ICMS 2021 SINO-MICRO 2021

海外华人微生物学会年会
暨国际代谢科学大会

2021 ANNUAL MEETING OF OVERSEAS CHINESE SOCIETY OF MICROBIOLOGY & INTENATIONAL CONFERENCE ON METABOLIC SCIENCES

会议手册

上海 · 中国

2021年10月25日-29日

Hosts & Organizers

Sponsors

Co-Organizers

- Chinese Society for Microbiology
- Joint International Research Laboratory of Metabolic and Developmental Sciences, Shanghai Jiao Tong University
- Shanghai Society for Microbiology
- Shanghai Synthetic Biology Innovation Strategic Alliance
- Shanghai Joint Innovation Center on Antibacterial Resistances, Shanghai Jiao Tong University
- Association of Chinese Virologists in America / Society of Chinese Bioscientists in America-Virology Division

Content

ICMS 2021

SINO-MICRO 2021

Welcome Messages

Dear Colleagues and Friends,

Zixin Deng
Shanghai Jiao Tong University
Academician of CAS

Under the circumstance of the global public health events in recent years, it's indeed my great pleasure to see so many microbiologists here, discussing the topic of "Addressing the unprecedented public health challenges: the essence of microbial sciences and global collaboration".

This conference is jointly organized by State Key Laboratory of Microbial Metabolism at Shanghai Jiao Tong University and Overseas Chinese Society of Microbiology.

Shanghai Jiao Tong University is one of the oldest institutions of higher education in China. On basis of the unremitting efforts throughout the past 125 years, SJTU has become one of the top 5 universities in China. The State Key Laboratory of Microbial Metabolism of Shanghai Jiao Tong University was established in 2011, and is investigating bioactive secondary metabolites by various state-of-the-art approaches involved in molecular biology, microbiology, biochemistry, genomics and so on. We are now striving to reveal the genetics and metabolic pathways of microorganisms and subsequently make use of it to improve antibiotic production and bioactivity.

The Overseas Chinese Society of Microbiology is originally a registered non-for-profit organization comprising overseas Chinese microbiology scientists. It is aimed to promote the discovery, exchange, and dissemination of knowledge and ideas in the field of microbiology, as well as the professional growth and career development of overseas Chinese microbiologists. In the framework of China-US academic cooperation, Sino-Micro is also dedicated to bridge the mutually beneficial relationship between the two countries, and to facilitate collaboration on global topics, from fundamental scientific understanding, public health, environmental sustainability to food safety.

The global public health events have had far-reaching impact. Now more than ever, there is demand for our scientists to intensify open cooperation and innovation in science and technology, and meet the challenges of our times. Here, I sincerely hope that all of you could engage in in-depth exchange of views to inspire each other and to come up with valuable recommendations for promoting global cooperation on science, technology and innovation.

I wish the conference a great success and all our guests a pleasant stay in Shanghai. Thank you!

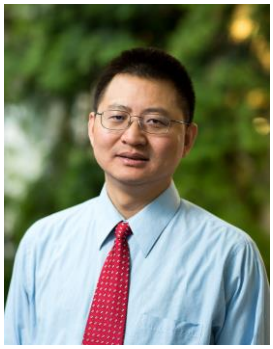
Sincerely,

Prof. Zixin Deng
Co-Chair, ICMS & SINO-MICRO 2021
Shanghai Jiao Tong University, Shanghai 200240, China

Welcome Messages

Welcome, colleagues and friends, to attend Sino-Micro 2021!

Yi-Wei Tang
Memorial Sloan-Kettering Cancer Center



Oliver Yongqun He
University of Michigan

The Overseas Chinese Society of Microbiology (Sino-Micro) is a registered non-profit organization formed by overseas Chinese scientists who study microbiology. Our goal is to promote the discovery, exchange, and dissemination of knowledge and ideas in the field of microbiology, and professional growth and career development of overseas Chinese microbiologists. Sino-Micro is also dedicated to bridge mutually benefiting relationship between world and China, and to facilitate collaboration on global topics, from fundamental scientific understanding, public health, environmental sustainability to food safety. Sino-Micro hosts annual meeting in US and China, in every alternate year. In addition, Sino-Micro supports other collaborative symposia and events with Chinese colleagues, when appropriate.

Sino-Micro and State Key Laboratory of Microbial Metabolism at Shanghai Jiao Tong University (SJTU) will co-host Annual Meeting of “Overseas Chinese Society of Microbiology (Sino-Micro 2021)” and “International Conference of Metabolic Sciences, ICMS 2021”, on October 25−29, 2021 in Shanghai. Scientists and practitioners in fundamental, clinical and environmental microbiology are invited to attend the event for communications and global collaborations. This meeting aims to address the unprecedented public health challenges during COVID-19 pandemic and highlight the essence of microbial sciences with global collaboration.

This meeting has been organized by many experts and groups in different areas of microbiology in mainland China and overseas. We appreciate their contributions, especially due to COVID-19 pandemic.

We wish you enjoy your time in Sino-Micro 2021!

Yi-Wei Tang, MD, PhD
President, Sino-Micro

Oliver Yongqun He, PhD
President-Elect, Sino-Micro

Welcome Messages

尊敬的各位来宾：

Ping Xu

Shanghai Jiao Tong University

大家好!我代表 2021 年海外华人微生物学会年会暨国际代谢科学大会的筹委会，向参与会议的各位老师、同学们表示热烈的欢迎，向关心、支持此次会议举办的各个单位、各位领导、同行、同学们表示衷心的感谢。作为上海交通大学微生物代谢国家重点实验室的一员，很荣幸能够参与到这一高水平而又隆重的学术会议中来。

2019 年的新冠肺炎疫情，打乱了无数国人的正常生活，也使学术界的“云上交流”变得常见，但我们今天能够在这里面对面地交流科学问题、碰撞思想火花，我想“生命科学”在其中发挥的作用是功不可没的，“生命科学”也又一次站在了所有人关注的焦点上，微生物科学与公共卫生的联系也引起了许多科研工作者的思考，因此此次大会的主题“应对前所未有的公共卫生挑战：微生物科学与全球合作的本质”恰逢其时。

华侨微生物学会作为海内外微生物领域极具影响力的非盈利组织之一，对推动微生物科学的新发现、新思想的交流和传播，促进微生物科学在世界范围内的合作起着至关重要的作用；而上海交通大学微生物代谢国家重点实验室作为国内微生物代谢领域极具影响力的学术组织之一，多年来在分解代谢、合成代谢、代谢互作等各个领域成果丰硕。我相信两个组织联合举办此次会议，一定能够取得圆满成功。

女士们、先生们，在全球疫情并未消散的今日，在生命科学，尤其是微生物科学引起广泛关注的今日，我们比任何时候都需要合作与交流，希望此次会议能够作为一座桥梁，连接起广大科研工作者，一起攻克新的科学高峰。最后，我代表筹委会向此次大会的志愿者、工作人员表示衷心的感谢，预祝会议取得圆满成功，预祝各位来宾在上海能有一段愉快的时光！

许平

ICMS & SINO-MICRO 2021 组织委员会主席

上海交通大学

Committees

Honorary Chairs

Yumei Wen, Shanghai Medicine College, Fudan University

Guoping Zhao, Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS

Conference Co-Chairs

Yi-Wei Tang, Memorial Sloan-Kettering Cancer Center

Zixin Deng, Shanghai Jiao Tong University

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George F. Gao (co-chair), Chinese Center for Disease Control and Prevention

Hua Wang (co-chair), The Ohio State University

Shuangjiang Liu, Institute of Microbiology, CAS

Feng Shao, National Institute of Biological Sciences

Wenyuan Shi, The Forsyth Institute

Chuanwu Xi, University of Michigan

Jianguo Xu, National Institute for Communicable Disease Control and Prevention

Frank Yang, Indiana University School of Medicine

Qijing Zhang, Iowa State University

Jizhong Zhou, University of Oklahoma

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Yongqun (Oliver) He (chair), University of Michigan

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Yan Feng, Shanghai Jiao Tong University

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Shuangjiang Liu, Institute of Microbiology, CAS

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Hong-Yu Ou, Shanghai Jiao Tong University

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Qijing Zhang, Iowa State University

Wenhong Zhang, Huashan Hospital affiliated to Fudan University

Guoping Zhao, Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS

Liping Zhao, Shanghai Jiao Tong University

Daoguo Zhou, Purdue University

Jizhong Zhou, University of Oklahoma

Ningyi Zhou, Shanghai Jiao Tong University

Jun Zhu, University of Pennsylvania School of Medicine

● Organization Committee

Ping Xu (chair), Shanghai Jiao Tong University

Shuyang Sun (co-chair), Shanghai Jiao Tong University

Yongqun (Oliver) He, University of Michigan

Hong-Yu Ou, Shanghai Jiao Tong University

Linquan Bai, Shanghai Jiao Tong University

Yi-Wei Tang, Memorial Sloan-Kettering Cancer Center

Xiaokui Guo, Shanghai Jiao Tong University

Jun Ni, Shanghai Jiao Tong University

Wenhong Zhang, Huashan Hospital affiliated to Fudan University

Organizer Introduction

- **Overseas Chinese Society for Microbiology**

Sino-Micro stands for The Overseas Chinese Society for Microbiology. Sino-Micro is an association established by and for overseas Chinese microbiologists.

Sino-Micro is formed to the promotion of discovery, exchange, and dissemination of knowledge and ideas in the field of microbiology and professional growth and career development of overseas Chinese microbiologists. Sino-Micro acts in two principal ways: 1) facilitating interaction between members; and 2) interaction between members and microbiologists in China. Sino-Micro accomplishes these objectives through meetings and symposia, dissemination of technical information, mentoring of students and young scholars, and participation in national and international research and educational programs.

Sino-Micro is a registered non-for-profit organization formed by overseas Chinese researchers who study microbiology. Our goal is to establish a social network that will facilitate the advancement of our research programs and the development of our careers. In addition, we wish to work as a group to create a platform for enhancing scientific interactions with our colleagues in China. Current Sino-Micro members are primarily principal investigators in the USA. However, our organization is open to all overseas Chinese microbiologists.

Sino-Micro

海外华人微生物学会

Overseas Chinese Society for Microbiology

Organizer Introduction

- **State Key Laboratory of Microbial Metabolism (上海交通大学微生物代谢国家重点实验室)**

State Key Laboratory of Microbial Metabolism (SKLMM) takes lead in researches on metabolic science and in diverse frontier areas of microbial metabolism, with a core interest to support China's strategic goal for sustainable development. SKLMM focuses on intensive and extensive investigation into mechanisms of microbial anabolism and catabolism, for unveiling the physiological functions, regulatory networks, and their complex interactions or connections with the environments. SKLMM aims to pave solid ways for optimizing and reprogramming metabolic pathways to maximize the metabolic potential of microorganisms, and therefore promoting the fundamental and technological innovations.

SKLMM has rapidly been developing with a common motto ‘erudition, creativity, dedication, and harmony’ for its faculty team, composed of internationally well-known scientists. Particularly, it has constantly energized with enthusiastic and outstanding young scholars through international recruitment and in-house training. Taking multi-disciplinary advantages of metabolic science, SKLMM tries to play important roles in microbial genetics, microbial ecology, microbial physiology, and biotechnology.

General Information

- **Theme and Topics**

Addressing the Unprecedented Public Health Challenges: The Essence of Microbial Sciences and Global Collaboration

Session I:	Synthetic Biology and Biotechnology
Session II:	Pathogen, Virus and Vaccine
Session III:	Applied and Environmental Microbiology
Session IV:	Antibiotics & Resistance
Session V:	Metabolic Sciences and Microbial Metabolism
Session VI:	Intestinal Microbiomes and Microbial Bioinformatics

- **Registration**

Date	Time	Location (上海松江开元名都大酒店)
Oct 25th	**14:00-20:00**	**Lobby**
Oct 26th	**7:30-17:00**	**Lobby**
Oct 27th	**7:30-17:00**	**Lobby**
Oct 28th	**7:30-17:00**	**Lobby**

- **Catering**

Catering	Time	Location (上海松江开元名都大酒店)
Lunch	**Oct 26th 12:00-13:30**	地中海餐厅（一楼）
Welcome Banquet	**Oct 26th 17:30-19:00**	开元厅（四楼）
Lunch	**Oct 27th 12:00-13:30**	地中海餐厅（一楼）
Dinner	**Oct 27th 18:00-19:00**	地中海餐厅（一楼）
Lunch	**Oct 28th 12:00-13:30**	地中海餐厅（一楼）
Dinner	**Oct 28th 18:00-19:00**	地中海餐厅（一楼）

General Information

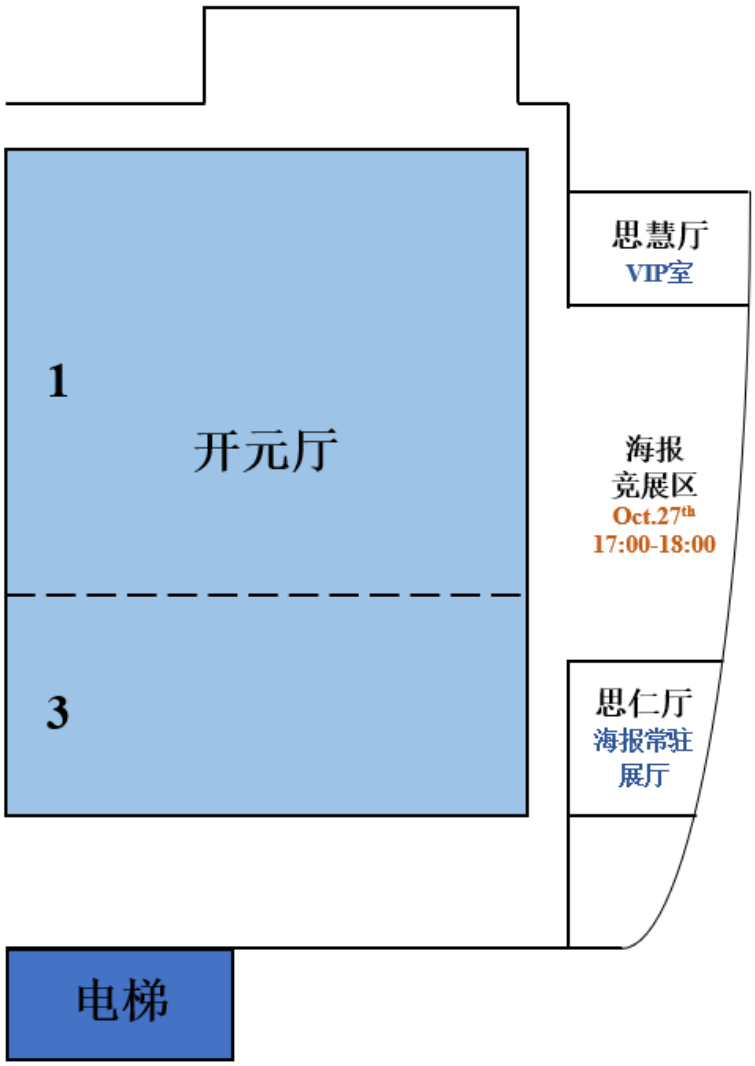
- **Contact**

If you have any questions, please contact the conference registration desk.

Telephone: +86-21-34204051 E-mail: service@icms-sjtu.org

- **Map**

上海松江开元名都大酒店



Sino-Micro & ICMS 2021

New Century Grand Hotel Songjiang (上海松江开元名都大酒店), 1799 Renmin North Road, Songjiang District, Shanghai

http://www.icms-sjtu.org October 25-29, 2021

Oct 25 Monday	
14:00	**Registration Open (Lobby)**
Oct 26 Tuesday	
Opening Ceremony (开元厅，四楼) Chair: **Yan Feng**, Shanghai Jiao Tong University & **Ping Xu**, Shanghai Jiao Tong University	
08:30-09:00	**Welcome Message from ICMS (Zixin Deng, conference co-chair)** **Welcome Message from Sino-Micro (Yiwei Tang, conference co-chair)** **Welcome Message from Scientific Committee (Yongqun He, scientific committee chair)** **Welcome Message from Organization Committee (Ping Xu, organization committee chair)**
Plenary Session (开元厅，四楼) Chair: **Yan Feng**, Shanghai Jiao Tong University & **Ping Xu**, Shanghai Jiao Tong University	
09:00-10:00	**Yumei Wen (CAE Academician)** "A Sandwich Therapeutic Approach for Treatment of Persistent Viral Infections" **Russ Higuchi (Cepheid Fellow & qPCR Inventor)** "Real-time PCR – Past, Present and Future"
10:00-10:30	**Photo & Coffee Break**
10:30-12:00	**Guoping Zhao (CAS Academician)** "TBA" **Feng Shao (CAS Academician)** "Pyroptosis in Antibacterial and Antitumor Immunity" **George F Gao (CAS Academician)** "TBA"
12:00-13:30	**Lunch (地中海餐厅，一楼)**

	Session I: Synthetic Biology and Biotechnology(开元厅 1，四楼) Chair: **Fengwu Bai**, Shanghai Jiao Tong University **Hongzhi Tang**, Shanghai Jiao Tong University	**Session II: Pathogen, Virus and Vaccine(开元厅 3，四楼)** Chair: **Yufeng Yao**, Shanghai Jiao Tong University School of Medicine **Haihua Liang**, Southern University of Science and Technology
13:30-15:00	**(K) Lixin Zhang (East China University of Science and Technology)** "Intelligent Manufacturing of Microbial Drugs" **(K) Jingwen Zhou (Jiangnan University)** "Towards the Customized Production of Flavonoids in Microorganisms" **Fuli Li (QIBEBT, CAS)** "Ethanol Metabolism Dynamics in *Clostridium ljungdahlii* Grown on Syngas" **Qiannan Hu (SINH, CAS)** "Data-driven *de novo* Biosynthesis Pathway Design Systems"	**(K) Yongqun He (University of Michigan)** "Rational COVID-19 Vaccine Design and Safety Evaluation Using Bioinformatics" **Chan Ding (SHVRI, CAAS)** "Newcastle Disease Virus Degrades SIRT3 via PINK1-PRKN Dependent Mitophagy to Reprogram Energy Metabolism in Infected cells" **Chao Gao (Shandong University)** **"**Microbial 2-Hydroxyglutarate Metabolism" **Qiyao Wang (East China University of Science and Technology)** "*Edwardsiella piscicida* Functional Genomics Investigation Illuminates Pathogenesis and Strategies for Heuristics Vaccine Design"
15:00-15:30	**Coffee Break**	
15:30-17:00	**(K) Chao Zhong (SIAT, CAS)** ""Living" Materials Enabled by Engineered Bacterial Biofilms" **(K) Yong Wang (CEMPS, CAS)** "Biosynthesis of Flavonoids via Manufacturing Self-Assembly Enzyme Reactor *in vivo*" **Yi Xiao (Shanghai Jiao Tong University)** "Bioconversion of Lignocellulose-derived *p*-Coumaric and Ferulic Acids into Value-added Aromatic Natural Products" **Xiao Yi (SIAT, CAS)** "Rapid Evolution of Macromolecules"	**(K) Luyan Ma (Institute of Microbiology, CAS)** "Intracellular Glycosyl Hydrolase PslG Shapes Bacterial Cell Fate, Signaling, and the Biofilm Development of *Pseudomonas aeruginosa*" **Jianping Xie (Southwest University)** "Novel Biomarkers for Tuberculosis Diagnosis and Treatment Management Tailored for Chinese Population" **Nan Song (Beijing Friendship Hospital, Capital Medical University)** "Tc Toxin-A Versatile Weapon Targeting Mammals" **Donglei Sun (Shanghai Jiao Tong University)** "Advanced Imaging Reveals the Fungal Pathogen *Cryptococcus neoformans* Invade the Brain via a Proliferation Dependent Manner"
17:30-19:00	**Welcome Banquet (开元厅，四楼)**	

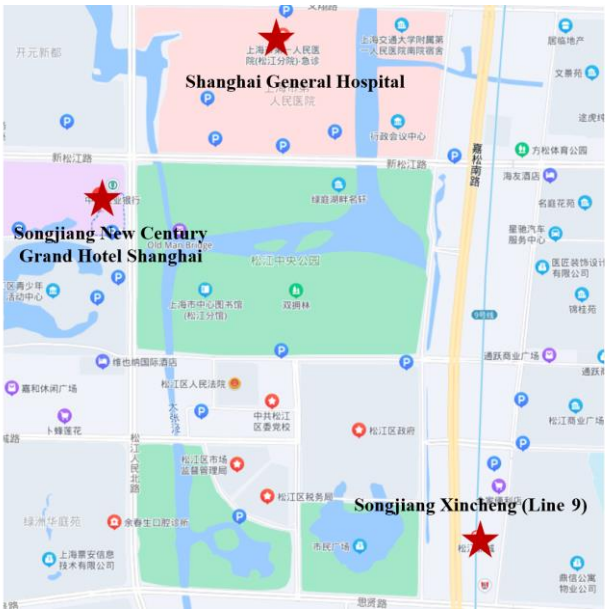
Oct 27 Wednesday	
Plenary Session(开元厅，四楼) Chair: **Shuangjiang Liu**, Institute of Microbiology, CAS & **Guanghua Huang**, Fudan University	
08:30-10:00	**Jizhong Zhou (University of Oklahoma)** "Feedback Responses of Grassland Soil Microbial Communities to Climate Warming" **Yuzhong Zhang (Shandong University)** "Mechanistic Insights into the Metabolism of Special One Carbon Compounds (DMSP, TMAO) by Marine Bacteria" **Sponsor Presentation**
10:00-10:30	**Coffee break**
10:30-12:00	**Chuanwu Xi (University of Michigan)** "What Can Environmental Surveillance of SARS-CoV-2 on a University Campus Tell Us?" **Pei-Yong Shi (University of Texas)** "SARS-CoV-2 Biology and Countermeasure Development" **Zhengli Shi (WIV, CAS)** "Key Factors Involved in Virus Spillover from Wildlife to Humans"
12:00-13:30	**Lunch (地中海餐厅，一楼)**

	Session III:Applied and Environmental Microbiology **(开元厅 1，四楼)** Chair: **Yuzhong Zhang**, Shandong University **Shuangjun Lin**, Shanghai Jiao Tong University	**Session IV: Antibiotics and Resistance** **(开元厅 3，四楼)** Chair: **Min Li**, Renji Hospital, SJTU School of Medicine **Liangdong Lyu**, Fudan University School of Medicine
13:30-15:00	**(K) Shuangjiang Liu (Institute of Microbiology, CAS)** "TBA" **(K) Xihui Shen (Northwest A&F University)** "t-T6SS Secretes an LPS-binding Effector to Recruit OMVs for Exploitative Competition and Horizontal Gene Transfer" **Tao Dong (Shanghai Jiao Tong University)** "Avoiding Traffic Jam: Quantity Control of the Type VI Secretion System Substrates in Response to the Functional Status" **Jiandong Jiang (Nanjing Agricultural University)** "Redundancy of 4-Hydroxybenzoate 3-Monooxygenase Genes Ensures the Catabolic Safety of 4-Hydroxybenzoate in *Pigmentiphaga* sp. H8"	**(K) Xingmin Sun (University of South Florida)** "Antibiotic Resistance of *Clostridioides difficile*" **Liangdong Lyu (Fudan University School of Medicine)** "Metabolic Regulation of *Mycobacterial* Persistence" **Xiaofei Jiang (Huashan Hospital of Fudan University)** "Research Progress on the Dissemination Mechanism of Bacterial Resistance" **Jie Feng (Institute of Microbiology, CAS)** "Solidarity in the Genetic World: A Single Integrase for the Mobilization of Two Genetic Elements Disseminating Antibiotic Resistance"
15:00-15:30	**Coffee Break**	
15:30-17:00	**(K) Jidong Gu (Guangdong Technion-Israel Institute of Technology)** "New Microbial Nitrogen Transformation Reactions on the Old Angkor Monuments" **(K) Haihua Liang (Southern University of Science and Technology)** "A Novel Signaling Network Regulates Biofilm Formation in *Pseudomonas aeruginosa*" **Kun Zhao (Tianjin University)** "MSHA Pili-assisted Surface Landing of *Vibrio cholerae* in a Viscoelastic Environment" **Qian Wang (Shandong University)** "Design, Construction and Precise Dynamic Control of an Unnatural Glycolysis Pathway"	**(K) Min Li (Renji Hospital, SJTU School of Medicine)** "Progress in Drug Resistance Mechanism of Gram Positive Bacteria" **Xinxin Feng (Hunan University)** "Chemical Biology of Multi-targeting Resistance-resistant Antibiotics" **Yang Fu (Southern University of Science and Technology)** "Identification of a Novel T6SS Effector Reveals a Brand New Mechanism Precisely Targeting Cholera Infection" **Ke Wang (Guangxi Medical University)** "Pleural Empyema Related Pathogens and Biofilms"
17:00–18:00	**Poster Session**	
18:00–19:00	**Dinner (地中海餐厅，一楼)**	

Oct 28 Thursday	
Plenary Session(开元厅，四楼) Chair: **Linquan Bai**, Shanghai Jiao Tong University & **Sibao Wang**, IPPE, CAS	
08:30-10:00	**John Leong (Tufts University)** "Microbial Tools to Characterize Age-associated Innate Immune Dysfunction" **Zhaoqing Luo (Purdue University)** "The ADP-Ribosylation Arsenals of *Legionella pneumophila*" **Yan Feng (Shanghai Jiao Tong University)** "Enzyme Evolution in Synthetic Biology: A Key Role from Proof-of-Concept towards Precision Function"
10:00-10:30	**Coffee break**
10:30-12:00	**Jiangchao Zhao (University of Arkansas)** "Translating Swine Gut Microbiome Research into Animal Production: Challenges, Opportunities and Future Directions" **Liping Zhao (Shanghai Jiao Tong University)** "Reference-free and Ecology-based Discovery of Microbiome Biomarkers" **Sibao Wang (IPPE, CAS)** "Mosquito Microbiota and Implications for Disease Control"
12:00-13:30	**Lunch(地中海餐厅，一楼)**

	Session V: Metabolic Sciences and Microbial Metabolism **(开元厅 1，四楼)** Chair: **Shengying Li**, Shandong University **Jianjiang Zhong**, Shanghai Jiao Tong University	**Session VI: Intestinal Microbiomes and Microbial Bioinformatics** **(开元厅 3，四楼)** Chair: **Hongwei Zhou**, Southern Medical University **Chenhong Zhang**, Shanghai Jiao Tong University
13:30-15:00	**(K) Lianrong Wang (Wuhan University)** "Characteristics of a New Type of DNA Phosphorothioate Modification System" **(K) Long Liu (Jiangnan University)** "Acid-stress Adaptation of Yeast for Natural Lactic Acid Production" **Yu Zhang (CEMPS, CAS)** "Structural Insights into the Intrinsic Transcription Termination in Bacteria" **Xuming Mao (Zhejiang University)** "Discovery of Semi-Pinacolases from Epoxide Hydrolase Family during Efficient Assembly of a Fungal Polyketide"	**(K) Hongwei Zhou (Southern Medical University)** "Multi-Center Design to Overcome the Regional Variation of Disease Microbiome Signatures on the CALM Platform" **Xingyin Liu (Nanjing Medical University)** "*Lactobacillus plantarum* Ameliorates Colorectal Tumorigenesis through Contributing to Priming the IFN-γ+CD8+ T Cell Immunity" **Chenhong Zhang (Shanghai Jiao Tong University)** "Nutritional Modulation of Gut Microbiota for Alleviation of Metabolic Diseases" **Wei Wang (Institute of Molecular Medicine, SJTU School of Medicine)** "In vivo Metabolic Labeling-based Chemical Biology Research of Gut Microbiota"
15:00-15:30	**Coffee Break**	
15:30-17:00	**(K) Tiangang Liu (Wuhan University)** "Intelligent Production and Innovative Discovery of Natural Products" **Wei Zhang (Shandong University)** "Biosynthesis of Sulfur-containing Antibiotic Chuangxinmycin Featuring a Deubiquitinase-like Sulfurtransferase" **Wei Ding (Shanghai Jiao Tong University)** "The Novel Post-translational Modifications in Biosynthesis of RiPP Natural Products" **Yingxiu Cao (Tianjin University)** "Genome-scale Target Identification and Programming of Microbes for High Production of Chemicals"	**(K) Zheng Zhang (Shandong University)** "Estimate of the Sequenced Proportion of the Global Prokaryotic Genome" **Bo Liu (IPBCAMS)** "The Construction of a Web Based Analysis Platform for Zoonotic and Vector-Borne Viruses" **Yi-Lei Zhao (Shanghai Jiao Tong University)** "PT-diet and Longevity" **Hong-Yu Ou (Shanghai Jiao Tong University)** "Identification of the Conjugative Transfer Modules of the Antibiotic Resistance Plasmids and Virulence Plasmids of *Klebsiella*"
17:00–17:30	**Closing Ceremony & Poster Award**	
18:00–19:00	**Dinner (地中海餐厅，一楼)**	

Location and Transportation



New Century Grand Hotel Songjiang (上海松江开元名都大酒店)

No.1799 Renmin North Road Songjiang District Shanghai 201620 China

~1.5 km from Songjiang Xincheng Subway Station (Line 9)

~30 km from Shanghai Hongqiao Airport (SHA) or Shanghai Hongqiao Railway Station, ~35 min by taxi

~65 km from Shanghai Pudong Airport (PVG), ~ 60 min by taxi

Opening Ceremony

Zixin Deng

Shanghai Jiao Tong University, China

Sino-Micro & ICMS 2021 Conference co-Chair

Zixin Deng is a Professor at Shanghai Jiao Tong University. He is the President of Chinese Society for Microbiology, member of Chinese Academy of Sciences, fellow of the World Academy of Sciences, fellow of the American Academy of Microbiology, and a fellow of Royal Society Fellow of Chemistry. He works on *Streptomyces* genetics, and the biochemistry and molecular biology of antibiotic biosynthesis, and the DNA backbone modification by sulfur (phosphorothiolation).

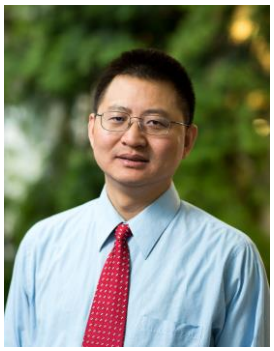
Yiwei Tang

Memorial Sloan-Kettering Cancer Center, USA

Sino-Micro & ICMS 2021 Conference co-Chair

Yiwei Tang is currently the Chief of the Clinical Microbiology Service at the Memorial Sloan Kettering Cancer Center and a Professor of Laboratory Medicine at the Weill Cornell Medical College in New York City, USA. He received his B.S. degree in medicine from Fudan University, Shanghai, China, in 1982, and a M.S. degree in Epidemiology from Fudan University, Shanghai, China, in 1986, and a Ph.D. in Microbiology and Immunology from the Vanderbilt University, USA, in 1996. Dr. Tang ranks among the top scientists in the field of clinical microbiology, as evidenced by his election as an Editor for the *J. Clin. Microbiol.* and a Fellow of the American Academy for Microbiology and of the Infectious Disease Society of America. He is mainly engaged in the fields of infectious disease epidemiology, clinical microbiology, immunology, and molecular biology.

Yongqun He



University of Michigan Medical School, USA

Scientific Committee Chair

Yongqun "Oliver" He, CCMB Affiliate Faculty, Associate Professor of Laboratory Animal Medicine, Associate Professor of Microbiology and Immunology Professor of Microbiology and Chemical Biology. He received his B.S. degree in Veterinary Med. from Jiangxi Agricultural Univ, Nanchang, China, in 1991, and a M.S. degree in Infect. Dis. & Veterinary Preventive Med. from China Agricultural University, Beijing, China, in 1996, and a Ph.D. in Molecular Immunology from Virginia Polytechnic Institute and State University, USA, in 2000. Dr. He's primary bioinformatics interests are development of biomedical ontologies and their applications in literature mining, Bayesian network modeling, microbial genomics, and vaccine informatics. His primary wet-lab research interests are in studying microbial pathogenesis and host-pathogen interaction using high-throughput technologies and developing vaccines against intracellular pathogens.

Ping Xu

Shanghai Jiao Tong University, China

Organization Committee Chair

Dr. Ping Xu is a distinguished professor of microbiology, biomolecular engineering and biochemical engineering as the deputy director of State Key Lab of Microbial Metabolism at Shanghai Jiao Tong University (SJTU). Dr. Xu has authored and co-authored over 220 research articles and over 80 issued and pending patents with several being licensed by industry. He received numerous research and teaching awards and honors, such as Winner of Young Asian Biotechnologist Prize of the Society for Biotechnology Japan (2007), and a Fellow of the American Institute of Medical and Biological Engineering (AIMBE, 2014). He has been elected a member of the US National Academy of Inventors (NAI, 2015) and a Fellow of American Academy of Microbiology (AAM, 2019). His primary research interests are in the seminal discovery of useful bacteria and using metabolic engineering for agricultural, biotechnological, clean-environmental engineering and waste treatment applications.

Plenary Session

Yumei Wen

Shanghai Medicine College, Fudan University, China

Yu-Mei Wen MD graduated from Shanghai Medical University in 1956, and has been a graduate student in the Department of Microbiology and Immunology in Shanghai Second Medical University. She was further trained as a research fellow in Immunology in the Chinese Academy of Medical Sciences. After the opening up, in 1979, she was a WHO fellow at London School of Hygiene and Tropical Medicine, and in 1981, a Fogarty visiting scholar at NIAID, National Institutes of Health, USA. Currently, she is appointed as the Chair of the Academic Committee of Fudan University, and Professor at the Institute of Medical Microbiology, Fudan University, and Professor at Key Laboratory of Medical Molecular Virology, Ministry of Education/Ministry of Health. Her interests are in research of molecular virology and immunology of hepatitis B virus, and in microbial functional genomics. She is one of the pioneers in basic and applied studies on therapeutic vaccine for chronic hepatitis B patients, and studies on bacterial biofilm formation. Recently, she was appointed Director of the National Engineering laboratory for Therapeutic vaccines. She has published around 300 articles in journals home and abroad, including *Lancet*, *Nature*, *Cancer Res.*, *J. Viro.* etc. and has edited and co-edited 8 books. She was elected member of the Chinese Academy of Engineering in 1999, was awarded in recognition of outstanding contribution in Medical Virology by Asian Pacific Society for Medical Microbiology (2006), and Honorary Doctorate by University of Duisburg and Essen, Germany (2009).

Russ Higuchi

Cepheid, USA

With more than 55 patents to his name, Russ Higuchi—Distinguished Fellow, Cepheid—has made substantial contributions to science and molecular diagnostics over the past 20+ years. Recognized for his integrity and strong work ethic, Russ joined Cepheid in 2008. Prior to Cepheid, Russ revolutionized molecular diagnostics with the invention of real-time polymerase chain reaction (real-time PCR)—a molecular diagnostic testing technique used to measure gene expression. With real-time PCR, Russ enabled a technique that was once limited to highly complex labs to be done anywhere, anytime, at any scale. In his 10+ years at Cepheid, Russ has contributed to multiple diagnostic assays for infectious disease and oncology, which have simultaneously helped patients and helped fuel Cepheid's significant growth. Core technology developed by Russ is used in all Cepheid products. With 30,000+ citations of his extensive body of published work, Russ was born with the innovator gene.

Real-time PCR – Past, Present and Future

This presentation will describe the early days of PCR – including a short detour into DNA from extinct species - and the invention of real-time PCR and real-time PCR instruments. Also discussed will be the application of real-time PCR to real-world problems including the Covid pandemic. Lastly, recent work will be presented on making PCR faster by reducing by more than half the number of thermal cycles needed. This is accomplished by increasing the rate of DNA replication from a doubling to up to a six-fold increase per thermal cycle.

Guoping Zhao

Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS, China

Guo-Ping Zhao was born in Shanghai in 1948. He obtained his B.S. of Microbiology from Fudan University, Shanghai, China in 1982 and Ph.D. of Biochemistry from Purdue University, W. Lafayette, Indiana, USA in 1990. He was the first production manager of Shanghai Promega Biological Products, Ltd. when he returned back to China in 1992. He joined the Shanghai Institute of Plant Physiology, CAS in 1995 as a professor, director of the Microbiology Laboratory and later the deputy director of the institute. He was the director of Shanghai Research Center of Biotechnology, CAS from 1997 to 1999. From 1999 to 2001, he was the vice president of SIBS responsible for research and planning. He was a member of the Advisory Committee for Biotechnology of the State High Technology Development Program (863) from 1996 to 2005 and was elected the academician of the CAS in 2005.

Prof. Zhao has been working on the structure function relationship and reaction mechanisms of microbial enzymes since his graduate studies. Based on these studies, he is also interested in developing microbial and/or protein engineering technology for industrial application of these enzymes. Prof. Zhao organized the genomic sequencing and annotation project for Leptospira interrogans. He organized the consortium responsible for the study of SARS molecular epidemiology and SARS CoV evolution. He successfully analyzed the molecular evolution of the virus employing the accurate and comprehensive data of epidemiology. Meanwhile, aided by the mechanism of viral genomic variation and evolution learned via this study, the animal origin of the pathogen was strongly supported, the molecular markers of the epidemiological phases of the pandemic were assigned and the critical amino acid residues related to the cross host infection of SARS CoV were characterized. This knowledge has laid down a strong foundation for searching the nature reservoir of SARS CoV and for further understanding the mechanism of cross host infection of emerging zoonotic. diseases.

Feng Shao

National Institute of Biological Sciences, China

Feng Shao, CAS, Investigator and Deputy Director for Academic Affairs in NIBS. He received his B.S. degree in Applied Chemistry from Peking University, Beijing, China, in 1996, and a M.S. degree in Molecular Biology from Institute of Biophysics, Chinese Academy of Sciences, Beijing, China, in 1999, and a Ph.D. in Biological Chemistry from University of Michigan Medical School, USA, in 2003. Dr. Feng Shao's laboratory is interested in studying molecular mechanisms of bacterial infection and host innate immunity defense. Meanwhile, Dr. Feng Shao's laboratory is also interested in how the host uses its innate immunity system to counteract bacterial infection, particularly the inflammasome pathway in macrophages.

Pyroptosis in Antibacterial and Antitumor Immunity

Pyroptosis is a highly proinflammatory form of cell death executed by a newly identified family of pore-forming proteins known as gasdermins, including gasdermin A to E in human. Among the family, gasdermin D (GSDMD) is cleaved by canonical inflammasome-activated caspase-1 and LPS-activated caspase-11/4/5. The cleavage unmasks the N-terminal pore-forming domain in GSDMD that perforates the plasma membrane. The GSDMD pores also serve as a conduit for IL-1/18 release upon canonical inflammasome activation. Thus, GSDMD plays a key and determining role in all inflammasome-mediate immune defenses. We found that GSDME is efficiently cleaved by caspase-3, and the presence of GSDME switches canonical apoptosis to pyroptosis, such as in DNA-damaging drugs activation of caspase-3 activation in cancer chemotherapy. Using a novel bioorthogonal chemical biology approach that allowed controlled delivery of an active gasdermin into tumors in mice, we found that pyroptosis of < 15% tumour cells was sufficient to clear the entire 4T1 mammary tumourgraft. The tumour clearance was absent in immune-deficient mice or upon T-cell depletion. A reduced ineffective dosage of gasdermin delivery could sensitize 4T1 tumours to the anti-PD1 checkpoint blockade therapy. Thus, pyroptosis-induced inflammation can stimulate potent and effective antitumour immunity. In immune-mediated tumor clearance, cytotoxic lymphocyte relies on granzymes to kill target tumor cells, which has been deemed via an apoptosis mechanism. We instead found that natural killer cells and cytotoxic T lymphocytes kill GSDMB-positive cells through inducing pyroptotic death, which is mediated by granzyme A (GZMA) cleavage of GSDMB. IFN-γ upregulates GSDMB expression and promotes the pyroptotic killing of cancer cells including that by CAR-T and TCR-T cells. Introducing GZMA-cleavable GSDMB into murine cancer cells promotes tumor clearance in mice in the presence of the anti-PD1 antibody. Thus, gasdermin-executed pyroptosis can serve as a cytotoxic lymphocyte killing mechanism, playing an important role in cancer immunotherapy.

George F. Gao

Chinese Center for Disease Control and Prevention, China

George F. Gao is an academician of the Chinese Academy of Sciences and The World Academy of Sciences, as well as a foreign associate of the US National Academy of Sciences and the US National Academy of Medicine. He received his M.S. degree in microbiology and veterinary epidemiology from Beijing Agricultural University, Beijing, China, in 1986, and a Ph.D. in biochemistry from Oxford University, England, in 1994. Dr. Gao's main research focus is on the mechanism of viral entry and release, especially the cross-species transmission (host jump) of the influenza virus. He also studies viral ecology, including the ecology of the flu virus in migratory birds and poultry markets. He was the first to describe the cross-species transmission mechanism of the H5N1 avian flu virus. Gao's research also involves public and global health policy. Gao has published 20 books or book chapters and over 500 peer-reviewed research papers, including those on newly discovered pathogenic viruses such as the SARS virus and the H7N9 avian flu virus.

Jizhong Zhou

University of Oklahoma, USA

Jizhong Zhou, Professor of Microbiology at University of Oklahoma. He has expertise in molecular biology, microbial genomics, microbial ecology, molecular evolution, theoretical ecology, metagenomics, and genomic technologies, as well as array-based bioinformatics for environmental studies. He has pioneered the development of array-based genomic technologies for environmental studies. His lab does much of the field sample processing for sequencing and as such is involved in multiple collaborations across the three aims where their packages/pipelines, mechanisms, and predictions of the microbiome and biogeochemical dynamics are used. He provides high-quality microbiome data to support the field and laboratory research, including amplicon sequencing of phylogenetic marker genes (e.g. 16S, 18S) and key functional genes (e.g. amoA), functional gene microarray test. He develops and applies statistical tools (particularly for network analysis, time series analysis, community assembly mechanisms), ecological models, and omics-enabled biogeochemical models to approach a mechanistic and predictive understanding of the subsurface microbiome dynamics and their functioning in biogeochemical processes.

Feedback Responses of Grassland Soil Microbial Communities to Climate Warming

The acceleration of global climate warming, a consequence of the buildup of atmospheric CO_2 and other greenhouse gases due to fossil fuel combustion and land use change, represents one of the greatest scientific and policy concerns in the 21st century. Understanding the mechanisms of biospheric feedbacks to climate change is critical to project future climate warming. Although microorganisms catalyze most of biosphere processes related to fluxes of greenhouse gases, the roles of microorganisms in regulating future climate change remain elusive. With time series data from a long-term climate change experiment, our results showed that microorganisms play central roles in regulating soil carbon dynamics through three primary feedback mechanisms, climate warming stimulates microbial temporal turnovers and divergent succession, enhances network complexity and stability, but reduces microbial diversity. Our results also demonstrated that incorporating microbial community information significantly improve the predictability of global change models. All these results have important implications in modeling and predicting future climate change, as well as for policy-making.

Yuzhong Zhang

Shandong University, China

Yuzhong Zhang, Professor, Director of the Marine Biotechnology Research Center of Shandong University. Professor Zhang Yuzhong's current main research direction is "Marine Microbiology and Marine Microbial Technology". The main research content includes: the diversity of cold-adaptive bacteria in the deep sea and polar regions (Antarctic and Arctic), physiological and biochemical and ecological adaptation mechanisms, and the development of cold-adaptive enzymes Catalytic mechanism and cold-adaptive evolution, resource development and utilization of cold-adaptive bacteria and protease. In addition, Professor Zhang Yuzhong has also carried out more systematic research on the physiology and biochemistry of photosynthesis of cyanobacteria and unicellular red algae. After more than 10 years of unremitting efforts, Professor Zhang Yuzhong has established a domestic research system featuring marine microbial enzymology and marine microbial biochemistry and has achieved a series of innovative and internationally influential research results, which have been published in *PNAS* and *J. Biol. Chem*., *ISME. J*., *PLoS One*, *Appl. Environ. Microbiol.* and other famous magazines in the field of microbiology and biochemistry.

Chuanwu Xi

University of Michigan, USA

Chuanwu Xi, Professor at University of Michigan. His research mainly focuses on biofilms, water quality and human health in three major inter-related areas: 1) molecular mechanisms of biofilm development; 2) characterization of biofilms in environmental, industrial and clinical settings; and 3) development of novel approaches for biofilm control for a variety of applications. His research has been supported by various sponsors including federal agencies, industry, and private foundations. Some of his research will not only contribute to the basic sciences but also improve the awareness of public of certain emerging public health issues and has a great translational potential to improve human health and industrial products.

What Can Environmental Surveillance of SARS-CoV-2 on a University Campus Tell Us?

Since the beginning of the pandemic of COVID-19 across the globe, a full knowledge about the SARS-CoV-2 has been lacking and public health policies and prevention approaches have evolved along the way. A limitation public health authorities often face is the non-optimal participation rate in public health measures such as clinical testing and vaccination by the public, which significantly impact the effectiveness of these measures. It is critical to understand the environmental transmission of the SARS-CoV-2 virus and determine the major transmission routes. In addition, tools to determine the overall burden of the spread of the virus prior to outbreaks and clinical interventions have become very valuable. In this talk, I will describe a comprehensive environmental surveillance program of SARS-CoV-2 on a public university campus. We have conducted longitudinal air, surface and wastewater sampling in a wide range of settings on and off-campus to quantify SARS-CoV-2 contamination levels using molecular methods. Air and surface samples were used to evaluate exposure risks and the probability of infection in these settings using quantitative microbial risk assessment (QMRA). Furthermore, wastewater data was used to evaluate the robustness of wastewater-based epidemiology (WBE) for early detection and evaluation of spread of infection in the university community. Our study and others have demonstrated that environmental public health surveillance has the potential to provide insight on real-life environmental exposure risks to infectious respiratory diseases, and WBE can be a valuable early warning alert and a helpful complementary surveillance tool to other public health and clinical measures.

Pei-Yong Shi

University of Texas, USA

Pei-Yong Shi is John Sealy Distinguished Chair in Innovations in Molecular Biology at University of Texas Medical Branch (UTMB). He works on RNA virus, drug discovery, and vaccine research. His unique expertise in public health laboratory (York State Department of Health), pharmaceutical companies (Novartis and Bristol-Myers Squibb), and academia (UTMB and Yale) allows him to work on both basic and translational research. He has published >300 peer-reviewed papers. His group developed the first reverse genetic systems for the epidemic West Nile virus and Zika virus and discovered flavivirus N7 and 2'O methyltransferase activities. His team also published the first peer-reviewed infectious clone and reporter virus for SARS-CoV-2. Besides academic excellence, he also has a stellar track record of senior leadership role at major pharmaceutical companies (e.g., Executive Director at Novartis Institute for Tropical Diseases) where he set up antiviral strategies and executed drug discovery and development. He contributed to the development of Fostemsavir, an FDA-approved HIV drug. Many of his technologies have been licensed to leading pharmaceutical companies for countermeasure development. A recent example is his reporter neutralization assay that has enabled the rapid development of Pfizer's COVID-19 vaccine, the first vaccine with 95% efficacy in humans.

SARS-CoV-2 Biology and Countermeasure Development

I will present two reverse genetic systems for studying SARS-CoV-2 biology and countermeasure development: 1) a full-length infectious cDNA clone and 2) a trans-complementation system that can be performed at a biosafety level-2 (BSL-2) laboratory. These systems were used to develop a high-throughput reporter neutralization assay to support vaccine development, leading to the approval of the first COVID vaccine from Pfizer/BioNTech. These systems were also used to prepare chimeric SARS-CoV-2 to 1) study the effect of variants on vaccine-elicited neutralizations and 2) provide laboratory dada for supporting a vaccine booster strategy. Finally, I will present mutations in the newly emerged variants that enhance viral replication and transmission.

Zhengli Shi

Wuhan Institute of Virology, CAS, China

Zhengli Shi, Ph.D., researcher. Outstanding postgraduate tutor of the Chinese Academy of Sciences. She is currently the director of the Wuhan Institute of Virology Research Center for Emerging Infectious Diseases, the deputy director of the Wuhan National Biosafety Laboratory (Level 4), the director of the Biosafety Level 3 Laboratory, the director of the Biosafety Working Committee, and the leader of the Emerging Virus Subject Group. She received a bachelor's degree in genetics from Wuhan University in 1987, a master's degree in virology from the Wuhan Institute of Virology, Chinese Academy of Sciences in 1990, and a doctorate in virology from Montpellier University II in France in 2000. She has long been engaged in the etiology research of new viruses and has rich research experience in the etiology, molecular epidemiology and infection mechanism of viruses transmitted by wild animals. Presided over the national major special projects of infectious diseases, the 973 plan, the major projects of the National Natural Science Foundation of China and other ongoing research projects. Published 84 international research papers such as *Nature* and *Science*, including 47 SCI papers, and obtained 3 authorized patents.

Tentative Title of Presentation: Key Factors Involved in Virus Spillover from Wildlife to Humans

Emerging infectious diseases (EID) threat the public health and cause economic losses in human society. More than 70% of the EIDs such as Ebola haemorrhagic fever, Nipah virus encephalitis, severe acute respiratory syndrome and the ongoing COVID-19 pandemic, originate in wildlife. Many factors are involved in the EIDs, which include virus diversity and evolution, ecological changes, land uses, urbanization, global trading and travelling. Wildlife carry enormous viruses which have more and more opportunity to spillover to human society with the increasing land use and decreasing habitats of wildlife. High density of animal and human populations allow the virus to rapidly mutate and adapt, and successfully to invade the human society. Global trading and travelling make the viruses spread without any barriers. In this talk, I'll focus on more the severe respiratory diseases caused by three coronaviruses and discuss how the viruses evolve in their natural reservoirs and transmitted to humans and what we need to do to prevent the next EID in the future.

John Leong

Tufts University, USA

Dr. Leong is Edith Rieva and Hyman S. Trilling Professor and Chair of the Department of Molecular Biology and Microbiology at Tufts University School of Medicine. He is Senior Leadership member of the Stuart B. Levy Center for Integrated Management of Antimicrobial Resistance (CIMAR), Tufts University and Tufts Medical Center. He received his B.A. degree in 1979, his Ph.D. degree in 1985 and his M.D. degree in 1987 from Brown University. His research focuses on the interaction of pathogenic Escherichia coli, Borrelia burgdorferi (the Lyme disease spirochete) and Streptococcus pneumoniae with host immune and epithelial cells in order to understand the infectious process and develop novel therapies to prevent or treat these infections.

Microbial Tools to Characterize Age-Associated Innate Immune Dysfunction

Elderly individuals are particularly susceptible to systemic infection after pulmonary infection by *Streptococcus pneumoniae* (pneumoncoccus), which is characterized by robust alveolar infiltration of polymorphonuclear cells (PMNs). We previously showed that pneumolysin (PLY), a cholesterol-dependent pore-forming toxin, elicits epithelial production of the PMN eicosanoid chemoattractant hepoxilin A3 and acute pulmonary inflammation, leading to systemic infection after pneumococcal lung challenge. Here, we examined *S. pneumoniae*-mediated epithelial barrier disruption using a stem cell-derived air-liquid interphase (ALI) polarized epithelial culture system. Comparison of wild-type and PLY-deficient pneumococcal strains revealed that PLY promotes the disruption of both the apical junctional complex (AJC) and tight junction (TJ), structures that maintain epithelial barrier integrity, resulting in diminished transepithelial electrical resistance and increased transepithelial protein leakage. The combination of PLY and hepoxilin A3-induced PMN transmigration was required for bacterial translocation across ALI monolayers. Upon pulmonary infection of mice, PLY-dependent epithelial junctional disruption and PMN airway infiltration combined to increase lung permeability and promote systemic bacterial spread. Compared to young mice, *S. pneumoniae*-infected aged (20- to 24-month-old) mice experienced higher levels of PMN infiltration, less robust apical junction complexes, and more severe bacteremia. Thus, junctional disruption, mediated by PLY and PMN transmigration, is more severe in aged mice and promotes systemic disease.

Zhaoqing Luo

Purdue University, USA

Dr. Zhao-Qing Luo is a Professor of Biological Sciences at Purdue University. He is the Director of Luo Lab, a center dedicated to researching the mechanisms of various bacterial processes. He received his B.S. degree in 1991 and M.S. degree in 1994 from Beijing Agricultural University and his Ph.D. degree from University of Illinois at Urbana-Champaign in 2001. He received NIH-NIAID Independent Scientist Award (2011-2015) and was selected as Fellow of the American Academy of Microbiology in 2019. He has authored numerous high-impact publications including *Nature*, *Nat. Microbiol*., *EMBO J.*, and *PNAS*. His laboratory is interested in understanding the mechanisms that allow microbial pathogens to survive and multiply within the hostile host cells and how host cells respond to infection.

The ADP-Ribosylation Arsenals of *Legionella pneumophila*

A prominent feature in *Legionella pneumophila* pathogenesis is the hundreds of effectors translocated by its Dot/Icm type IV secretion system, which extensively modulate host function to create an intracellular niche permissive for its replication in phagocytes. Among the extremely diverse biochemical mechanisms displayed by Dot/Icm effectors, ADP-ribosylation has recently emerged as a versatile tool to regulate key cellular processes important for bacterial virulence. For example, our earlier studies have revealed that ADP-ribosylation was used to activate ubiquitin to induce phosphoribosyl ubiquitination and a recent study has demonstrated the targeting of host basic metabolism by inactivating the glutamate dehydrogenase by an ADP-ribosyltransferase. In this presentation, I will discuss our recent finding on the modulation of host energy metabolism by reversible ADP-ribosylation induced by a pair of effectors, which use unique mechanisms to recognize the target proteins and the ADPR moiety. The role of modulating host cell energy production in bacterial virulence will be also discussed.

Yan Feng

Shanghai Jiao Tong University, China

Dr. Yan Feng is Distinguished Professor of Shanghai Jiao Tong University, Deputy Director of State Key Laboratory of Microbial Metabolism, and Executive Director of Chinese Society of Biochemistry and Molecular Biology. Her research interests include molecular enzymology and synthetic biology. By exploring the molecular mechanisms of microbial enzymes such as the relationship between structure and function, high-temperature enzyme stability and substrate specificity, her laboratory has developed new molecular modification strategies such as rational design of enzyme activity center and coevolution of enzyme family, and established mutant libraries superior to natural enzymes to promote the biosynthesis of drugs and natural products. She has published numerous publications including *Nat. Commun., Angew. Chem., JACS, JBC, ACS Synth. Biol.*

Jiangchao Zhao

University of Arkansas, USA

Dr. Jiangchao Zhao has been an assistant professor (April 2015-July 2019) and an associate professor (July 2019 to present) in the Department of Animal Science in University of Arkansas. His research focuses on human and animal microbiome, the collection of all the microorganisms in a specific niche (e.g. gut microbiome), which plays important roles in different aspects of human and animal health. Dr. Zhao's group uses interdisciplinary approaches such as multi-omics (e.g. metagenomics, metatranscriptomics, metabolomics), bioinformatics, statistics, and mixed culture to understand the roles that human and animal microbiome play in health and different diseases. His research mainly focuses on humans, pigs and beef cattle and are interested in, more specifically, the microbiome of the respiratory and GI-tract. Dr. Zhao has published 68 papers including several high-impact papers on human gut microbiome in healthy aging and swine gut microbiome in animal production.

Translating Swine Gut Microbiome Research into Animal Production: Challenges, Opportunities, and Future Directions

The advent of next-generation sequencing has substantially improved our understanding of the animal gut microbiome, which plays essential roles in almost every aspect of animal production such as animal nutrition and health. The ban of growth-promoting antibiotics in production animals has made it crucial to identify alternatives to antibiotics. Modulation of the gut microbiome and development of probiotics are considered efficient ways to replace antibiotics. However, little progress has been made in translating animal microbiome into production due to the lack of basic research and the descriptive nature of most studies. In my presentation, I will discuss these challenges. I will also demonstrate a pathway from basic research, big data analysis to the identification, cultivation, and validation of a probiotic bacterial species that could remarkably increase the growth performance of pigs and be used as alternatives to antibiotics. Our study also shows causality rather than just association between the swine gut microbiome and animal phenotypes. I will also discuss several future directions in this field.

Liping Zhao

Shanghai Jiao Tong University, China

Liping Zhao is currently the Eveleigh-Fenton Chair of Applied Microbiology at Rutgers University and Distinguished Professor of Microbiology at Shanghai Jiao Tong University. He is a fellow of American Academy of Microbiology. He is a senior fellow of Canadian Institute for Advanced Research (CIFAR). He serves on Scientific Advisory Board for the Center for Microbiome Research and Education of American Gastroenterology Association (AGA). His team has pioneered the approach of applying metagenomics-metabolomics integrated tools and dietary intervention for systems understanding and predictive manipulation of gut microbiota to improve human metabolic health. Following the logic of Koch's postulates, Liping has found that an endotoxin-producing opportunistic pathogen isolated from an obese human gut can induce obesity in germfree mice. Their clinical trials published in Science and EBioMedicine showed that dietary modulation of gut microbiota can significantly alleviate metabolic diseases including a genetic form of obesity in children and type 2 diabetes in adults. The Science magazine featured a story on how he combines traditional Chinese medicine and gut microbiota study to understand and fight obesity.

Reference-Free and Ecology-Based Discovery of Microbiome Biomarkers

Gut microbiome is not the "-ome of all microbial genes" but the "biome of all microbes" living in human gut. As a microbial ecosystem, microbiome is a complex adaptive system in which strains, as the most basic building blocks, organize themselves into a higher-level structure called guilds. Guilds are functional units that consist of strains with diverse taxonomic backgrounds yet work together to contribute to community level emergent functions relevant to human health. Co-abundance analysis of amplicon sequence variants (ASVs) of 16S rRNA gene or high-quality draft genomes assembled from metagenomic datasets can help identify key guilds whose ecological behavior correlates with host phenotypes. Different from taxon-based and gene-centric approaches, this strategy does not need any prior databases and can discover ecologically robust microbiome biomarkers.

Sibao Wang

Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS, China

Prof. Sibao Wang received Ph.D. degree from Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences in 2007. He was a postdoctoral research associate in Prof. Raymond St Leger lab at University of Maryland from 2007 to 2009, and a postdoctoral research fellow in Prof. Marcelo Jacobs-Lorena lab at Johns Hopkins University School of Public Health, Department of Molecular and Immunology from 2009 to 2013. From 2013, he is a Principal Investigator and the head of the Laboratory of Vector Insect-Microbe Interactions at Institute of Plant Physiology & Ecology, Chinese Academy of Sciences. Dr. Wang's research interests focus on the molecular interactions between the mosquito, gut microbiome and pathogens, and develop novel strategies to contain the spread of vector-borne diseases.

Mosquito Microbiota and Implications for Disease Control

Malaria is a life-threatening disease caused by *Plasmodium* parasites, which are transmitted to people through the bites of female Anopheles mosquitoes. The mainstay of current malaria control programs relies on insecticide to control vector mosquito population and antimalarial drugs to treat infections. However, the emergence and increasing spread of mosquito insecticide resistance and parasite drug resistance have stalled the progress against malaria over the past few years, and call for new intervention strategies. Blocking malaria parasites in the vector mosquito before they are transmitted to humans is a novel strategy to prevent malaria transmission. As part of this effort, we have been exploring a new strategy, termed paratransgenesis, for controlling transmission of malaria via genetic engineering of mosquito symbionts to deliver antipathogen effector molecules. Whilst engineered symbiotic bacteria have been shown to confer mosquito resistance to parasite infection, a major challenge for field implementation is to address regulatory concerns. To overcome the major roadblock, we recently identified a naturally occurring *Plasmodium*-blocking symbiotic bacterium, *Serratia ureilytica* Su_YN1, isolated from the midgut of wild *Anopheles sinensis* in China that inhibits malaria parasites via secretion of an antimalarial lipase. This bacterium has three important properties: 1) when it colonizes the mosquito gut, it strongly inhibits development of the malaria parasite, while imposing no fitness load to the mosquito; 2) this bacterium is transmitted vertically from female mosquitoes to the progeny and horizontally from male to female mosquitoes, signifying that it can naturally spread through mosquito populations by vertical and horizontal transmission; 3) this bacterium renders mosquitoes resistant to infection by the human parasite *Plasmodium falciparum* or the rodent parasite *Plasmodium berghei* via secretion of a lipase that selectively kills parasites at various stages. These findings show that Su_YN1 provides a potential tool for driving mosquito refractoriness to *Plasmodium* infection and thus blocking malaria transmission in the field.

Session I

Synthetic Biology and Biotechnology

Lixin Zhang

East China University of Science and Technology, China

Prof. Lixin Zhang served as the Director of National Key Laboratory of Bioreactor Engineering at East China University of Science and Technology. His research focused on: Taxonomy guided diversification of a marine microbial natural product library; screening for synergistic medicines in a high throughput manner; increasing the production of drugable secondary metabolites from microbial producers by synthetic biology. His avermectin project won National Award for "Excellence to improve science and technologies". He was a Chief Scientist of a "973 Program" and an Awardee of the National Science Fund for Distinguished Young Scholars, China. He worked in 3 pharmaceutical companies in USA and published seven books, 298 papers and holds 28 Chinese patents and 16 PCT patents. He served as the President of the International Chemical Biology Society (ICBS) during 2016-8. He has been appointed as an Editor-in-Chief for *Synth. Syst. Biotechnol.*, Associate Editor-in-Chief for *Appl. Microbiol. Biotechnol.*, etc. He also served as an Executive Board Member of International Committee on the Biology of Actinomycetes (ISBA) and the GIM (Genetics of Industrial Microorganisms). He is also on the SYNBIOCHEM External Advisory Board for the Manchester Institute of Biotechnology.

Intelligent Manufacturing of Microbial Drugs

Microbial strains are amazingly clever by homeostasis of their own survival and optimization for the accelerated evolution. As an example, the overproduction of a desired phenotype e.g. drugable secondary metabolites is achieved through coordination of key genes overexpression and media optimizations. Besides their pesticide activities, avermectins (AVMs) are identified as potent antibiotic agents for a wide range of drug-resistant pathogens by a high-throughput synergy screening strategy. To rewire the genetic circuitry controlling low yields, we summarized the work on balancing the biological chassis with functional parts, and optimized their dynamical process, as well as predicted favorable effective overproduction of AVMs by 5Ms strategy. The cellular triacylglycerol (TAG) pool enables more carbon flux to be redirected towards polyketide biosynthesis9. AVMs are exclusively made in China now and intelligences learned from the success of AVMs will help transform microbes into a true power-house of innovation.

Jingwen Zhou

Jiangnan University, China

Jingwen Zhou is mainly engaged in microbial metabolic engineering and synthetic biology intensified microbial synthesis of plant natural products and other related research, mainly responsible for the teaching of “metabolic pathway engineering”, “synthetic biology” and other courses. He undertook and completed 10 scientific research projects such as the 863 Program and the National Natural Science Foundation of China Youth/General Project. He has published 98 SCI papers in mainstream authoritative journals in bioengineering and applied microorganisms such as *Microbiol. Mol. Biol. Rev., Trends in Biotechnol., Biotechnol. Adv., Green Chem., Metab. Eng. and ACS Synth. Biol.*, and authorized 32 invention patents. Related work has realized the industrial production of a number of fermented products.

Towards the Customized Production of Flavonoids in Microorganisms

Flavonoids are a group of important phytochemicals that have extensive applications. They could be regarded as the derivatives from naringeine or pinocembrin by a series of enzyme modifications. Production of flavonoids by microorganisms has been extensively investigated in last several decades. Almost all of the common derivative enzymes for flavonoids have been reported, and some of them were applied for the metabolic engineering of microorganisms for the production of complciated flavonoids. Besides, along with the development of metabolic engineering and synthetic biology tools, the titer and the yield of flavonoids production by microorganisms are keeping increasing. Mining of more enzymes from plants and assembly of the more complicated pathways in microorganisms facilitate the production of more flavonoids with higher titer and yield. In order to achieve the efficient biosynthesis of more flavonoids in microorganisms, different modification enzymes from plants that could efficient accumulate corresponding flavonoids with specific modifications have been either chemical synthesized according to transcriptomics data or PCR amplified from cDNA of the plants. These modification enzymes include glycotransferase, hydroxylase, methyltransferase, prenyltransferase, isoflavonoid synthease, etc. By assembling these enzymes with suitable promoters and inserted into the genome of *Saccharomyces cerevisiae* engineered for the enhanced supply of flavonoid precursors *p*-coumaric acid and malonyl-CoA, production of common flavonoids with ideal titer could be achieved. Collection of more enzymes could finally achieve the customized production of flavonoids by microorganisms.

Fuli Li

Qingdao Institute of Bioenergy and Bioprocess Technology, CAS, China

Fuli Li graduated from Lanzhou University in 1998 and obtained his PhD degree in microbiology from the State Key Laboratory of Microbial Technology of Shandong University in 2003. From September 2005 to September 2007, he was engaged in post-doctoral research at the Max Planck Institute of Microbiology in Germany, and from October to December 2009, he conducted collaborative research at the Institute of Microbiology of the Technical University of Munich. First discovered the flavin-based electron disproportionation reaction (Flavin-based electron bifurcation, FBEB; *J. Bacteriol.*, 2008, 190:843). His team is dedicated to the study of microbial biochemistry and molecular biology, especially the catalytic mechanism of polysaccharide degradation enzymes of thermophilic microorganisms, and the construction of high-efficiency cell factories for the production of biofuels. Provide upstream process and technical support for the development of bio-energy.

Ethanol Metabolism Dynamics in *Clostridium ljungdahlii* Grown on Syngas

Carbon one industry flux gas generated from fossil fuels, various industrial and domestic waste, as well as lignocellulosic biomass provides an innovative raw material to lead the sustainable development. Through the chemical and biological processing, the gas mixture composed of CO, CO_2, and H_2, also termed as syngas, is converted to biofuels and high-value chemicals. Bioethanol production from syngas using acetogenic bacteria has attracted considerable attention in recent years. However, low ethanol yield is the biggest challenge that prevents the commercialization of syngas fermentation into biofuels using microbial catalysts. The present study demonstrated that ethanol metabolism plays an important role in recycling NADH/NAD^+ during autotrophic growth. Deletion of bifunctional aldehyde/alcohol dehydrogenase (*adh*E) genes leads to significant growth deficiencies in gas fermentation. Using specific fermentation technology in which the gas pressure and pH were constantly controlled at 0.1 MPa and 6.0, respectively, we revealed that ethanol was formed during the exponential phase, closely accompanied by biomass production. Then, ethanol was oxidized to acetate via the aldehyde ferredoxin oxidoreductase pathway in *Clostridium ljungdahlii*. A metabolic experiment using ^{13}C-labeled ethanol and acetate, redox balance analysis, and comparative transcriptomic analysis demonstrated that ethanol production and reuse shared the metabolic pathway but occurred at different growth phases. Clarification of the mechanism of ethanol oxidation and biosynthesis can provide an important reference for generating high-ethanol-yield strains of *C. ljungdahlii* in the future.

Qiannan Hu

Shanghai Institute of Nutrition and Health, CAS, China

In response to the national strategic needs of healthy China 2030 and the main battlefield of the national economy, Dr. Qiannan Hu is committed to creating a new data-driven synthetic biology innovation model. The team has big data on food, medicine, virus, health, biochemical reaction, biological pathway, etc., enzyme discovery technology based on molecular structure transformation, biological element sequence to function prediction model, biosynthetic pathway design, biosynthetic potential mining, industrial microbial strain optimization, and made outstanding achievements in one-stop design technology integration.

Data-driven *de novo* Biosynthesis Pathway Design Systems

A proliferation of chemical, reaction and enzyme databases, new computational methods and software tools for data-driven rational synthetic biology design have emerged in recent years.

a) Synthetic biology big data: We implemented ChemHub, a knowledgebase containing >90,000 chemicals and their functions, along with related biosynthesis information for these chemicals. We present a web server named as Cell2Chem which accelerates the search for explored compounds in organisms, facilitating investigations of biosynthesis in unexplored chemical spaces. We collected more than 300,000 biochemical reactions, more than 8,000 organisms and more than 60,000 molecules biosynthesized from more than 600,000 biosynthetic/biodegradation publications.

b) Synthetic biology pathway design tools: We built a user-friendly web server, novoPathFinder, to design novel pathways integrated with GEM-models. We established a biological reasoning system for appropriate chassis host selection by coupling with various GEM-models. We developed a user-friendly Web server named EcoSynther to search pathways.

c) Chemo-/Bio-informatics novel tools: We describe Transcriptor, a novel platform for annotating transcripts encoding enzymes. We established a new knowledge base called EnzyMine, through which we propose to elucidate enzymatic reaction features and then link them with sequence and structural annotations. A computational system, BCSExplorer, is proposed to discover the unexplored chemical space using nature's biosynthetic potential. We present Bio2Rxn as a web-based tool to provide putative enzymatic reaction predictions for uncharacterized protein sequences. We present RxnBLAST as a web-based tool for analyzing scaffold transformations and reactive chemical environment features in bioreactions. We present PrecursorFinder, a computational tool that explores biosynthetic precursors for the query target molecules.

d) Data-driven ‘dry’ and ‘wet’ integrative R&D research model achievements: We constructed a novel platform that integrates the technical aspects of toxin biotransformation methods. The synthetic biology design tools have been successfully applied in more than 30 industrial nutrition and health chemical production applications.

Chao Zhong

Shenzhen Institute of Advanced Technology, CAS, China

Chao Zhong joined the School of Material Science and Technology of ShanghaiTech University in July 2014 as an assistant professor. His research field is to integrate the long-term research interests of the bio-inspired molecular engineering laboratory, which is based on the principles of bio-inspired engineering, and is oriented to the major issues of health, energy and environment faced by contemporary society, and is committed to the next generation of bio-inspiration. Development and practical application of materials, bio-nanotechnology or devices. Specifically include the following aspects: 1) the exploration of the intersection of biological and non-biological interfaces and the development of related cutting-edge technologies; 2) the development of new biologically inspired materials, biomimetic nanotechnology and its application in medicine and other important technical fields; 3) Development and application of biologically inspired molecular devices and devices based on molecules, cells and tissues.

“Living” Materials Enabled by Engineered Bacterial Biofilms

Many biological material systems—such as skeletal tissues, marine adhesives and biofilms—grow, self-repair and adapt to the environment and possess distinctive ‘living’ attributes that are beyond the reach of the vast majority of existing synthetic materials. Harnessing these attributes to create dynamic, environmentally responsive, and evolvable ‘living materials’ has been of keen interest and becomes one of the major research focuses in the emerging interdisciplinary field of Materials Synthetic Biology. In this talk, I will introduce our recent efforts in creating a highly flexible and tunable living materials platform based on engineered bacterial biofilms by leveraging the power of synthetic biology. We show that such programmable bacterial biofilms enable a radically different paradigm of materials synthesis and performance, and provide new opportunities for constructing living materials with dynamic and environmentally responsive features. Specific examples demonstrated thus far include but not limited to: 1) programming light-sensing bacterial to fabricate living composites via gradient mineralization of patterned biofilms; 2) creating smart living cellular glues for autonomous damage repairs. Notably, the engineered biofilms have the viscoelastic behaviors of hydrogels and can be precisely fabricated into microstructures having a diversity of three-dimensional (3D) shapes using 3D printing and microencapsulation techniques. This new tunable platform offers previously unattainable properties for a variety of living materials having applications in biomaterials, biotechnology, bioenergy and biomedicine.

Yong Wang

Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS, China

Yong Wang graduated from East China University of Science and Technology with a PhD in 2004. Since January 2005, he has been doing post-doctoral research at Massachusetts Institute of Technology and Tufts University in the United States. Since September 2008, he has been a professor at the State Key Laboratory of Bioreactor Engineering at East China University of Science and Technology; since September 2010, he has been a researcher at the Key Laboratory of Synthetic Biology, Chinese Academy of Sciences. The main research direction is the synthetic biology of natural products: by analyzing the biosynthetic pathways of natural products, using the ideas and methods of synthetic biology, based on engineering design and construction, improving the biosynthesis efficiency of complex natural products and their production methods, The development of natural or non-natural complex natural product active ingredients is the core content of our research.

Yi Xiao

Shanghai Jiao Tong University, China

Dr. Yi Xiao received his BSc from Huazhong University of Science and Technology, China, and PhD from Wuhan Institute of Virology, CAS, China. Yi Xiao's research interests focus on developing biotechnology tools for basic research and applied research. We design and construct genetically-encoded biosensors and CRISPR-associated tools. Using these tools, we modify cell genomes and reprogram cell behaviors to explore metabolism and enhance biosynthesis.

Bioconversion of Lignocellulose-derived *p*-Coumaric and Ferulic Acids into Value-added Aromatic Natural Products

lignocellulose-derived *p*-coumaric and ferulic acids are highly underutilized aromatic renewable resources. There is a need to upgrade them to make them economically feasible. Value-added plant-derived aromatic natural products, are widely used in the nutraceutical, pharmaceutical, and cosmetic industries. However, their complex aromatic structures make their efficient biosynthesis a challenging process. To overcome this issue, we created several novel synthetic cascades to convert *p*-coumaric and ferulic acids to various value-added aromatics, including phenolic glycosides (gastrodin, arbutin, and salidroside), tyrosol, hydroxytyrosol, homovanillyl alcohol, 4-hydroxyphenylacetic acid, homovanillic acid, and 3,4-dihydroxyphenylacetic acid. Because the *p*-coumaric and ferulic acids directly provide aromatic units, these cascades enabled efficient biosynthesis. Given the ubiquity of the aromatic structure in natural products, the use of lignocellulose-derived aromatics should facilitate efficient biosynthesis of numerous aromatic natural products.

Xiao Yi

Shenzhen Institute of Advanced Technology, CAS, China

Xiao Yi was born in Changsha, Hunan. He obtained an undergraduate degree from the Biology Base Class of Sun Yat-Sen University and then went to the United States to study. Under the tutelage of Professor Antony Dean, a molecular evolutionist at the University of Minnesota, he studied population genetics and ecology. During the Ph.D. period, he cooperated with his supervisor to develop a set of new theories on biodiversity and provide evidence through experiments: traditionally believed that seasonal changes that are not important to the formation of biodiversity can actually explain the coexistence of species. In the post-doctoral period, he became interested in the physical and molecular mechanisms of life phenomena, and tried to independently explore the relationship between evolutionary processes and functional mechanisms. During the postdoctoral period, his interest extended to engineering applications: how to use the evolutionary process. Construct an experimental platform to realize the rapid evolution of target proteins in living cells. Next, he hopes to apply this system to solve scientific research or production problems.

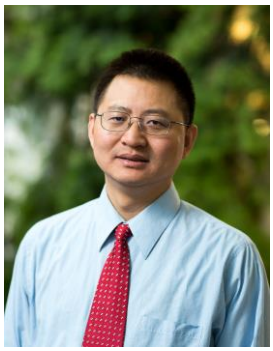
Rapid Evolution of Macromolecules Using a Targeted Artificial DNA Replisome

Extensive exploration of a protein’s sequence space for improved or new molecular functions requires in vivo evolution with large populations. But disentangling the evolution of a target protein from the rest of the proteome is challenging. Here, we designed a protein complex of targeted artificial DNA replisome (TADR) that operates in live cells to processively replicate one strand of a plasmid with errors. It enhanced mutation rates of target plasmid up to 2.3 × 105–fold with only a 78-fold increase in off-target mutagenesis. It was used to evolve itself to increase error rate and increase the efficiency of an efflux pump while simultaneously expanding the substrate repertoire. TADR enables multiple simultaneous substitutions to discover functions inaccessible by accumulating single substitutions, affording potential for solving hard problems in molecular evolution and developing biologic drugs and industrial catalysts.

Session II

Pathogen, Virus and Vaccine

Yongqun He



University of Michigan, USA

Yongqun "Oliver" He, CCMB Affiliate Faculty, Associate Professor of Laboratory Animal Medicine, Associate Professor of Microbiology and Immunology Professor of Microbiology and Chemical Biology. He's primary bioinformatics interests are development of biomedical ontologies and their applications in literature mining, Bayesian network modeling, microbial genomics, and vaccine informatics. His primary wet-lab research interests are in studying microbial pathogenesis and host-pathogen interaction using high-throughput technologies and developing vaccines against intracellular pathogens.

Rational COVID-19 Vaccine Design and Safety Evaluation Using Bioinformatics

The COVID-19 pandemic represents one of the greatest crisis in recent history. The development of successful vaccines within one year represents one of the greatest triumphs in medical history. While existing vaccines are in general successful, the next-generation of COVID-19 vaccines are continuously being pursued, and vaccine safety requires careful investigation.

Reverse vaccinology is a vaccine development strategy that starts with comparative genomics analysis to predict protective vaccine antigens. We have developed the first web-based reverse vaccinology method Vaxign based on the filtering method and recently the Vaxign-ML machine learning method. Using Vaxign and Vaxign-ML methods, we were able to predict the SARS-CoV-2 S protein being the highest ranked protective antigen, which is consistent with the current COVID-19 vaccine development status. Meanwhile, five SARS-CoV-2 non-structural proteins (nsp3, 5, and 8-10) were predicted to be adhesins, which are crucial to the viral adhering and host invasion. The S, nsp3, and nsp8 proteins were also predicted by Vaxign-ML to induce high protective antigenicity. Our further analysis confirmed the potential of nsp3 being a valuable protective antigen for COVID-19 vaccine development. We also propose that an “Sp/Nsp cocktail vaccine” containing a structural protein(s) (Sp) and a non-structural protein(s) (Nsp) would stimulate effective complementary immune responses.

To address the S protein mutations, SARS-CoV-2 S protein may be engineered to contain more immune epitopes. Based on this design, we developed a new structural vaccinology method to rationally design new SARS-CoV-2 S proteins to maintain the same surface structure while updating the core sequence of the S protein so that more T cell epitopes are generated. The maintenance of the surface structure keeps the same antibody epitopes for antibody generation. The addition of new T cell epitopes is hypothesized to enhance T cell responses. These predicted results are worth experimental verification.

To support COVID-19 vaccine annotation and vaccine safety evaluation, the Cov19VaxKB COVID-19 vaccine knowledgebase (http://www.violinet.org/cov19vaxkb) is developed. Cov19VaxKB stores COVID-19 vaccine adverse event case reported downloaded from the VAERS database and allows users to perform dynamic statistical analysis to find statistically enriched vaccine adverse events.

Chan Ding

Shanghai Veterinary Research Institute, CAAS, China

Chan Ding, Deputy Director and doctoral Supervisor of Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences, received his doctorate in microbiology/biochemistry from Yamaguchi University in Japan. His team's main research interests are: Newcastle disease virus and its evolutionary mechanism, the interaction mechanism between avian viruses such as infectious bronchitis virus and host, and the construction of new vaccines based on the reverse genetic system of Newcastle disease virus. He has successively presided over and participated in 35 key projects of the National 13th five-year Plan, National Natural Science Foundation and 863 projects, and won 7 provincial and ministerial awards. More than 300 research papers have been published in professional journals at home and abroad, of which more than 100 have been collected by SCI and 4 monographs have been published.

Newcastle Disease Virus Degrades SIRT3 via PINK1-PRKN Dependent Mitophagy to Reprogram Energy Metabolism in Infected Cells

Lacking a self-contained metabolism network, viruses have evolved multiple mechanisms for rewiring the metabolic system of their host to hijack the host’s metabolic resources for replication. Newcastle disease virus (NDV) is a paramyxovirus, as an oncolytic virus currently being developed for cancer treatment. However, how NDV alters cellular metabolism is still far from fully understood. In this study, we show that NDV infection reprograms cell metabolism by increasing glucose utilization in the glycolytic pathway. Mechanistically, NDV induces mitochondrial damage, elevated mitochondrial reactive oxygen species (mROS) and ETC dysfunction. Infection of cells depletes nucleotide triphosphate levels, resulting in elevated AMP:ATP ratios, AMP-activated protein kinase (AMPK) phosphorylation, and MTOR crosstalk mediated autophagy. In a time-dependent manner, NDV shifts the balance of mitochondrial dynamics from fusion to fission. Subsequently, PINK1-PRKN-dependent mitophagy was activated, forming a ubiquitin chain with MFN2 (mitofusin 2), and molecular receptor SQSTM1/p62 recognized damaged mitochondria. We also found that NDV infection induces NAD+-dependent deacetylase SIRT3 loss via mitophagy to engender HIF1A stabilization, leading to the switch from oxidative phosphorylation (OXPHOS) to aerobic glycolysis. Overall, these studies support a model that NDV modulates host cell metabolism through PINK1-PRKN-dependent mitophagy for degrading SIRT3.

Chao Gao

Shandong University, China

Chao Gao, professor of State Key Laboratory of Microbial Technology (Microbial Technology Institute), Shandong University, got his bachelor and Ph.D. degree in Shandong University. After graduation from Shandong University in 2009, he performed his postdoctoral work in Shanghai Jiao Tong University from 2009 to 2012. His research interests include microbial physiology and biochemistry, microbiome and metabolic interaction, synthetic biology and biocatalysis. He has published many research papers in famous magazines such as *Nat. Commu.*, *Proc. Natl. Acad. Sci. U. S. A.*, *Green Chem.*, *ACS Sustainable Chem. Eng.*, etc.

Microbial 2-Hydroxyglutarate Metabolism

2-Hydroxyglutarate (2-HG) accumulation may promote the tumorigenesis and carcinogenesis of numerous cancers. It was thus previously viewed as an abnormal metabolite with no physiological function and 2-HG conversion to 2-ketoglutarate by 2-HG dehydrogenase seems to be a process of metabolite repair. However, we recently revealed that 2-HG production in microorganisms is not meaningless without physiological purpose. 2-HG production actually participates in many core metabolic processes like L-serine production and L-lysine catabolism. This oral presentation summarizes our recent researches related to the diverse distributed microbiol metabolic processes involving 2-HG (*Proc. Natl. Acad. Sci. U.S.A.* 2017, 114:E7574; *J. Biol. Chem.* 2018, 293:15513), the regulation mechanism of 2-HG metabolism (*Nat. Commun.* 2018, 9:2114) and development of 2-HG biosensors for the clinical quantitation of 2-HG (*mBio.* 2019, 10:e1570-19; *Nat. Commun.* 2021, 12:3619).

Qiyao Wang

East China University of Science and Technology, China

Wang Qiyao, Ph.D., professor and doctoral supervisor of State Key Laboratory of Bioreactor Engineering. He is currently the vice Dean of School of Biotechnology, East China University of Science and Technology. He is also a part-time researcher at Qingdao National Laboratory of Marine Science and Technology. He was selected as the scientist and functional director of disease prevention and control post in National Marine-culture Industries of China Agricultural Research System, Shanghai Science and Technology Star Talent Plan, Shanghai Pujiang Talent Plan, and a member of the 2nd Expert Committee on Aquaculture Disease Prevention and Control of the Ministry of Agriculture. From December 2013 to December 2014, he was a visiting scholar in Harvard Medical School/Howard Hughes Medical Research Institute. He is an associate editor of Microbiol. Res. At present, he has published more than 80 academic papers and granted 20 patents in magazines such as Proc. Natl. Acad. Sci. U.S.A., *Nat. Commun.*, *iScience*, *Nucleic Acids Res.*, *PLOS Pathog.*, *mBio.*, *Environ. Microbiol*. His team has been licensed two Class I vaccines against fish diseases.

Edwardsiella Piscicida Functional Genomics Investigation Illuminates Pathogenesis and Strategies for Heuristics Vaccine Design

Edwardsiella piscicida is a leading bacterial pathogen threatening worldwide aquaculture industries. Illuminating the genes essential for its in vivo growth and combating the stressful niches is important for understanding its pathogenesis and therapeutics development. We have devised pattern analysis of gene essentiality (PACE) algorithm combined with transposon insertion sequencing technology (TIS) to globally explore in vivo conditional essential genes as well as their fitness patterns that is useful for heuristics vaccine design. In addition, we identified several novel regulators and interrogated their regulatory mechanisms on the key virulence determinants including Type III and VI secretion systems (T3/T6SS). We highlighted a novel nucleoid associated protein (NAP) EnrR that is putatively horizontally acquired and a unique NAP playing a role as an H-NS-antagonizing virulence activator and provided insights into the mechanisms by which EnrR recognizes AT-rich DNA. We showed that bacteria have evolved to leverage xenogeneic regulator to recognize foreign DNA and fine tune their expression.

Luyan Ma

Institute of Microbiology, CAS, China

Luyan Ma, professor of Molecular Microbiology, Institute of Microbiology, Chinese Academy of Sciences, graduated from the School of Biology of Beijing Agricultural University in 1991, received her Doctor of Science degree from China Agricultural University in 1996, and was employed as an associate professor in the Department of Microbiology of China Agricultural University in 1999. She has worked as a postdoctoral and senior visiting scholar at the Institute of Pasteur in France, Connecticut University and Wake Forest University in the United States. She has worked at Ohio State University since 2008, and has been engaged in the study of the molecular mechanism of bacterial biofilm. Her primary research interests are to explore and define molecular mechanisms for biofilm persistence and eventually to design therapies for control of biofilm-related complications in medical, industrial, and environmental settings. The current research focuses are: 1. how does a biofilm matrix form? 2. the role of extracellular proteins in biofilm formation and persistence; 3. programmed cell death and autolysis in biofilms; 4. the biofilms of nitrogen-fixing bacteria and its applications.

Intracellular Glycosyl Hydrolase Pslg Shapes Bacterial Cell Fate, Signaling, and the Biofilm Development of *Pseudomonas Aeruginosa*

Biofilm formation is one of most important causes leading to persistent infections. Exopolysaccharides are usually a main component of biofilm matrix. Genes encoding for glycosyl hydrolases are often found in gene clusters that are involved in the exopolysaccharide synthesis. It remains elusive about the functions of intracellular glycosyl hydrolase and why a polysaccharide synthesis gene cluster requires a glycosyl hydrolase. Here we systematically studied the role of intracellular PslG, a glycosyl hydrolase that is co-transcribed with 15 *psl* genes, which is responsible for the synthesis of exopolysaccharide Psl (ePsl), a key biofilm matrix polysaccharide in opportunistic pathogen *Pseudomonas aeruginosa*. We showed that lacking of PslG in this opportunistic pathogen alters the signaling function and structure of ePsl, changes the relative level of cyclic-di-GMP within daughter cells during cell division and shapes the localization of ePsl on bacterial periphery, thus results in long chains of bacterial cells, fast-forming and compact biofilm microcolonies. Our results reveal the important roles of intracellular PslG on the cell fate and biofilm development.

Jianping Xie

Southwest University, China

Jianping Xie, professor of School of Life Sciences, Southeast University, got his Ph.D. in Fudan University in 2002. He is mainly engaged in the study of pathogenic mechanism of microorganism and new drugs development. His scientific research includes: 1) Mechanism of pathogenicity and drug resistance, new vaccines or drugs, new diagnostic techniques and methods of *Mycobacterium tuberculosis* and other main pathogenic bacteria in human and economic animals. 2) System biology study on regulation of key metabolites of important *i*ndustrial microorganism. 3) Construction and application of expression *s*ystem of *Saccharomyces cerevisiae* and other genetically engineered drug-producing microorganisms.

Novel Biomarkers for Tuberculosis Diagnosis and Treatment Management Tailored for Chinese Population

Tuberculosis (TB) remains a formidable public health threat. Precise and prompt diagnosis and monitoring of treatment responses are urgently needed for clinical management. To pursue novel biomarkers meet the World Health Organization (WHO) and Foundation for Innovative New Diagnostics (FIND) target product profiles (TPPs) for non-sputum-based diagnostic tests for the diagnosis of active tuberculosis (ATB) disease and for predicting the progression from latent tuberculosis infection (LTBI) to ATB, we customized a bioinformatic pipeline by integrating differentially expressed genes, a gene co-expression network, and short time-series analysis to mine the published transcriptomes derived from whole blood of TB patients in the GEO database, followed by validating the diagnostic performance of biomarkers in both independent datasets and blood samples of Chinese patients using quantitative real-time PCR (qRT-PCR). We shortlisted four genes, namely UBE2L6 (Ubiquitin/ISG15-conjugating enzyme E2 L6), BATF2 (Basic leucine zipper transcriptional factor ATF-like), SERPING1 (Plasma protease C1 inhibitor), and VAMP5 (Vesicle-associated membrane protein 5), which had high diagnostic value for active TB. The transcription levels of these four gene combinations can reach up to 88% sensitivity and 78% specificity (average) for the diagnosis of active TB; the highest sensitivity can achieve 100% by parallel of BATF2 and VAMP5, and the highest specificity can reach 89.5% through a combination of SERPIG1, UBE2L6, and VAMP5, which were significantly higher than 75.3% sensitivity and 69.1% specificity by T-SPOT.TB in the same patients. Quite unexpectedly, the gene set can assess the efficacy of anti-TB response and differentiate active TB from Latent TB infection. The data demonstrated these four biomarkers might have great potency and advantage over IGRAs in the diagnosis of TB.

Nan Song

Beijing Institute of Tropical Medicine, China

Nan Song, Ph.D. trained at Tsinghua University from 2006-2012. Then he worked at the Academy of Military Medical Sciences as a Postdoc under the supervision of Prof. Xue-Min Zhang, and pursued studies of key regulations of the host innate immune responses, with a major emphasis on the post-translational modifications of NLRP3 and MAVS. In June 2018, Dr. Song moved to the Beijing Institute of Topical Medicine, Capital Medical University. As an independent principal investigator, he continues to pursue studies aimed at elucidating the identification, distribution, structure, role and impact of diverse bacterial toxins that are involved in infectious diseases.

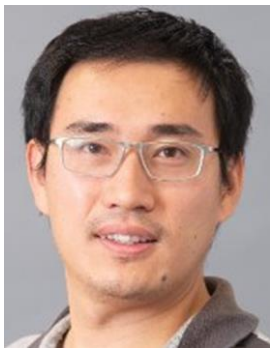
Tc Toxin: a Versatile Weapon Targeting Mammals

Bacterial toxin plays a critical role during pathogen infections, thus characterization of the pathogenic mechanism of bacterial toxins will facilitate the prevention and control of the related infectious diseases. Toxin complex, also referred to as Tc toxin, is an ABC-type toxin that is firstly characterized in entomopathogenic bacteria *Photorhabdus* in 1998. We have performed a comprehensive genome- wide analysis, and established a database that includes 1,608 identified Tc loci containing 2,528 TcC proteins in 1,421 bacterial genomes. We found that Tc toxins are widely distributed among Gram-negative and positive bacterial genomes. Our findings reveal that, as a new polymorphic toxin systems, Tc toxins encode hundreds of different toxic domains, including over 100 as yet uncharacterized domains. By a higher resolution analysis of TcC proteins identified in genomes of *Salmonella* and *Yersinia* strains, we proposed a two-level evolutionary process that can explain the taxonomical specific distribution pattern of TcC HVRs.

Structural analysis revealed that TcA can form homopentamer that mediates the cellular recognition and delivery processes, thus contributing to the host tropism of Tc toxin. We performed two independent genome-wide CRISPR-Cas9 screens, and have validated glycans and sulfated glycosaminoglycans (sGAGs) as Tc toxin receptors. Based on the Tc database we previously established, we have analyzed all available TcA homologues, and classified them into 5 subfamilies, which show a good correlation with the taxonomic origin of the genomes. In the current study, we have identified a series pathways that can mediate the host targeting of Tc toxins, offering the potential to decipher the host specificity and possible future biomedical applications of Tc toxins.

Donglei Sun

Shanghai Jiao Tong University, China



Donglei Sun, Associate Professor of School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, got his doctorate in University of Maryland, College Park in 2018 and worked as a post doctor from 2018 to 2020. His research interests are immunity, infection and major diseases. With monocytes/macrophages as the center, a variety of imaging techniques were used to study the recruitment, differentiation and function of monocytes/macrophages from different sources in animal disease models. Another research direction is the regulation and intervention of monocyte/ macrophage function to make it function effectively while avoiding tissue damage. He has published many papers in important magazines such as *Nat. Commun.*, *Proc. Natl. Acad. Sci. U.S.A*.

Advanced Imaging Reveals the Fungal Pathogen *Cryptococcus Neoformans* Invade The Brain via a Proliferation Dependent Manner

Cryptococcus neoformans is the causative agent of fatal cryptococcal meningoencephalitis. How the fungal pathogen crosses the blood brain barrier (BBB) has been one of the leading questions in the field. Previous studies used transwell assays to evaluate fungal brain transmigration and proposed multiple theories. Our lab, taking advantage of advanced imaging methods especially intravital microscopy, provided a brand-new view of this critical process and proposed a theory that is different than existing theory. We found that most mother cells do not physically transmigrate, instead, the daughter cells transmigrate across the capillary vessels after proliferation. The initially trapped mother cells disrupt the BBB structure within the capillary vessel allowing the daughter cells to grow directly into the brain parenchyma. In addition, we found brain microglial cells are recruited to the fungi rapidly, a process requiring fungal phospholipase B and capsule production. Interestingly, microglia do not respond to the fungi themselves, but to the leaking blood vessel. Cell depletion further confirmed the negative role of microglia during fungal brain invasion. Conclusively, this work provided a brand-new view of fungal brain invasion using advanced imaging techniques.

Session III

Applied and Environmental Microbiology

Shuangjiang Liu

Institute of Microbiology, CAS, China

Shuangjiang Liu, researcher, served as director of Institute of Microbiology, Chinese Academy of Sciences; Director of Environmental Biotechnology Center; Deputy Secretary of the Party committee and director of the Environmental Biotechnology Center. Winner of national fund for Distinguished Young Scholars and winner of "Hundred Talents Program" of Chinese Academy of Sciences. The environmental microbiology research group focuses on the microbial transformation and degradation of aromatic compounds, the microbial transformation of sulfur under extreme acid and heat conditions, microbial diversity and bioremediation technology in specific environment, and carries out the research on the relationship between microorganisms and environment, as well as the research on environmental biotechnology based on microbiology theory. Remarkable achievements have been made in the microbial degradation of aromatic compounds and their application in the treatment of polluted environment. More than 60 SCI articles and 2 authorized patents have been published in domestic and foreign magazines.

Xihui Shen

Northwest A&F University, China

Shen Xihui, Professor, is mainly engaged in the research of agricultural and environmental microbiology. He has made outstanding achievements in the functional research and effector protein identification of bacterial six type secretion system, bacterial biofilm formation and motility regulation, plant symbiotic microbiome and its growth promoting and drought resistance function on crops, and the degradation mechanism of aromatic compounds. Academic leader of agricultural and environmental microbiology research team, academic backbone of State Key Laboratory of Crop Stress Biology for Arid Areas, first candidate of "youth talent training program" of Northwest University of agriculture and forestry science and technology, and approved the project of National Science Fund for distinguished young people in 2017. He served as a member of the general microbiology Professional Committee of the Chinese society of Microbiology, CO editor of the special issue of *Front. Microbiol.*, an international journal, and reviewer of more than ten international journals of microbiology. He was invited to make general assembly reports and keynote reports at international and domestic academic conferences for many times.

T6SS Secretes an LPS-binding Effector to Recruit OMVs for Exploitative Competition and Horizontal Gene Transfer

Outer membrane vesicles (OMVs) can function as nanoscale vectors that mediate bacterial interactions in microbial communities. How bacteria recognize and recruit OMVs inter-specifically remains largely unknown, thus limiting our understanding of the complex physiological and ecological roles of OMVs. Here, we report a ligand-receptor interaction-based OMV recruitment mechanism, consisting of a type VI secretion system (T6SS)-secreted lipopolysaccharide (LPS)-binding effector TeoL and the outer membrane receptors CubA and CstR. We demonstrated that *Cupriavidus necator* T6SS1 secretes TeoL to preferentially associate with OMVs in the extracellular milieu through interactions with LPS, one of the most abundant components of OMVs. TeoL associated with OMVs can further bind outer membrane receptors CubA and CstR, which tethers OMVs to the recipient cells and allows cargo to be delivered. The LPS-mediated mechanism enables bacterial cells to recruit OMVs derived from different species, and confers advantages to bacterial cells in iron acquisition, interbacterial competition and horizontal gene transfer (HGT). Moreover, our findings provide multiple new perspectives on T6SS functionality in the context of bacterial competition and HGT, through the recruitment of OMVs.

Tao Dong

Shanghai Jiao Tong University, China

Dong Tao is a professor of Shanghai Jiao Tong University. He is now the Chair of the Department of Biochemistry and Molecular Biology. He has successively served as an assistant professor and associate professor at Ph.D., Harvard University and the University of Calgary Study and work. His research focus is on the molecular adaptation mechanism of bacteria in uncomfortable environment and complex flora environment. His main research directions include: 1) The mechanism of competition between bacteria and the role of protein secretion system; 2) The mechanism and solution of drug resistance; 3) The regulation mechanism of environmental adaptability regulatory factors; 4) Using synthetic biological means to develop tools for the study of environmental adaptability and pathogen treatment mechanism.

Avoiding Traffic Jam: Quantity Control of the Type VI Secretion System Substrates in Response to the Functional Status

The type VI secretion system (T6SS) is a widespread spear-like molecular machine that can translocate diverse toxic effectors into eukaryotic and prokaryotic neighboring cells. The T6SS spear consists of a long hexameric tube Hcp and a spike complex made of a VgrG trimer and a cone-shaped PAAR protein. Effectors are often loaded to the T6SS secretion apparatus through direct interaction with the spear proteins PAAR, VgrG, and Hcp. T6SS secretion is an energetically expensive process costing several hundred copies of the carrier protein Hcp per secretion event, to deliver just a few effector proteins. Therefore, it is important to control the secretion process to adjust to the changing cellular demand. Here we report two key regulatory mechanisms that ensure effectors are loaded prior to secretion and prevent the wasteful accumulation of secreted proteins when the T6SS is inactivated, respectively. Such regulation is crucial to ensure the efficiency of the T6SS and the resulting fitness in T6SS-mediated interspecies competition.

Jiandong Jiang

Nanjing Agricultural University, China

Jiandong Jiang, Professor, Dean of School of life sciences, Nanjing Agricultural University, mainly focuses on environmental and soil microbiology, and his research direction is microbial degradation and remediation of pesticide persistent organic pollutants. Presided over national key R & D special projects, National Natural Science Foundation of China (excellent youth, China Israel international cooperation project, China Europe international cooperation project), Jiangsu outstanding youth fund, New Century Excellent Talents Project of the Ministry of education, National 863 high tech plan project, social development project of Jiangsu Science and technology support plan and other projects, and published more than 70 papers in domestic and foreign journals, As the first author or corresponding author, he has published more than 80 papers in SCI journals such as *ISME J.*, *Mol. Microbiol.*, *Environ. Microbiol.*, *J. Bacteriol.*, *Appl. Environ. Microbiol.*, and won the second prize of National Scientific and Technological Progress Award (the 9th finisher), the second prize of Technological Invention Award of the Ministry of Education (the 5th finisher) and the third prize of Bumper Harvest of Agriculture, Animal Husbandry and Fishery of the Ministry of Agriculture (item 8) 1 each.

Redundancy of 4-Hydroxybenzoate 3-Monooxygenase Genes Ensures the Catabolic Safety of 4-Hydroxybenzoate in *Pigmentiphaga* sp. H8

Genetic redundancy is prevalent in organisms and its selective advantages have caused great interests of many biologists. In this study, three redundant 4-hydroxybenzoate-3-monooxygenase (PHBH) genes (phbh1, phbh2 and phbh3), were found in the versatile halo-aromatics degrading strain of *Pigmentiphaga* sp. H8, which catabolized 3-Br-4-HB via the unexpected protocatechuic acid pathway. Comparative transcriptome and proteome analysis showed that phbh1 and phbh2 instead of pbbh3 were significantly up-regulated in the presence of 3-bromo-4-hydroxybenzoate (3-Br-4-HB). Genetic, physiological and biochemical assays confirmed that PHBH1 and PHBH2 were mostly responsible for the catabolism of 3-Br-4-HB, while PHBH3 was primary for the catabolism of 4-hydroxybenzoate (4-HB), the abundant compound in nature. In vitro and in vivo assays showed that 3-Br-4-HB inhibited the 4-HB catabolic activity of PHBH3, while this inhibition could be relieved due to the removal of 3-Br-4-HB catalyzed by PHBH1 and PHBH2. Therefore, the selective advantages of the genetic redundancy of phbh1 and phbh2 were to enhance the adaptability of strain H8 to environments mixed with 3-Br-4-HB and ensure the catabolic safety for the important compound 4-HB.

Jidong Gu

Guangdong Technion-Israel Institute of Technology, China

Jidong Gu, Professor, has long been engaged in the research on pollutant degradation, microbial metabolism and metabolic pathway, molecular mechanism of biological fouling and new biological control methods, and has accumulated rich experience in the fields of microbial degradation, biological corrosion, degradation and fouling control. Especially in the degradation of phthalate lipids and polycyclic aromatic hydrocarbons, which is a hot environmental topic in the world, it is at the international forefront.

New Microbial Nitrogen Transformation Reactions on the Old Angkor Monuments

Sandstone monuments/temples of the Angkor Empire in the Southeast Asia are important UNESCO World Cultural Heritage. Majority of these monuments suffer severe deterioration from weathering caused by a combination of physical, chemical and (micro)biological processes. Current information on deterioration of sandstone is mainly driven by emerging technologies, including DNA sequencing for community composition as an example, but the mechanisms to the damage of these temples/monuments are still lacking. In this presentation, the latest discoveries on high concentration of nitrate and accumulation on these temples are presented with the microbial reactions responsible and a conceptual framework to explain this phenomenon by multiple groups of microorganisms to maintain a surface colonized biofilm community. Ammonia-oxidizing archaea (AOA), ammonia-oxidizing bacteria (AOB) and complete ammonia oxidation (Comammox) bacteria oxidize ammonia/ammonium to nitrite/nitrate and, at the same time, sequest CO_2 onto the stone as biomass, and this process is in turn supported by dissimilatory nitrate reduction to ammonium (DNRA) to provide the substrate ammonia/ammonium from abundant nitrate available for a cyclic reaction to take place continuously between ammonium/ammonia and nitrate. This internal N cycle modifies the surface properties of stone and promote colonization of diverse microorganisms over time. In addition to the metagenomics and transcriptomics, stable isotope N-15 analysis was performed to gain further insights on the multiple reactions involved. Because of these, an innovative approach is required to understand the mechanisms involved for protection of Angkor sandstone temples and architecture.

Haihua Liang

Southern University of Science and Technology, China

Haihua Liang is a Professor at Southern University of Science and Technology. He works on the functional genomics, pathogenicity and drug resistances of pathogenic bacteria. He focuses on the two important signal systems in Pseudomonas aeruginosa, quorum sensing system and second messenger signal molecules(c-di-GMP). He has published more 40 papers in the international journals, such as *PNAS*, *EMBO J.*, *Nucleic Acids Res*., *JACS* and *Elife*.

Kun Zhao

Tianjin University, China

Kun Zhao, Professor, School of Chemical Engineering and Technology, Tianjin University. Dr. Zhao received his Bachelor’s degree in Physics from Beijing University in China and earned his Ph.D. in Condensed Matter Physics at Princeton University. After receiving his doctorate, he trained as a postdoctoral fellow at the University of California, Los Angeles, where he investigated complex pattern formation in two model systems: complex fluids of anisotropic shaped colloids and biofilms. In 2014, he joined Tianjin University as a Professor in the School of Chemical Engineering and Technology. Now he is the project leader of the national key R & D plan, mainly engaged in cutting-edge cross research in the field of soft matter physics and microbiology.

MSHA Pili-assisted Surface Landing of *Vibrio cholerae* in a Viscoelastic Environment

Mannose-sensitive hemagglutinin (MSHA) pili and flagellum are critical for the surface attachment of *Vibrio cholerae*, a human pathogen that causes the debilitating disease cholera. However, the cell landing mechanism remains largely unknown, particularly in viscoelastic environments such as the mucus layers of intestines. In this talk, I will show our recent work on quantitatively characterizing the landing of *V. cholerae* by directly observing both pili and flagellum of cells in a viscoelastic solution consisting of 2% Luria-Bertani and 1% methylcellulose (LB+MC). We found that MSHA pili are evenly distributed along the cell length. More interestingly, MSHA pili are observed to act as a brake and anchor during cell landing which include three phases: running, lingering, and attaching. Importantly, loss of MSHA pili results in a more dramatic increase in mean path length in LB+MC than in 2% LB only or in 20% Ficoll solutions, indicating that the role of MSHA pili during cell landing is more apparent in viscoelastic fluids than viscous Newtonian ones. Our work provides a detailed picture of the landing dynamics of *V. cholerae* under viscoelastic conditions, which can provide insights into ways to better control *V. cholerae* infections in real mucus-like environment.

Qian Wang

Shandong University, China

Qian Wang, a doctoral supervisor of Shandong University, graduated from Shandong Agricultural University with a bachelor's degree, and graduated with a Ph.D. from the State Key Laboratory of Microbial Technology of Shandong University. From 2015 to 2020, she served as an associate professor of the National Sugar Engineering Technology Research Center of Shandong University, and is currently a professor and doctoral supervisor of the National Sugar Engineering Technology Research Center of Shandong University. In 2016, she was selected as the talent support program of Shandong University "Young Scholars Future Plan".

Design, Construction and Precise Dynamic Control of an Unnatural Glycolysis Pathway

The existing natural pathways, such as the phosphoketolase pathway and the synthetic non-oxidative glycolysis (NOG) pathway, can avoid the decarboxylation of pyruvate, completely converting glucose into acetyl-CoA, and reduce the release of CO_2. However, it cannot satisfy cell growth and cannot provide reducing power, thus they are difficult to be applied for chemicals production. Through the analysis of the E. coli metabolic network, combining the pentose phosphate pathway, EMP pathway and bifid shunt, we designed and constructed an artificial glycolysis "EP-bifido pathway". In this pathway, bi-functional phosphoketolase Fxpk from bifidobacteria was introduced, 6-phosphofructokinase PfkA, phosphogluconate dehydratase Edd and acetate kinase AckA were knocked out. Through 13C metabolic flux analysis and CO_2 detection, the effectiveness of the EP-bifido pathway was verified. To verify this approach, this pathway was applied for PHB, mevalonate and fatty acid production. Meanwhile, a glycolysis biosensor was constructed for dynamic control and optimize the "EP-bifido pathway", achieving the precise tuning of central carbon metabolic flux. Our study provided an effective strategy to realize the effective adaptation of unnatural heterologous pathways to the host's natural pathways.

Session IV

Antibiotics & Resistance

Xingmin Sun

University of South Florida, USA

Dr. Xingmin Sun is an Associate Professor with tenure in the Department of Molecular Medicine, College of Medicine at the University of South Florida (USF). He holds courtesy appointments in the Department of Internal Medicine, Department of Cell Biology, Microbiology & Molecular Biology, Department of Chemistry at USF and USF Genomics. He was an NIH (National Institutes of Health) Career Development K01 Awardee. he served as an associate editor for *Mol. Med.*, associate topic editor for *Front. Microbiol.*, and editorial boards for *Infect. Immun.* and *Appl. Environ. Microbiol*. He received the “Tufts Institute for Innovation Inaugural Award” in 2014. He chaired the Research Committee of College of Medicine at USF from 2019 to 2020. In 2018, he was awarded the "Faculty Outstanding Research Achievement Award" at USF. In 2019, he was awarded the "Excellence in Innovation Award" at USF.

Antibiotic Resistance of *Clostridioides difficile*

Clostridioides difficile is one of the top five urgent antibiotic resistance threats in USA. There is a worldwide increase in multidrug resistance (MDR) of *C. difficile*, with emergence of novel strains which are often more virulent and MDR. Antibiotic resistance in *C. difficile* is constantly evolving with acquisition of novel resistance mechanisms, which can be transferred between different species of bacteria and among different *C. difficile* strains present in the clinical setting, community, and environment. Therefore, understanding the antibiotic resistance mechanisms of *C. difficile* is important to guide optimal antibiotic stewardship policies and to identify novel therapeutic targets to combat *C. difficile* as well as other bacteria. Epidemiology of *C. difficile* is driven by the evolution of antibiotic resistance. Prevalence of different *C. difficile* strains and their characteristic resistomes show distinct global geographical patterns. Understanding epidemiologically driven and strain-specific characteristics of antibiotic resistance is important for effective epidemiological surveillance of antibiotic resistance and to curb the inter-strain and -species spread of the *C. difficile* resistome. *C. difficile* has developed resistance to antibiotics with diverse mechanisms such as drug alteration, modification of the antibiotic target site and extrusion of drugs via efflux pumps. In this talk, I will summarize the most recent advancements in the understanding of mechanisms of antibiotic resistance in *C. difficile* and analyze the antibiotic resistance factors present in genomes of a few representatives well known, epidemic and MDR *C. difficile* strains found predominantly in different regions of world.

Liangdong Lyu

Fudan University, China

Liangdong Lyu is an Associate Professor in Shanghai Medical College of Fudan University. He works on Mycobacterium and Escherichia coli to develop persistent infection, drug tolerance mechanism and bacterial resistance. He has published many articles in international journals such as *PNAS, PLoS Pathog., EMI* and *JBC*.

Metabolic Regulation of *Mycobacterial* Persistence

The ability to remodel the metabolism within the host environment is critical for *Mycobacterium tuberculosis* (Mtb) to persist in the face of prolonged multidrug therapy and immune response. Increasing evidence indicates that maintaining the integrity of cell envelops and genetic content is a pivotal function of mycobacterial metabolic adaptation. Host-derived fatty acids are an important carbon source for pathogenic mycobacteria during infection. We identified a TetR-family transcriptional factor, FdmR, as the key regulator of fatty acid catabolism in the pathogen *Mycobacterium marinum*. We found that the *fdmR*-deficient mutant of *M. marinum* was severely attenuated in zebrafish larvae and adult zebrafish. FdmR was identified as a long-chain acyl-coenzyme A (acyl-CoA)–responsive repressor of genes involved in fatty acid degradation and modification. By combining use of transcriptomics, chromatin immunoprecipitation followed by sequencing, dynamic ^{13}C-based flux analysis, metabolomics, and lipidomics, we found that FdmR suppresses degradation of long-chain acyl-CoAs endogenously synthesized through the type I fatty acid synthase. By modulating the supply of long-chain acyl-CoAs for lipogenesis, FdmR controls the abundance and chain length of virulence-associated lipids and mycolates and plays an important role in the impermeability of the cell envelope. Deficiency of *fdmR* results in increased susceptibility to hydrophobic antimicrobials. In another study, we showed that prevention of DNA double-strand breaks (DSBs) through elimination of oxidation of dCTP by *mazG*-encoded (d)NTP pyrophosphohydrolase underlies antibiotic tolerance of stationary-phase mycobacteria. Deletion of *mazG* in Mtb or *Mycobacterium smegmatis* potentiates antibiotic killing of stationary-phase bacilli, but did not affect antibiotic efficacy in exponentially growing cultures. Critically, the effect of *mazG* deletion on potentiating antibiotic killing is associated with antibiotic-induced ROS and accumulation of lethal DSBs. We provided genetic evidence that 5-OH-dCTP is incorporated into genomic DNA via error-prone DNA polymerase DnaE2 and repair of 5-OH-dC lesions via the endonuclease Nth leads to the generation of lethal DSBs. Therefore, understanding of the ultimate mechanism underlying bacterial survival by metabolism adaptation may provide us new targets for the development of anti-tuberculosis strategies.

Xiaofei Jiang

Huashan Hospital, Shanghai Medical College, Fudan University, China

Xiaofei Jiang, Researcher, doctoral supervisor, head of the microbiology group of the Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University. He has published more than 60 articles in academic journals at home and abroad. He participated in the editing of "National Clinical Laboratory Operation Manual (Fourth Edition)", "Standardized Operation of Clinical Microbiology Laboratory (ISO15189 Accreditation Guide)", "Laboratory Diagnosis and Clinical Treatment of Bloodstream Infections" and many other monographs. Now he is a member of the editorial board of "Laboratory Medicine".

Jie Feng

Institute of Microbiology, CAS, China

Jie Feng is a Professor in the Institute of Microbiology of the Chinese Academy of Sciences (IMCAS). Dr. Jie Feng's group at State Key Laboratory of Microbial Resources of IMCAS focuses on the research of diversity and dispersion of antibiotics resistance in environment, exploration of new mechanism of resistance in nonpathogen and mobile genetic element-associated transmission of antibiotic resistance determinants. Since 2016, she has been a member of the Environmental Microbiology Committee of the Chinese Society of Microbiology.

Solidarity in the Genetic World: A Single Integrase for the Mobilization of Two Genetic Elements Disseminating Antibiotic Resistance

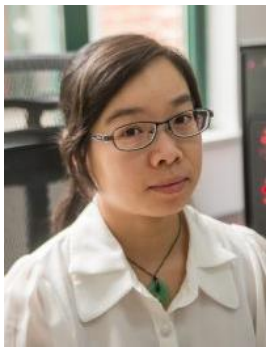
In the worldwide health threat posed by antibiotic resistant bacterial pathogens, mobile genetic elements (MGEs) play a critical role in favoring the dissemination of resistance genes. Among them, the GI*sul2* genomic island and its embedded CR2-*sul2* unit are believed to participate to this dissemination. However, the mobility of GI*sul2* or of the CR2-*sul2* unit has not yet been demonstrated. Here, we show that the integrase of GI*sul2* is functional and mediates the site-specific recombination between the attachement (*att)* sites of GI*sul2* and plasmid-located or chromosomal *attB* sites. Moreover, we show that the integrase can also perform the excision of GI*sul2* and of the CR2-*sul* unit independently, albeit at low efficiency under our standard culture conditions, and their re-integration into a free *attB* site. Our findings provide the first experimental characterization of the mobility of the GI*sul2* element. They also suggest a potential and unappreciated role of integrases related to those of GI*sul2* in the dissemination of the CR2-*sul2* unit.

Min Li

Renji Hospital, Shanghai Jiao Tong University School of Medicine, China

Min Li, Professor, director of the Department of Laboratory Medicine, Renji Hospital, Shanghai Jiao Tong University School of Medicine. She works on pathogenic mechanism and rapid diagnosis of important pathogenic microorganisms. She has published more than 80 articles in international journals such as *Nat. Med.* and *Cell Host Microbe*. As a Shanghai molecular diagnostic technology review expert, she participated in the review of Shanghai clinical molecular diagnostic laboratories.

Xinxin Feng



Hunan University, China

Xinxin Feng is an Associate Professor worked in the School of Chemistry and Chemical Engineering, State Key Laboratory of Chemobiological Sensing and Metrology, Hunan University. Dr. Feng Xinxin relies on the general direction of Oldfield's research topics, focusing on the study of the structure and function of polyprenyl transferases (polyprenyl transferases) and the development of new antibiotics. She has published more than 20 papers in the international journals, such as *Proc. Natl. Acad. Sci. U.S.A.* and *J. Am. Chem. Soc*. These work results provide an important structural basis for the study of the mechanism of polyprenyl transferase and the rational design of its inhibitors, and lay a foundation for the development of new drug-resistant antibiotics based on "multi-targeting".

Chemical Biology of Multi-targeting Resistance-resistant Antibiotics

The increasing number of infections caused by multi-drug resistance (MDR) bacteria is an omen of a new global challenge. With antibiotic resistance being a major threat to human health, one of the countermeasures under development is multi-targeting antimicrobial agents that are resistant to resistance generation. By combining multiple antimicrobial mechanisms, such as membrane lysis, DNA binding, enzyme inhibition, ROS attack etc., our group has recently developed several strategies for the design of such multi-targeting antimicrobial agents via new chemical entity synthesis, drug combination, and chemical conjugation. Chemical biology investigation of these strategies has revealed previously unknown synergy between different antimicrobial mechanisms, which may provide insights for the discovery of next generation resistance-resistant antibiotics that have longer lifespan in clinical use.

Yang Fu

Southern University of Science and Technology, China

Fu Yang is a doctoral supervisor and researcher at the School of Medicine of Southern University of Science and Technology. He works on pathogenic biology, intestinal pathogen-host-symbiotic microbiome. In recent years, more than 16 papers have been published in international authoritative academic journals, such as *Cell Host Microbe*, *Sci. Transl. Med.* and *PNAS*. He has won the Fogarty Global Health Fellowship Award.

Identification of A Novel T6SS Effector Reveals A Brand New Mechanism Precisely Targeting Cholera Infection

The Type VI secretion system (T6SS) is a bacterial nanomachine widely used by bacteria to delivers toxic effectors into neighbor cells. However, the modes of action of many effectors remain unknown. Here, we report a novel effector VtsE, an anti-bacterial effector encoded by a ~32 kb size genomic island (VPI-VI) of the non-toxigenic *Vibrio cholerae*, which specifically targets *Vibrio* species but not *E. coli*, *E. aerogenes*, *A. hydrophilia* and other common T6SS sensitive gram-negative bacterial species. Full characterization of this protein demonstrated that VtsE functions as a pore-forming toxin on an artificial bimolecular lipid membrane and is delivered by the VgrG1, VgrG2 and VgrG4 spike complex into prey cells. Using *in vitro* assays, we also indicate that genomic island VPI-VI can be excised from chromosome, circulated and transferred into toxigenic *V. cholerae* strain. Collectively, VtsE-mediated toxicity enables us to precisely control toxigenic vibrio both in the environment and human host.

Ke Wang

Guangxi Medical University, China

Ke Wang, Professor, respiratory physician of the First Affiliated Hospital, Guangxi Medical University, China. He has published more than 20 papers in the international journals, such as *CHEST* and *J. Clin. Microbiol.* The report on the diagnosis of invasive fungal disease by galactomannan and β-D-glucan has become the evidence-based medicine basis for the relevant guidelines formulated by the American Society of Infectious Diseases, the British Thoracic Society, and the European Society of Leukemia-Related Infections.

Pleural Empyema Related Pathogens and Biofilms

Pleural empyema is a purulent infection, and is still associated with high morbidity and mortality. The key factor leading to the lack of treatment progress may be that the pathogenesis that we do not fully understand, such as the causative microbiota and the role of biofilm formation. Firstly, we firstly carried out a metagenomic snapshot of the pleural effusion from 45 empyema patients by Illumina sequencing platform to assess its taxonomic. We found that the variation of microbiota in the pleural effusion is generally stratified, not continuous. *Staphylococcus aureus* was the most abundant species, appearing in almost all samples, and all specimens of empyema were mixed infections. Secondly, we used *Pseudomonas aeruginosa* or *S. aureus* to establish two different rabbit empyema models to determine whether they can independently form biofilms in the pleural cavity. We found that both *P. aeruginosa* and *S. aureus* can form biofilms. In addition, c-di-GMP signaling molecules played an important role for *P. aeruginosa* in biofilm formation in the pleural cavity.

Session V

Metabolic Sciences and Microbial Metabolism

Lianrong Wang

Wuhan University, China

Dr. Lianrong Wang is Distinguished Professor of Wuhan University and the Director of Luo Lab. She received postdoctoral degree at Department of Bioengineering, Massachusetts Institute of Technology in 2011. She won Outstanding Youth Fund of the National Foundation of China in 2021. Her research interests include impact of genomic phosphorothioate modification on bacterial and archaeal physiology and epigenetic and biomedical applications. She has published numerous publications including *Nat. Microbiol., PNAS, Nat. Commun., Nucleic Acids Res., Small, mBio, Med. Res. Rev., Cell Death & Dis., Anal. Chem., Biotechnol. J.*

Characteristics of a New Type of DNA Phosphorothioate Modification System

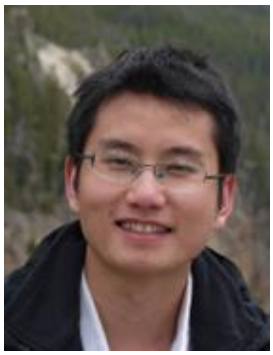
DNA phosphorothioate (PT) modification with the non-bridging oxygen in the DNA sugar-phosphate backbone replaced by sulfur physiologically occurs in diverse bacteria and archaea in a sequence-selective and Rp configuration-specific manner governed by DndABCDE five proteins. DndABCDE-mediated PTs predominantly occur as double-stranded modifications in a variety of 4-bp consensus sequences. Interestingly, we recently identified a new type of SspABCD–SspE PT system which exhibits distinct genetic organization, biochemical functions and phenotypic behavior compared to that of Dnd system. SspABCD confers single-stranded and high-frequency PTs with SspB acting as a nickase and possibly introducing nicks to facilitate sulfur incorporation and SspE uses DNA PT modification as a recognition tag to distinguish and destroy non-PT invasive phage DNA. Surprisingly, SspE senses sequence-specific PT modification by virtue of its PT-stimulated NTPase activity, which subsequently regulates its C-terminal nickase activity to inhibit phage propagation, rendering SspABCD-SspE an unusual epigenetic PT-sensing bacterial defense barrier. However, single-molecule optical mapping of DNA PT epigenetics reveals that PT profiles vary markedly from molecule to molecule, with different PT locations and spacing distances between PT pairs, even in the presence of SspE. The features point to special target selection mechanisms of DNA PT modification systems.

Long Liu

Jiangnan University, China

Dr. Long Liu is a Professor at School of Biotechnology at Jiangnan University. He is currently the dean of the Industrial Technology Research Institute of Jiangnan University. His research mainly uses synthetic biology technology to carry out the rational design of the model industrial microorganism *Bacillus subtilis* chassis cells, the construction of complex gene circuits, and the research of dynamic metabolic engineering, including the mining and creation of metabolic elements, the optimization of metabolic pathway design, and the reconstruction of metabolic network modeling, etc. , To construct food cell factory seeds to efficiently produce milk-derived key active components (milk-derived proteins, breast milk oligosaccharides, fat-soluble vitamins, structural fats, etc.). Some products such as acetylglucosamine, vitamin K2, phosphatidylserine, etc. have been industrialized Production has produced significant social and economic benefits. As a corresponding author, he has published more than 100 SCI papers in journals including *Nat. Chem. Biol.*, *Nucleic Acids Res.*, *Nat. Commun.*, *Trend Biotechnol.*

Yu Zhang



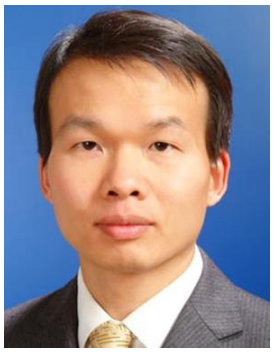
Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS, China

Dr. Yu Zhang is a professor in Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, CAS. He received bachelor degree in Life Sciences at Fudan University and got Ph.D degree in drug design at Shanghai Institute of Materia Medica, CAS. His current projects include: 1) Molecular mechanism of bacterial transcription initiation. 2) Transcription regulation by alternative initiator “sigma” factors. 3) Molecular mechanism of transcription-coupled DNA repair. 4) Molecular mechanism of bacterial transcription termination. (5) Discovery and mechanism study of new RNAP regulatory proteins and (6) Discovery of new antibiotics targeting bacterial RNA polymerase. Dr. Zhang has numerous papers published in well-known journals including *Science*, *Nature*, *Cell*, *eLife*, and *Nucleic Acid Res.*

Structural Insights into the Intrinsic Transcription Termination in Bacteria

Termination is the last step of gene transcription. Two modes of transcription termination exit in bacteria, the factor-dependent termination (Rho-dependent termination) and the factor-independent termination (intrinsic termination). The bacterial intrinsic termination occurs when RNA polymerase (RNAP) reaches the terminator sequence typically encoding a GC-rich hairpin followed by a poly-U tail. We have captured key intermediate structures of the intrinsic termination process using the single particle cryo-EM approach. The structures show that the poly-U tail pauses transcription by inducing a half-translocated conformation of the RNA-DNA hybrid in the active center of RNAP. The pause allows RNA hairpin to fold in the RNA exit channel of RNAP, a key step required for RNA release. The structures further show that RNA is rapidly released but the template double-stranded DNA remains retained on RNAP after termination.

Xuming Mao



Zhejiang University, China

Xuming Mao is a Professor of Institute of Pharmaceutical Biotechnology, Zhejiang University School of Medicine. He studied under the School of Life Sciences of Fudan University, and graduated from the Shanghai Institute of Biological Sciences, Chinese Academy of Sciences with a Ph.D., and had a two-year (2013-2015) exchange research collaboration at the University of California, Los Angeles. UCLA Exchange research. His team is interested in researches including: 1) Innovative drug research and development: i) Discovery of new active natural products in microorganisms, analysis of biosynthetic mechanism and evaluation of druggability; ii) Realize structural modification of active natural products based on biosynthesis and improve druggability. 2) Modification of generic drugs: i) Remodeling of production bacteria to achieve high-efficiency synthesis of a large variety of microbial drugs; ii) Using heterologous expression to achieve high-efficiency biosynthesis of low-yield and high-value-added microbial drugs. In recent years, as the first author or corresponding author, he has published many researches on famous SCI journals in the field of microbial biochemistry and chemistry, including *Nat. Commun.*, *J. Am. Chem. Soc.*, *Angew Chem. Int. Ed. Engl.*, *J. Biol. Chem.*, etc.

Discovery of Semi-Pinacolases from Epoxide Hydrolase Family during Efficient Assembly of a Fungal Polyketide

Semi-pinacol rearrangement (SPR) is highly useful in asymmetric synthesis of complex compounds. In biological systems, only several semi-pinacolases belonging to few families have been identified to catalyze SPR on alkaloids. Here based on the biosynthesis of a fungal mycotoxin asteltoxin, two semi-pinacolases AstD/MrvD were identified from the epoxide hydrolase family to catalyze type III SPR on the polyketide backbone. They were proposed to unprecedentedly catalyze efficient regio-selective hydrolysis on the bis-epoxide and 2,3-migration on the epoxide alcohol for the rearrangement. Based on the comprehensive mutations and chemical calculations, a critical Asp residue was identified as an acid for the coupled catalysis of selective epoxide collapse and subsequent SPR, while other critical residues facilitated efficient hydrolysis and protected carbocation for SPR. Thus, this study expanded the SPR biocatalyst family and provided new understanding of the catalytic mechanisms of these bi-functional semi-pinacolases.

Tiangang Liu

Wuhan University, China

Tiangang Liu is a Professor at Wuhan University. His research interests are the natural products overproduction and discovery, focusing on overproduction of value-added chemicals by engineering of the interested pathways, overproduction of pharmaceuticals and its precursors by using synthetic biology strategies and high throughput genome mining of new compounds utilizing synthetic biology strategies. In last several years, he was collaborating with many companies to improve their strain performances. He also applies his precursor supply systems both in vivo and in vitro for natural products mining. Tiangang Liu received several awards and funding in China, including National Natural Science Funds for Excellent Young Scholar and "Ten thousand plan" national high level talents special support plan “Top-Notch Young Talents”, and "Ten thousand plan" - national high level talents special support plan “Leading Scientists”. He is associate editor for *Metab. Eng. Commun.*, and serve as editorial board for *ACS Synth. Biol*., *Biotechnol. J.*, *Syst. Synth. Biotechnol.*, etc.

Intelligent Production and Innovative Discovery of Natural Products

Our group developed a principle technical system called “Efficient Microbial Chassis-based Natural Product Overproduction (EMC-NPO)”.

The main achievements in the last 5 years are as follows: 1) Reconstitute the mevalonate (MVA) pathway for terpenoid overproduction in vitro. This information guided the successful overproduction of farnesene, lycopene, astaxanthin, taxadiene, etc. Recently, the proposed the use of farnesene as a precursor to synthesize isophytol, and then vitamin E. This proposal was made tested under the supervision of the speaker. The large facility was launched in Hubei,China. This new technique completely changed the vitamin E industry and has generated a revenue of 2 billion RMB since its initiation at the end of 2017. 2) The speaker successfully commercialized lycopene production by Saccharomyces cerevisiae fermentation. 3) The “EMC-NPO” strategy was also expanded to natural product discovery. Based on previous work on the MVA pathway, robust precursor supplying platforms were constructed. The terpene synthase of interest was cloned and introduced to fully release the potential power of these enzymes. A new series of terpenes with a novel skeleton was discovered based on this platform. This platform has helped achieve the most efficient and shortest semi-synthesis of the complex bioactive sesquiterpenoid englerin A. 4) “EMC-NPO” strategy not only provided an important research platform and tool for basic biochemistry research on metabolic pathways but has also had a major impact on the industry by facilitating the development of several successful industrial applications for natural products.

Wei Zhang

Shandong University, China

Wei Zhang was previously an assistant researche of Qingdao Institute of bioenergy and process, Chinese Academy of Sciences (2012-2014), an associate researcher, Chinese Academy of Sciences (2014-2018), a postdoctoral fellow of Vanderbilt University in the United States (2016-2017), having been a professor, Shandong University. Professor Zhang has long been engaged in the natural product biosynthesis and synthetic biology; design and reconstruction of synthetic pathways of important pharmaceutical compounds and P450 monooxygenase and activity improvement of natural products, etc. In recent three years, he published more than 10 papers in *J. Biol. Chem.*, *ACS Catal.*, *J. Am. Chem. Soc.* and other journals. He presided over 8 programs and projects of the National Natural Science Foundation of China and other funds.

Biosynthesis of Sulfur-containing Antibiotic Chuangxinmycin Featuring a Deubiquitinase-like Sulfurtransferase

Chuangxinmycin is a sulfur-containing antibiotic with a unique thiopyrano[4,3,2-cd]indole (TPI) skeleton and selective inhibitory activity against bacterial tryptophanyl-tRNA synthetase (TrpRS). It draws continuing attention on drug development since there has not been any clinical antibiotic targeting bacterial TrpRS. With respect to its biogenesis, the biochemical basis for construction of the unique TPI scaffold is of special interest for further understanding the sulfur metabolism during natural product biosynthesis. However, the knowledge on sulfur incorporation mechanism involved in sulfur-containing molecule biosynthesis remains limited.

Here, we resolved the central biosynthetic problem by in vitro biochemical characterization of the key enzymes, and reconstituted the TPI skeleton in a one-pot enzymatic reaction. Particularly, we reveal that the JAMM/MPN+ protein Cxm3 functions as a deubiquitinase-like sulfurtransferase to catalyze a non-classical sulfur-transfer reaction by interacting with the ubiquitin-like sulfur carrier protein Cxm4GG. This finding adds a new mechanism for sulfurtransferase in nature.

Wei Ding

Shanghai Jiao Tong University, China

Wei Ding, previously a postdoctoral fellow, Department of pharmaceutical biotechnology, Saarland University, Germany (2010-2012), associate professor and master student supervisor, School of life Sciences, Lanzhou University (2013-2018), has been an associate professor and Ph.D. student advisor, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University. Professor Wei Ding focused on the biosynthesis mechanism and synthetic biology of natural products, the discovery of active small molecules and efficient enzymes in extreme environmental microorganisms, the diversity and directed evolution of enzyme catalytic mechanisms, the biocatalysis of important clinical drug intermediates and the metabolic engineering of microbial industrial strains. And He has published nearly 10 SCI papers in mainstream chemical journals such as *Nat. Commun.* and *Angew. Chem. Int. Ed*.

Yingxiu Cao

Tianjin University, China

Yingxiu Cao is an associate professor and doctoral supervisor in the School of Chemical Engineering, Tianjin University. Her main research field is the development of genomic manipulation tools and strategies to improve microbial biosynthesis capability. I have published 16 SCI papers as the first author or corresponding author in the international journals such as *Nat. Commun.*, *Metab. Eng.*, *ACS Catal.* and etc. She has gained 7 national and provincial research projects. She has also gained the Young Elite Scientists Sponsorship Program by Tianjin, and has won the China Petroleum and Chemical Industry Federation-Science and Technology Progress Award (third prize) for her works in the area of metabolic engineering and synthetic biology.

Genome-scale Target Identification and Programming of Microbes for High Production of Chemicals

Microbial biosynthesis of a desired product is constantly in the control of a complex intracellular network. In addition to synthetic pathways, many seemingly unrelated cellular processes also greatly affect the synthesis of products. Therefore, there are a large number of potential gene targets that can promote product synthesis in the whole genome. However, traditional metabolic engineering mainly manipulates the pathways that directly related to product synthesis, but the connections between product synthesis and other cellular processes remains unexplored. We are committed to unlock the full potential of microbial biosynthesis by developing genomic manipulation tools and strategies, enabling identification and engineer of deep gene targets. Take free fatty acids (FFAs) biosynthesis as an example, we identified 56 novel beneficial gene targets on genome-scale by employing CRISPRi-omics technologies. Through combinatorial perturbations of the identified genes, 30.0 g L−1 of FFAs were produced in fed-batch, which is the highest FFAs titer in E. coli to date. Our study provides new insights into digging the linkages between cell functions and product biosynthesis, providing avenues for the construction of a superior microbial cell factory for biochemical overproduction.

Session VI

Intestinal Microbiomes and Microbial Bioinformatics

Hongwei Zhou

Southern Medical University, China

Hongwei Zhou Southern Medical University, China Hongwei Zhou is the Director of Laboratory Medicine Department of Zhujiang Hospital of Southern Medical University, PI of Southern Medical University Microbiology Medical Center, PI of State Key Laboratory of Organ Failure Prevention and Treatment and Chief Editor of *Med. Microecol.* (Elsevier). He works on human microbiome and new technology of omics inspection. He has published many researches on the international journals, such as *Nat. Method*, *Microbiome*, and *EBioMedicine*.

Multi-Center Design to Overcome the Regional Variation of Disease Microbiome Signatures on the CALM Platform

It is often to obtain different microbiome signatures for the same disease from different studies. Although technical biases are possibly involved, we demonstrate that regional variation is a crucial factor using a cross-sectional study with over 7000 participants. This regional variation is correlated with the prevalence of hypertension and explains more than the age and BMI etc. We further build the Chinse Association for clinical Microbiome (CALM) platform and start multi-center microbiome studies for pregnancy, stroke, CRC etc.

Xingyin Liu

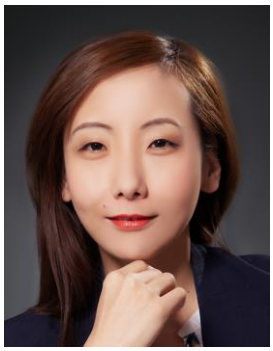
Nanjing Medical University, China

Xingyin Liu is a professor at Nanjing Medical University. She received her Ph.D. degree from Sun Yat-Sen University in 2006. From 2006 to October 2010, she worked on the signal transduction mechanism of the interaction between enteric pathogenic microbes and host at University of Rochester in the United States. From 2010 to 2015, she was engaged in epigenetic research on genes associated with autism at Einstein College of Medicine in the United States. Since October 2015, she has worked on Nanjing Medical University. She is currently the leader of the gut microecological system innovation team of Nanjing Medical University, mainly dedicated to basic research on the association between gut microbes and human diseases including autism and colorectal cancer. She has published more 30 paper in the international journals, such as *Cell Host & Microbe, Cell Reports, Gut Microbes, and Genomics, Proteomics & Bioinformatics.*

Lactobacillus plantarum Ameliorates Colorectal Tumorigenesis Through Contributing to Priming the IFN-γ+CD8+ T Cell Immunity

Previous studies have showed that probiotics, including *Lactobacillus* and *Bifidobacterium* species have function of ameliorating colorectal tumorigenesis in mouse model. An recent epidemiological survey showed that the incidence of cancer in people who often drink yogurt containing some probiotics is lower than that in people who do rarely drink yogurt. However, the underlying mechanisms of probiotics resisting caner remain unclear. Here, we found a probiotic stain, *Lactobacillus plantarum* L168(L168) and it's metabolite, 3ILA(indole-3-lactic acid) administration ameliorates intestinal inflammation and CRC. We found L168/ILA (indole-3-lactic acid) treatment can improve the disorder of intestinal microecological system in CRC mice. Furthermore, we provided evidences that L168/ILA treatment accelerated dendritic cells for IL-12 production though epigenetics regulation that contributed to priming the IFN-γ+CD8+ T cell immunity against tumor growth in vivo and in vitro. Recent studies implicated that the elevated cholesterol level in tumor tissue accelerate depletion of the IFN-γ+CD8+T cells. Based on this, so we further demonstrated L168 and 3HLA can reduce cholesterol concentrations of tumor tissue through regulating expression of 3aa3, an important gene for initiation of adipose tissue, accordingly, L168 and 3HLA inhibited the depletion of IFN-γ+CD8+T cells in tumors. Together, our findings suggest L168/ILA has the high potential to develop probiotic-based therapeutic strategies to resist CRC.

Chenhong Zhang



Shanghai Jiao Tong University, China

Chenhong Zhang is a professor at the State Key Laboratory of Microbial Metabolism, Shanghai Jiao Tong University. She has conducted nearly 10 years of research in the field of the relationship between intestinal flora and obesity and other metabolic diseases, and has made outstanding achievements in improving obesity and type 2 diabetes through nutritional regulation of intestinal flora. She has published more 30 papers in the international journals, such as *Science*, *Nat. Commun.*, and *ISME J.*

Nutritional Modulation of Gut Microbiota for Alleviation of Metabolic Diseases

Human microbiome plays an important role in maintaining human health by providing essential functions that may not be encoded in our own genome. Bioactive substances produced by gut bacteria can impact host immunity and metabolism. Under the conceptual framework of Koch's postulates and guided by ecological theory, we employed high-throughput metagenomic sequencing with multivariate statistical method, to have revealed that diet plays a more dominating role in shaping gut microbiota than host genetics and identified specific bacterial species/strains that may be contributory to obesity, insulin resistance and inflammaging in mice. Moreover, the applicant has made critical contributions in clinical alleviation of simple obesity, childhood genetic obesity and type 2 diabetes with nutritional modulation of gut microbiota.

Wei Wang

Shanghai Jiao Tong University School of Medicine, China

Wei Wang is an Associate Professor at Shanghai Jiao Tong University School of Medicine. He received a bachelor's degree in medicine from Shandong University School of Medicine in 2008 and he received a Ph.D. in Biochemistry from the University of Missouri, USA in 2014. His main research direction is chemical microbiology. Through the development and use of chemical probe tools, the microbial activities and corresponding physiological and pathological functions related to the health of the host can be studied at the overall level of the flora. He has published numerous papers in the international journals, including *Gut Microbes*, *ACS Chem. Biol.* and *Cell Death Dis.*

In vivo Metabolic Labeling-based Chemical Biology Research of Gut Microbiota

Traditional gut microbiota research strategies, which are mostly based on DNA sequencing, bacterial culture and isolation, and genetic engineering, have encountered a series of bottlenecks in the further study of the complicated functions of this complex microbial system. In this presentation, I would like to introduce several new chemical tools and methods that we have developed in recent years for studying gut microbiotas. These include a series of gut microbiota studies using a D-amino acid fluorescent probe (FDAA)-based in vivo metabolic labeling strategy: 1) fluorescence imaging of the in vivo division modes of different intestinal bacteria (including those that cannot be separately cultured in vitro) using sequential FDAA-labeling; 2) a new in vivo metabolic status quantification methodology developed by combining FDAA-labeling and fluorescence *in situ* hybridization (FISH); 3) in situ three-dimensional single cell-resolution imaging of mucosa associated microbiota using CUBIC-based tissue clearing and a new in vivo FDAA-labeling protocol. These new tools and methods not only open a new research field of chemical biology, but also provide new research strategies and perspectives for the in-depth understanding of microflora, the "dark matter" in the intestine.

Zheng Zhang

Shandong University, China

Zheng Zhang is a Professor in the Institute of Microbial Technology of Shandong University. He focused on the mechanism of microbial evolution, the mining of microbial toxin immune protein system and the global distribution of prokaryotic genes based on biological information big data. And He has published more 30 papers in the international journals, such as *Microbiol. Spectr.* and *Microbiome.*

Estimate of the Sequenced Proportion of the Global Prokaryotic Genome

More than 300,000 bacterial and archaeal complete or draft genomes have been uploaded to the public databases resulting from the development of sequencing technology and the decrease in costs. However, what is the cells or taxa proportion of genome-sequenced bacteria or archaea on earth? We conducted a large-scale sequence alignment between the data released by the Earth Microbiome Project (EMP) and the sequenced bacterial or archaeal genomes in the public database, showed the present situation of prokaryotic genome sequencing in the earth biomes for the first time.

We found that the majority of the biomes were occupied by a few predominant taxa with high relative abundance and much higher genome-sequenced proportions than numerous rare taxa. On this basis, we provided a new approach to investigate the global distribution of prokaryotic functional genes, and focused on the global distribution of prokaryotic glycoside hydrolase (GH) systems. We revealed that approximately 1% of genes in the global prokaryotic gene pool encoded GHs, and the median number of GH families in prokaryotic communities was 105. The GH genes in host-associated prokaryotic communities were more abundant than those in free-living communities, but the free-living environments had a wider variety of GH families. The GH complexity was correlated with the alpha diversity index, consistent with the assumed carbohydrate supplies. The prokaryotes occurring in wider environments normally encoded more GH genes and families; most GH families had complex and diverse taxonomic sources. This GH panorama provides the global functional potentials of carbohydrates degradation and an exploration guide for new GHs.

Bo Liu

Institute of Pathogen Biology, CAS, China

Liu Bo, male, is a doctor who graduated from Ilmenau University of Technology in Germany and Peking Union Medical College in China. He is currently working at the Key Laboratory of Ministry of Health, Institute of Pathogen Biology, Chinese Academy of Medical Sciences and Peking Union Medical College. He has been engaged in bioinformatics research related to pathogen genomics for a long time. He has participated in "National Key Research and Development Program", "National Natural Science Foundation of China", and "Medical and Health Science and Technology Innovation Project of Chinese Academy of Medical Sciences". Currently, as the first or joint first author, he has published 9 academic papers in SCI journals such as Nucleic Acids Res., Microbiome and Front. Microbiol., among which “VFDB 2019: a comparative pathogenomic platform with an interactive web interface” published on Nucleic Acids Res. was included in the list of "China's 100 Most Influential International Academic Papers" in 2019. In 2017, he was awarded the First Prize for Outstanding Achievements in Scientific Research of Colleges and Universities by the Ministry of Education of China.

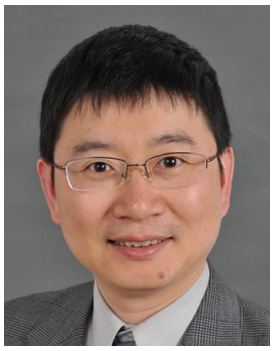
The Construction of a Web Based Analysis Platform for Zoonotic and Vector-Borne Viruses

Current times call for more efficient eco-epidemiological approaches for the rapid identification of novel pathogens by genome sequencing and phylogenetic tracing studies to detect potential interspecies spillover. Therefore, it is critical to setup a comprehensive and integrative resource center for zoonotic and vector-borne viruses worldwide.

Build upon two of our previously released databases, DBatVir and DRodVir for bat- and rodent-associated viruses respectively (Database 2014. 2014:bau021; J Genet Genomics 2017. 44:259), we further collects up-to-date knowledge on mosquito- and tick-associated viruses. We conducted an exhaustive search within the nucleotide and literature databases of NCBI. We constructed a comprehensive resource for zoonotic and vector-borne viruses, namely ZOVER (http://www.mgc.ac.cn/ZOVER).

As of August 2021, the database currently collects 39,339 viruses of 34 viral families identified from 957 species of bats/rodents/mosquitos/ticks distributed in 151 countries worldwide. All the incorporated information and devoted tools for online analysis and visualization facilitate ZOVER as a valuable resource for researchers to better understand the diversity and dynamics of zoonotic and vector-borne viruses to conduct effective surveillance to monitor and trace the current and future emerging zoonotic diseases.

Yi-Lei Zhao



Shanghai Jiao Tong University, China

Yi-Lei Zhao is a Professor in the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University. He focused on computational biochemistry, such as the double helix structure perturbation and chemical property changes caused by DNA phosphorylation, and the relationship between the reaction potential energy surface of biological synthase and industrial enzyme mutation and catalytic efficiency. And he has published more than 90 SCI papers in the international journals, such as *JACS* and *ACS Catal.*

Insights into Substrate Selectivity and Catalytic Mechanism of the Nocardicin Bifunctional Thioesterase

D-amino acid introduction in peptides can enrich their biological activities and pharmacological properties as potential drugs. This achievement of stereochemical inversion usually owes to an epimerase or racemase. Interestingly, a unique bifunctional thioesterase (NocTE), which is incorporated in nonribosomal peptide synthetase (NRPS) NocA-NocB assembly line for the biosynthesis of monocyclic β-lactam antibiotic nocardicin A, can control the generation of D-products with high stereochemical purity. However, the molecular basis of NocTE selectivity on substrate and product is still unclear. Herein, we constructed a series of systems with different peptide chirality, length and composition to investigate the substrate selectivity. The studies on binding affinities and loading conformations analyses elucidated the important roles of peptide length and β-lactam ring in substrate selectivity. Through energy decomposition and interaction analyses, some key residues involved in substrate selectivity were captured. On the other hand, natural product undergoing epimerization was found to be liberated from the active pocket more easily in comparison with its diastereomer (epi-nocardicin G), explaining the superiority of nocardicin G. These results provide detailed molecular insights into the exquisite control of substrate and product scopes, and encourage to diversification of substrates and final products for NRPS assembly line.

Hong-Yu Ou

Shanghai Jiao Tong University, China

Hong-Yu Ou is a Professor in the School of Life Sciences & Biotechnology, Shanghai Jiao Tong University. He has employed genome sequencing, bioinformatics, and genetics experiments to elucidate what poles the conjugative elements play in the horizontal transfer of antimicrobial resistance genes and virulence genes in bacterial pathogens. He has also developed a series of open-access databases and tools for mobilome analysis. He has >70 peer-reviewed publications in both microbiology and bioinformatics, including *Nucleic Acids Res.* (11 articles), *Brief. Bioinform.* and *Genome Med.*

Identification of the Conjugative Transfer Modules of the Antibiotic Resistance Plasmids and Virulence Plasmids of *Klebsiella pneumoniae*

Bacterial conjugative plasmids have been highlighted as important vehicles for the dissemination of antibiotic-resistance determinants and pathogenesis. The conjugative transfer regions of the self-transmissible plasmids typically consist of four modules: an origin of transfer (oriT) region, relaxase gene, type IV coupling protein (T4CP) gene, and gene cluster for the bacterial type IV secretion system (T4SS) apparatus. Interestingly, non-conjugative plasmids carrying functional oriT sequences can be mobilized by conjugative plasmids. The identification of these modules in plasmid sequences is important to investigate the self-transfer or mobilizing transfer capability of plasmids.

Here, we report a web tool, named ‘oriTfinder’, as a public resource for in silico detection of conjugative transfer modules in bacterial plasmid sequences. It outputs a simple list and generates a graphic overview of not only the predicted transfer-related functional modules (oriT region, relaxase genes, T4CP genes, T4SS gene clusters) but also the extended putative virulence or acquired antibiotic resistance genes. With the aid of oriTfinder, we elucidated the acquisition of a self-transferable blaDHA-1-carrying plasmid by a *Klebsiella pneumoniae* ST23 strain, and the mobilization of the non-conjugative virulence plasmid from hypervirulent *Klebsiella pneumoniae*. The oriTfinder might facilitate the rapid detection of various conjugative regions in the dynamic plasmids of bacterial pathogens.

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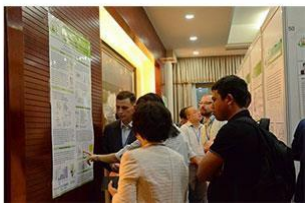
ICMS Conference Archives

- **ICMS 2015**

- **ICMS 2016**







- **ICMS 2019**