-Wei Huang, Chung-Yen Lin, Chih-hao Hsieh, and Hon-Tsen Yu*. (2018). Functional characteristics of the flying squirrel's cecal microbiota under a leaf-based diet, based on multiple meta-omic profiling. ***Frontiers in Microbiology*** 8: 2622.
6. Wenxue Wu, **Hsiao-Pei Lu**, Akash Sastri, Yi-Chun Yeh, Gwo-Ching Gong, Wen-Chen Chou, and Chih-Hao Hsieh*. (2018). Contrasting the relative importance of species sorting and dispersal limitation in shaping marine bacterial versus protist communities. ***The ISME Journal*** 12: 485-494.

7. **Hsiao-Pei Lu***, Yi-Chun Yeh, Akash Sastri, Fuh-Kwo Shiah, Gwo-Ching Gong, and Chih-hao Hsieh. (2016). Evaluating community-environment relationships along fine to broad taxonomic resolutions reveals evolutionary forces underlying community assembly. ***The ISME Journal*** 10: 2867-2878.
8. **Hsiao-Pei Lu**, Yung-Chih Lai, Shiao-Wei Huang, Huang-Chi Chen, Chih-hao Hsieh, and Hon-Tsen Yu*. (2014). Spatial heterogeneity of gut microbiota reveals multiple bacterial communities with distinct characteristics. ***Scientific Reports*** 4: 6185.
9. **Hsiao-Pei Lu**, Yu-bin Wang, Shiao-Wei Huang, Chung-Yen Lin, Martin Wu, Chih-hao Hsieh, and Hon-Tsen Yu*. (2012). Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (*Petaurista alborufus lena*). ***BMC Genomics*** 13: 466.

The Application of Metagenomics, Metatranscriptomics, and Metabolomics on Ecological Issues

Hsiao-Pei Lu
Department of Biotechnology and Bioindustry Sciences,
National Cheng Kung University, Tainan, Taiwan

Recent technological advances, including high-throughput sequencing and mass spectrometry platforms, have allowed us to thoroughly characterize the diversity and composition of genetic materials and chemical compounds; however, due to the complexity of organisms and their derivatives in natural environments, it is still difficult to apply multi-omics approaches on ecological issues. Here, I will introduce two case studies to share experiences in data analysis of metagenomics, metatranscriptomics, and metabolomics for investigating microbe-compound relationships.

In the first case, we focus on forest ecosystems, using the gut microbiota of leaf-eating flying squirrels as a model to explore how symbiotic microbes help the host adapt to a high-fiber, toxin-rich diet. In the second case, we focus on ocean ecosystems, using the marine bacterioplankton as a model to explore how microbes respond to nutrient upwelling and further affect the flux of dissolved organic matter. These exploratory studies based on metagenomics, metatranscriptomics, and metabolomics would provide new insights which allow to form molecular-based hypotheses regarding functional contributions of microorganisms in natural environments.

Shih Sheng Jiang, Ph.D. (江士昇)

Current position and professional experiences

2017/7 ~ Present	**Assistant Investigator**, National Institute of Cancer Research, NHRI
2011/3 ~ 2017/6	**Project Assistant Investigator**, National Institute of Cancer Research, NHRI
2015/8 ~ Present	**Adjunct Assistant Professor**, Biotechnology Center/Ph.D. Program in Tissue Engineering and Regenerative Medicine, National Chung Hsing University, Taichung, Taiwan
2012/8 ~ Present	**Adjunct Assistant Professor**, Graduate Institute of Life Sciences, National Defense Medical Center, Taipei, Taiwan
2006/1 ~ 2012/6	**Research Associate**, National Institute of Cancer Research, NHRI
2003/9 ~ 2005/12	**Research Associate**, President's Laboratory, NHRI
2000/5 ~ 2003/8	**Postdoctoral Fellow**, Division of Molecular and Genomic Medicine, NHRI

Research interest

1. Cancer genomics
2. Bioinformatics
3. Cancer biology
4. Molecular biology
5. Cancer immunology

Short research summary

Dr. Shih Sheng Jiang is a Principal Investigator of National Institute of Cancer Research at the National Health Research Institutes (NHRI), Taiwan. Dr. Jiang received his Ph.D. degree from the National Tsing Hua University, Taiwan and has been involved in genomic researches for more than 15 years. Dr. Jiang's research focuses on the utilization of genomics and bioinformatics approaches to identify biomarkers of cancers for early detection, diagnosis, and prognosis, as well as to unveil the underlying mechanisms of those cancer biomarkers to pave the way for better cancer treatments.

Publications

1. Li, Y. L., Chen, C. H., Chen, J. Y., Lai, Y. S., Wang, S. C., Jiang, S. S.*, and Hung, W. C.* (2020) Single-cell analysis reveals immune modulation and metabolic switch in tumor-draining lymph nodes. Oncoimmunology 9, 1830513
2. Kuo, C. L., Chou, H. Y., Chiu, Y. C., Cheng, A. N., Fan, C. C., Chang, Y. N., Chen, C. H., Jiang, S. S., Chen, N. J., and Lee, A. Y. (2020) Mitochondrial oxidative stress by Lon-PYCR1 maintains an immunosuppressive tumor microenvironment that promotes cancer progression and metastasis. Cancer Lett 474, 138-150
3. Wu, Y. J., Ko, B. S., Liang, S. M., Lu, Y. J., Jan, Y. J., Jiang, S. S., Shyue, S. K., Chen, L., and Liou, J. Y. (2019) ZNF479 downregulates metallothionein-1 expression by regulating ASH2L and DNMT1 in hepatocellular carcinoma. Cell Death Dis 10, 408
4. Lin, C. Y., Wang, B. J., Chen, B. C., Tseng, J. C., Jiang, S. S., Tsai, K. K., Shen, Y. Y., Yuh, C. H., Sie, Z. L., Wang, W. C., Kung, H. J., and Chuu, C. P. (2019) Histone Demethylase KDM4C Stimulates the Proliferation of Prostate Cancer Cells via Activation of AKT and c-Myc. Cancers (Basel) 11
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Dissecting Tumor Microenvironment Using Gene Expression Profiling Data for Prognostic Biomarkers of OSCC

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Oral squamous cell carcinomas (OSCC) are squamous cell carcinomas of the head and neck occurring at the oral cavity. OSCC are among the most prevalent malignancies in the world. The five-year survival rates range from 30% to 60%, making it among the worst for all types of cancers. Despite the advances in therapeutic methods, the prognosis of OSCC has not been significantly improved during the past several decades, mainly due to lack of effective biomarkers for predicting prognosis and proficient treatment strategies. To address such issues, it is advised to i) obtain biomarkers capable of identifying patients at high risk of disease progression and ii) to better understand the cellular and molecular mechanisms via which those biomarkers are functionally involved in the disease progression, and eventually one can invent tailored treatment strategies accordingly. In this talk, I will share our experience on prognosis biomarker development for OSCC of advanced stage based on genome-wide analyses of both bulk-tissue gene expression profiling (microarray, NanoString and RNAseq) data as well as single-cell RNAseq data. Pathway analysis at single-cell resolution has provided us insights into the mechanisms how alteration in cellular function or abundance of some candidate cell types could possibly account for poor prognosis and/or disease progression of OSCC.

H. Sunny Sun, Ph.D. (孫孝芳)

Current position and professional experiences

2016/8 ~ Present	**Director/Professor**, Institute of Molecular Medicine, National Cheng Kung University
2011/8 ~ Present	**Director**, Center for Genomic Medicine, National Cheng Kung University
2015/2 ~ 2016/7	**Associated Vice President**, Office of Research and Development, National Cheng Kung University

Research interest

1. Genomic medicine
2. Bioinformatics
3. Molecular genetics
4. Comparative genomics

Short research summary

Dr. Sunny Sun is a Professor and Director of Molecular Medicine at the National Cheng Kung University (NCKU), Taiwan. Dr. Sun received her Ph.D degree from the University of Wisconsin-Madison in the United State and has been involved in genomic researches for the past ~20 years. Dr. Sun's research interest focuses on the application of computational strategy and advanced molecular biology techniques to identify genes responsible for various human diseases and study the regulation of gene expression in physiological and pathological conditions. In addition to her primary role in the University, Dr. Sun is also the Director of Center for Genomic Medicine in NCKU, in which she leads a team to provide services for clinical diagnosis and supports for clinical research.

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Hsueh-Fen Juan, Ph.D. (阮雪芬)

Current position and professional experiences

2020/7 ~ Present **Distinguished Professor**, Department of Life Science, Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University (NTU), Taiwan

2020/4 ~ Present **Key Director**, Taiwan AI Labs

Research interest

1. Systems biology
2. Proteomics
3. Bioinformatics
4. Transcriptomics
5. Synthetic biology
6. Cancer biology

Short research summary

Dr. Hsueh-Fen Juan is Distinguished Professor of National Taiwan University. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU). She worked as a research scientist at Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) and a postdoctoral research fellow at Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan). She started her academic career as an assistant professor at Department of Chemical Engineering, National Taipei University of Technology and as an adjunct assistant professor at Department of Computer Science and Information Engineering at NTU in 2002. She moved to NTU as an assistant professor at Department of Life Science in 2004. She was promoted to associate professor in 2006, full professor in 2009 and became distinguished professor at Department of Life Science and Graduate Institute of Biomedical Electronics and Bioinformatics in 2020. Dr. Juan studied synthetic biology with Professor Hirotada Mori (NIST, Japan) in 2006 and Dr. James C. Liao (UCLA, USA) during 2007-2008. Dr. Juan joined the national teams for repurposed drugs against SARS in 2003 and SARS-CoV-2 in 2020 using bioinformatics and big data analysis. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy, she received several awards “Taiwan's Ten Outstanding Young Persons”, FY2011 JSPS Invitation Fellowship Program for Research in Japan, K. T. Li Breakthrough Award by Institute of Information and Computing Machinery, USA Emerging Information and Technology Association (EITA) Service Award, and Ministry of Science and Technology (MOST) Outstanding Research Award. She serves as the editor of Scientific Reports (Nature Research).

Publications

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5. Wang, W.-H., Hsu, C.-L., Huang, H.-C.*, Juan, H.-F.* (2020) "Quantitative phosphoproteomics reveals cell alignment and mitochondrial length change under cyclic stretching in lung cells" International Journal of Molecular Sciences 21(11):E4074.
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AI for Drug Repositioning

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Taiwan AI Labs, Taipei, Taiwan

In the big data era, the artificial intelligent (AI) and network medicine offer cutting-edge applications to drug repositioning. Drug repositioning is the process of finding new uses for existing approved drugs, and is believed to offer great benefits over de novo drug discovery. The current state of the COVID-19 pandemic is a global health crisis; drug repositioning enables rapid clinical trials and regulatory review for COVID-19 therapy. One of the best-known ways is to block enzymes essential for virus replication. By performing molecular docking analyses, we develop a drug database for SARS-CoV2, named as DockCoV2 which focuses on predicting the binding affinity of FDA-approved and Taiwan National Health Insurance (NHI) drugs with seven proteins including spike, 3CLpro, PLpro, RdRp, N protein, ACE2 and TMPRSS2. DockCoV2 also provides validation information to help users understand which drugs have already been reported to be effective against MERS or SARS-CoV. DockCoV2 is available at https://covirus.cc/drugs/. Additionally, by systematically analyzing a large compendium of compound-perturbed data obtained from the Library of Integrated Network-based Cellular Signatures (LINCS), a project initiated by the US National Institute of Health, we identified potentially effective drugs for COVID-19 and experimentally confirmed that the predicted compounds significantly inhibited SARS-CoV-2 replication at nanomolar, non-toxic concentrations.

Chien-Yu Chen, Ph.D. (陳倩瑜)

Current position and professional experiences

2013/8 ~ Present	**Professor**, Department of Biomechatronics Engineering, National Taiwan University
2019/2 ~ 2020/1	**Chief Scientist**, Genomic AI team, Taiwan AI Labs
2008/8 ~ 2013/7	**Associate Professor**, Department of Biomechatronics Engineering, National Taiwan University
2005/8 ~ 2008/7	**Assistant Professor**, Department of Biomechatronics Engineering, National Taiwan University

Research interest

1. Bioinformatics
2. Machine learning
3. Regulatory networks
4. Genomic medicine

Short research summary

Chien-Yu Chen received the B.S. degree in Electrical Engineering from National Taiwan University in 1996, the M.S. degree in Electrical Engineering from the Stanford University in 1998, and the Ph.D. degree in Computer Science and Information Engineering from National Taiwan University in 2003. She is currently a Professor of the department of Biomechatronics Engineering, National Taiwan University. Dr. Chen's lab mainly focuses on developing machine learning-based algorithms to solve problems of molecular biology, including predicting pathogenicity of regulatory variants, haplotyping, quantifying transcript expression, predicting cell type-specific enhancer activity, etc.

Publications

1. Ting-Fu Chen#, Yu-Chuan Chang#, Yi Hsiao#, Ko-Han Lee#, Yu-Chun Hsiao, Yu-Hsiang Lin, Yi-Chin Ethan Tu, Hsuan-Cheng Huang, **Chien-Yu Chen***, Hsueh-Fen Juan*, DockCoV2: a drug database against SARS-CoV-2, ***Nucleic Acids Research***, gkaa861, 2020.
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3. Jou-Ho Shih, Hsin-Yi Chen, Shin-Chih Lin, Yi-Chen Yeh, Roger Shen, Yaw-Dong Lang, Dung-Chi Wu, **Chien-Yu Chen**, Ruey-Hwa Chen, Teh-Ying Chou, and Yuh-Shan Jou*, Integrative analyses of noncoding RNAs reveal the potential mechanisms augmenting tumor malignancy in lung adenocarcinoma, ***Nucleic Acids Research***, Volume 48, Issue 3, 1175–1191, 2019.
4. Ping-Han Hsieh, Yen-Jen Oyang, and **Chien-Yu Chen***, Effect of *de novo* transcriptome assembly on transcript quantification, ***Scientific Reports***, 9:8304, 2019.
5. Yu-Yu Lin, Ping Chun Wu, Pei-Lung Chen, Yen-Jen Oyang, Chien-Yu Chen*, HAHap: a read-based haplotyping method using hierarchical assembly, ***PeerJ*** 6:e5852, 2018.
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Whole Genome Sequencing Data Analysis Using Deep Learning

Chien-Yu Chen
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In recent years, deep learning has been largely applied to analyzing various types of epigenomic data owing to its capability in capturing complicated structural patterns in regulatory regions. This facilitates the process of annotating abundant non-coding variants discovered in personal whole genome sequencing (WGS) data. In this talk, I will present a deep neural network model that utilizes DNase data to predict the H3K27ac peaks as the active enhancers in selected cell types. We propose joint training of multiple cell types to boost the model performance in predicting cross-cell type enhancer activities. The results demonstrated that by incorporating more datasets across different cell types, the complex regulatory patterns could be captured by the deep learning models and the prediction accuracy can be largely improved. In addition, I will also present an autoML framework, ezGeno, that can further improve the prediction performance by automatically searching the best network architecture. In the end of the talk, how the constructed models can be used in annotating the variants derived from WGS will be briefly explained.

Jia-Ming Chang, Ph.D. (張家銘)

Current position and professional experiences

2016/02 ~ Present	**Assistant Professor**, Department of Computer Science, National Cheng Chi University
2014/01 ~ 2016/01	**Post-doc**, Institute of Human Genetics (IGH), CNRS, France
2008/10 ~ 2013/03	**PhD**, Centre for Genomic Regulation and UPF, Spain

Research interest

1. Sequence analysis
2. Phylogenetics
3. Bioinformatics
4. Comparative genomics

Short research summary

Dr. Jia-Ming Chang is an Assistant Professor of Department of Computer Science at the National Cheng Chi University (NCCU), Taiwan. Dr. Chang received his Ph.D degree from Center of Genomic Regulation in Barcelona, Spain and has been involved in bioformatics researches for the past ~10 years. Dr. Chang's research interest focuses using computational approach to predict protein function prediction, the effect of multiple sequence analysis on downstream phylogenetics reconstruction and computational epigenetics.

Publications

1. Yang Ming Lin, Ching-Tai Chen, Jia-Ming Chang* (2019, Dec). MS2CNN: Predicting MS/MS spectrum based on protein sequence by Deep Convolutional Neural Networks. *BMC Genomics*, 20, 906.
2. Naihui Zhou et al. (include Jia-Ming Chang) (2019, Nov). The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 20, 244.
3. Jia-Ming Chang*, Evan W. Floden, Javier Herrero, Olivier Gascuel, Paolo Di Tommaso, Cedric Notredame* (2019, Feb). Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. Bioinformatics, https://doi.org/10.1093/bioinformatics/btz082.
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5. Quentin Szabo, Daniel Jost, Jia-Ming Chang, Diego I. Cattoni, Giorgio L. Papadopoulos, Boyan Bonev, Tom Sexton, Julian Gurgo, Caroline Jacquier, Marcelo Nollmann, Frédéric Bantignies, Giacomo Cavalli (2018, Feb). TADs are 3D structural units of higher-order chromosome organization in Drosophila. Science Advances, 4(2), eaar8082.
6. Diego I. Cattoni , Andrés M. Cardozo Gizzi, Mariya Georgieva, Marco Di Stefano, Alessandro Valeri, Delphine Chamousset, Christophe Houbron, Stephanie Déjardin, Jean-Bernard Fiche, Inma González, Jia-Ming Chang, Thomas Sexton, Marc A. Marti-Renom, Frédéric Bantignies, Giacomo Cavalli, Marcelo Nollmann (2017, Nov). Single-cell absolute contact probability

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8. Evan W. Floden, Paolo Di Tommaso, Maria Chatzou, Cedrik Magis, Cedric Notredame, Jia-Ming Chang* (2016, Jul). PSI/TM-Coffee: a web server for fast and accurate multiple sequence alignments of regular and transmembrane proteins using homology extension on reduced databases. Nucleic Acids Research, 44 (W1): W339-W343.
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Computational Protein Function Prediction

Jia-Ming Chang
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Biological data has grown explosively with the advance of next-generation sequencing. However, annotating protein function with wet lab experiments is time-consuming. Fortunately, computational function prediction can help wet labs formulate biological hypotheses and prioritize experiments. We have developed, GODoc, a novel and effective strategy to incorporate a training procedure into the k-nearest neighbor algorithm (instance-based learning) which is capable of solving the Gene Ontology (GO) multiple-label prediction problem, which is especially notable given the thousands of GO terms. In the CAFA3 competition (68 teams), GODoc ranks 10th in Cellular Component Ontology. In the term-centric task, GODoc performs third and is tied for first for the biofilm formation of Pseudomonas aeruginosa and the long-term memory of Drosophila melanogaster, respectively. Besides GO prediction, we present PSLCNN, a model using deep neural networks to predict protein subcellular localization for eukaryotes and prokaryotes. Compared with the state-of-the-art tools, PSLCNN achieves the best performance for prokaryotes and is comparable for eukaryotes.

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  - 2019 BMC bioinformatics GODoc: A High-Throughput Protein Function Prediction using the Novel k-nearest-neighbor and Voting algorithms
- PSLCNN
  - 2019 TAAI PSLCNN: Protein Subcellular Localization Prediction for Eukaryotes and Prokaryotes Using Deep Learning
  - 2013 PLoS one Efficient and interpretable prediction of protein functional classes by Correspondence Analysis and Compact Set Relations
  - 2008 Proteins PSLDoc: Protein subcellular localization prediction based on gapped-dipeptides and probabilistic latent semantic analysis

Chau-Ti Ting, Ph.D. (丁照棣)

Current position and professional experiences

2020 ~ Present	**Professor**, Department of Life Science, National Taiwan University, Taiwan
2006 ~ 2020	**Associate Professor**, Department of Life Science, National Taiwan University, Taiwan
2004 ~ 2006	**Associate Professor**, Department of Life Science, National Tsing Hua University, Taiwan
2000 ~ 2004	**Assistant Professor**, Department of Life Science, National Tsing Hua University, Taiwan

Research interest

1. Molecular evolution
2. Population genetics and genomics
3. Speciation
4. *Drosophila* genetics

Short research summary

Dr. Chau-Ti Ting is a Professor of Department of Life Science at the National Taiwan University, Taiwan. Dr. Ting received her Ph.D. degree from the National Taiwan University and has been involved in population genetics and genomics researches for more than 20 years. Dr. Ting's research interest focuses on the genetics changes during species formation and her team has applied advanced molecular genetic techniques to investigate the phenotypic consequences and fitness differences. Her work on population genomics has also revealed the evolutionary dynamics of segmental duplications and the evolutionary forces acting on these segmental duplications. In addition to her primary role in research and teaching, Dr. Ting is also the Director of Center for International Academic Exchanges in College of Life Science.

Publications

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2. Li J, Jiang L, Wu CI, Lu X*, Fang S*, and **Ting CT***. 2019. Small segmental duplications in *Drosophila*—High rate of emergence and elimination. *Genome Biol Evol* 11: 486–496. (doi.org/10.1093/gbe/evz011)
3. Chen, C K, Yu CP, Li SC, Wu SM, Lu MJ, Chen JH, Chen RD, Ng SC, **Ting CT***, and Li WH*. 2017. Identification and evolutionary analysis of long non-coding RNAs in zebra finch. *BMC Genomics* **18**: 117. (doi: 10.1186/s12864-017-3506-z)
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Hurng-Yi Wang, Ph.D. (王弘毅)

Current position and professional experiences

2015/8 ~ Present	**Professor**, Graduate Institute of Clinical Medicine, National Taiwan University
2010 ~ 2015	**Associate Professor**, Graduate Institute of Clinical Medicine, National Taiwan University
2006 ~ 2010	**Assistant Professor**, Graduate Institute of Clinical Medicine, National Taiwan University

Research interest

1. Population genetics
2. Molecular genetics
3. Comparative genomics
4. Virology

Short research summary

Dr. Hurng-Yi Wang is a Professor of Graduate Institute of Clinical Medicine at the National Taiwan University (NTU), Taiwan. Dr. Wang received his Ph.D degree from the National Taiwan Normal University. The researches in Dr. Wang's lab are concentrated on molecular evolution and population genetics. Currently, there are two major domains in his lab. The first one is virus related research. He focuses on patterns of viral diversity change within host, rate of viral evolution, and interaction between pathogen and host. The second domain is to understand the mechanisms that drive population differentiation including nature as well as tumor cell populations.

Publications

1. Chaw SM, Tai JH, Chen SL, Hiseh CH, Chang SY, Yeh SH, Yang WS, Chen PJ, **Wang HY***. The origin and underlying driving forces of the SARS-CoV-2 outbreak. Journal of Biomedical Science. 2020 27(1):1-12 (IF=5.762; Medicine, Research, and Experimental 20/136=12%)
2. Hsieh CH, Huang, CG, Wu WJ, **Wang HY***. A rapid insect species identification system using mini-barcode pyrosequencing. Pest Management Science 2020 76 (4), 1222-1227 (IF: 3.750; Entomology 7/101=7%)
3. Chen PY, Chuang YC, Wu UI, Sun HY, Wang JT, Sheng WH, Lo HJ, **Wang HY**, Chun YC, Chang SC. Clonality of fluconazole-nonsusceptible Candida tropicalis in bloodstream infections, Taiwan, 2011–2017. Emerging Infectious Diseases, 2019 25(9): 1668. (IF:6.259, Infectious Disease 7/93=8%)
4. Chen YA, Lien JC, Tseng LF, Cheng CF, Lin WY, Wang HY, Tsai KH. Effects of indoor residual spraying and outdoor larval control on *Anopheles coluzzii* from São Tomé and Príncipe, two islands with pre-eliminated malaria. Malaria journal, 2019, 18(1): 405. (IF:2.631, Infectious Disease, 53/93=57%)
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Gastroenterology and hepatology 6/88=7%)

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8. **Wang HY**, Chen Y, Tong D, Ling S, Hu Z, Tao Y, Lu X and Wu CI*. "Is the evolution in tumors Darwinian or non-Darwinian?" National Science *Review.* 2018, 5: 15-17. (IF: 16.693; Multidisciplinary Sciences 3/71=4%)
9. Zhang Y, Shen X, Li Y, Zhu T, Tao Y, Li T, Wang D, Li X, Ma Q, Lu X*, **Wang HY***, Wu CI. Genetic load in cancer cell populations. Cancer Research, 2017, 77(13) Supplement: 514 (IF:9.727, Oncology, 19/244=8%)
10. Lin YY, Hsieh CH, Chen JH, Lu X, Kao JH, Chen PJ, Chen DS, **Wang HY***. "*De novo* assembly of highly polymorphic metagenomic data using in situ generated reference sequences and a novel BLAST-based assembly pipeline." *BMC Bioinformatics*. 2017, 18(1):223. (IF: 3.242; Mathematical and computational biology 9/59=15%)
11. **Wang HY***. Revealing the time-dependent evolution of the hepatitis B virus from a chain of sequentially infected chronic carriers. *Genes & Genetic Systems.* 90 (6), 359-359 (IF: 0.917; Genetics and Heridity 164/177=92%)
12. Wu CI*, **Wang HY**, Ling S, Lu X. "The Ecology and Evolution of Cancer: The Ultra-Microevolutionary Process." *Annual Review of Genetics*. 2016, 50:347-369. (IF: 11.146; Genetics and heredity 5/177=3%)
13. Chiou HY, Jeng CR, **Wang HY**, Inoue S, Chan FT, Liao JW, Chiou MT, Pang VF*. "Pathology and molecular detection of rabies virus in ferret badgers associated with a rabies outbreak in Taiwan." *Journal of Wildlife Diseases.* 2016, 52(1): 57-69. (IF: 1.187; Veterinary Sciences 66/142=46%)
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The Origin and Underlying Driving Forces of the SARS-CoV-2 Outbreak

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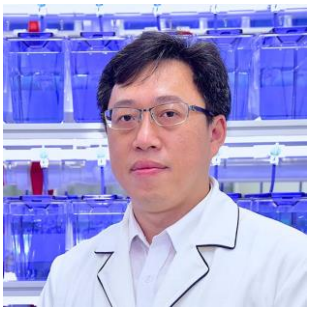
The spread of SARS-CoV-2 since December 2019 has become a pandemic and impacted many aspects of human society. In this study, genetic variation of SARS-CoV-2 genomes and its related coronaviruses was analyzed. After correction for mutational bias, the excess of low frequency mutations on both synonymous and nonsynonymous sites was revealed which is consistent with recent outbreak of the virus. In contrast to adaptive evolution previously reported for SARS-CoV in its brief epidemic in 2003, our analysis of SARS-CoV-2 genomes shows signs of relaxation of selection. The sequence similarity of the spike receptor binding domain between SARS-CoV-2 and a sequence from pangolin is probably due to an ancient intergenomic introgression approximately occurred 40 years ago. The current outbreak of SARS-CoV-2 was estimated to have originated on 12/11/2019 (ranging 11/13/2019−12/23/2019). The effective population size of the virus showed approximately 20-fold increase from the onset of the outbreak to the lockdown of Wuhan (1/23/2020) and ceased to increase afterwards, demonstrating the effectiveness of social distancing on preventing virus spread. Genetic diversity of SARS-CoV-2 collected from China in early pandemic was two time higher than those derived from the rest of the world. In network analysis, haplotypes collected from Wuhan were at interior and have more mutational connections, both of which are consistent with the observation that the outbreak of cov-19 was originated from China. Among huge amount of mutations, there are 16 mutations with frequencies higher than 10%. Based on these 16 mutations, we defined three clusters. Cluster I includes C8782T, C17747T, A17858G, C18060T, and C28144T. Cluster II contains G11083T, C14805T, and G26144T. Cluster III, which contains C3037T, C14408T, and A23403G, is the largest cluster and can be divided into 2 subclusters, IIIa and IIIb. Cluster IIIa includes C1059T and G25563T, and IIIb has 3 consecutive mutations, G28881A, G28882A, and G28883C. While effect of A23403G (D614G in spike protein) has been demonstrated, the impact for the result of mutations require further investigations.

Ming-Der Lin, Ph.D. (林明德)



Current position and professional experiences

2016/8 ~ Present	**Associate Professor**, Department of Molecular Biology and Human Genetics, Tzu Chi University
2010/2 ~ 2016/7	**Assistant Professor**, Department of Molecular Biology and Human Genetics, Tzu Chi University
2007/2 ~ 2010/1	**Assistant Professor**, Department of Life Sciences, Tzu Chi University

Research interest

1. Developmental biology
2. Molecular genetics

Short research summary

Dr. Ming-Der Lin is an Associate Professor of the Department of Molecular Biology and Human Genetics at the Tzu Chi University, Hualien, Taiwan. Dr. Lin received his Ph.D. degree from the National Taiwan University. One of Dr. Lin's research interests focuses on the germline development of *Drosophila*, biting midge, and other insects. Also, Dr. Lin adopts the zebrafish model to study traditional Chinese medicine's therapeutic effect on osteoporosis; and performs functional analyses on disease-causing genes by using both *Drosophila* and zebrafish as models.

Publications

1. Chun-I Chiu, Aaron J. Mullins, Kuan-Chih Kuan, Ming-Der Lin, Nan-Yao Su, Hou-Feng Li* (2020, Sep). Termite salinity tolerance and potential for transoceanic dispersal through rafting. *Ecological Entomology*, https://doi.org/10.1111/een.12946. (SCI, 26/101, Entomology).
2. Rui-Yi Chen, Bui Thi Ngoc Hieu, Gilbert Audira, Bao Lou*, Ming-Der Lin*, and Chung-Der Hsiao* (2020, Jul). Meta-Transcriptomic Analysis of RNAseq Data Reveals Pacu and Loach Fish with Unusually High Levels of Myoglobin Expression in Skeletal Muscles. *Animals*, 10(7), 1130. (SCI, 14/142, Veterinary Sciences).
3. Yi-Mei Lee, Po-Hsun Chiang, Jen-Ho Cheng, Wei-Hong Shen, Chao-Han Chen, Mei-Ling Wu, Yi-Lu Tian, Chao-Heng Ni, Ting-Fang Wang, Ming-Der Lin*, and Tze-Bin Chou* (2020, May). *Drosophila* decapping protein 2 modulates the formation of cortical F-actin for germ plasm assembly. *Developmental Biology*, https://doi.org/10.1016/j.ydbio.2020.01.013. (SCI, 13/43, Developmental Biology).
4. Rakesh Roy, Ren-In You, Ming-Der Lin, and Nien-Tsung Lin* (2020, Apr). Mutation of the Carboxy-Terminal Processing Protease in Acinetobacter baumannii Affects Motility, Leads to Loss of Membrane Integrity, and Reduces Virulence. *Pathogens*, 9(5), 322. (SCI, 45/133, Microbiology).
5. Szu-Chieh Wang, Yung-Hao Ching, Preethi Krishnaraj, Guan-Yu Chen, Anna Shiny Radhakrishnan, Hsien-Min Lee, Wu-Chun Tu, and Ming-Der Lin* (2020, Feb). Oogenesis of Hematophagous Midge *Forcipomyia taiwana* (Diptera: Ceratopogonidae) and Nuage Localization of Vasa in Germline Cells. *Insects*, 11(2), 106. (SCI, 18/101, Entomology).
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7. Preethi Krishnaraj, Yu Chang, Tsung-Jung Ho, Nai-Chen Lu, Ming-Der Lin*, Hao-Ping Chen* (2019, Jan). In vivo pro-angiogenic effects of dracorhodin perchlorate in zebrafish embryos: A novel bioactivity evaluation platform for commercial dragon blood samples. *Journal of food and drug analysis*, Volume 27, Issue 1, January 2019, Pages 259-265. (SCI, 13/139, Food Science and Technology).
8. Wan-Yu Liao, Lee-Fong Lin, Ming-Der Lin, Sheng-Che Hsieh, Althea Yi-Shan Li, Yueh-Shiah Tsay, and Ming-Lun Chou* (2018, Jul). Overexpression of Lilium formosanum MADS-box (LFMADS) Causing Floral Defects While Promoting Flowering in Arabidopsis thaliana, Whereas Only Affecting Floral Transition Time in Nicotiana tabacum. *International Journal of Molecular Sciences*, 19:2217-2244. (SCI, 90/292, Biochemistry and Molecular Biology).
9. Yu-Chung Lin, Kuan-Ting Wu, Zhe-Rui Lin, Elena Perevedentseva, Artashes Karmenyan, Ming-Der Lin, Chia-Liang Cheng* (2016, Apr). Nanodiamond for biolabelling and toxicity evaluation in the zebrafish embryo in vivo. *J Biophotonics*, Volume 9, Issue 8, Pages 827–836; doi: 10.1002/jbio.201500304. (SCI, 10/90, Optics).
10. Szu-Chieh Wang, Hao-Jen Hsu, Gee-way Lin, Ting-Fang Wang, Chun-che Chang*, Ming-Der Lin* (2015, Sep). Germ plasm localisation of the HELICc of Vasa in *Drosophila*: analysis of domain sufficiency and amino acids critical for localisation. *Scientific Reports*, 5:14703. (SCI, 5/57, Multidisciplinary Sciences).

The Genome of *Prorhinotermes Flavus*: A Termite Species with High Salinity Tolerance

Ming-Der Lin
Department of Molecular Biology and Human Genetics, Tzu Chi University, Hualien, Taiwan
Department of Life Sciences, Tzu Chi University, Hualien, Taiwan
Institute of Medical Sciences, Tzu Chi University, Hualien, Taiwan

Prorhinotermes flavus is a dampwood termite with unique habitats. They are found in coastal areas of islands or continents ranging over the Indian and the Pacific Ocean, including Taiwan. Though a few genomes of termite species have been sequenced, a high salinity tolerant termite species has not been explored. Here, we performed *de novo* assembly of *P. flavus* by using a hybrid assembly pipeline. The high-quality genome was obtained by 1. Building a genome draft by 10X Genomic Supernova assembly, 2. Scaffolding by SSPACE (Illumina mate-pair) and SSPACE-LongRead (PacBio longread), 3. Error correction using Illumina reads by Pilon, 4. Inter scaffolding and gap filling by Hi-C and our developing tool Tinker. The final assembly of the *P. flavus* genome is about 974 Mb. The scaffold N50 length is 29 Mb, and 32 scaffolds can comprise 90 % of the genome. Accordingly, we established a *P. flavus* database that provides a user-friendly interface for visualization of the genomic structure together with the information of transcriptome profiling among different castes and sexes. While *P. flavus* can be easily cultured on Petri dishes and produce a substantial amount of progenies, our high-quality genome assembly could grant *P. flavus* a great potential to be an emerging model of eusocial insects for exploring basic biological questions related to caste development, developmental processes of hemimetabolous insect, and termite eusociality.

Chuan Ku, Ph.D. (顧銓)

Current position and professional experiences

2019/1 ~ Present	**Assistant research fellow**, Institute of Plant and Microbial Biology, Academia Sinica
2020/8 ~ Present	**Adjunct assistant professor**, Institute of Ecology and Evolutionary Biology, National Taiwan University
2020/8 ~ Present	**Jointly appointed assistant professor**, Genome and Systems Biology Degree Program, National Taiwan University and Academia Sinica

Research interest

1. Eukaryote evolution
2. Giant viruses
3. Marine microalgae
4. Comparative genomics

Short research summary

Dr. Chuan Ku is an Assistant Research Fellow at Institute of Plant and Microbial Biology, Academia Sinica, Taiwan. He received his doctoral degree in 2016 from the University of Düsseldorf, Germany where his research focused on the prokaryotic origins of eukaryotic genes. Later Dr. Ku did his postdoctoral research as an EMBO long-term fellow at Department of Plant and Environmental Sciences, Weizmann Institute of Science, Israel, where he started to work on marine calcifying microalgae and giant viruses of eukaryotes. His current research focuses on ancient evolution of giant viruses and eukaryotes, genomics of microalgae, host-virus interactions, and single-cell omics of expression regulation.

Publications

1. **Chuan Ku**, Uri Sheyn, Arnau Sebé-Pedrós, Shifra Ben-Dor, Daniella Schatz, Amos Tanay, Shilo Rosenwasser, Assaf Vardi (2020): A single-cell view on alga-virus interactions reveals sequential transcriptional programs and infection states. *Science Advances* 6(21): eaba4137. DOI: 10.1126/sciadv.aba4137
2. **Chuan Ku***, Tsu-Wang Sun (2020): Did giant and large dsDNA viruses originate before their eukaryotic hosts? *Proceedings of the National Academy of Sciences of the United States of America* 117(6): 2747-2748. DOI: 10.1073/pnas.1919860117
3. **Chuan Ku***, Arnau Sebé-Pedrós***** (2019): Using single-cell transcriptomics to understand functional states and interactions in microbial eukaryotes. *Philosophical Transactions of the Royal Society B* 374(1786): 20190098. DOI:10.1098/rstb.2019.0098
4. **Chuan Ku**, Noa Barak-Gavish, Mark Maienschein-Cline, Stefan J. Green, Assaf Vardi (2018): Complete genome sequence of *Sulfitobacter* sp. strain D7, a virulent bacterium isolated from an *Emiliania huxleyi* algal bloom in the North Atlantic. *Microbiology Resource Announcements* 7(19): e01379-18. DOI:10.1128/MRA.01379-18
5. Noa Barak-Gavish, Miguel Frada, **Chuan Ku**, Peter A. Lee, Giacomo R. DiTullio, Sergey Malitsky, Asaph Aharoni, Stefan J. Green, Ron Rotkopf, Elena Kartvelishvily, Uri Sheyn, Daniella Schatz, Assaf Vardi (2018): Bacterial virulence against an oceanic bloom-forming phytoplankter is mediated by algal DMSP. *Science Advances* 4(10): eaau5716. DOI: 10.1126/sciadv.aau5716

6. William F. Martin, Mayo Roettger, **Chuan Ku**, Sriram G. Garg, Shijulal Nelson-Sathi, Giddy Landan (2017): Late mitochondrial origin is an artefact. *Genome Biology and Evolution* 9(2): 373-379. DOI:10.1093/gbe/evx027
7. **Chuan Ku***, William F. Martin* (2016): A natural barrier to lateral gene transfer from prokaryotes to eukaryotes revealed from genomes: the 70% rule. *BMC Biology* 14:89. DOI:10.1186/s12915-016-0315-9
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9. **Chuan Ku**, Shijulal Nelson-Sathi, Mayo Roettger, Sriram Garg, Einat Hazkani-Covo, William F. Martin (2015): Endosymbiotic gene transfer from prokaryotic pangenomes: Inherited chimerism in eukaryotes. *Proceedings of the National Academy of Sciences of the United States of America* 112(33): 10139-10146. DOI:10.1073/pnas.1421385112

Genome Content Evolution in Giant Viruses of Eukaryotes

Chuan Ku
Institute of Plant and Microbial Biology, Academia Sinica, Taiwan

The expanding collection of giant viruses discovered to date has revolutionized our view of viral genomes. The Nucleo-Cytoplasmic Large DNA Viruses (NCLDVs), which cause smallpox, African Swine Fever, algal deaths, and other diseases, have the largest genomes among viruses (up to 2.8 Mb) and infect diverse eukaryotic hosts across various ecosystems. While several hypotheses have been proposed on their origin(s) and evolution, most analyses to date have been limited to phylogenetic reconstruction using a few core genes and do not take into account the vast majority of the protein-encoding sequences. To provide a comprehensive view of the relationships among NCLDVs, we integrated comparative and network analyses of gene clusters to complement phylogenetic inferences based on individual genes. Despite extreme variation in their gene contents, we detected significant sharing of gene clusters between NCLDV families that are distant in the core gene tree. Notable differences exist between the core gene phylogenies and gene sharing patterns among genomes of giant viruses infecting aquatic amoebae and algae. Our results shed light upon the roles of host factors on the expansive genome evolution of eukaryotic giant viruses.

受邀演講 Invited Speeches

台灣基因醫學暨生物標記學會 (TGMBS)
Taiwan Genomics Mdeicine and Biomarker Society

台灣精準醫學學會 (TPMS)
Taiwan Precision Medicine Society

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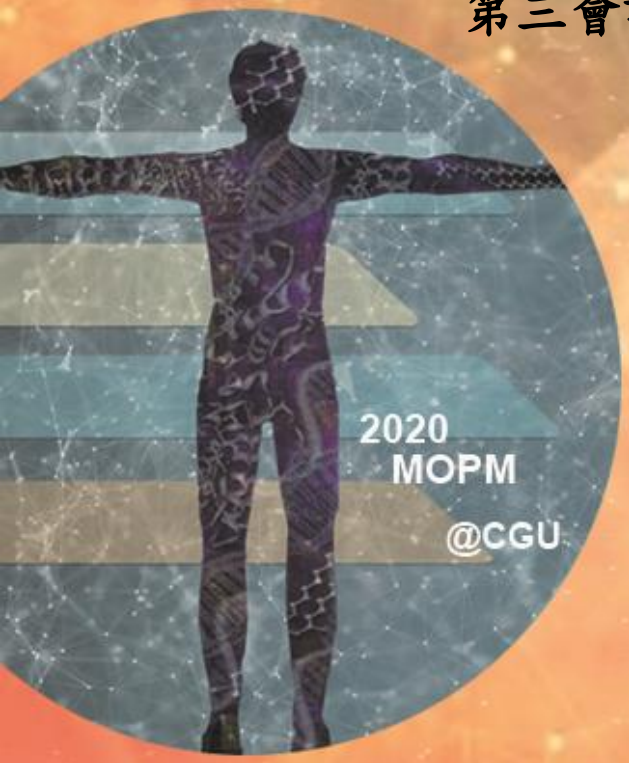

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Wan-Chi Tsai, Ph.D. (蔡婉琪)

Current position and professional experiences

2019/8 ~ Present **Associate Vice President**, Global Affairs/ **Director**, Division of Planning & Development, Office of Global Affairs, Kaohsiung Medical University

2017/8 ~ Present **Associate Professor**, Department of Medical Laboratory Science and Biotechnology, Kaohsiung Medical University

Research interest

1. Tumor biology
2. Natural products
3. Molecular genetics

Short research summary

Dr. Wan-Chi Tsai, is an Associate Professor of the Department of Medical Laboratory Science and Biotechnology of Kaohsiung Medical University (KMU), Taiwan. She received her bachelor's degree from KMU in 2000 and the Ph.D. degree from National Cheng Kung University in 2006. She conducted her postdoctoral fellowship at College of Pharmacy of Ohio State University in U.S. for two years to study the therapeutic potential of small molecules against prostate, breast, and pancreatic cancer. She served as an assistant professor at Chung Shan Medical University from 2008 to 2010, and transferred to KMU in 2011. Her primary research focus is on the therapeutic advantages of marine/herbal natural products and synthetic ruthenium-based small molecules in the treatment of oral and pancreatic cancer.

Publications

1. Wen-Chi Yang*, Sheng-Fung Lin, Shu-Chen Wang, Wan-Chi Tsai, Chun-Chieh Wu and Shih-Chi Wu. The Effects of Human BDH2 on the Cell Cycle, Differentiation, and Apoptosis and Associations with Leukemia Transformation in Myelodysplastic Syndrome. International Journal of Molecular Sciences. 2020; 21: 3033.
2. Ming-Hui Yang, Marcelo Chen, Hsiao-Hsuan Mo, Wan-Chi Tsai, Yu-Chi Chang, Chin-Chuan Chang, Ko-Chin Chen, Hsin-Yi Wu, Cheng-Hui Yuan, Che-Hsin Lee, Yi-Ming Arthur Chen* and Yu-Chang Tyan*. Utilizing Experimental Mouse Model to Identify Effectors of Hepatocellular Carcinoma Induced by HBx Antigen. Cancers (Basel). 2020 Feb 10;12(2).
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4. Wan-Chi Tsai, Hui-Fang Tsai, Yinuan Wong, Jui-Yen Hong, Shwu-Jen Chang, Ming-Wei Lee*. Preparation and characterization of Gellan gum/Glucosamine/Clioquinol film as oral cancer treatment patch. Mater Sci Eng C Mater Biol Appl. 2018 Jan 1;82:317-322.
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9. Wen-Hung Wang†, Yu-Hsuan Kuo†, Ling-Ya Chu, Chia-Ying Lee, Yu-Chang Tyan, Zong-Shiow Chen and Wan-Chi Tsai*. Anti-cancer Effects of Salvia miltiorrhiza Alcohol Extract on Oral Squamous Carcinoma Cells. Evidence-Based Complementary and Alternative Medicine. 2017;2017:5364010.
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Thai-Yen Ling, Ph.D. (林泰元)

Current position and professional experiences

Present	**Associate Professor**, Institute of Pharmacology, College of Medicine, National Taiwan University
2005 ~ 2006	**Postdoctoral Fellow**, Genomics Research Center, Academia Sinica, Taipei, Taiwan
2003 ~ 2005	**Postdoctoral Fellow**, Institute of Cellular and Organismic Biology, Academia Sinica, Taipei, Taiwan
2000 ~ 2002	**Postdoctoral Fellow**, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan

Research interest

1. Stem cell biology
2. Regeneration medicine
3. Tissue engineering
4. Signal transduction

Honors

第 17 屆國家新創獎 - 學研新創續獎
第 16 屆國家新創獎 - 學研新創
2012- ISSCR Travel Ward
Honorable Mention Award for “Competition for Originality in Biotechnology”: by the Industrial Development Bureau, Ministry of Economic Affairs, 2009
Post-doctoral research fellow scholarship, Academia Sinica 2003-2005

Publications

1. Huang AP, Hsu YH, Wu MS, Tsai HH, Su CY, **Ling TY**, Hsu SH, Lai DM. (2020) Potential of stem cell therapy in intracerebral hemorrhage. Mol Biol Rep. Jun;47(6):4671-4680. doi: 10.1007/s11033-020-05457-9. Epub 2020 May 15.
2. Tsai TH, Ling TY, Lee CH. (2020) Adoption of Regulations for Cell Therapy Development: Linkage Between Taiwan and Japan. Clin Transl Sci. May 14. doi: 10.1111/cts.12813.
3. Sun YJ, Hsu CH, **Ling TY,** Liu L, Lin TC, Jakfar S, Young IC, Lin FH. (2020) The preparation of cell-containing microbubble scaffolds to mimic alveoli structure as a 3D drug-screening system for lung cancer. Biofabrication. Mar 27;12(2):025031. doi: 10.1088/1758-5090/ab78ee.
4. Chiu PC, Liou HC, **Ling TY**, Shen LJ. (2020) Development of a Neuroprotective Erythropoietin Modified With a Novel Carrier for the Blood-Brain Barrier. Neurotherapeutics. Mar 6. doi: 10.1007/s13311-020-00845-2.
5. Chao TL, Gu SY, Lin PH, Chou YT, **Ling TY**, Chang SY. (2020) Characterization of Influenza A Virus Infection in Mouse Pulmonary Stem/Progenitor Cells. Front Microbiol. Jan 21;10:2942.
6. Lin SC, Liou YM, **Ling TY**, Chuang YH, Chiang BL. (2019) Placenta-Derived Mesenchymal Stem Cells Reduce the Interleukin-5 Level Experimentally in Children with Asthma. Int J Med Sci. 20;16(11):1430-1438.
7. Weng CF, Chen LJ, Lin CW, Chen HM, Lee HH, **Ling TY**, Hsiao FY. (2019) Association between the Risk of Lung Cancer and Influenza: A Population-Based Nested Case-Control Study. Int J Infect Dis. pii: S1201-9712(19)30315-7.

8. Su LJ, Lin HH, Wu MS, Pan L, Yadav K, Hsu HH, **Ling TY**, Chen YT, Chang HC. (2019) Intracellular Delivery of Luciferase with Fluorescent Nanodiamonds for Dual-Modality Imaging of Human Stem Cells. Bioconjug Chem. 30(8):2228-2237.
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12. Cheng NC, Lin WJ, **Ling TY,** Young TH. (2017) Sustained Release of Adipose-Derived Stem Cells by Thermosensitive Chitosan/Gelatin Hydrogel for Therapeutic Angiogenesis. Acta Biomater., S1742-7061 (17): 30069-7.
13. Tsao PN, Matsuoka C, Wei SC, Sato A, Sato S, Hasegawa K, Chen HK, **Ling TY**, Mori M, Cardoso WV, Morimoto M. (2016) Epithelial Notch signaling regulates lung alveolar morphogenesis and airway epithelial integrity. Proc Natl Acad Sci U S A., 113(29): 8242-7.
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17. Chang TS, Wu YC, Chi CC, Su WC, Chang PJ, Lee KF, Tung TH, Wang J, Liu JJ, Tung SY, Kuo LM, Ho HN, **Ling TY**, Huang YH. (2015) Activation of il6/igfir confers poor prognosis of hbv-related hepatocellular carcinoma through induction of oct4/nanog expression. Clin Cancer Res., 21(1): 201-10.
18. **Ling TY**, Liu YL, Huang YK, Gu SY, Chen HK, Ho CC, Tsao PN, Tung YC, Chen HW, Cheng CH, Lin KH, Lin FH. (2014) Differentiation of lung stem/progenitor cells into alveolar pneumocytes and induction of angiogenesis within a 3D gelatin--microbubble scaffold. Biomaterials, 35(22): 5660-9.
19. Chen WJ, Ho CC, Chang YL, Chen HY, Lin CA, **Ling TY**, Yu SL, Yuan SS, Chen YJ, Lin CY, Pan SH, Chou HY, Chen YJ, Chang GC, Chu WC, Lee YM, Lee JY, Lee PJ, Li KC, Chen HW, Yang PC. (2014) Cancer-associated fibroblasts regulate the plasticity of lung cancer stemness via paracrine signalling. Nat Commun.,5: 3472.
20. Huang YH, Lin MH, Wang PC, Wu YC, Chiang HL, Wang YL, Chang JH, Huang YK, Gu SY, Ho HN, **Ling TY*** (2014) Hypoxia inducible factor 2α/insulin-like growth factor receptor signal loop supports the proliferation and Oct-4 maintenance of mouse germline stem cells. Mol Hum Reprod., 20(6): 526-37.
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23. Chang JH, Au HK, Lee WC, Chi CC, **Ling TY**, Wang LM, Kao SH, Huang YH, Tzeng CR.(2013) Expression of the pluripotent transcription factor OCT4 promotes cell migration in endometriosis. Fertil Steril., 99(5): 1332-39.
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ectodermal organogenesis in real time bioengineered organ manipulation. Cell Commun Signal., 10(1): 34.
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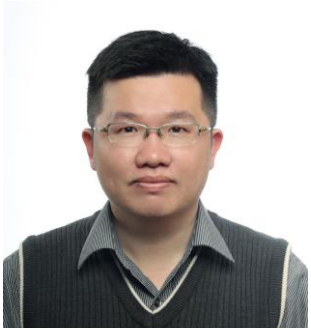
The Pharmacology of Cellular Therapy

Thai-Yen Ling
Department of Pharmacology, College of Medicine, NTU, Taiwan

In the past years, the concept of “a drug” has been regarded as low molecular weight organic compounds, so-called “small molecules” and larger biomolecules, such as peptide drugs and monoclonal antibodies. However, over the past decade, these traditional concepts have been improved on the development of new drugs based upon cells, which we refer to here as cellular therapies. The examples were tisagenlecleucel (CTL019, Kymriah) and axicabtagene ciloleucel (Yescarta), which were approved by FDA in August and October, 2017, respectively. In Pharmaceutical industry, drugs used in the clinical setting require production that adheres to current Good Manufacturing Practices (cGMP) to ensure the safety, purity, and potency from batch to batch. Like all drugs, understanding the pharmacology for the products of cellular therapies is critical to their effective application in the clinical setting.

Kuo-Hsiang Chuang, Ph.D. (莊國祥)



Current position and professional experiences

2017 ~ Present	**Associate Professor**, Graduate Institute of Pharmacognosy, Taipei Medical University, Taiwan
2012 ~ 2017	**Assistant Professor**, Graduate Institute of Pharmacognosy, Taipei Medical University, Taiwan

Research interest

1. Antibody engineering
2. Immunotherapy
3. Autoimmune disease
4. Molecular imaging

Short research summary

Dr. Kuo-Hsiang Chuang completed his Ph.D. degree in Kaohsiung Medical University in 2010, and his advisor is Dr. Tian-Lu Cheng. Dr. Chuang has 18-year experiences on genetic engineering and antibody drug development technology. After entering Taipei Medical University as an assistant professor in February 2012, he is committed to the development of multifunctional antibody drugs, novel tumor-specific T cell technology platform, novel protein drugs for treatment of autoimmune diseases, and a variety of tandem-repeated protein technologies that can be applied to enhance the sensitivity of immunoassay technology. Currently, Dr. Chuang is an associate professor at Taipei Medical University and the CEO and founder of CytoArm Co., Ltd.

Publications

1. Chen YJ, Chen M, Cheng TL, Roffler SR, Lin SY, Hsu HL, Wang CH, Chen CY, Kao AP, Cheng JJ, **Chuang KH ***. Simply mixing poly-protein G with detection antibodies enhances the detection limit and sensitivity of immunoassays. ***Analytical Chemistry*** 2019 Jul 2;91(13):8310-8317 **IF: 6.35** [7/84 (7.7%); CHEMISTRY, ANALYTICAL]
2. Lu YC, Chuang CH, **Chuang KH (3rd)**, Chen IJ, Huang BC, Lee WH, Huang HE, Li JJ, Cheng YA, Cheng KW, Wang JY, Hsieh YC, Lin WW, Cheng TL*. Specific activation of pro-Remicade enhances selectivity and safety of rheumatoid arthritis therapy. ***PLOS Biology*** 2019 Jun 13;17(6):e3000286. **IF: 8.386** [3/87 (2.9%); BIOLOGY]
3. Chen YJ, Chen M, Hsieh YC, Su YC, Wang CH, Cheng CM, Kao AP, Wang KH, Cheng JJ, **Chuang KH***. Development of a highly sensitive enzyme-linked immunosorbent assay (ELISA) through use of poly-protein G-expressing cell-based microplates. ***Scientific Reports*** 2018 Dec 14;8:17868 **IF: 4.011** [15/69 (21.1%); MULTIDISCIPLINARY SCIENCES]
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5. Lee CJ, Wang CC, Chen M, **Chuang KH (4th)**, Cheng TL, Jian TY, Wang YM, Huang TH, Liao KW, Tzou SC. Development of an inflammatory tissue-selective chimeric TNF receptor. ***Cytokine*** 2019 Jan;113:340-346. **IF: 3.078** [113/193 (58.3%); CELL BIOLOGY]

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7. Hao WR, Chen M, Chen YJ, Su YC, Cheng CM, Hsueh HY, Kao AP, Hsieh YC, Chang J, Tseng MY, **Chuang KH***. Poly-protein G-expressing bacteria enhance the sensitivity of immunoassays. ***Scientific Reports*** 2017 Apr 20;7(1):989. **IF: 4.011** [15/69 (21.1%); MULTIDISCIPLINARY SCIENCES]
8. Su YC, Burnouf PA, **Chuang KH (3rd)**, Chen BM, Cheng TL, Roffler SR. Conditional internalization of PEGylated nanomedicines by PEG engagers for triple negative breast cancer therapy. ***Nature communications*** 2017 Jun 8;8:15507. **IF: 11.878 [5/69 (6.5%)**; MULTIDISCIPLINARY SCIENCES]
9. Hsieh YC, Cheng TC, Wang HE, Li JJ, Lin WW, Huang CC, Chuang CH, Wang YT, Wang JY, Roffler SR, **Chuang KH***, Cheng TL*. Using anti-poly(ethylene glycol) bioparticles for the quantitation of PEGylated nanoparticles. ***Scientific Reports*** 2016 Dec 19;6:39119. **IF: 4.011** [15/69 (21.1%); MULTIDISCIPLINARY SCIENCES]
10. Huang WC, Burnouf PA, Su YC, Chen BM, **Chuang KH (5th)**, Lee CW, Wei PK, Cheng TL, Roffler SR. Engineering Chimeric Receptors To Investigate the Size- and Rigidity-Dependent Interaction of PEGylated Nanoparticles with Cells. ***ACS Nano***. 2016 Jan 26;10(1):648-62. **13.903** [14/172 (7.8%), CHEMISTRY & MULTIDISCIPLINARY]
11. Lin WW, Hsieh YC, Cheng YA, **Chuang KH (4th)**, Huang CC, Chuang CH, Chen IJ, Cheng KW, Lu YC, Cheng TC, Wang YT, Roffler SR, Cheng TL. Optimization of an Anti-poly(ethylene glycol) (anti-PEG) Cell-Based Capture System To Quantify PEG and PEGylated Molecules. ***Analytical Chemistry*** 2016 Dec 20;88(24):12371-12379. **IF: 6.35** [7/84 (7.7%); CHEMISTRY, ANALYTICAL]
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Novel Anti-cancer Armed T Cell Therapeutic Technology

Kuo-Hsiang Chuang
Graduate Institute of Pharmacognosy, Taipei Medical University, Taiwan

Chimeric antigen receptor (CAR) T cell technology has been the most well-known cellular immunotherapy in recent years due to its substantial success in the treatment of hematological tumors in clinical practice. However, the gene transfer technology used in current CAR T cells is still mainly based on retrovirus or lentivirus systems, which poses a potential carcinogenic risk. Additionally, the laborious protocols for manufacturing and quality control of CAR T cell products take almost 30 days, and some patients may die before the products are completed.

In this study, we present a non-genetic engineering technology for rapidly manufacturing cancer-specific T cells. By using anti-cancer/anti-CD3 bispecific antibody with the unique structure to culture human peripheral blood mononuclear cells, cancer-specific BsAb-armed T cells can be rapidly generated with a purity of over 90% in 7 days. The BsAb-armed T cells efficiently accumulated at tumor sites in vitro and in vivo. The release of cytotoxins (perforin and granzyme) and cytokines (TNF-α and IFN-γ) from the BsAb-armed T cells dramatically increased after they contacted cancer cells, causing the effective elimination of the cells in vitro and in vivo. Importantly, the BsAb-armed T cells did not cause obvious cytokine release syndrome or tissue toxicity in mouse models.

Collectively, the BsAb-armed T cell technology, as compared to current CAR-T cell technology, represents a simple, time-saving, highly safe, and economical method to generate highly pure cancer-specific effector T cells, thereby providing an affordable T cell immunotherapy to patients

Chi-Kuan Chen, M.D., Ph.D. (陳冀寬)

Current position and professional experiences

2019/12 ~ Present	**General Manager**, ProMD Inc
2019 ~ Present	**Secretory General**, Taiwan Precision Medicine Society
2013 ~ 2019	**Director**, Department of Laboratory Medicine, Mackay Memorial Hospital, Taipei and Tamsui, Taiwan
2017 ~ 2019	**Director**, Precision Medicine Center, MacKay Memorial Hospital, Taipei
2018 ~ 2019	**Director**, Department of Pathology, School of Medicine, Mackay Medical College

Research interest

1. Hematopathology
2. Molecular diagnosis & precision medicine
3. Immunomodulation and immune cell therapy
4. Bioethic and biobanking
5. IVDD clinical trial
6. Quality system for ISO 9001, ISO 13485, ISO 14971, ISO 15189, ISO 17025

Short research summary

Dr. GQ Chen is a Medical Physician professional with proven experience in surgical pathology, laboratory medicine, molecular pathology, and precision medicine. He has strong expertise in translating medicinal science into clinical practice, bridging basic biotechnology into laboratory application, introducing medical knowledge to common people. He also well experienced in planning and connecting R&D discipline to clinical trial and IND.

Industrial Cooperation Projects

1. Invented and filed patents over the field of histopathology, molecular pathology, implanted medical device, medical ethic, and biomedical database.
2. In charged of Molecular Diagnostic R&D Lab & Pilot Manufacturing Project, came out ten more oncogenic somatic mutations detecting kits, sold to local medical centers molecular pathology labs, and directed some medical device clinical trials.
3. Became specialized on ISO 9001, ISO 15189, ISO 17025, ISO 14155, ISO 13485, and ISO 14971, covering regulations from basic quality system, good laboratory practice, good clinical trial practice, and good manufacturing practice in medical device.
4. Served as the science and technology topic of the Ministry of Economic Affairs "Infectious Diseases Intelligent Automation Inspection System Development Project"(A+ Project) General Counsel, about to produce the world's first unmanned microbiological testing automation system for clinical testing laboratories

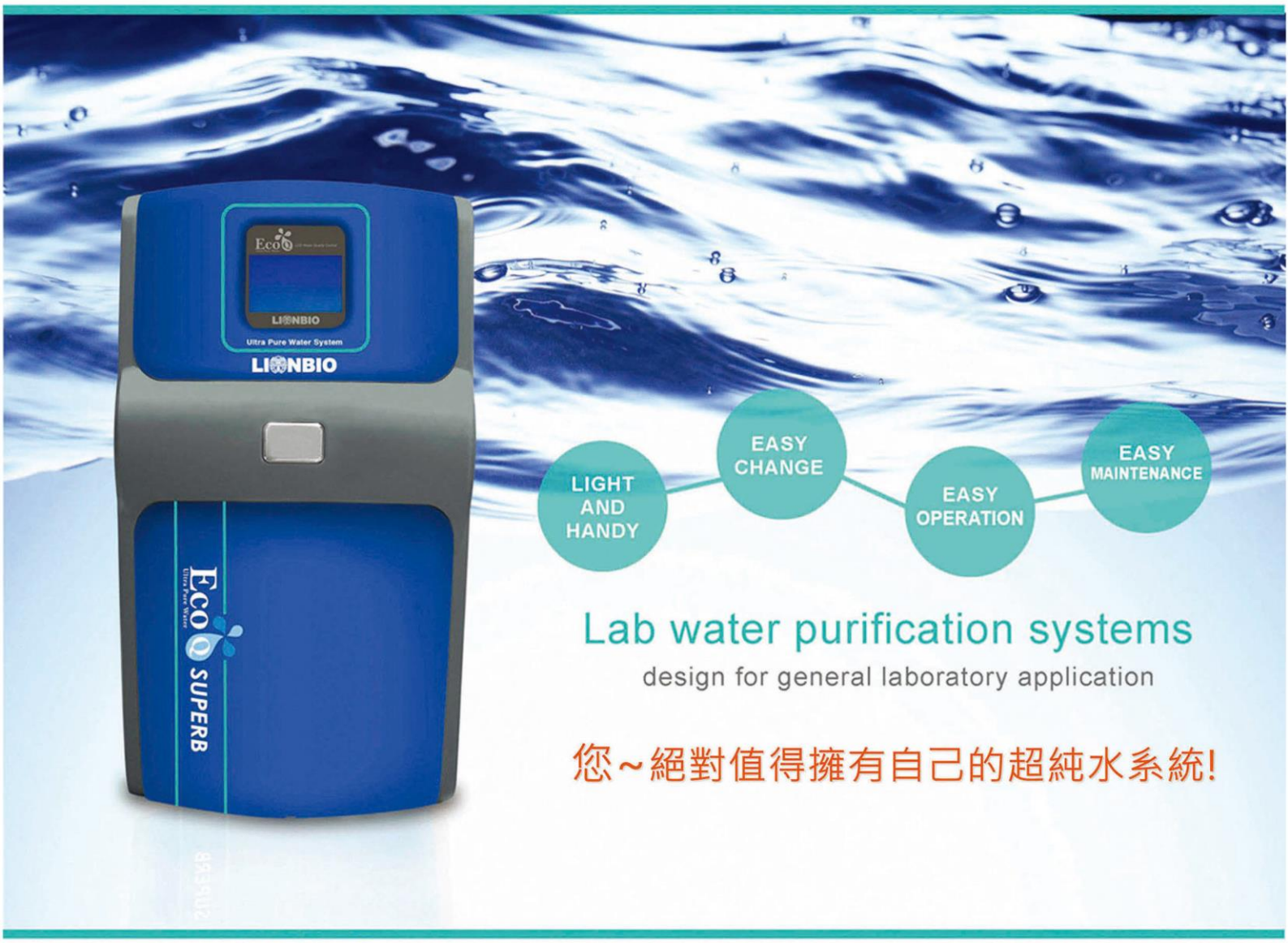
Pitfalls in Autologous Immune Cell Therapy

Chi-Kuan Chen
BioRay Health Group, Taiwan

Autologous immune cell therapy takes the patient's own immune cells, increases the number through in vitro cell culture technology, and then transfuses them to the patient's circulation vessels. It is a way to passively enhance the number and activity of immune cells. It has been widely used in cancer adjuvant treatment, balance self immunity, and even prevent cancer. Immune cells drawn from patients are usually in a chaotic and abnormal microenvironment. In a relatively nutritious and healthy culture situation in vitro, they can usually recover their activity and increase their number smoothly. Once the immune cells are reinfused into the patient, they are again exposed to the same adverse microenvironmental effects. These proliferated immune cells usually cannot survive smoothly, and the cell survival half-life is usually no more than one week. Therefore, the effect of autologous immune cell therapy in clinical adjuvant treatment of cancer will be greatly limited. We will discuss how to improve the improper immune microenvironment in patients and enhance the clinical effect of autologous immune cell therapy.

實驗室級超純水系統

EcoQ
Ultra Pure Water



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Ming-Yii Huang, M.D., Ph.D. (黃旼儀)

Current position and professional experiences

2019/9 ~ Present	**Associate Dean**, School of Medicine, Kaohsiung Medical University
2016/2 ~ Present	**Professor**, College of Medicine, Kaohsiung Medical University
1999/8 ~ Present	**Attending stuff**, Department of Radiation Oncology, Kaohsiung Medical University Hospital
2014/8 ~ 2018/7	**Vice Director**, Center for Biomarkers and Biotech Drugs (CBBD), Kaohsiung Medical University

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Research interest

1. Radiation oncology
2. Molecular biology
3. Pharmacogenomics
4. Radiation biology

Short research summary

Dr. Ming-Yii Huang is a Professor and Medical Doctor at the Kaohsiung Medical University (KMU), Taiwan. Dr. Huang received her MD, Ph.D degree from the KMU and has been involved in cancer researches for the past ~18 years. Dr. Huang's research interest focuses on the develop mRNA molecular markers for the detection of circulating tumor cells in various human cancers. And identification of novel genes involved in the carcinogenesis, the therapeutic efficacy prediction of various human cancers receiving radiation therapy.

Publications

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Chun-Ying Wu, M.D., Ph.D., M.P.H., L.L.M., L.L.B. (吳俊穎)

Current position and professional experiences

2019/8 ~ Present **Director**, Professor, Institute of Biomedical Informatics, National Yang-Ming University

2017/10 ~ Present **Chief**, Division of Translational Research, Taipei Veterans General Hospital

2014/8 ~ Present **Joint Appointment Researcher**, National Institute of Cancer Research, National Health Research Institutes

Research interest

1. Digestive cancers translational research
2. Big data research and health outcome assessment
3. Microbiome research and bionanochip development
4. Empirical study of medical malpractice

Short research summary

Prof. Wu establishes Taiwan Microbiome Consortium and currently serves as the first President in the consortium. Prof. Wu is now the Editor-in-Chief of Advances in Digestive Medicine (the joint official journal of GEST, DEST & TASL), editorial member of Gut, Vice-Secretary General of the Digestive Endoscopy Society of Taiwan, the executive of the Taiwan Liver Cancer Association, and the control board of the Taiwan Evidence-based Medicine Association. Prof. Wu has published many articles in top ranking journals such as JAMA, J Clinical Oncology, Gastroenterology, JAMA Intern Med, Gut, J of Hepatology, Hepatology, Annals of Surgery, Gastrointest Endoscopy, Radiology, Biosens Bioelectron, etc. Prof. Wu owns several patents, such as gastric cancer screening, hepatitis B virus quantitative detection methods, microbiota to treat metabolic syndrome, etc. Prof. Wu is the winner of “2016 National Innovation Award”, Taiwan Institute for Biotechnology & Medicine Industry; “2015 Outstanding Research Award”, Ministry of Science & Technology; and “2015 Emerging Leadership Award”, Asia-Pacific Digestive Week.

Publications

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   Exp Dermatol 2018 Dec;27(12):1336-43 (SCI, IF **3.368**, 15/68)
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10. Hsu YC, Yip TCF, Ho HJ, Wong VWS, Huang YT, El-Serag HB, Lee TY, Wu MS, Lin JT, Wong GLH, **Wu CY***. Development of a scoring system to predict hepatocellular carcinoma in Asians on antivirals for chronic hepatitis B. **J Hepatol** 2018 Aug; 69(2): 278-85 (SCI, **IF 20.582**, 2/88)
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12. Yeo YH, Shiu SI, Ho HJ, Zou B, Lin JT, Wu MS, Liou JM, **Wu CY***. First-line *Helicobacter pylori* eradication therapies in countries with high and low clarithromycin resistance: a systematic review and network meta-analysis. **Gut** 2018 Jan; 67(1): 20-7 (SCI, **IF 19.819**, 3/88)
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    Biosens Bioelectron 2016 Mar 15; 77:603-8 (SCI, IF **10.257**, **2/27**, Electrochemistry).
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    Sci Rep 2016 Feb 10; 6:20701 (SCI, IF **4.122**, 12/64)

Gut Microbiota, FMT and Human Diseases

Chun-Ying Wu
Director, Institute of Biomedical Informatics, National Yang-Ming University, Taiwan
Chief, Division of Translational Research, Taipei Veterans General Hospital, Taiwan

Human intestinal tract harbors a complex microbial community with approximately 100 trillion cells, about 10 times of the number of human cells and 100 times of the number of human genes. This complex microbial community is called gut microbiota. The development of next generation sequencing technologies makes it possible to explore the composition of gut microbial community, most of them are not cultivable. Human microbiota can be considered as the second genome of human beings.

Gut microbiota is stabilized in the first years after birth via the vertical transmission from parents and close contract with family members. Environmental factors, such as diet, medication, exercise, etc., further shape gut microbiota characteristics thereafter. Each subject's gut microbiota is unique, but changes with time. Gut microbiota interacted with human immune system and triggers several inflammatory related pathways, which are associated with many human diseases, such as obesity, metabolic syndrome, cancers, autoimmune diseases, cardiovascular diseases, neurological and psychiatric diseases, etc.

Fecal microbiota transplantation (FMT) is the translocation of gut microbiota to treat human diseases by re-colonization of normal gut microbiota in patients. A couple of human diseases have been treated successfully by FMT in recently randomized clinical trials. FMT has been demonstrated to be superior than traditional antibiotics treatment in patients with refractory pseudomembranous colitis, infected by Clostridium difficile. FMT is also approved to be effective in some subset of patients with inflammatory bowel diseases. There are many ongoing clinical trials to examine the efficacy and safety of FMT in treating obesity, metabolic diseases, psychiatric diseases, cancer and autoimmune diseases.

Gut microbiota plays important roles in shaping and treating human diseases. Exploring the complicated interactions between gut microbiota and human diseases will provides many new diagnostic and therapeutic methods for human diseases and will be the most exciting fields of 21st century.

Ching-Hung Tseng, Ph.D. (曾景鴻)

Current position and professional experiences

2017/9 ~ Present **General Manager**, Germark Biotechnology Co., Ltd

2016/9 ~ 2017/8 **Research and Development Manager**, Germark Biotechnology Co., Ltd

Research interest

1. Gut microbiome
2. Microbial metagenomics
3. Comparative genomics
4. Bioinformatics

Short research summary

Dr. Tseng is now the General Manager in Germark Biotechnology Co., Ltd., Taichung, which provides the total solution to microbiome research from sample collection, DNA extraction, NGS sequencing, to downstream analysis with scientific rigor. Dr. Tseng received his Ph.D. degree from the Bioinformatics Program jointly hold by Taiwan International Graduate Program (TIGP) and National Yang-Ming University (NYMU) and involved in environmental microbiome studies during his Ph.D pursuit. Dr. Tseng's research interest focuses on the application of computational strategy to resolve microbial functionality, ecology, and interactions to their host environments, including human body.

Publications

1. Shan-Hua Yang, Ching-Hung Tseng, Hsueh-Ping Lo, Pei-wen Chiang, Hsing-Ju Chen, Jia-Ho Shiu, Hung-Chun Lai, Kshitij Tandon, Naoko Isomura, Takuma Mezaki, Hiromi Yamamoto and Sen-Lin Tang. (2020) Locality effect of coral-associated bacterial community in the Kuroshio Current from Taiwan to Japan. Front Ecol Evol, accepted. (as co-first author)
2. Li-Lin Liang, **Ching-Hung Tseng**, Hsiu J. Ho and Chun-Ying Wu. (2020) Covid-19 mortality is negatively associated with test number and government effectiveness. *Sci Rep*, 10:12567.
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6. **Ching-Hung Tseng** and Chun-Ying Wu. (2018) The gut microbiome in obesity. *J Formos Med Assoc*, doi: 10.1016/j.jfma.2018.07.009.
7. Yu-Ting Wu, Cheng-Yu Yang, Pei-Wen Chiang, **Ching-Hung Tseng**, Hsiu-Hui Chiu, Isaam Saeed, Bayanmunkh Baatar, Denis Rogozin, Saman Halgamuge, Andrei Degermendzhi and Sen-Lin Tang. (2018) Comprehensive insights into composition, metabolic potentials, and interactions among archaeal, bacterial, and viral assemblages in meromictic Lake Shunet in Siberia. *Front Microbiol*, 9:1763.

8. Jia-Ho Shiu, Jiun-Yan Ding, **Ching-Hung Tseng**, Shueh-Ping Lou, Takuma Mezaki, Yu-Ting Wu, Hsiang-Iu Wang and Sen-Lin Tang. (2018) A newly designed primer revealed high phylogenetic diversity of Endozoicomonas in coral reefs. *Microbes Environ*, 33(2):172-85.
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11. Bayanmunkh Baatar, Pei-Wen Chiang, Denis Yu Rogozin, Yu-Ting Wu, **Ching-Hung Tseng**, Cheng-Yu Yang, Hsiu-Hui Chiu, Bolormaa Oyuntsetseg, Andrey G. Degermendzhy and Sen-Lin Tang. (2016) Bacterial communities of three saline meromictic lakes in central Asia. *PLoS ONE*, 11(3): e0150847.
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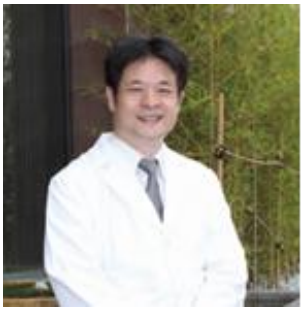
The Gut Microbiome in Human Health and Diseases, a Recent Perspective

Ching-Hung Tseng
Germark Biotechnology Co., Ltd, Taichung, Taiwan

In the past two decades, the sheer number of studies tackling the intestinal microbiota reveals its immense intimacy to human health, and to disease pathogenesis when it is disrupted. Descriptive microbiota association investigations have motivated the integration of multi-omics approaches into this nascent field to resolve causative mechanisms behind observed association. With the supports from techniques in metagenomics, metabolomics, culturomics, and animal inoculation, microbiome-derived metabolites have been discovered one after another as central messengers mediating host metabolism. To translate these discoveries into real-world applications, several microbiome-directed interventions (including targeted and untargeted) have been continuously put on trial for validation. In addition to academic progress, an overview of contemporary microbiome industry will be discussed, together with future challenges and potential needs for microbiome therapy development to address interpersonal response variation.

Ting-Yuan Hsu M.D., O.M.D., Ph.D. (許庭源)



Current position and professional experiences

2018 ~ Present	**Consulting Physician**, An-Ho Clinic, Kaohsiung, Taiwan
2011/12 ~ 2018/7	**Director**, BioRay Biotec Inc
1997/6 ~ 2011/6	**Associate Professor**, Chinese Medicine Institute, China Medical University, Taichung, Taiwan
1996/6 ~ 2001/6	**Director**, Pediatric Department, Hua Ji Hospital, Chiayi, Taiwan
1993/9 ~ 1996/5	**Attending Physician**, Pediatrics, St. Paul Hospital, Taoyuang, Taiwan
1990/6 ~ 1993/8	**Residency**, Mackay Memorial Hospital, Taipei
1987/6 ~ 1988/5	**Internship**, Mackay Memorial Hospital, Taipei

Research interest

1. Immunology
2. Pediatrics
3. Division of rheumatology

Short research summary

1. Establishment of an animal model for the study of atopic dermatitis I led a team established first animal model for atopic dermatitis induced by allergen
2. Prevention and treatment of allergic disease by direct allergen-gene transfer I led a team successfully demonstrated that direct gene transfer (gene therapy) could treat and prevent IgE-mediated allergenic diseases including atopic dermatitis and airway hyperreactivity. This is a major breakthrough in the treatment of allergic diseases
3. To investigate the working mechanisms of tradition Chinese medicine in the treatment of allergic diseases
4. To select anti-allergy probiotic strain for clinical application
5. Development of Cordyceps and Taiwanfungus in the good agriculture practice
6. To develop biomarkers for heat pattern diagnosis by microarray technology

Publications

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3. Hsu CH, Chen MR, Hwang FY, Kao HA, Hung HY, and Hsu CH. Efficacy of plasmin-treated Intravenous Gamma-globulin for therapy of Kawasaki Syndrome. Pediatr Infect Dis J 1993;12:509-12.SCI
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5. Hsu CH, Chua KY, Huang SK, Chiang IP, and Hsieh KH. Development and Characterizations of a murine Dermatitis Model. J Allergy and Clin Immunol 1995;95:806.SCI
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15. Yu MC , Lee CH, Lai CH ,Chiang IP ,Wang YY, and Hsu CH. The hepatoprotective effect of traditional Chinese medicine in galatosamine –induced acute hepatotoxicity . J Chin Med 2003; 14 :99-108.
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21. Hsu CH, Lu CM,Chang TT. Efficacy and safety of modified Mai-Men-Dong-Tang for treatment of allergic asthma. Pediatr Allergy Immunol. 2005;16:76-81. SCI
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24. Chang TT, Huang CC, Hsu CH. Inhibition of mite-induced immunoglobulin E synthesis, airway inflammation, a;nd hyperreactivity by herbal medicine STA-1. Immunopharmacology and Immunotoxicology. 2006;28: 683-95. SCI
25. Production of Active Nonglycosylated Recombinant B-Chain of Type-2 Ribosome-Inactivating Protein from Viscum articulatum and Its Biological Effects on Peripheral Blood Mononuclear Cells. Evid Based Complement Alternat Med. Lu TL, Chuang JY, Yang JS, Chiu ST, Hsiao NW, Wu MC, Hsu CH. 2011;2011:283747-16. SCI
26. Daily Intake of Probiotics with High IFN-γ/IL-10 Ratio Increases the Cytotoxicity of Human Natural Killer Cells: A Personalized Probiotic. J. Immun. Research. Yu-Hsuan Ho, Yu-Chiu Lu,

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Integrative Treatments of Advanced Cancers by Combined Both Cytokine-induced Killer Cell and Personalized Probiotic Ttherapy

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Many studies have demonstrated that cytokine-induced killer cells (CIK) have potent cytotoxic activities against both solid and hematologic tumors such as leukemia, lung cancer, hepatoma, and ovarian cancer in a MHC-unrestricted cytolytic effect, and having potential synergy with surgery, chemotherapy and radiotherapy. In addition, side effects of CIK infusions were very minor. However, there are some obstacles impeding treatment efficacy: (1) biological response to gut microbes may vary in different individuals; this responses can enhance clinical curative effects? (2) insufficient amount and short life span of effector CIK cells may compromise therapeutic efficacy; (3) sensitive examination for real-time evaluating the efficacy is not accessible.

To solve aforementioned problems and create groundbreaking immunotherapy, we accordingly established T-cell antigen reviving system (T-CARS), Kinetic Amplified Cytokine induced Killer cell (KA-CIK) and circulating tumor cells (CTC) assay. T-CARS utilizes our patented microfluidic system to identify quickly personalized probiotic antigen to effectively facilitate T-cell activity. Oral administration of personalized probiotic strain can double CIK cytotoxicity activity after 30-day treatment and most importantly prolong CIK cells life span to 90-day after infusion in patients. KA-CIK technology simulates virtual circulation to yield remarkably higher amount of anti-tumor active CIK cells than traditional culture method which provided standardized system to produce high qualities and quantities of cell for treatment within 14 days. Besides, high sensitivity CTC assay employs as low as 7.5 ml blood to determine free tumor cells in patients peripheral blood circulation. We therefore use KA-CIK system to provide patient with advanced cancers more than 1×10^{10} cells for each infusion that are enhanced by T-CARS from individual probiotic strain, and followed by measurement of the changes of CTC in peripheral blood after each infusion.

Our integrative CIK cell-based immunotherapy including T-CARS and KA-CIK has demonstrated potential in improving clinical outcomes and relieving the major side effects for standard treatment options. However, the number of transfused CIK cells and frequency of transfusion seem to play an important role in enhancing anti-tumor activity. The optimal protocol for each patient needs to be elucidated. And challenges are under investigation for synergy with other immunotherapy approaches, target therapies or even conventional chemotherapy.

Hei-Jen Jou, M.D., Ph.D. (周輝政)

Current position and professional experiences

2018/7 ~ Present	**Principal Investigator**, Circulating Tumor Cell (CRC) & Genetic Laboratory, Taiwan Adventist Hospital (TAH)
2018/2 ~ Present	**Senior Vice President**, Taiwan Adventist Hospital (TAH)
2011/1 ~ Present	**Chief Strategy Officer**, Taiwan Adventist Hospital (TAH)
1996/7 ~ Present	**Attending Physician**, Department of Obstetrics and Gynecology, Taiwan Adventist Hospital (TAH)
2012/8 ~ Present	**Adjunct Associate Professor**, Graduate Institute of Nurse-Midwifery, National Taipei University of Nursing and Health Sciences (NTUNHS)
2004/2 ~ Present	**Adjunct Assistant Professor**, College of Medicine, National Taiwan University (NTU)

Research interest

1. Circulating rare cell
2. Microfluidic chip

Short research summary

Dr. Jou Hei-Jen is the Senior Vice President and Chief Strategy Officer of the Taiwan Adventist Hospital (TAH), and the attending physician in obstetrics and gynecology. Dr. Jou obtained a bachelor's degree in medicine from the Department of Medicine of National Taiwan University (NTU) in 1985, and a master's degree in finance from the EMBA of NTU in 2001. He is currently a doctoral candidate in the International College of Semiconductor Technology, National Chiao Tung University.

In the past five years, Dr. Jou has been committed to the research of microfluidic chips and circulating rare cells. In addition to his primary roles in the Hospital, he is also a principal investigator of the circulating tumor cell and genetic laboratory in TAH, in which he leads a team to provide supports for clinical research and the development of precision medicine.

Publications

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3. **Jou, H. J.**, Siao, R. Y., Tsai, Y. S., Chen, Y. T., Li, C. Y., & Chen, C. C. (2014). Postdischarge rehospitalization and in-hospital mortality among Taiwanese women with hip fracture. *Taiwan J Obstet Gynecol, 53*(1), 43-47. doi: 10.1016/j.tjog.2012.04.042

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7. **Jou, H. J.**, Hung, H. W., Yan, Y. H., & Wu, S. C. (2012). Risk factors for blood transfusion in singleton pregnancy deliveries in Taiwan. *Int J Gynaecol Obstet, 117*(2), 124-127. doi: 10.1016/j.ijgo.2011.11.028
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10. **Jou, H. J.**, & Huang, H. T. (2009). Metabolic syndrome: menopausal women and the health care challenge. *Taiwan J Obstet Gynecol, 48*(3), 205-209. doi: 10.1016/S1028-4559(09)60291-6

Hung-Cheng Lai, M.D., Ph.D. (賴鴻政)

Current position and professional experiences

2013/11 ~ Present	**Director/Professor**, Department of Obstetrics and Gynecology, School of Medicine, College of Medicine, Taipei Medical University
2013/11 ~ Present	**Vice Superintendent**, Shuang Ho Hospital, Taipei Medical University
2014/8 ~ 2020/7	**Chair**, Department of OB/ GYN, Shuang Ho Hospital, Taipei Medical University

Research interest

1. Epigenetic biomarker
2. Cancer organoids
3. Robotic surgery

Short research summary

My research interest focuses on two themes: “Epigenetics “and “Cancer Stem Cells”. The long term goal is to discover novel diagnostic markers and therapeutic targets. In epigenetics, we are using genome-wide approaches to discover novel DNA methylation in Gynecological cancers, and trying to translate these DNA methylation markers to clinical diagnostics. Novel genes of interest undergo functional characterization from molecular biology to cell biology and animal studies. In addition, we have successfully established cancer organoids from primary tumors. Translational investigation of cancer organoids is ongoing. Clinically, I am a board-certified Gynecologic Oncologist and a pioneer robotic gynecological surgeon in Asia.

Publications

1. Liew PL, Huang RL, Wu TI, Liao CC, Chen CW, Su PH, Wang HC, Weng YC, Lai HC*. Combined genetic mutations and DNA-methylated genes as biomarkers for endometrial cancer detection from cervical scrapings. Clinical Epigenetics. 2019 Nov 28;11(1):170
2. Wu TI, Huang RL, Su PH, Mao SP, Wu CH, Lai HC*. Ovarian Cancer Detection by DNA Methylation in Cervical Scrapings. Clinical Epigenetics. 2019 Nov 27;11(1):166
3. Su PH, Lai HC, Huang RL, Chen LY, Wang YC, Wu TI, Chan MWY, Liao CC, Chen CW, Lin WY, Chang CC. Paired Box-1 (PAX1) Activates Multiple Phosphatases and Inhibits Kinase Cascades in Cervical Cancer. Sci Rep. 2019 Jun 24;9(1):9195.
4. Chung VY, Tan TZ, Ye J, Huang RL, Lai HC, Kappei D, Wollmann H, Guccione E, Huang RY. The role of GRHL2 and epigenetic remodeling in epithelial-mesenchymal plasticity in ovarian cancer cells.Commun Biol. 2019 Jul 24;2(1):272.
5. Chen CW, Chang HC, Huang TF, Liao CC, Huang RL, Lai HC. Transition from multiport to single-site surgery: A single institution experience in robotic supracervical hysterectomy for benign gynecological diseases. Taiwan J Obstet Gynecol. 2019 Jul;58(4):514-519.
6. Li SS, Ip CKM, Tang MYH, Tang MKS, Tong Y, Zhang J, Hassan AA, Mak ASC, Yung S, Chan TM, Ip PP, Lee CL, Chiu PCN, Lee LTO, Lai HC, Zeng JZ, Shum HC, Wong AST. Sialyl Lewisx-P-selectin cascade mediates tumor-mesothelial adhesion in ascitic fluid shear flow. Nat Commun. 2019 Jun 3;10(1):2406.
7. Chen LY, Huang RL, Chan MW, Yan PS, Huang TS, Wu RC, Suryo Rahmanto Y, Su PH, Weng YC, Chou JL, Chao TK, Wang YC, Shih IM, Lai HC*.TET1 reprograms the epithelial ovarian cancer

epigenome and reveals casein kinase 2α as a therapeutic target. J Pathol. 2019 Mar 18.
8. Cheng FHC, Lin HY, Hwang TW, Chen YC, Huang RL, Chang CB, Yang W, Lin RI, Lin CW, Chen GCW, Mai SY, Lin JMJ, Chuang YM, Chou JL, Kuo LW, Li C, Cheng ASL, Lai HC, Wu SF, Tsai JC, Chan MWY. E2F6 functions as a competing endogenous RNA, and transcriptional repressor, to promote ovarian cancer stemness. Cancer Sci. 2019 Mar;110(3):1085-1095.
9. Su PH, Hsu YW, Huang RL, Chen LY, Chao TK, Liao CC, Chen CW, Wu TI, Mao SP, Balch C, Lai HC*. TET1 promotes 5hmC-dependent stemness, and inhibits a 5hmC-independent epithelial-mesenchymal transition, in cervical precancerous lesions. Cancer Lett. 2019 May 28;450:53-62.
10. Mase S, Shinjo K, Totani H, Katsushima K, Arakawa A, Takahashi S, Lai HC, Lin RI, Chan MWY, Sugiura-Ogasawara M, Kondo Y. ZNF671 DNA methylation as a molecular predictor for the early recurrence of serous ovarian cancer. Cancer Sci. 2019 Mar;110(3):1105-1116.
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12. Maggie Tang, Patrick Yue, Philip Ip, Huang RL, Lai HC, Annie NY Cheung, Ka Yu Tse, Hextan Ngan, and Alice Wong. Soluble E-cadherin promotes tumor angiogenesis and localizes to exosome surface. Nature Communication. 11 June 2018
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23. Lin CK, Bai MY, Hu TM, Wang YC, Chao TK, Weng SJ, Ma KH, Lai HC*. Preclinical evaluation of a

nano-formulated, antihelminthic niclosamide in ovarian cancer. Oncotarget 2016 Feb 23;7(8):8993-9006. doi: 10.18632/oncotarget.7113.
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27. Chang CC, Huang RL, Liao YP, Su PH, Hsu YW, Wang HC, Tien CY, Yu MH, Lin YW, Lai HC*.Concordance analysis of methylation biomarkers detection in self-collected and physician-collected samples in cervical neoplasm. BMC Cancer. 2015 May 19;15(1):418.
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王子豪教授紀念講座 (Memorial Lecture for Prof. Tzu-Hao Wang)

FemTech: Precision Women Health

Hung-Cheng Lai
Department of Obstetrics and Gynecology, School of Medicine, Collega of Medicine,
Taipei Medical University, Taiwan

Technology developed for female health (Female technology; FemTech) is burgeoning. Cancer and infertility are two crucial diseases threatening women's health. The concept and development of precision diagnostics may lead to a new cancer screening and reproduction assessment. Using methylomic approaches, we have developed DNA methylation biomarkers for cervical cancer screening, which has been approved by TFDA in 2016 (Cervi-M). Recently, a registration trial of DNA methylation biomarkers for endometrial cancer, an increasing incidence in Taiwan and worldwide, was completed with an expected positive result (MPap). The latest research reveals a potential panel for implantation prediction after an embryo transfer in infertility treatment, which may substantially improve assisted reproduction technology's efficiency. Precision diagnostics by DNA methylation biomarkers are paving a new way in women's health and create an opportunity for a startup.

Ni-Chung Lee, M.D., Ph.D. (李妮鍾)

Current position and professional experiences

2016 ~ Present **Clinical Associate Professor**, Department of Pediatrics, National Taiwan University Hospital, Taipei, Taiwan

2006 ~ Present **Attending Physician**, Department of Medical Genetics and Pediatrics, NTUH

Research interest

1. Molecular genetics
2. Gene therapy

Short research summary

Dr. Ni-Chung Lee is a Clinical Associate Professor at the National Taiwan University Hospital (NTUH). She had her PhD degree from NTU. Her research interests include the diagnosis and treatment of pediatric patients with rare diseases. In the diagnosis, she involves in the clinical application of next generation sequencing for pediatric rare diseases. About the treatment, she conducted gene therapy researches for AADC deficiency, Pompe disease and several rare diseases.

Publications

1. Kuo CW, Hwu WL, Chien YH, Hsu C, Hung MZ, Lin IL, Lai F, Lee NC*. Frequency and spectrum of actionable pathogenic secondary findings in Taiwanese exomes. Mol Genet Genomic Med. 2020 Aug 14:e1455.
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3. Fan SP, Lee NC, Lin CH. Novel Phenotype of 6p25 Deletion Syndrome Presenting Juvenile Parkinsonism and Brain Calcification. Mov Disord. 2020 Aug;35(8):1457-1462.
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兒童罕病的精準醫療 – 機會與挑戰
Precision Medicine for Critically Ill Children – Opportunities and Challenges

Ni-Chung Lee
Department of Pediatrics and Medical Genetics, National Taiwan University Hospital, Taipei, Taiwan

Critical illness in infants and children, especially those caused by genetic diseases, is one of the most challenging fields in maternal and children health. In the intensive care units patients are threatened by death or serious sequelae; but specific diagnosis won't be established. Because precise managements in respective of the disease are not possible, the prognosis of patients can be poor even though large amount of medical resources are consumed. Our team employs rapid whole exome sequencing (WES), for in time diagnosis of critical illness in infants and children. The work flow encompasses collaboration between clinical and bench work, establishment of clinical network, WES technical improvements to increase speed and efficiency, clinical reading of WES, and development of WES clinical reading program with artificial intellegence assistance We run trio (patient and parents) samples to increase diagnostic yields. The time from sample collection to pivotal report is 6 working days with a diagnostic yield around 50%. We create a new standard for clinical care for critically ill children in Tawian. With this, we hope to improve the care of our children.

Pi-Yueh Chang, Ph.D. (張璧月)

Current position and professional experiences

2019/6 ~ Present **Technical Director**,
Department of laboratory medicine, Linkou Chang Gung Memorial Hospital

2018/3 ~ Present **Assistant professor**,
Department of Medical Biotechnology and Laboratory Science, Chang Gung University

2008/7 ~ 2019/5 **Deputy Chief Technologist**,
Department of laboratory medicine, Linkou Chang Gung Memorial Hospital

Research interest

1. Clinical molecular diagnosis
2. Tumor marker exploration
3. ELISA kit development

Short research summary

Pi-Yueh Chang is a Director at Department of Laboratory Medicine in Linkou Chang Gung Memorial Hospital and an Assistant Professor at the Department of Medical Biotechnology and Laboratory Science, Chang Gung University. Mrs. Chang has been in charge the Clinical Molecular Diagnostic Lab for the past 15 years and implemented more than 30 laboratory-developed molecular tests for clinical use, such as molecular tests for emerging infectious pathogens and tests for single-gene caused rare diseases. In recent year, her team turned to develop multigene tests for common diseases such as epilepsy, obesity, gout, heart disease, cleft palate, or deafness by next generation sequencer or MassArray platform. And her research interests focus on exploration of genetic cancer markers especially for colorectal cancer.

Publications

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2. Chao-Hua Fu, Wei-ting Chen, **Pi-Yueh Chang ***, Ming-Ta. Michael Lee, Ming-Shien Wen. Revalidation of CoaguChek XS Plus System for INR Monitoring in Taiwanese Patients: Effects of Clinical and Genetic Factors. Biomed J 2014;37:380-5 * Corresponding
3. Ying-Hao Wen, **Pi-Yueh Chang**, Chen-Ming Hsu, Hsin-YaoWang, Cheng-Tang Chiu, Jang-Jih Lu. Cancer screening through a multi-analyte serum biomarker panel during health check-up examinations: results from a 12-year experience. Clin Chim Acta 2015;450:273-76
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5. **Pi-Yueh Chang**, Cheng-Tao Yang, Ching-Hui Cheng, Kuang-Hui Yu. Diagnostic Performance of Anti-cyclic Citrullinated Peptide and Rheumatoid Factor in Patients with Rheumatoid Arthritis. Int J Rheum Dis 2016;19(9):880-6
6. **Pi-Yueh Chang**, Chia-Chun Chen, Yu-Sun Chang, Wen-Sy Tsai, Jeng-Fu You, Geng-Ping Lin, Ting-Wen Chen, Jinn-Shiun Chen, Err-Cheng Chan. MicroRNA-223 and microRNA-92a in stool and

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10. **Pi-Yueh Chang**, Jinn-Shiun Chen, Shih-Cheng Chang, Mei-Chia Wang, Nai-Chung Chang, Ying-Hao Wen, Wen-Sy Tsai, Wei-Hsiu Liu, Hsiu-Ling Liu and Jang-Jih Lu. Acquired somatic TP53 or PIK3CA mutations are potential predictors of when polyps evolve into colorectal cancer. Oncotarget 2017;8(42):72352-62.
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13. Wei-Hsiu Liu; **Pi-Yueh Chang#**; Shih-Cheng Chang; Jang-Jih Lu; Che-Ming Wu. Mutation Screening in Non-syndromic Hearing Loss Patients with Cochlear Implant by Massive Parallel Sequencing in Taiwan. PLOS ONE 2019,14(1) : e0211261, https://doi.org./10.1371/journal.pone.0211261, # co-first author
14. **Pi-Yueh Chang**, Chia-Chun Chen , Jy-Ming Chiang , Shih-Cheng Chang, Mei-Chia Wang , Jinn-Shiun Chen , Wen-Sy Tsai , Jeng Fu You and Jang-Jih Lu. A Simple and Highly Specific MassARRAY-Based Stool DNA Assay to Prioritize Follow-up Decisions in Fecal Immunochemical Test-Positive Individuals. Cancers 2019, 11, 423; doi:10.3390/cancers11030423
15. **Pi-Yueh Chang**, Shih-Cheng Chang, Mei-Chia Wang, Jinn-Shiun Chen, Wen-Sy Tsai, Jeng Fu You, Chia-Chun Chen, Hsiu-Ling Liu, Jy-Ming Chiang. Pathogenic germline mutations of DNA repair pathway components in early-onset sporadic colorectal polyp and cancer patients 2020 (under revision)

我會得癌症嗎？遺傳性癌症基因檢測經驗分享
Am I Susceptible to Cancer?

Pi-Yueh Chang
Department of Laboratory Medicine, Chang Gung Memorial Hospital at LinKou Taoyuan, Taiwan

Sometimes, certain types of cancer seem to run in some families because family members share certain behaviors or exposures such as smoking or obesity. However, in some cases the cancer is caused by an abnormal gene that is being passed along from generation to generation and we often referred it to”inherited cancer”. Only about 5% to 10% of all cancers result directly from gene defects inherited from a parent. In this talk, I will introduce: (1) Clinical definition of family cancer syndrome which considering the onset age, how many cases of the same type of cancer in the pedigree, whether more than one type of cancer occurred in a single person et al. (2) Genes specifically associated with inherited cancer, using hereditary breast and ovarian cancer syndrome and Lynch syndrome as examples. (3) How do we identify cancer-predisposed individuals by multigene panel testing on next generation sequencing platform? What‘s the optimal gene content in the panel? How do we make sure the high complexity genetic testing been performed accurately? How do we interpretate the gene test results for risk assessment? (4) What is the clinical performance of the hereditary cancer panel test based on sensitivity and cost-effectiveness point of view? Finally, I will share the experience of offering inherited cancer panel service in Linkou Chang Gung Memorial Hospital.

Jang-Jih Lu, M.D., Ph.D. (盧章智)

Current position and professional experiences

2011 ~ Present	**Director and Professor**, Department of Laboratory Medicine, LinKou Chang Gung Memorial Hospital
2019 ~ 2021	**President**, Taiwan Precision Medicine Society
2012 ~ 2018	President, Taiwan Society of Clinical Pathologist and Laboratory Medicine
2012 ~ 2015	**President**, Taiwan Association of Histocompatibility
2001 ~ 2021	**Executive Council**, Taiwan Society of Microbiology
2008 ~ 2011	**Director and Professor**, Department of Laboratory Medicine, China Medical University Hospital, Taichung
2003 ~ 2008	**Director and Professor**, Division of clinical Pathology, Department of Pathology, Tri-Service General Hospital

Research interest

1. Clinical microbiology
2. Infectious diseases
3. Molecular epidemiology, antimicrobial drug resistance and molecular diagnosis
4. Laboratory management and accreditation

Short research summary

My main research contributions focus on the field of clinical microbiology to address the clinical and epidemiological important questions involving in bacterial infectious diseases. I continuously investigate many clinically significant bacterial pathogens including gram-positive bacteria (methicillin-resistant *Staphylococcus aureus*, *S. lugdunensis*, *S. haemolyticus,* Group B S*treptococcus* and vancomycin-resistant *Enterococcus faecium*), *Campylobacter spp.*, and *Candida albicans*. My another main research is to develop and validate a rapid and accurate method for detecting antimicrobial resistance or typing strainsby using matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry andartificial intelligence /machine learning (ML) methods. One of my major achievements was to use tumor markers and ML technology for more accurate and subjective cancer screening. The results of the study had been patented（Pub. No. 發明第 **I630501**, Pub. date：2018/07/21） (**USA,** Filing No. **15/382,212**, Filing date：**2016/12/16)** and transferred to **20/20 GeneSystems Inc**.

Publications

1. Wang HY, Chung CR, Wang Z, Li S, Chu BY, Horng JT, **Lu JJ***, Lee TY. A large-scale investigation and identification of methicillin-resistant Staphylococcus aureus based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. Brief Bioinformation. 2020. Jul 16:bbaa138. Doi: 10.1093/bib/bbaa138. Online ahead of print. PMID: 32672791.
2. Wang HY, Chen CH, Shi S, Chung CR, Wen HY, Wu MH, Lebowitz MS, Zhou J, **Lu JJ***. Improving Multi-Tumor Biomarker Health Check-up Tests with Machine Learning Algorithms. Cancers (Basel). 2020 Jun 1;12(6)1442. doi: 10.3390/cancers12061442. PMID: 32492934.
3. Lin LC, Ge MC, Liu TP, **Lu JJ*** 2020. Molecular epidemiological survey of prophages in MRSA isolates in Taiwan. Infect Drug Resist. 2020 Feb 24;13:635-641.

4. Wang SH, Chen CC, Lee CH, Chen XA, Chang TY, Cheng YC, Young JJ, **Lu JJ***. 2020. Fungicidal and anti-biofilm activities of trimethylchitosan-stabilized silver nanoparticles against Candida species in zebrafish embryos. Int J Biol Macromol. 2020 Jan 15;143:724- 731.
5. Yang SL, Wen YH, Wu YS, Wang MC, Chang PY, Yang S, **Lu JJ***. 2019. Diagnosis of Pneumocystis pneumonia by real-time PCR in patients with various underlying diseases. J Microbiol Immunol Infect. 2019 Oct 7. pii: 1684-1182(19)30147-1. doi: 10.1016/j.jmii.2019.08.012. [Epub ahead of print] PMID 31635929
6. Chung CR, Wang HY, Lien F, Tseng YJ, Chen CH, Lee TY, Liu TP, Horng JT, **Lu JJ***. 2019. Incorporating Statistical Test and Machine Intelligence Into Strain Typing of *Staphylococcus haemolyticus* Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. Front Microbiol. 2019 Sep 13;10:2120. doi: 10.3389/fmicb.2019.02120. eCollection 2019. PMID 31572327
7. Wang HY, Hung CC, Chen CH, Lee TY, Huang KY, Ning HC, Lai NC, Tsai MH, Lu LC, Tseng YJ, **Lu JJ***. 2019. Increase Trichomonas vaginalis detection based on urine routine analysis through a machine learning approach. Sci Rep. 2019 Aug 19;9(1):11074. doi: 10.1038/s41598-019-47361-8. PMID 31423009.
8. Tsai MH, Lin LC, Hsu JF, Lai MY, Huang HR, Chiang MC, **Lu JJ***.2019. Rapid identification of invasive fungal species using sensitive universal primers-based PCR and restriction endonuclease digestions coupled with high-resolution melting analysis. J Microbiol Immunol Infect. 2019 Oct;52(5):728-735.
9. Chang SC, Lin LC, Ge MC, Liu TP, **Lu JJ***.2019. Characterization of a novel, type II staphylococcal cassette chromosome mec element from an endemic oxacillin-resistant Staphylococcus lugdunensis clone in a hospital setting. J Antimicrob Chemother. 2019 May 18. pii: dkz189. doi: 10.1093/jac/dkz189. [Epub ahead of print]
10. Tseng YJ, Huang CE, Wen CN, Lai PY, Wu MH, Sun YC, Wang HY, **Lu JJ***.2019. Predicting breast cancer metastasis by using serum biomarkers and clinicopathological data with machine learning technologies. Int J Med Inform. 2019 Aug;128:79-86. doi:10.1016/j.ijmedinf. 2019.05.003. Epub 2019 May 7.
11. Chang PY, Chen CC, Chiang JM, Chang SC, Wang MC, Chen JS, Tsai WS, You JF, **Lu JJ***. 2019. A Simple and Highly Specific MassARRAY-Based Stool DNA Assay to Prioritize Follow-up Decisions in Fecal Immunochemical Test-Positive Individuals. Cancers (Basel). 2019 Mar 25;11(3). pii: E423. doi: 10.3390/cancers11030423.
12. Tsai MH, Hsu JF, Lai MY, Lin LC, Chu SM, Huang HR, Chiang MC, Fu RH, **Lu JJ***. 2019. Molecular Characteristics and Antimicrobial Resistance of Group B Streptococcus Strains Causing Invasive Disease in Neonates and Adults. Front Microbiol. 2019 Feb 18;10:264. doi: 10.3389/fmicb.2019.00264. eCollection 2019.
13. Yeh HC, **Lu JJ***, Chang SC, Ge MC. 2019. Identification of microbiota in peri-implantitis pockets by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Sci Rep. 2019 Jan 28;9(1):774. doi: 10.1038/s41598-018-37450-5.**(Equally contributed with first author)**
14. Liu WH, Chang PY, Chang SC, **Lu JJ***, Wu CM. 2019. Mutation screening in non-syndromic hearing loss patients with cochlear implantation by massive parallel sequencing in Taiwan. PLoS One. 2019 Jan 25;14(1):e0211261. doi: 10.1371/journal.pone.0211261. eCollection 2019.
15. Ge MC, Kuo SF, Chang SC, Chien CC, You HL, **Lu JJ***. 2019. Antimicrobial Susceptibility and Virulence Surveillance of Campylobacter spp. Isolated From Patients in Two Tertiary Medical Centers in Taiwan. Front Microbiol. 2019 Jan 7;9:3186. doi: 10.3389/fmicb.2018.03186. eCollection 2018.
16. Wang HY, **Lu JJ**, Chang CY, Chou WP, Hsieh JC, Lin CR, Wu MH. 2019. Development of a high sensitivity TaqMan-based PCR assay for the specific detection of Mycobacterium tuberculosis complex in both pulmonary and extrapulmonary specimens. Sci Rep. 2019 Jan 14;9(1):113. doi: 10.1038/s41598-018-33804-1. **(Equally contributed with first author)**

Chen-Wen Yen, Ph.D. (嚴成文)

Current position and professional experiences

Professor, Deparment of Mechanical and Electro-Mechanical **Engineering**, Sun Yat-Sen Univeristy, Kaoshing, Taiwan

Research interest

1. Machine learning
2. Sleep medicine
3. Intelligent medical diagnostic systems
4. Physiological signal processing

Short research summary

1. 2011, 2011, 2015, 2017, Distinguished Teaching Award, National Sun Yat-sen University
2. 2013, 2014, National Instrument Engineering Impact Awards
3. 2018, Two National Innovators Awards
4. 2018, Associate Vice President for Research & Development, National Sun Yat-sen University
5. Excellent Teacher Award, Ministry of Education, Taiwan

Publications

1. Hong CY, Guo LY, Song R, Nagurka ML, Sung JL, Yen CW, 2016, “Assessing postural stability via the correlation patterns of vertical ground reaction force components,” Biomed Eng Online. Vol. 15, 90.
2. Hong CY, Guo LY, Song R, Nagurka ML, Sung JL, Yen CW, 2017, “Developing a low cost treadmill vi dynamic modeling,” Journal of Healthcare Engineering, Article ID 9875471.
3. Lin NH, Hsu CY, Luo Y, Nagurka ML, Sung JL, Hong CY, Yen CW, 2107, “Detecting rapid eye movement sleep using a single EEG signal channel,” Expert Systems with Applications, 2017, Vol. 87, 220-227.
4. Liu CH, Lee PL, Chen YL, Yen CW, 2020, “Developping postural stability measures by using Kinect to assess body joint coordinatin patterns,” Sensors (Basel). Vol. 20(5).

睡眠醫學遇上機器學習
When Sleep Medicine Meets Machine Learning

嚴成文
高雄國立中山大學 機械與機電工程學系

對機器學習而言，睡眠既是目的也是手段。以手段而言，機器學習的挑戰主在於建立評估睡眠品質的客觀指標，幫助大家了解自己的各項作為是否有助於達到一夜好眠的目的。所以以目的而言，由於許多疾病都會影響睡眠，機器學習的主要功能在於如何由睡眠中的各項生理訊號萃取出能客觀評估疾病嚴重度的量化特徵，追蹤病情的變化，進而協助規劃有效的介入方式。報告中將以多個實例來說明研究的規劃，並具體描述目前的困難。

Chin-An Yang, M.D., Ph.D. (楊晶安)

Current position and professional experiences

2019/8 ~ Present	中國醫藥大學醫學系實驗診斷科專任副教授(院校合聘)
2018/12 ~ Present	中國醫藥大學新竹附設醫院檢驗科主任
2018/12 ~ Present	中國醫藥大學新竹附設醫院臨床病理科暨兒科(過敏免疫風濕次專科)主治醫師
2019/8 ~ Present	中國醫藥大學新竹附設醫院教學部主任
2019 ~ Present	台灣臨床病理暨檢驗醫學會中區副秘書長 台灣精準醫學會中區副秘書長
2020/2 ~ Present	國立清華大學生醫工程與環境科學系合聘副教授
2007/9 ~ 2011/1	德國柏林洪堡大學醫學免疫研究所博士
2011/7 ~ 2014/7	台大醫院小兒部住院醫師

Research interest

1. Laboratory medicine
2. Immunology
3. Molecular genetics
4. Bioinformatics

Short research summary

My research focuses on complex immune diseases and cancers using multi-cohort and multi-omics approaches. The aims of our studies are to understand the underlying mechanisms, to identify diagnostic biomarkers, and to build up prognostication models. Another part of my research is related to clinical laboratory automation.

Publications

1. Yang CA, Li JP, Yen JC, Lai IL, Ho YC, Chen YC, Lan JL, Chang JG (2018, Sep). lncRNA NTT/PBOV1 Axis Promotes Monocyte Differentiation and Is Elevated in Rheumatoid Arthritis. International Journal of Molecular Sciences, 2018 Sep 18;19(9).pii: E2806.
2. Yang CA, Bauer S, Ho YC, Sotzny F, Chang JG, Scheibenbogen C (2018, Aug). The expression signature of very long non-coding RNA in myalgic encephalomyelitis/chronic fatigue syndrome. Journal of Transnational Medicine, 2018 Aug 17;16(1):231.
3. Yang CA, Chou IC, Cho DY, Lin CY, Huang HY, Ho YC, Liu TY, Li YH, Chang JG. (2018, May). Whole exome sequencing in Dandy-Walker variant with intellectual disability reveals an activating CIP2A mutation as novel genetic cause. Neurogenetics, 2018 Aug;19(3):157-163.
4. Yang CA, Huang HY, Yen JC, and Chang JG. (2018, May). Prognostic value of RNASEH2A-, CDK1-, and CD151-related pathway gene profiling for kidney cancers. International Journal of Molecular Sciences, 2018 May 28;19(6).
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6. Chin-An Yang, Jiunu-An Lin, Ci-Wen Chang, Kang-Hsi Wu, Su-Peng Yeh, Cheng-Mao Ho, Jan-

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精準用藥：從高維度次世代定序資訊分析談起

Drug Selection Using High-dimensional NGS Data Analysis

楊晶安
中國醫藥大學新竹附設醫院, 台灣

在精準醫學時代，執行次世代定序相較以前方便很多，臨床醫師有機會利用此項技術為病人的檢體做多體學的分析。每位病人都是獨立的個體，即使得到同一種感染，或是得到同一種癌症，也可能有著不同的生理特徵及藥物反應，甚至同一人體內不同微環境內的細胞，隨著時間，也可能產生不同的變化。以多體學的角度分析這些異質性，能提供臨床寶貴的資訊，用以達到個人化醫療。但次世代定序的資料十分龐大，如何從中分析出真正與疾病相關的用藥資訊是關鍵。本演講將從精準醫學檢驗和臨床醫師的角度討論高維度次世代定序資訊分析可能遇到的判讀問題，提供次世代定序與臨床癌症指引整合的癌症範例，分享尋找癌症替代路徑相關標的的過程，並討論如何利用免疫高通量分析尋找嚴重新冠肺炎病人可能的診斷及治療方式。

Eric Pok Yang, Ph.D. (楊博鈞)

Current position and professional experiences

2020/9 ~ Present	**Chief Business Officer**, Quark Biosciences, Inc.
2018/5 ~ Present	**Secretary General**, Precision Medicine & Molecular Diagnostics Industry Association (PMMD Taiwan)
2016/8 ~ 2020/8	**Vice President**, Quark Biosciences, Inc.
2015/6 ~ 2016/7	**Director**, Application and Business Development, Quark Biosciences, Inc.
2015/1 ~ 2015/5	**Manager**, Business Development, Quark Biosciences, Inc.
2005 ~ 2007	**Howard Hughes Postdoctoral Fellow**, Harvard Medical School

Research interest

1. Clinical diagnostics tools
2. Cancer biomarkers
3. Non-coding RNA

Short background summary

Dr. Eric Pok Yang joined Quark Biosciences in 2015 and was appointed Chief Business Officer in 2020. As a serial entrepreneur passionate in building world class brands, he currently oversees the company's marketing strategy and corporate development. Since joining Quark, Dr. Yang has successfully launched a number of products in precision oncology and reproductive healthcare.

Dr. Yang majored in Biochemistry at the University of California, Los Angeles (UCLA). After receiving his bachelor's degree, he joined the laboratory of Guillaume Chanfreau at UCLA to further his studies in Molecular Biology and Biochemistry. His doctoral thesis focused on deciphering the biogenesis of essential non-coding RNAs responsible for the modifications of ribosomal RNAs. Dr. Yang continued his research in long non-coding RNAs as a Howard Hughes Medical Institute Scholar at Harvard Medical School.

Publications

1. A Novel Multi-Gene Detection Platform for the Analysis of miRNA Expression. Science Report.Chia-Hsun Hsieh, Wei-Ming Chen , Yi-Shan Hsieh, Ya-Chun Fan, **Pok Eric Yang**, Shih-Ting Kang 3, Chun-Ta Liao.
2. miPrimer: an empirical-based qPCR primer design method for small noncoding microRNA. RNA. Shih-Ting Kang, Yi-Shan Hsieh, Chi-Ting Feng, Yu-Ting Chen , **Pok Eric Yang**, Wei-Ming Chen.
3. MSL complex is attracted to genes marked by H3K36 trimethylation using a sequence-independent mechanism. Molecular Cell. Erica Larschan, Artyom A Alekseyenko, Andrey A. Gortchakov, Shouyong Peng, Bing Li, **Pok Yang**, Jerry L Workman, Peter J Park, Mitzi I Kuroda
4. Noncoding RNAs and intranuclear positioning in monoallelic gene expression. Cell. **Pok Kwan Yang**, Mitzi I Kuroda.
5. Cotranscriptional recruitment of the pseudouridylsynthetase Cbf5p and of the RNA binding protein Naf1p during H/ACA snoRNP assembly. Molecular and Cellular Biology. **Pok Kwan Yang**, Coralie Hoareau, Carine Froment, Bernard Monsarrat, Yves Henry, Guillaume Chanfreau
6. The Shq1p.Naf1p complex is required for box H/ACA small nucleolar ribonucleoprotein particle

biogenesis. Journal of Biological Chemistry. **Pok Kwan Yang**, Giuseppe Rotondo, Tanya Porras, Pierre Legrain, Guillaume Chanfreau.

7. Localization of deletion to a 300 Kb interval of chromosome 11q13 in cervical cancer. Oncogene.Eri S Srivatsan, Rita Chakrabarti, Kayvan Zainabadi, Svetlana D Pack, Payam Benyamini, Marc S Mendonca, **Pok Kwan Yang**, Kevin Kang, Daria Motamedi, Mark P Sawicki, Zhengping Zhuang, Rachel A Jesudasan, Ulla Bengtsson, Chi Sun, Bruce A Roe, Eric J Stanbridge, Sharon P Wilczynski, J Leslie Redpath.

The Various Diagnostic Technologies for Precision Target Therapy

Eric P. Yang
Quark Biosciences, Taiwan

In the past few years, targeted therapy has become a mainstay in cancer treatment. With increasing amount of genomic data being generated, more cancer drugs are being developed each targeting specific gene alteration. As a result of the many options available, the goal for the clinicians is to identify patients with the alteration that will benefit from the treatment. While traditional methodologies are most used, newer and more sophisticated molecular diagnostic tools are now at the physicians' disposal. Here we examined various novel technologies that can be employed to detect mutations/rearrangements to aid precision target therapy.

科技新知分享

New Frontiers in the Development of Science and Biotechnology

日　　期 Date	11 月 14 日 Nov. 14	時　　間 Time	12:40-13:20	地　　點 Position	第一會議廳 Lecture Hall I
公司名稱	台灣賽默飛世爾科技股份有限公司 Thermo Fisher				
演講主題	**Orbitrap Exploris™ Mass Spectrometry – The Preferred Platform for Proteomics**				
演 講 人	**簡芷薇 Chih-Wei Chien, PhD** Application Scientist Center of Excellence for Applications & Training, SEA & TW Chromatography & Mass Spectrometry Division, Thermo Fisher Scientific, Taiwan Dr. Chien received her Ph.D. in Chemistry from National Tsing-Hua University, Taiwan in 2013. She worked as a postdoctoral researcher at Carnegie Institution for Science, Stanford, CA, USA in 2016, working on Immuno-precipitation–Mass Spectrometry (IP-MS) approach in the study of protein-protein interactome, related to brassinosteroid signaling in Arabidopsis. She has extensive experience in MS-based approaches to study quantitative proteomics in various biological specimens analysis as well as biomarker discovery in cancers. Prior to joining the biotechnology industry, she then joined Meribank Biotechnology Co., Ltd and was mainly responsible for the precision medicine project in maternal diseases. She has delineated stem cell multi-omic profiling in preterm birth and discovered the novel biomarkers for further in-vitro diagnostic application. She joined Thermo Fisher Scientific to explore more innovative applications and marketing in life science mass spectrometry.				
演講摘要	The new benchmark for proteomics requires the precise quantitation of all identified proteins, setting the foundation for bolder hypotheses and deeper understanding. Orbitrap mass spectrometers offer leading mass spectrometry (MS) technology for identifying and quantifying complex proteomics samples over a wide dynamic range. With established sample preparation, chromatographic separation and integrated data analysis tools, Orbitrap mass spectrometers enable researchers to successfully analyze diverse sample matrices with industry-leading sensitivity. Herein, we present the Orbitrap Exploris™ high-resolution, accurate-mass (HRAM) LCMS, with the power of built-in intelligence, sensitivity and selectivity delivers depth of analysis, to the lowest levels. Besides, the FAIMS Pro™ interface works seamlessly with next-generation MS technologies to enhance selectivity and enable the identification and quantitation of higher numbers of proteins than ever before. Combining HRAM instrumentation with differential ion mobility methods and orthogonal gas-phase separation techniques can reduces the complexity of accumulating and analyzing precursor ions, increasing proteome coverage, decreasing interference and improving quantitative confidence. The Orbitrap Exploris™ mass spectrometer can be helpful to obtain high confidence identifications, deeper proteome coverage, and enhanced biological knowledge generation.				

日　　期 Date	11 月 14 日 Nov. 14	時　　間 Time	12:40-13:20	地　　點 Position	第三會議廳 Lecture Hall III
公司名稱	台灣科睿唯安股份有限公司 Clarivate™				
演講主題	使用 AI 工具加速研究創新				
演 講 人	**趙宇薇** 科睿唯安 解決方案顧問 現為科睿唯安生命科學解決方案顧問，提供生命科學及智權的市場數據收集、分析及解讀，協助客戶解析靶點評估、產品選題、市場調查及競爭產品監控等商業決策。在加入科睿唯安之前，趙顧問曾任職於專利事務所及企業，參與專利申請、授權、技轉等業務。趙顧問於臺灣大學生物化學暨分子生物學研究所取得碩士學位，並在 2014 年通過中國專利代理人考試。近期報告： • 《2018 年監管審批與世界接軌》 • 《罕見病藥物的機會與挑戰》 • 《2018 年全球新藥觀察暨 2019 年重磅預測》 • 《2020 最值得關注的重磅藥物》 • 《重磅藥物的研發早期特徵與授權獲利模式》 • 《新藥開發商品化之考慮-市場研究、競爭者分析、價值主張》				
演講摘要	使用 AI 工具不僅是進年來各大藥廠的趨勢，實務上在早期 pathway 及靶點選擇時即可導入 AI 工具，將繁瑣的數據評估工作交由 AI 代勞。在本演講及新知分享中，趙顧問將以實例說明研究者使用 AI 工具及可加速選擇合適的標的及研究設計；此外，AI 工具亦可應用在藥物上市成功率及時程預估，幫助給予計劃補助的單位合適並謹慎評估補助對象及其競品上市時程及成功率差異，合理調整補助產品組合(Portfolio)以達成最優效益。				

日　　期 Date	11 月 15 日 Nov. 15	時　　間 Time	12:30-13:10	地　　點 Position	第一會議廳 Lecture Hall I
公司名稱	法德利科技股份有限公司 VtR Inc./Groupe Dassault				
演講主題	全球疫情帶來的醫藥產業新秩序—數據為王、有「它」就強！				
演 講 人	李佩力 博士 美國伊利諾大學厄巴納-香檳分校植物病理學研究所 博士 現職：法德利科技股份有限公司 科學長 經歷：創源生物科技股份有限公司 副總經理、分子視算股份有限公司 副總經理、法國達梭系統 (Dassault Systèmes BIOVIA)全球生物資訊與科學資訊首席講師、國際藥物工程學會(International Society for Pharmaceutical Engineering, ISPE)會員				
演講摘要	數位時代的現代醫藥產業 Tidal Change – Modern Pharma in the Digital Age 數據、大數據、數據科學、數據分析學 – 你搞懂了嗎？ From Data, Big Data to Data Science and Data Analytics – Your precious data is worth more than you think 疫情如何改變了醫藥產業 – 而且回不去了？ Life before pandemic and how COVID-19 changes everything – Pharma's perspective 「它」如何幫助你度過難關並在產業新常態中勝出 What you can do about it and how Tableau can help?				

日　　期 Date	11 月 15 日 Nov. 15	時　　間 Time	12:30-13:10	地　　點 Position	第三會議廳 Lecture Hall III
公司名稱	凱杰生物科技有限公司 QIAGEN				
演講主題	**QIAGEN 實現 NGS 樣本定序到數據分析解決方案** **QIAGEN Digital DNA sequencing, a total NGS solution to rapid diagnosis and annotate complex variants from oncology and hereditary disease.**				
主 持 人	**翁振哲先生** 凱杰生物科技業務經理				
演 講 人	**張量凱先生** 凱杰生物科技應用技術支援專員				
演講摘要	**Somatic cancer：** 針對不同表型之乳癌病患篩選位點並提供用藥資訊– a live case study **Hereditary disease：** 以 Trio 家族性遺傳性分析評斷多表型遺傳症狀之變異位點 – a live case study				

學會資訊
Information of Societies

台灣蛋白體學會
Taiwan Proteomics Society

關於學會

台灣蛋白體學會自 2003 年成立以來，透過積極推動各項教育訓練與籌辦學術會議達到：落實專業人才的培育、提供國內學生與學者展現研究成果的平台、促進國際合作與交流的機會、提升產業界與學術界之間的連結。為提升年輕學者的學術國際觀，學會每年也提撥預算，用以補助年輕學者參與此領域之重要國際會議。誠摯歡迎蛋白質體與代謝體領域的新血加入，支持學會之永續經營，以推廣更豐富多元的學術活動。

109 年度會員大會與第七屆理監事選舉

- 今年度會員大會因疫情因素延期，並視情況擇日舉行。
- TPS 第六屆理監事三年任期將於 2020 年 12 月結束，因疫情因素，第七屆理監事將採通訊投票選出。選票預計 11/20 前寄發給當年度已繳交年費之非學生有效會員，請會員收到選票後一週內寄回。選舉結果將以 email 告知會員並同時公佈於學會網站。

會員與會費

	一般會員		團體會員
	社會人士	學生	
入會費	0	0	0
常年會費	1,050 元 / 年	550 元 / 年	10,000 元 / 年

*歡迎登入學會網站線上填寫會員資料及繳費 https://reurl.cc/RdRZY9

*會員參與國際會議可申請學會獎助金補助 (相關辦法公布於學會網站)

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秘 書	蔡淑娟	(03) 211-8800 ext. 3130						

https://www.proteomics.org.tw/

https://www.facebook.com/TPSpost/

台灣生物資訊與系統生物學會

Taiwan Bioinformatics and Systems Biology Society

學會緣起

21 世紀藉由基因體及蛋白質體技術的蓬勃發展，人們解開了生物系統內龐大且複雜的核酸及蛋白質數據，而這些傲人成果的背後，代表著海量數據的運算。生物資訊學迅速結合後基因體多項新技術發展，解開生物系統內龐大而復雜的數據，引發生物科技與分子醫學研究方法的革命，並產生多方面巨大之影響，其中包括著人類在生物及醫學領域的新契機與面臨的新挑戰。『台灣生物資訊與系統生物學會』於 2000 年 12 月建立，成立的宗旨即是希望透過跨領域的合作與資源整合，加速台灣生物資訊學的發展及推廣，進而提昇台灣在生技醫學領域的研發能量，如精準醫療、健康醫療大數據應用、基因檢測及微生物菌相分析等領域之研究。有鑒於此，我們誠摯邀請所有對生物資訊及系統生物學有興趣的人、系所與公司行號加入我們的行列。讓大家都能藉此平台進行交流及利用本學會各項資源。

入會方式

入會資格：凡年滿十八歲、贊同本會宗旨、並完成會費繳交者。
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近期活動

APBC2021 The 19th Asia Pacific Bioinformatics Conference
February 3rd-5th, 2021
National Cheng Kung University, Tainan, Taiwan
活動網址: http://www.binfo.ncku.edu.tw/APBC2021/

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台灣基因醫學暨生物標記學會

Taiwan Genomic Mdeicine and Biomarker Society

各位會員、先進們大家好！

「2020 多體學及精準醫學聯合會議 暨 109 年台灣基因醫學暨生物標記學會年會」將於今日在林口長庚大學舉辦。此次大會活動得以順利籌辦，要特別感謝主辦的台灣蛋白體學會，與協辦的台灣生物資訊暨系統生物學會、台灣演化與計算生物學會、台灣精準醫學學會、與台灣胞外體學會。在這全球受到新冠肺炎疫情的嚴重衝擊的一年，本著維繫學術交流的考量，堅持舉辦本次的會議，相當的不容易。一個活動能夠順利籌辦，要感激的人實在太多太多。剩下的，就是希望踴躍參與活動的會員、學員及各界先進，在親臨現場之後，能仔細感受到活動籌辦團隊的用心，給予指教與鼓勵。

有鑑於近年來生物醫學研究發展急遽，人類及各種生物基因體遺傳因子也持續完成解碼，基因醫學及生物標記等相關研究更彰顯其重要性；本會係以推動國內基因醫學暨生物標記研究，並建構完善應用發展平台，落實各項基因醫學新知與新技術之臨床醫學診治應用，有效協助國人健康維護、提升臨床醫療照護成效，啟動現代醫學全新紀元為宗旨。本會成立轉眼已經多年，一直以來得以穩步成長，除了顧問的指導，所有理監事對學會的發展，集思廣益，熱情參與外，全體會員積極參與每個活動與學員們的支持與鼓勵，更是推動學會進步的最大動力。歡迎有志一同之學、研、業界人士加入本學會，共同為台灣基因醫學暨生物標記學會的未來發展而努力。

在此，謹代表學會感激所有對本會支持或有所批評指導的各界人士，有了大家的支持與督促，學會將會更加努力前進，在未來發展的過程中，加倍凝聚會員的力量，激發所有潛在的爆發力。最後，謹以最誠摯的心，歡迎並感激所有參與籌辦及蒞臨與會的嘉賓，更預祝此次大會順利圓滿，與會者都能滿載而歸，不虛此行。

學會報名網址：

台灣基因醫學暨生物標記學會理事長

鄭添祿

台灣演化與計算生物學會

Taiwan Society of Evolution and Computational Biology

學會簡介

本學會為非營利之社會團體。旨在推廣演化及計算生物學相關之技術研發、教育及應用。現代演化論應用到許多計算技巧，而計算生物學亦需要有演化的理念基礎。本學會亦將致力於聯繫國內外相關組織並推動學術及技術之國際交流平台。促進國內相關之知識管理及生技產業發展。

本次會議演講

特別演講：Genomic Evolution and Adaptation in Africa: Implication for Health and Disease
時間：2020/11/15 (日) 9:10-10:00
講者：Prof. Sarah A. Tishkoff
David and Lyn Silfen University Professor, Department of Genetics, Univeristy of Pennsylvania

Section I Population Genomics 時間：2020/11/14 (六) 10:40-12:05
Section IV Genomics of Pathogens 時間：2020/11/15 (日) 13:30-14:55

入會方式

個人會員：凡贊同本會宗旨、年滿二十歲、具有行為能力、從事或有志於演化或計算生物學研究與應用之個人，為個人會員。
團體會員：凡贊同本會宗旨之公私機構或團體，從事或有志於演化或計算生物學研究教學與應用之公私機構或團體，為團體會員。
入會費：

	個人會員			團體會員
	一般個人	助理及學生會員	博士後會員	
入會費	NT 100-	NT 100-	NT 100-	NT 10,000-
常年會費	NT 1,000-	NT 300-	NT 500-	NT 10,000-
終身會員	NT 12,000-	NA	NA	NT 120,000-

現任理監事

理 事 長 丁照棣
常務理事 丁照棣 阮雪芬 莊樹諄
理 事 黃禎祥 呂美曄 陳倩瑜 蔡怡陞 廖本揚 張家銘
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秘 書 長 王弘毅

台灣胞外體學會
Taiwan Society for Extracellular Vesicles

關於學會

胞外體在動植物和微生物的基礎科學重要性越來越被顯現，提供科學家對於解釋生命現象不同的角度和視窗；同時，也開始被應用在產業上，包含液態檢體之生物標識、藥物傳輸系統甚至治療。台灣有許多優秀的學者、活力創新的學生、高度的跨領域合作能量、完整的研究資源和基礎，要在胞外體的研究上或是產業應用開發上，我們應該非常有競爭力。台灣胞外體學會(TSEV)自 2017 開始籌劃、2018 年成立自今，逐漸成長; 期間，學會舉辦和推廣許多國內外有關胞外體的學術活動及工作坊，推廣胞外體相關前瞻研究進展和產業資訊，逐漸看到了胞外體研究在台灣的迅速擴散，實現了台灣胞外體學會的宗旨。同時，台灣投入胞外體研究的學者和成果也在國際逐漸曝光和受到肯定，也成為亞太胞外體學會成員之一。台灣胞外體學已成台灣在胞外體研究和國際及產業鏈結的重要推手，目標和責任越趨重大。正如胞外體做為體內細胞間交流的重要媒介，每一位參與胞外體研究的人，絕對不吝嗇相互的交流，也是必然的性格特性。

入會方式

入　會　資　格：贊同本會宗旨，檢附資料並完成會費繳交者。
入會費(新台幣)：個人會員參佰元、學生會員壹佰元、團體會員參仟元。
常年會費(新台幣)：個人會員參佰元，一次繳交新台幣貳仟元得成為終身會員，不需再繳交常年會費、學生會員壹佰元、團體會員參仟元。
收　款　行：華南銀行台大分行
收　款　帳　號：154-10-009245-1
戶　　名：台灣胞外體學會

匯款完成後請 email 至學會信箱 tsevtw@gmail.com，請註明【入會費用】

現任理監事

理事長	沈湯龍	理　事	郭文宏
常務理事	湯銘哲	理　事	徐瑋萱
常務理事	賴品光	常務監事	黃富楠
理　事	張金堅	監　事	何佳安
理　事	陳致真	監　事	許藝瓊
理　事	林劭品		

台灣精準醫學學會
Taiwan Precision Medicine Society

學會簡介

「台灣精準醫學學會」，英文名稱為「Taiwan Precision Medicine Society (TPMS)」，於 2015 年成立，為從事精準醫學之專家學者及臨床從業人員組成的非營利團體。以聯絡從事精準醫學之相關人士，共同促進精準醫學之研究發展及臨床應用，以及提高精準醫學範疇所涉及之疾病診療與研究水準為宗旨。本學會致力於提升精準醫學之水準，並舉辦精準醫學之教育訓練及舉辦學術演講與討論會，促進精準醫學之研究發展與應用及建立精準醫學之專科醫師與諮詢師制度與資格審核。

加入學會

入會費：個人會員貳千元，團體會員貳萬元，於入會時繳納。
常年會費：個人會員壹仟元，團體會員貳萬元，於入會時繳納。
個人會員、團體會員、學生會員、終身會員入會方式請參考學會網站。

精準醫學專科醫師/諮詢師訓練與認證

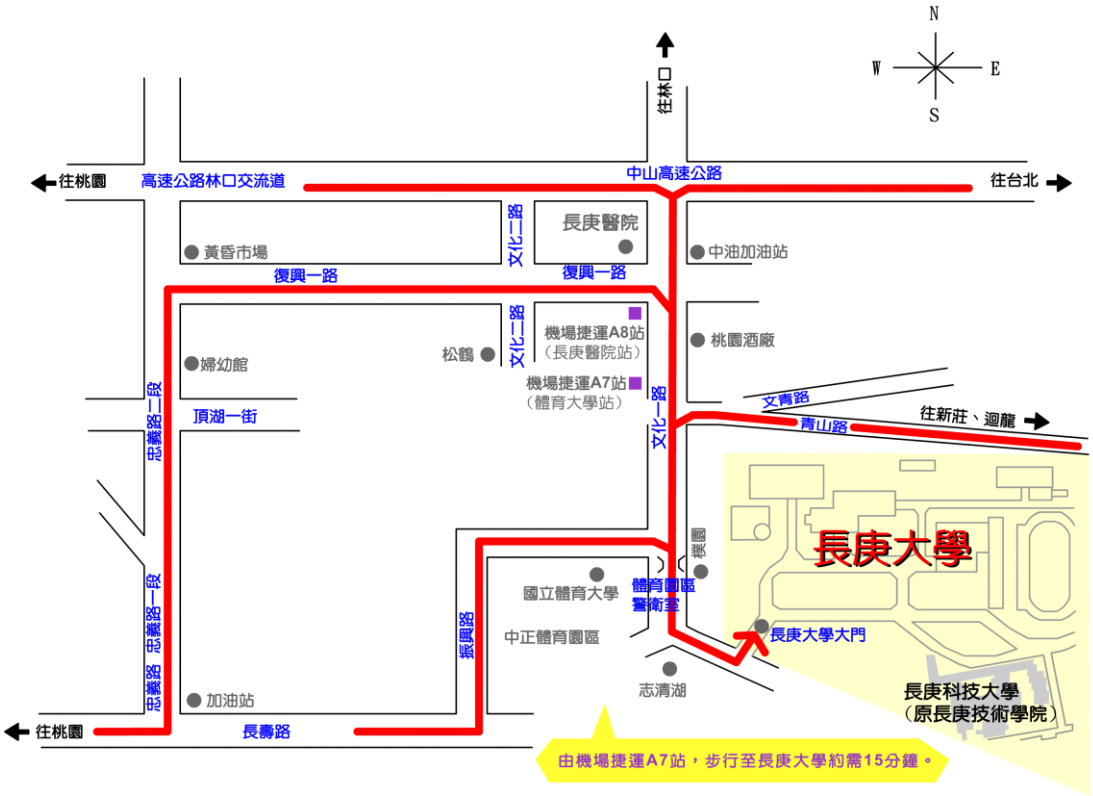
110 年精準醫學專科醫師/諮詢師訓練開始報名。
早鳥報名有優惠，詳細報名辦法請上學會網站查詢!

台灣精準醫學學會
會址：33305 桃園市龜山區復興街 5 號 K 棟 B1（林口長庚醫院檢驗醫學部）
電話：0966-630-686 / 03-3281200-5140
http://www.tpms.org.tw

交通地圖
Maps

交通地圖 Maps

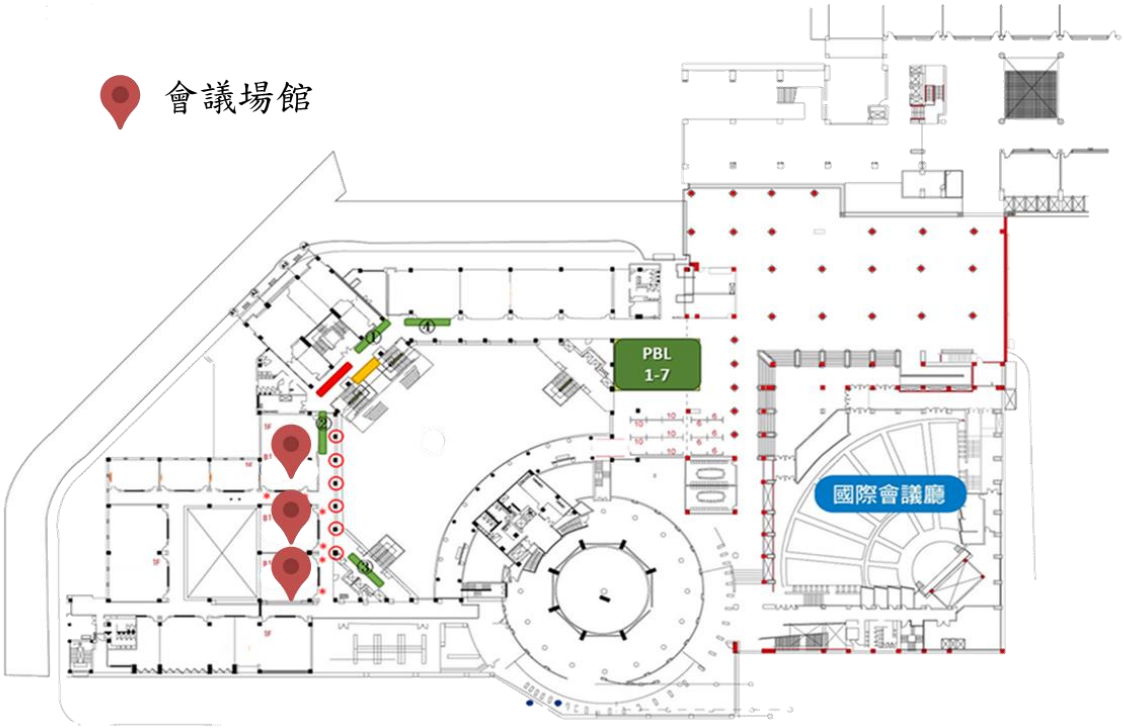
交通資訊（長庚大學）



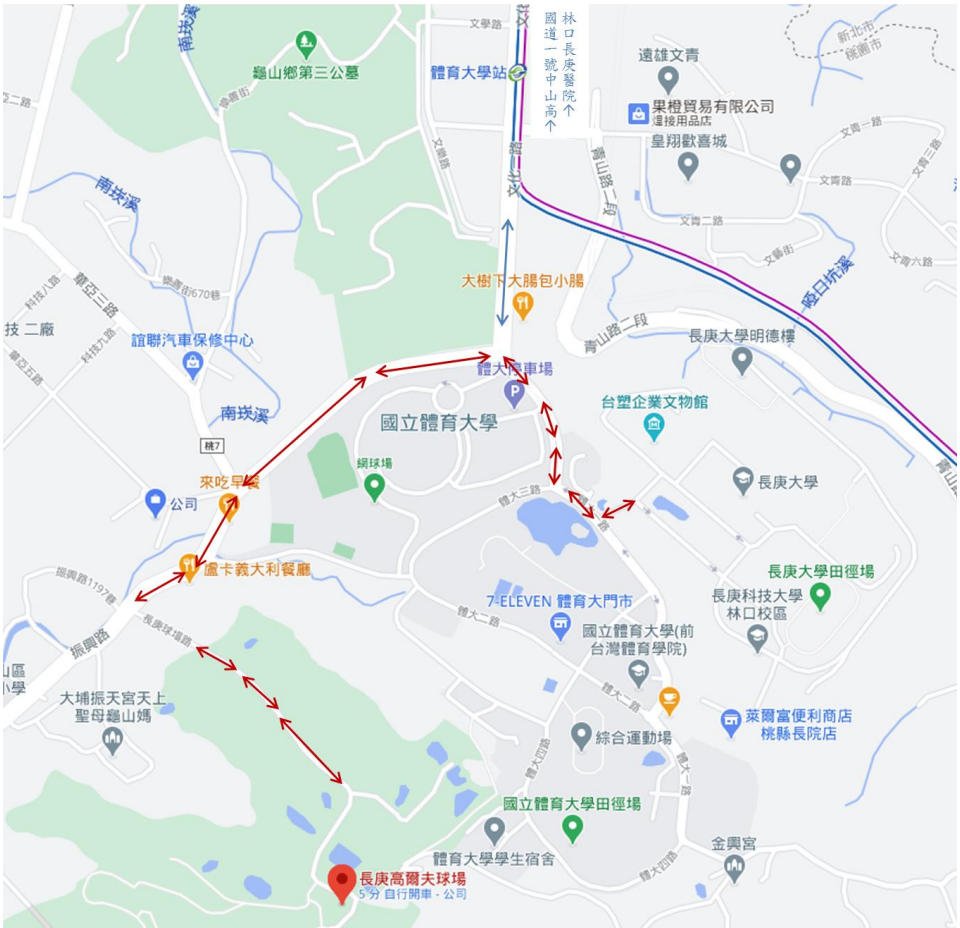
校園平面圖

交通地圖 Maps

會場：第二醫學大樓



晚宴：長庚高爾夫球場



校車時刻表

Linkou branch ⟷ Chang Gung University Shuttle Bus Time Table

項次	星期一至星期五(Mon.~Fri.)		星　期　六 (Sat.)		星期(例假)日(Sun.and Holidays)	
	總　院 Linkou branc	校　區 Chang Gung University	總　院 Linkou branc	校　區 Chang Gung University	總　院 Linkou branc	校　區 Chang Gung University
1	06:20	06:30	06:20	06:30	*07:00	*07:20
2	06:30	06:40	*06:50	*07:15	⊕07:30	⊕07:40
3	06:40	06:50	*07:35	*07:55	*08:00	*08:20
4	*06:50	*07:10	08:15	08:25	⊕09:20	⊕09:30
5	⊕07:15	⊕07:25	08:45	08:55	⊕09:50	⊕10:00
6	*07:35	*07:55	09:20	09:30	⊕10:20	⊕10:30
7	⊕07:40	⊕07:50	*09:25	*09:45	*10:50	*11:10
8	⊕08:10	⊕08:20	09:50	10:00	*12:00	*12:20
9	08:15	08:25	10:20	10:30	*12:50	*13:10
10	08:45	08:55	10:50	11:00	*14:00	*14:20
11	09:20	09:30	*11:00	*11:20	*15:10	*15:30
12	09:50	10:00	11:20	11:30	15:40	15:50
13	10:20	10:30	*11:40	*12:00	*16:10	*16:30
14	10:50	11:00	⊕*12:05	⊕*12:25	16:10	16:20
15	⊕11:20	⊕11:30	*12:20	*12:40	16:40	16:50
16	*11:50	*12:10	⊕*12:40	⊕*13:00	*17:15	*17:35
17	12:30	12:40	*12:50	*13:10	17:40	17:50
18	⊕*12:40	⊕*13:00	*13:00	*13:20	18:10	18:20
19	13:20	13:30	⊕*13:15	⊕*13:35	*18:20	*18:40
20	13:50	14:00	13:40	13:50	18:40	18:50
21	14:20	14:30	14:10	14:20	*19:25	*19:45
22	14:50	15:00	14:40	14:50	19:40	19:50
23	⊕15:00	⊕15:10	*15:10	*15:30	20:10	20:20
24	⊕15:10	⊕15:20	*15:40	*16:00	*20:30	*20:50
25	*15:20	*15:40	*16:10	*16:30	20:40	20:50
26	⊕15:55	⊕16:05	16:30	16:40	21:10	21:20
27	⊕16:05	⊕16:15	17:00	17:10	*21:35	*21:55
28	*16:10	*16:30	17:30	17:40	22:10	22:20
29	16:20	16:30	⊕18:00	⊕18:10	*22:15	*22:35
30	⊕16:35	⊕16:45	18:30	18:40	22:40	23:00
31	16:50	17:00	*18:40	*19:00	*22:50	*23:10
32	17:10	17:20	19:00	19:10	23:10	23:30
33	17:20	17:30	19:30	19:40	*23:25	*23:45
34	⊕17:35	⊕17:45	20:00	20:10	23:40	23:50
35	17:50	18:00	*20:20	*20:40	00:10	00:20
36	18:20	18:30	21:00	21:10	*00:25	*00:45
37	18:50	19:00	21:40	21:50		
38	19:20	19:30	*21:50	*22:10		
39	19:45	19:55	22:10	22:20		
40	20:15	20:25	22:40	22:50	收假專車(林口總院發車)	
41	*20:50	*21:10	23:10	23:20		
42	21:00	21:10	23:40	23:50	◎13:10	◎17:55
43	21:30	21:40	00:10	00:20	◎13:40	◎18:25
44	*21:55	*22:15	*00:25	*00:45	◎14:25	◎18:55
45	21:55	22:05			◎14:55	◎19:50
46	22:20	22:30			◎15:25	◎20:20
47	22:45	22:55			◎15:55	◎20:50
48	23:10	23:20			◎16:55	◎21:20
49	●23:40	●23:50			◎17:25	
50	00:10	00:20			◎以上專車僅於星期例假日及連續假期之收假日行駛	
51	*00:25	*00:45				

代號說明：

＊：總院→社區→校區→總院	◎：收假日行駛
⊕：支援車輛，非社校區本線班車	●：總院→校區→社區

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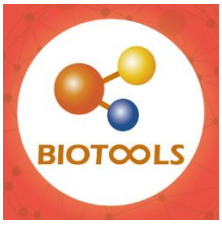
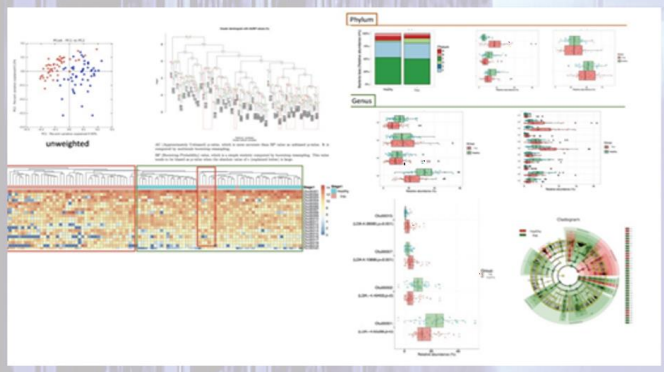
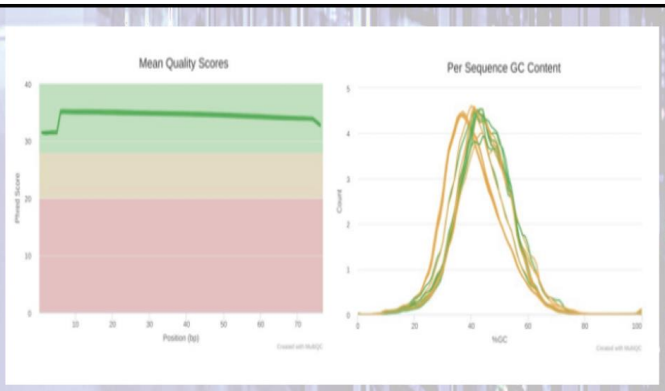
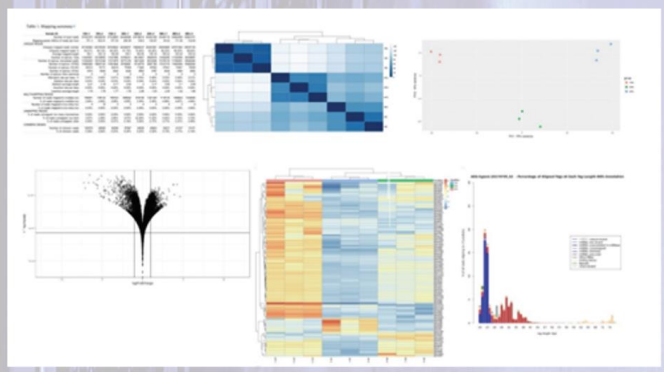


生物資訊分析平台

服務內容	1. RNA-seq data 標準分析 2. Small RNA sequencing data 標準分析 3. 外顯子定序(WES) data 標準分析 4. 全基因體定序(WGS) data 標準分析 5. Panel平台分析 6. 16S metagenome sequencing data 標準分析 7. Pathway analysis 標準分析 8. 生物資訊客製化分析/整合(電洽)
平台特色	➢ 由多名博士後研究員及資深分析工程師專案進行分析 ➢ 提供客製化分析與視覺化的整合 ➢ 專業高速運算叢集伺服器系統，提供最快速的服務 ➢ 多種跨體學生醫大數據之整合分析 ➢ 分析技術開發合作及產學合作







長庚大學分子醫學研究中心
Chang Gung Molecular Medicine Research Center

單位：生物資訊暨體學數據應用核心實驗室
網址： https://cgmmrc.cgu.edu.tw/p/412-1029-9988.php
聯絡人：張益峯 博士 (分機：3941)
Email：ianyfchang@mail.cgu.edu.tw

蛋白質體服務平台

Proteomics Core Lab Service

質譜分析與多重蛋白質同步定量

Sample preparation

- Tryptic digestion[1]
- Sample desalting[2]
- TiO_2 enrichment[3]

Mass spectrometry

- 1D LC-MS/MS[4]
- 2D LC-MS/MS[5]
- Data analysis[6]

Luminex-based immunodetection

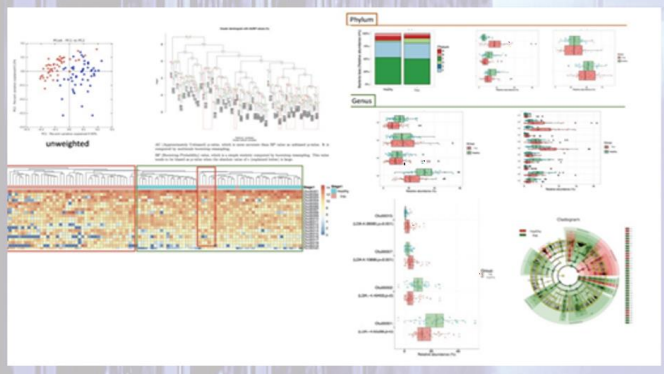
- Protein detection[7]
- Autoantibody detection[8]

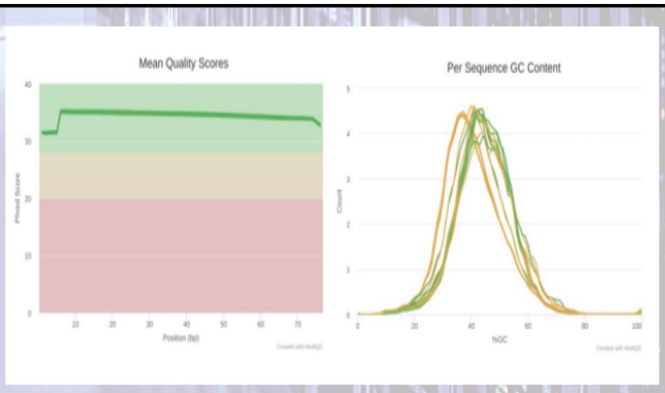
[1]接受PAGE膠體內或水溶液樣品，目前預設為Trypsin切割蛋白體，若有其他需求可先告知。[2]接受使用者已經切割完成的胜肽，但須經過去除鹽類的處理。[3]用於磷酸化蛋白體的分析。[4]預設使用的質譜儀機型為Thermo Fisher LTQ ORBITRAP XL。[5]使用者須先完成SILAC、iTRAQ、TMT...蛋白質或胜肽的同位素標定。[6]報告以MicroSoft Office Excel形式發送。[7]使用BioRad、R&D、Luminex或相同原理的檢測試劑測定蛋白濃度。[8]使用者需提供重組蛋白做為自體抗原以偵測自體抗體的相對量。

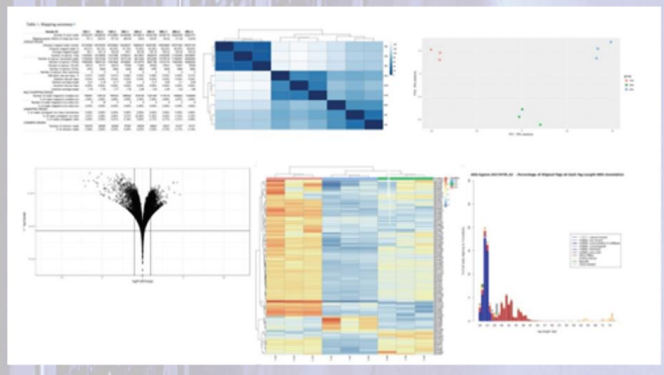
長庚大學分子醫學研究中心
Chang Gung Molecular Medicine Research Center
213
單位：蛋白質體核心實驗室
網址：https://cgmmrc.cgu.edu.tw/p/412-1029-9961.php
聯絡人:張育勳 (分機 :3542)
Email: proteomics@mail.cgu.edu.tw

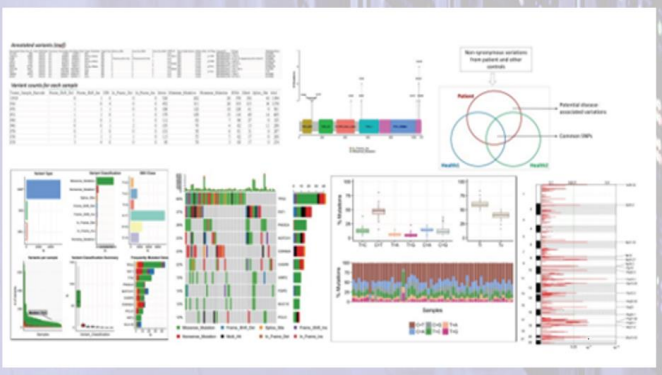
生物資訊分析平台

服務內容	1. RNA-seq data 標準分析 2. Small RNA sequencing data 標準分析 3. 外顯子定序(WES) data 標準分析 4. 全基因體定序(WGS) data 標準分析 5. Panel平台分析 6. 16S metagenome sequencing data 標準分析 7. Pathway analysis 標準分析 8. 生物資訊客製化分析/整合(電洽)
平台特色	➢ 由多名博士後研究員及資深分析工程師專案進行分析 ➢ 提供客製化分析與視覺化的整合 ➢ 專業高速運算叢集伺服器系統，提供最快速的服務 ➢ 多種跨體學生醫大數據之整合分析 ➢ 分析技術開發合作及產學合作









長庚大學分子醫學研究中心
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單位：生物資訊暨體學數據應用核心實驗室
網址： https://cgmmrc.cgu.edu.tw/p/412-1029-9988.php
聯絡人：張益峯 博士 (分機：3941)
Email：ianyfchang@mail.cgu.edu.tw

基因體定序服務平台

Next Generation Sequencing Service

NGS core lab service

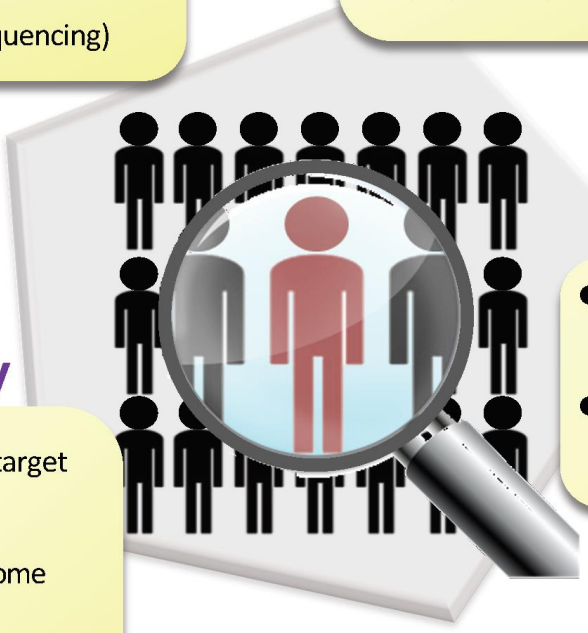
- Nucleic acid extraction
- Library preparation
- Sequencing
- Data reports

DNA sequencing

- 全外顯子組測序 (Whole exome sequencing)
- DNA甲基化測序 (Methylation sequencing)
- 標的基因測序 (Targeted re-sequencing)
- 染色質免疫沉澱測序 (ChIP sequencing)

RNA sequencing

- PolyA RNA sequencing
- 核醣體RNA測序 (Ribominus RNA sequencing)
- Coding RNA sequencing (capture-based RNA sequencing)
- 微小RNA測序 (Small RNA sequencing)



Metagenomics

- 細菌16S測序 (Bacterial 16S sequencing)
- 全基因組測序 (Whole genome sequencing)

Liquid biopsy

- 細胞外游離DNA測序 (cfDNA target sequencing)
- 外吐小體微小RNA測序 (Exosome small RNA sequencing)
- 免疫譜測序 (Immune repertoire sequencing)
- 單細胞轉錄體測序 (Single cell RNA sequencing)

Precision Medicine

- 藥物代謝基因檢測
- 腸道菌群定序分析
- 乳癌與卵巢癌基因篩檢
- 液態切片基因檢測
- 癌症標靶治療基因定序服務
- 心臟病用藥基因檢測
- 家族性高血脂基因檢測
- 心血管疾病基因檢測

長庚大學分子醫學研究中心 215
Chang Gung Molecular Medicine Research Center

單位: 次世代定序基因體核心實驗室
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聯絡人:郭鈺屏博士(分機：5529)
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病理核心實驗室服務平台
Pathology Service Platform

服務項目

1. 免疫組織化學染色 (Immunohistochemistry. IHC)
2. 顯色原位雜交染色 (Chromogen In Situ Hybridization. CISH)
3. 玻片掃描服務

服務特色

1. 提供免疫組織化學染色抗體測試結果之病理科醫師諮詢服務
2. 提供免疫組織染色常用抗體，減少查詢抗體及測試時間
3. 採用全自動化染色系統，減少人為染色誤差與縮短染色時間
4. 使用Leica compact polymer試劑組，提高偵測敏感度與降低非特異性背景訊號
5. 五片式全自動玻片掃描，可完成20X/40X高品質切片影像掃描

使用設備

1. Leica Bond MAX自動化免疫染色系統
2. Aperio ScanScope CS2病理組織切片全相式影像掃描儀
3. OLYMPUS DP71數位化顯微影像分析系統

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定量代謝體服務平台

Quantitative Metabolomics Service

收件評估

客製化流程

樣品前處理

樣品檢測

數據分析

報告產出

服務對象

長庚體系研究單位、各大專院校學研單位及廠商

檢測標的

小分子(< 2000 Dalton)代謝物檢測

服務項目

1. 代謝物衍生化: 化學同位素標定之樣品前處理 (Chemical isotope labeling)
2. 特定小分子及代謝物定量檢測
3. 客製化代謝體學檢測平台 (metabolomics profiling analysis)

服務特色

1. 提供唾液、尿液、組織及細胞等多樣化檢體萃取平台
2. 與國外實驗室技術合作，利用化學同位素標定方法，可全面性的分析代謝體學，並提供定性與準確定量的結果
3. 提供特定代謝物之定量分析

儀器設備

Agilent 1290, Infinity II LC system

Waters ACQUITY, UPLC

Bruker ion trap, HCT ultra

Bruker Qq-Tof, Impact II

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