iMeta Conference 2024 Agenda

iMeta Conference 2024– Detailed Agenda				
November 11-13, 2024 Conference Center, 3rd Floor, Administration Building, Nanshan District People's Hospital, Shenzhen				
3rd Floor Conference Center - 496 seats (Main Conference) / 3rd Floor Lecture Hall – 120 seats (Special Session)				
Time	**Name**	**Affiliation**	**Report Title**	**Session Chair**
October 11 (Friday) All Day 9:00 AM - 21:00 PM Registration				
October 11 (Friday) 14:00 PM-18:30 PM - Cutting-edge Technology				
14:00-14:20	Yu Xia	Southern University of Science and Technology	Genome Enrichment of Rare and Unknown Species from Complicated Microbiome by Nanopore Selective Sequencing	Kang Ning Huazhong University of Science and Technology
14:20-14:40	Bing Li	Tsinghua University	Using Metagenomic Approaches to Investigate Antibiotic Resistance in “One Health” Framework	
14:40-15:00	Yongchao Su	Chief Architect for Tencent Health Southern Region	Tencent's Medical Large Model Supports the Digital and Intelligent Upgrade of Healthcare	
15:00-15:20	Zhencheng Fang	Southern Medical University	AI Language Models and Microbiomes	Weihua Chen Huazhong University of Science and Technology
15:20-15:40	Yulin Wang	Shandong University	From Microbial Association Network Prediction to Interaction Validation	
15:40-16:00	Yan Ni	Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center for Child Health	Integrated Analysis Methods and Strategies for Gut Microbiome and Metabolome	
16:00-16:30	**Coffee Break**			
16:30-16:50	Jun Wang	Institute of Microbiology, Chinese Academy of Sciences	Characterization and Functional Analysis of Microbial Macromolecules	Zhipeng Liu Biotree Metabolomics Technology Research Center
16:50-17:10	Tong Chen	National Resource Center for Chinese Materia Medica, China Academy of Chinese Medical Sciences	High-Quality Online Data Analysis, Visualization, and Figures for Reserch Papers	
17:10-17:30	Huizeng Sun	Zhejiang University	Advances and Perspectives in Single-Cell Transcriptomics of Microbes.	
17:30-17:50	Wei Liu	Anhui Agricultural University	Analyzing Host Regulation of Microbial Metabolism and Pathogenic Heterogeneity Based on Bacterial Co-Cultures and Single-Cell RNA-Seq Technology	Xiaoqian Su Qingdao University
17:50-18:10	Zhichao Zhou	Shenzhen University	Tools and Research Advances in Environmental Viromics	
18:10-18:25	Chihmin Chang	Magigene/Sun Yat-sen University	Empirical Analysis of Data Quality and Characteristics of Multi-Platform Sequencing in the Field of Microbiomics	

18:25-18:30	Guangyi Zeng	Director of South China Region, BGI Intelligent Manufacturing	BGI Genomics CycloneSEQ Nanopore Sequencing Technology Scientific Empowerment Program Southern China Launch Event	
October 11 (Friday) 19:00 PM - 21:00 PM Welcome Dinner				
iMeta Conference 2024– Detailed Agenda				
November 11-13, 2024, Conference Center, 3rd Floor, Administration Building, Nanshan District				
3rd Floor Conference Center - 496 Seats (Main Conference) / 3rd Floor Lecture Hall - 120 Seats				
October 12 (Saturday) 9:00 AM - 12:00 PM - Keynote Speeches				
9:00-9:25	Opening Ceremony		Promotional Video, Host, and Speeches by Special Guests	Yongxin Liu Agricultural Genomics Institute at Shenzhen (Dapeng Bay Laboratory)
	Tieying Hou	Director/Secretary of Nanshan Hospital	Speech	
	Hua Yang	Executive Deputy Director of Xianghu Laboratory	Speech	
	Shuangjiang Liu	Editor-in-Chief of the iMeta Journal	Speech	
9:25-9:30	Conference Group Photo			
9:30-10:00	Yulong Yin	Chinese Academy of Sciences, Subtropical Agricultural Ecology Research Institute (Academician)	Regulation of Gut Microbiota Response and Antibiotic Alternatives	
10:00-10:25	Jun Yu	The Chinese University of Hong Kong	Journey and Insights in Microecology and Tumor Research	Lei Dai Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences
10:25-10:50	Fangqin Zhao	Beijing Institute of Life Sciences, Chinese Academy of Sciences	Development and Data Mining of Single-Cell Spatial Omics Technology	
10:50-11:10	**Coffee Break**			
11:10-11:35	Shuangjiang Liu	Institute of Microbiology, Chinese Academy of Sciences / Shandong University	Koch's Postulates--- From Microorganisms to Microbiomes	Yanliang Bi Institute of Feed Research, Chinese Academy of Agricultural Sciences
11:35-12:00	Hongwei Liu	Institute of Microbiology, Chinese Academy of Sciences	Research on the Mechanisms of Microbiota-Host Interactions Driven by Chemical Molecules	
October 12 (Saturday) 14:00 PM-17:30 PM - Conference Reports				
14:00-14:25	Wenkai Ren	South China Agricultural University	Amino Acid Metabolism and Immune Cell Fate in Piglets	Shifu Chen Hopeland Bio
14:25-14:50	Robert Schlaberg	Illumina	Solutions for Sequencing-based pathogen and AMR identification and profiling	
14:50-15:15	Diwei Zheng	Institute of Process Engineering, Chinese Academy of Sciences	Bacterial Biomaterials	Changzheng Du Tsinghua University
15:15-15:40	Hubing Shi	West China Hospital, Sichuan University	Immune Surveillance and Evasion Mechanisms in Tumor Metastasis	
15:40-16:10	**Coffee Break**			
16:10-16:30	Shuangxia Jin	Huazhong Agricultural U	Development of Cotton Gene Editing Tools and Applications in Molecular Breeding	Guihai Feng

16:30-16:50	Liang Li	Southern University of Science and Technology	Research on Microbiota-Host Interactions and Drug Development Based on Clinical Sample Cultures and Human Organ-like Platforms of Major Organs	Institute of Zoology, Chinese Academy of Sciences
16:50-17:10	Bangzhou Zhang	TreatGut Biotechnology Co., Ltd	Microecological Medicine and Research Translation Platform	Jiang Chao Zhejiang University
October 12 (Saturday) 14:00 PM-15:40 PM - Biotechnology Session				
14:00-14:20	Yongcheng Wang	Zhejiang University	Development and Application of High-Throughput Single-Cell and Single-Bacterium RNA Sequencing Technologies	Leyuan Li National Center for Protein Sciences (Beijing)
14:20-14:40	Dijun Chen	Nanjing University	Single-Cell and Spatial Omics Technologies Reveal the Heterogeneity and Molecular Mechanisms of Tumor Metastasis	
14:40-15:00	Shengguo Zhao	Chinese Academy of Agricultural Sciences	In Situ Targeted Isolation Techniques for Functional Microorganisms	Junya Zhang Center for Ecological and Environmental Research, Chinese Academy of Sciences
15:00-15:20	Lin Shi	Shanxi Normal University	Multi-Omics Integration for Analyzing Gut Microbiota and Cardiovascular Metabolic Health in Qinghai Plateau Populations	
15:20-15:40	Meiqing Yuan	Institute of Forensic Science of China	Advancements in Forensic Soil Microbiology Research and Case Applications	
15:40-16:10	**Coffee Break**			
October 12 (Saturday) 4:10 PM - 5:30 PM - Medical Session				
16:10-16:30	Xinxia Wang	Zhejiang University	Quercetin Induces Akkermansia to Regulate Host Bile Acid Metabolism and Alleviate Obesity	Wenping Gong The Eighth Medical Center of PLA General Hospital
16:30-16:50	Mingbang Wang	Longgang District Maternity & Child Healthcare Hospital of Shenzhen City	The gut microbiome and autism: —moving from correlation to causation?	
16:50-17:10	Xin Hong	Southern University of Science and Technology	Research on Circulating Tumor Cells (CTC) Biology and Clinical Applications	Cheng Lu Guangdong Provincial People's Hospital
17:10-17:30	Jianquan He	TreatGut Biotechnology S	Clinical Applications of Precision Microbiota Transplantation	
October 12 (Saturday) 19:00 PM-21:00 PM - Editorial Board Meeting: Discussion and Issuance of				
19:00-19:20	Yongxin Liu	Agricultural Genomics Institute at Shenzhen (Dapeng Bay Lab)	Progress Report and Future Plans for the iMeta Series Journals	Chunlin Shi Executive Editor of iMeta
19:20-19:40	Awards Presentation by Editors-in-Chief		Issuance of certificates for Executive Deputy Editors, Young Editorial Board Members, and Outstanding Reviewers	
19:40-20:40	Editorial Board Discussion			
20:40-21:00	Summary Remarks by the Editor-in-Chief			

October 13 (Sunday) 9:00 AM-12:00 PM - Gut Microbiota				
9:00-9:20	Jixin Zhong	Huazhong University of Science and Technology	DPP4 Regulates Gut Microbiota and Immune Dialogue	Kun Jiang Shandong University
9:20-9:40	Yi Duan	University of Science and Technology of China	From Clinic to Clinic— Analyzing the Closed-Loop Model of Clinical Basic Research from the Perspective of Gut Microbiota	
9:40-10:00	Zhemin Zhou	Soochow University	Long-Term and Medium-Term Evolutionary Studies of Microorganisms Driven by Human Activities	Fuyong Li Zhejiang University
10:00-10:20	Qi Su	The Chinese University of Hong Kong	Gut Microbiota and Irritable Bowel Syndrome	
10:20-10:40	Jin Wang	Southeast University	The Impact of Breast Milk Probiotics and Short-Chain Fatty Acid Interventions on Gut Microbiota Structure and the Immunological Mechanisms for Alleviating Food Allergies	Xueli Zhang Guangdong Provincial People's Hospital
10:40-11:00	**Coffee Break**			
11:00-11:20	Yi Hu	Nanchang University	Vonoprazan-based Dual Therapy for Eradication of Helicobacter pylori	
11:20-11:40	Xingxing Jian	Central South University	Study on the Mechanism by Which Nitrogen Source Cycling Gut Microbiota Accelerates the Progression of Multiple Myeloma and Induces Resistance to Bortezomib	Xuemeng Li Guangdong Medical University
11:40-12:00	Liangliang Wang	Institute of Microbiology, Chinese Academy of Sciences	Mechanism of Interaction Between Probiotics and Immune Cells	
October 13 (Sunday) 9:00 AM-12:00 PM - Health Session				
9:00-9:20	Shaolin Wang	China Agricultural University	The Impact of Antibiotic Use on Antibiotic Resistance Groups in Aquaculture Environments	Guodong Cao Anhui Medical University
9:20-9:40	Yichen Liu	Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences	Cheese from the Bronze Age Reveals the Interaction Between Humans and Lactic Acid Bacteria on an Evolutionary Scale	
9:40-10:00	Shaohua Gu	Peking University	The Co-evolution of Iron Carrier Synthase and Receptor Genes Reveals Bacterial Iron Interaction Networks Specific to Habitat and Pathogens	
10:00-10:20	Yangyu Liu	Harvard Medical School	Rational Design of Biologics for Living Organisms (Online)	Huang Shi The University of Hong Kong
10:20-11:00	**Coffee Break**			

11:00-11:20	Guangyu Liu	Hangzhou Normal University	Quality Control of Respiratory Chain Complex Orphan Proteins Mediated by Shigella sonnei Rhomboid Protease	Jianyu He Zhejiang Ocean University
11:20-11:40	Zhimin Xu	Research Institute of Subtropical Agriculture, Chinese Academy of Sciences	Research on the Environmental Geochemical Behavior and Ecotoxicological Effects of Microplastics	
11:40-12:00	Junqing Huang	Jinan University	Study on the Mechanism and Material Basis of Compound Xiaoyao Powder in Alleviating Depression by Reshaping the C3/CR3 Complement Cascade through Gut Metabolism	
October 13 (Sunday) 14:00 PM-15:30 PM - Journal Forum				
14:00-14:15	Hongling Zhou	Academic Editor of GigaScience	Introduction to the Journal 'GigaScience' and Submission Review Tips	Tong Chen China Academy of Chinese Medical Sciences
14:15-14:30	Yuxia Jiao	Executive Editor of GPB, National Center for Bioinformatics	To be a GPBee (Online)	
14:30-14:45	Lei Lei	Wiley	Advanced science and wiley life & health sciences	
14:45-15:00	Yongxin Liu	Agricultural Genomics Institute at Shenzhen (Dapeng Bay Lab)	Introduction to the iMeta Journal: Characteristics of High-Impact Articles	
15:00-15:30	Shuangxia Jin	Huazhong Agricultural University	Discussion: The Future of Academic Journals in China	
15:30-16:00	**Coffee BreaK**			
October 13 (Sunday) 14:00 PM-16:40 PM - Omics Session				
14:00-14:20	Moyang Liu	Shanghai Jiao Tong University	Development and Application of Gene Functional Evolution Methods Utilizing Public Data Resources	Sanqi An Guangxi Medical University
14:20-14:40	Lei Dong	Sun Yat-sen University	Exploring Microbial Dark Matter in Desert and Evaluation of Their Metabolic Potential	
14:40-15:00	Qi Wang	Guizhou University	Digitalization and Intelligence of Plants, Pests, and Pesticides	Zhuobin Liang Shenzhen Bay Laboratory
15:00-15:20	Qiang Sun	Zhejiang University	Identification of RNA Selective Splicing and its Functional Analysis	
15:20-15:40	Weipeng Zhang	Ocean University of China	Research on the Life Characteristics of Marine Biofilm Bacteria and their Resource Development and Applications	
15:40-16:00	**Coffee Break**			
16:00-16:20	Yang Liu	Southern University of Science and Technology	The Mechanism by Which DNA Methyltransferases and Their Modification Patterns Affect Bacterial Virulence Phenotypes	Xiaodong Li Nanshan District

16:20-16:40	Chong Yin	North Sichuan Medical College	The Mechanobiological Mechanism of PPL in Promoting Bone Formation through Phase Separation and Binding to HuR	People's Hospital, Shenzhen
October 13 (Sunday) 16:00 PM-17:30 PM - International Program				
16:00-16:15	Leyuan Li	National Center for Protein Sciences (Beijing)	International Guidelines for Metaproteomics Research	Renyou Gan Hong Kong Polytechnic University
16:15-16:30	Yunyun Gao	Shenzhen Genomics Institute, Chinese Academy of Agricultural Sciences	Metagenomics Guidelines Alliance (EasyAmplicon / EasyMetagenome / Microbiome Handbook)	
16:30-16:45	Shifu Chen	Haplox	fastplong: Ultra-fast Preprocessing for Long Reads	
16:45-17:00	**Closing Ceremony**			

iMeta大会2024日程大纲			
2024年11-13日 深圳南山区人民医院行政楼三层会议中心			
三楼会议中心-496座(大会)/三楼阶梯教室-120座(专场)			
日期	**上午**(9:00-12:00)	**下午**(14:00-17:30)	**晚上**(19:00-21:30)
10月11日(周五)	注册报到	前沿技术	欢迎晚宴
10月12日(周六)	特邀报告	大会/专场报告	编委会/聘书
10月13日(周日)	大会/专题报告	期刊/专题+国际计划	离会

iMeta大会2024详细日程				
2024年11-13日 深圳南山区人民医院行政楼三层会议中心				
三楼会议中心-496座(大会) / 三楼阶梯教室-120座(专场)				
时间	**姓名**	**单位**	**报告题目**	**主持人**
10月11日 (周五) 全天9:00-21:00 签到				
10月11日 (周五) 下午14:00-18:30 前沿技术				
14:00-14:20	夏雨	南方科技大学	复杂微生物群落中稀有物种的纳米孔选择性宏基因组富集测序研究	宁康 华中科技大学
14:20-14:40	李炳	清华大学	Using Metagenomic Approaches to Investigate Antibiotic Resistance in “One Health” Framework	
14:40-15:00	苏永超	腾讯健康南区架构师负责人	腾讯医疗大模型助力医疗健康数智化升级	
15:00-15:20	方臻成	南方医科大学	AI语言模型与微生物组	陈卫华 华中科技大学
15:20-15:40	王玉琳	山东大学	从微生物关联网络预测到相互作用验证	
15:40-16:00	倪艳	国家儿童健康与疾病临床医学研究中心，浙江大学医学院附属儿童医院	肠道微生物和代谢整合分析方法及策略	
16:00-16:30	**茶歇**			
16:30-16:50	王军	中国科学院微生物研究所	微生物大分子的表征和功能分析	

16:50-17:10	陈同	中国中医科学院中药资源中心	高颜值在线数据分析绘图和论文组图	刘志鹏 上海百趣代谢组学
17:10-17:30	孙会增	浙江大学	微生物单细胞转录组研究进展与展望	
17:30-17:50	刘威	安徽农业大学	基于细菌混池和单细胞RNA-seq技术解析宿主调控微生物组代谢与致病异质性	苏晓泉 青岛大学
17:50-18:10	周之超	深圳大学	环境病毒组学工具和研究进展	
18:10-18:25	张智闵	美格基因/中山大学	实测解析多系列测序平台在微生物组学领域的数据质量与特性	
18:25-18:30	曾广怡	华大智造华南战区总监	华大智造CycloneSEQ纳米孔测序技术科研赋能计划华南区发布会	
10月11日 (周五) 晚上19:00-21:00 欢迎晚宴				
iMeta大会2024详细日程				
2024年11-13日 深圳南山区人民医院行政楼三层会议中心				
三楼会议中心-496座(大会) / 三楼阶梯教室-120座(专场)				
10月12日(周六) 上午9:00-12:00 特邀报告				
9:00-9:25	开幕式		宣传片、主持人、特邀嘉宾致辞	刘永鑫 深圳基因组所/大鹏湾实验室
	侯铁英	南山医院院长/书记	致辞	
	杨华	湘湖实验室常务副主任	致辞	
	刘双江	iMeta期刊主编	致辞	
9:25-9:30	大会合影			
9:30-10:00	印遇龙	中国科学院亚热带农业生态研究所(院士)	肠道微生物群体反应调控与抗生素替代	
10:00-10:25	于君	香港中文大学	微生态和肿瘤研究的历程和体会	戴磊 中科院深圳先进院
10:25-10:50	赵方庆	中国科学院北京生命科学研究院	单细胞空间组学技术开发及数据挖掘	
10:50-11:10	**茶歇**			
11:10-11:35	刘双江	中国科学院微生物研究所/山东大学	科赫法则---从微生物到微生物组	毕研亮 中国农业科学院饲料所
11:35-12:00	刘宏伟	中国科学院微生物研究所	化学分子驱动的菌群与宿主互作机制	
10月12日(周六) 下午14:00-17:30 大会报告				
14:00-14:25	任文凯	华南农业大学	仔猪氨基酸代谢与免疫细胞命运	陈实富 海普洛斯
14:25-14:50	Robert Schlaberg	Illumina	Solutions for Sequencing-based pathogen and AMR identification and profiling	
14:50-15:15	郑迪威	中国科学院过程工程研究所	细菌生物材料	杜长征 清华大学
15:15-15:40	石虎兵	四川大学华西医院	肿瘤转移过程中的免疫监控与逃逸机制	
15:40-16:10	**茶歇**			
16:10-16:30	金双侠	华中农业大学	棉花基因编辑工具开发及分子育种应	冯桂海 中科院动物所
16:30-16:50	李亮	南方科技大学	基于临床样本培养和主要脏器人源类器官平台的微生物-宿主互作研究与药物研发	
16:50-17:10	张帮周	承葛医药集团	微生态医疗与研究转化平台	蒋超 浙江大学

10月12日(周六) 下午14:00-15:40 生物技术专场				
14:00-14:20	王永成	浙江大学	高通量单细胞和单细菌RNA测序技术的开发与应用	李乐园 国家蛋白质科学中心（北京）
14:20-14:40	陈迪俊	南京大学	单细胞与空间组学技术揭示肿瘤转移的异质性及分子机制	
14:40-15:00	赵圣国	中国农业科学院	功能微生物的原位靶向分离技术	张俊亚 中国科学院生态环境研究中心
15:00-15:20	施琳	陕西师范大学	多组学融合解析青海高原人群肠道微生态与心血管代谢健康	
15:20-15:40	苑美青	公安部鉴定中心	法医土壤微生物研究进展及案例应用	
15:40-16:10	**茶歇**			
10月12日(周六) 下午16:10-17:30 医学专场				
16:10-16:30	王新霞	浙江大学	槲皮素诱导阿克曼菌调节宿主胆汁酸代谢以缓解肥胖	龚文平 解放军总医院第八医学中心
16:30-16:50	王明帮	深圳市龙岗区妇幼保健院	肠道微生物群与孤独症：从“相关”到“因果”——从相关到因果?	
16:50-17:10	洪鑫	南方科技大学	循环肿瘤细胞（CTC）生物学研究以及临床应用	陆铖 广东省人民医院
17:10-17:30	何剑全	上海承葛生物	精准菌群移植的临床应用	
10月12日(周六) 晚上19:00-21:00 编委会——讨论和颁发聘书				
19:00-19:20	刘永鑫	深圳基因组所	iMeta系列期刊进展报告和未来规划	施春林 iMeta执行编辑
19:20-19:40	各位主编颁奖		颁发执行副主编、青年编委、优秀审稿人聘书	
19:40-20:40	编委发言讨论			
20:40-21:00	主编总结发言			
10月13日(周日) 上午9:00-12:00 肠道菌群				
9:00-9:20	钟继新	华中科技大学	DPP4调控肠道菌群和免疫对话	姜昆 山东大学
9:20-9:40	段屹	中国科学技术大学	“从临床中来，回临床中去”——肠道菌群角度解析临床型基础研究闭环范例	
9:40-10:00	周哲敏	苏州大学	人类活动驱动微生物的中长期进化研究	李福勇 浙江大学
10:00-10:20	苏奇	香港中文大学	肠道菌群与肠易激综合征	
10:20-10:40	王进	东南大学	母乳益生菌与短链脂肪酸干预对肠道微生物结构的影响及缓解食物过敏的免疫机制	张学礼 广东省人民医院
10:40-11:00	**茶歇**			
11:00-11:20	胡奕	南昌大学	伏诺拉生二联方案根除幽门螺杆菌	
11:20-11:40	简星星	中南大学	氮源循环肠道微生物加速多发性骨髓瘤进程且诱导硼替佐米耐药的机制研究	李雪萌 广东医科大学
11:40-12:00	王亮亮	中国科学院微生物研究所	益生菌与免疫细胞互作机制	
10月13日(周日) 上午9:00-12:00 同一健康专场				
9:00-9:20	王少林	中国农业大学	抗菌药物使用对养殖环境耐药组的影响	曹国栋 [illegible]
9:20-9:40	刘逸宸	中国科学院古脊椎动物与古人类研究所	青铜时期奶酪揭示人类与乳酸菌在演化尺度下的相互作用	

9:40-10:00	顾少华	北京大学	铁载体合成酶-受体基因协同演化揭示了栖息地和病原体特异性的细菌铁相互作用网络	安徽医科大学
10:00-10:20	刘洋彧	哈佛医学院	活体生物药的合理设计 (线上)	黄适 香港大学
10:20-11:00	**茶歇**			
11:00-11:20	刘广宇	杭州师范大学	宋内志贺菌（Shigella sonnei）菱形蛋白酶介导呼吸链复合体孤儿蛋白的质控	何建瑜 浙江海洋大学
11:20-11:40	徐智敏	中国科学院亚热带农业生态研究所	微塑料的环境地球化学行为及生态毒性效应研究	
11:40-12:00	黄俊卿	暨南大学	复方逍遥散通过肠道代谢重塑调控C3/CR3补体级联缓解抑郁机制及物质基础研究	
10月13日(周日) 下午14:00-15:30 期刊论坛				
14:00-14:15	周红玲	GigaScience学术编辑	《GigaScience》期刊介绍与投审稿技巧	陈同 中国中医科学院
14:15-14:30	焦玉霞	国家生物信息中心GPB执行主编	To be a GPBee (线上)	
14:30-14:45	雷蕾	威立出版集团	Advanced Science and Wiley Life & Health Sciences	
14:45-15:00	刘永鑫	大鹏湾实验室	iMeta期刊介绍和高影响力文章特点	
15:00-15:30	金双侠	华中农业大学	讨论：学术期刊的未来在中国	
15:30-16:00	茶歇			
10月13日(周日) 下午14:00-16:40 组学专场				
14:00-14:20	刘默洋	上海交通大学	基于公共数据资源的基因功能演化方法的开发与应用	安三奇 广西医科大学
14:20-14:40	董雷	中山大学	沙漠微生物暗物质挖掘及其代谢潜能勘探	
14:40-15:00	王崎	贵州大学	植物-有害生物-农药的数字化与智能化	梁卓斌 深圳湾实验室
15:00-15:20	孙强	浙江大学	RNA 选择性剪接的鉴定及其功能解析	
15:20-15:40	张伟鹏	中国海洋大学	海洋被膜细菌生命特征研究与资源开发应用	
15:40-16:00	**茶歇**			
16:00-16:20	刘洋	南方科技大学	DNA甲基转移酶及其修饰模式影响细菌毒力表型的机制	李晓东 深圳市南山区人民医院
16:20-16:40	印崇	川北医学院	PPL通过相分离和结合HuR促进骨形成的力生物学机制	
10月13日(周日)下午(16:00-17:30)国际项目				
16:00-16:15	李乐园	国家蛋白质中心	国际宏蛋白组学研究指南	甘人友 香港理工大学
16:15-16:30	高云云	中国农业科学院深圳基因组研究所	宏组学指南联盟(易扩增子/易宏基因组/微生物组手册)	
16:30-16:45	陈实富	海普洛斯	fastplong: ultra-fast preprocessing for long reads	
16:45-17:00	闭幕式			

Conference Abstracts

(Sort in chronological order of submission)

CAT-BLAST: Engineered Bacteria for Precision Targeting and Elimination of Cancer-Associated Fibroblasts

Mengdi Xu[1, 3], Ehsan Hashemi [3], Hui Gao[3], Qumar Zaman [3], Yi Ma[1], Jufang Wang[1], Wenjun Mao [2], Zhuobin Liang[3*]

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Abstract

Cancer-associated fibroblasts (CAFs) within the tumor microenvironment (TME) create a protective barrier that promotes tumor growth, metastasis, and hinders the efficacy of current therapies. To address this challenge, we introduce CAT-BLAST (CAF-Targeting Bacteria for Localized and Suppressive Therapy), a novel bacteria-based platform designed to specifically target and eliminate CAFs. We strategically engineered E. coli BL21 (EcB1) bacteria, removing type I fimbriae for enhanced safety and incorporating synthetic adhesins (SAs) for precise CAF targeting. These SAs utilize optimized surface-anchoring domains from natural adhesins (intimin and YeeJ) fused with a FAP-specific nanobody. We further engineered EcB1 to secrete the therapeutic cytolysin A (ClyA), inducing targeted apoptosis in both CAFs and adjacent tumor cells. In vitro, our engineered bacteria demonstrated superior adherence to FAP+ CAFs and ClyA-mediated cell death. Importantly, in a murine colorectal cancer model, these bacteria colonized tumors with improved specificity and efficiency, suppressing tumor growth. This study highlights CAT-BLAST's potential as a potent tool to overcome CAF-mediated obstacles in tumor therapies.

Keywords: Tumor microenvironment, Cancer-associated fibroblasts, Fibroblast activating protein, Bacteria-based cancer therapy, Synthetic adhesin

ENSURE: The encyclopedia of suppressor tRNA therapeutics with AI assistant

Yi-Feng Zhang[1#], Ou-Yang Zhuo[1#], Xu-Dong Zeng[1], Fan Feng[1], Xuan Bu[1], Yang Sun[1], Jian-Hua Yang[1], Liang-Hu Qu[1], Ling-Ling Zheng[1*]

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Abstract

In recent years, the potential of tRNA in treating genetic diseases, especially those related to mutations in mRNA translation, has garnered widespread attention. By engineering suppressor tRNAs (sup-tRNAs) to read through premature termination codons (PTCs), protein synthesis and function can be restored. However, the field of tRNA therapeutics is still in its early stages, lacking dedicated data resources for natural and engineered sup-tRNAs. This limitation hinders both fundamental research and therapeutic applications.

To address this urgent need, we have established ENSURE: The Encyclopedia of Suppressor tRNA Therapeutics with AI Assistant(https://trna.lumoxuan.cn/). This platform offers the following key features and significance:

1. **Point Mutation Information:** ENSURE includes mutation events occurring in genetic diseases and cancers, encompassing missense, nonsense, and frameshift mutations. This provides researchers with a rich resource of mutation information, facilitating the study and treatment of related diseases using tRNA therapeutics.
2. **Classification of Natural sup-tRNAs**: ENSURE catalogs hundreds of natural sup-tRNAs, detailing their source species, sequences, and structures. This aids in a deeper understanding of the diversity and function of natural sup-tRNAs.
3. **Records of Existing tRNA Therapies**: ENSURE compiles current research on tRNA therapies, including pathogenic genes, mutation sites, sup-tRNA sequences and structures, as well as data on the efficiency and safety of these therapies. By comparing the sequence similarity between sup-tRNAs and original tRNAs through BLAST, it highlights the modification sites of engineered sup-tRNAs and predicts their secondary and tertiary structures.
4. **Functional Element Analysis**: The platform thoroughly summarizes the key elements on tRNA molecules (including sequences, structures, and modifications) that influence their functions. It also establishes an interactive tRNA binding map, showcasing the binding sites of tRNAs with three classes of aminoacyl-tRNA synthetases (AARS), elongation factor Tu (EF-Tu), and the ribosomal E, P, and A sites.
5. **Virtual Assistant Yingying**: Based on ENSURE's data, we have trained a virtual assistant named Yingying, based on the GPT-4o model. Yingying can answer various questions regarding tRNA therapeutics, enhancing research and clinical application efficiency.

The establishment of the ENSURE platform not only provides researchers with tools for quickly exploring the biological mechanisms and application scope of sup-tRNAs but also offers a rich data resource and analysis platform for the design of engineered tRNAs. This is of significant importance in advancing the field of tRNA therapeutics.

Keywords: suppressor tRNA, therapy, AI, premature termination codons (PTCs)

Hosts manipulate metabolism and pathogenicity heterogeneity of microbiome based on bacterial bulk and single-cell RNA-seq technique

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Abstract

Major animals have complicating interactions with their resident microbes that profoundly affect many aspects of host physiopathology. However, the reversible influence of the host on the component and function of the microbiome has received less attention. Using Drosophila-symbiant model, we found that *Drosophila* larvae efficiently outcompete their symbionts by reducing bacterial loads in the niche. Furthermore, Drosophila larvae reshape the transcriptomic and metabolic profiles of symbionts. Bacteria manifest phenotypic heterogeneity among individual bacterial cells, but gene expression of bacterial cells has been traditionally investigated in bulk or on a population level. Bacterial single-cell RNA-seq technique is revolutionizing the study of phenotypic cell-to-cell variations. Indeed, the host alters pathogenicity and heterogeneity of *S. marcescens* at the single-cell resolution. Altogether, our findings provide an insight into the pivotal roles of the host in harnessing the life history and heterogeneity of symbiotic bacterial cells, advancing knowledge of advance fundamental concepts of precise manipulation of bacterial communities.

Keywords: Bacterial single-cell RNA-seq; Transcriptomics; Microbiome; Heterogeneity; Pathogenicity

Lifestyle of Marine Biofilm Bacteria and Antimicrobial Resource Mining

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Abstract

Microorganisms are important components of the marine ecosystem. For a long time, microorganisms living in plankton have been studied extensively. However, a growing body of research shows that the species and functional diversity of attached-living microorganisms is severely underestimated and largely unknown. Our work in recent years has been directed on "Marine Biofilm Species-Functional Diversity and Resource Mining", including: 1) Marine biofilm species diversity and core functions; 2) Energy metabolism of typical biofilm bacteria; 3) Development of biofilm resources based on artificial intelligence. Through global sampling and metagenomic analysis, we constructed the world's first marine biofilm strain and core gene library, and systematically interpreted the species and functional diversity. We isolated rosebacters from marine biofilms and established a new model organism to study biofilm formation, bacterial energy metabolism, and carbon source utilization. It was found that Roseobacter can be oxidized under facultative anaerobic conditions through the sox gene cluster. The reduced sulfur element was used to obtain energy, and the regulatory mechanism of biofilms adapting to temperature changes was explored. On the basis of understanding the diversity of marine biofilms and the life characteristics of typical species, our recent work has established a biofilm culturable bacterial catalog and discovered more than 300 antibacterial peptide molecules with activity against pathogenic bacteria.

Keywords: marine biofilms, biodiversity, roseobacter, antimicrobial peptide

Clinical Glycoproteomics: Methods and Diseases

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Abstract

Glycoproteins, which constitute a significant proportion of post-translational products, play pivotal roles in various biological processes, such as signal transduction, cell construction, and immune response. Abnormal glycosylation may lead to structural and functional changes of glycoprotein, which is closely related to the occurrence and development of various diseases. Recent advancements in mass spectrometry-based clinical glycoproteomics have improved our ability to identify abnormal glycoproteins in clinical samples, thereby enhancing disease diagnosis and treatment strategies. In this review, we systematically summarize the progress of clinical glycoproteomic methodologies and discuss the typical characteristics, underlying functions, and mechanisms of glycoproteins in various diseases, such as brain diseases, cardiovascular diseases, cancers, kidney diseases and metabolic diseases. In addition, we highlighted potential avenues for future development in clinical glycoproteomics. This review will deepen the understanding of clinical glycoproteomic methods and diseases and promote the discovery of novel diagnostic biomarkers and therapeutic targets.

Keywords: clinical glycoproteomics, glycosylation, method, disease, mass spectrometry

PlantDRAW: a web tool for fast image-based phenomics recognition and analysis of disease in plant science

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Abstract

Plant diseases pose an enormous challenge globally, with the potential to cause 100 % yield loss and threaten global food security. Early detection and prediction of diseases can significantly reduce food losses due to diseases. For this reason, researchers have endeavored to develop high-throughput phenotyping methods for disease detection. However, the lack of integration of these existing methods for plant disease detection has led to poor rapid recognition detection of diseases. To improve the efficiency of disease detection, we have introduced PlantDRAW (Plant Disease Recognition and Analysis Web), a web-based plant disease recognition and analysis platform. PlantDRAW has valuable features such as rapid intelligent diagnostics, disease data, and efficient disease detection and control. PlantDRAW categorizes 60 crops and 384 diseases and performs disease detection and apple leaf disease segmentation tasks. Our web platform efficiently reduces photo analysis time to under 30 seconds, providing users with rapid calculation of disease-affected areas and comprehensive insights across 120 diverse metrics, achieving an impressive 94.78% accuracy in disease recognition. With its user-friendly interface and functional design, PlantDRAW has great potential to enhance plant disease control research. PlantDRAW is freely available at http://plantdraw.samlab.cn.

Keywords: Plant Disease Recognition, Plant Phenomics, Web Tool

Microbiome and mycotoxins distribution patterns of wheat grains from major wheat producing areas in China

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Abstract

Cereal grains are prone to mold, significant nutrient loss, and mycotoxin contamination, which poses a significant threat to food safety. It is estimated that China's annual food loss due to such problems is as high as 31 million tons, equivalent to 4.5% of the country's total food production. In-depth analysis of the microbiome on food grains is strategically important for the prevention and control of harmful microorganisms and their associated mycotoxins.

In this study, 485 samples were collected from the main production areas of wheat in China. Nationwide data analysis revealed significant geographical differences in grain microbial communities, with greater microbial diversity recorded in the southern regions compared to the northern ones. We confirmed that *Aspergillus flavus* (*Af*), *A. parasiticus* (*Ap*), *Fusarium graminearum* (*Fg*), *F. culmorum* (*Fc*), and *F. pseudograminearum* (*Fp*) were the main mycotoxin-producing fungi in these major wheat production areas. The Random Forest model could accurately predict mycotoxin contaminations, and we identified key biomarkers capable of predicting these contaminants. In addition, we found that the average temperature, rainfall, and grain moisture were the key factors regulating the distribution of mycotoxins and microbial communities.

Using cultureomics, we obtained more than 2,000 endophytic fungi and 2,000 bacteria from wheat seeds. Based on the core taxa and keystone species analysis, seven fungal and three bacterial species with high efficiency in antagonizing *Aspergillus flavus* were screened out. Among these, *Streptomyces* S54, which showed complete inhibition of *Aspergillus flavus* (100% inhibition), was particularly notable. The genome map of *Streptomyces* S54 has been completed, with a genome size of 7.7 Mbp, GC content of 72.2%, and encoding 6,514 genes. Bafilomycin and valinomycin produced by *Streptomyces* S54 are the primary functional molecules inhibiting *Aspergillus flavus*. This study provides a scientific foundation for the early detection of mycotoxin contamination and the prevention of mycotoxin outbreaks in wheat grain from harvest through storage.

Keywords: Cereal grain microbiome, Cereal mycotoxins, Seed microorganisms, Aflatoxins, Mycotoxin warning and control

Multi-omics insights on the gut microbial community associated with cardiometabolic health in Tibetans: a cross-sectional cohort study in Qinghai- Plateau Area in China

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Abstract

Variations in gut microbiota composition interact with host-exogenous factors such as diet, geography, and anthropometrics, exerting a pivotal role in human health. Nonetheless, there is a scarcity of in-depth understanding regarding intricate relationships between host-gut microbiome and cardiometabolic health in Tibetans who adapt to the high-altitude environment. Here, we characterized the composition and metabolic functions of the gut microbiome in 539 Tibetans residing at 2800 meters above sea level (high altitude) or residing above 4000 meters (ultrahigh altitude).Four distinct microbial community profiles (CPs) were identified peculiar to Tibetans, characterizing variability in microbial composition and functions across individuals. Variations in microbial compositions were predominantly explained by age, sex, body fat indices, serum alanine aminotransferase, uric acid, and habitual diet, with these factors diversely associated with CPs. Notably, we found associations between microbial CPs and cardiovascular phenotypes, i.e., hypertriglyceridemia, metabolic syndrome and obesity, with altitude serving as an effecting factor: *Blautia* and *Ruminococcus*-dominated CP and *Prevotella*-dominated CP were more prevalent in participants with hypertriglyceridemia, particularly those residing at high altitude. *Bacteroides* dominated CP negatively associated with hypertriglyceridemia in participants residing at high altitude. People had *Clostridum, Collinsella* and *Slakia* dominated CP were prone to be obesity and overweight at ultrahigh altitude. Similar trends were observed for CP-specific functional genes, particularly those involved in pyrimidine metabolism, purine metabolism, oxidative phosphorylation and fatty acid metabolism. Besides, potential causal links between CP-related genera and cardiovascular outcomes were verified using a two sample Mendelian randomization. Furthermore, we established novel connections between gut microbiota and specific lipoprotein sub-fractions, and elucidated the mediating role of lipoproteins, particularly low-density lipoproteins and its sub-fractions, in linking microbial CPs to cardiovascular outcomes. Our findings emphasize the clinical significance of microbial profiles, offering new perspectives on the interplay between host-exogenous factors and gut microbiota, as well as their link to cardiometabolic health in high-altitude populations.

Keywords: Gut microbiota, Microbial metabolism, Altitude, Metabolome, Mediation analysis, Plasma metabolome, Cardiometabolic health

Exploration and analysis of functional gene related to stem rot resistance in *Anoectochilus roxburghii*

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Abstract

In the cultivation of medicinal plants, pathogens often infect the plants, severely disrupting and damaging their normal growth, development, and metabolic processes. This results in a range of symptoms, including spots, rot, and wilting, ultimately leading to plant wilt and death. Stem rot is a destructive fungal infection affecting *Anoectochilus roxburghii*. While plant endophytes have been shown to play a role in diseases development, the interactions among pathogens, endophytes, and the plant are complex. Here, the dynamic changes and ecological functions of endophytic communities and the immune response mechanism of *A. roxburghii* were investigated through 16S rRNA gene and transcriptome sequencing. The results showed that stem rot altered the richness, diversity, and composition of endophytic communities, and reduced network complexity. Evolutionary tree analysis of transcriptome data identified six relevant genes: ArMAPK2, ArMAPK20, ArWRKY8, ArWRKY9, ArWRKY10, and ArWRKY18. Functional analysis using the yeast two-hybrid (Y2H) system revealed four pairs of interactions. Further investigation with the firefly luciferase (Luc) reporter assay showed that only ArWRKY9 and ArMAPK20 interact. Subcellular localization studies indicated that ArWRKY9 is located in the nucleus, ArMAPK20 is found in both the nucleus and cell membrane, and both genes are capable of nuclear localization. This provides a spatial possibility for the interaction between the two proteins.

Keywords: *Anoectochilus roxburghii*, Stem rot, Transcriptome, Yeast two-hybrid, Luciferase, Subcellular localization

BEEx: An Open-source Batch Effect Explorer for Medical Image-based Multicenter Studies

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Abstract

The batch effect is a nonbiological variation that arises from technical differences across different batches of data during the data generation process for acquisition-related reasons such as curating images from different sites or obtained by different scanners. This phenomenon can affect the robustness and generalizability of computational pathology- or radiology-based cancer diagnostic models, especially in multicenter studies. To address this issue, we introduce an open-source platform, Batch Effect Explorer (BEEx), that is designed to qualitatively and quantitatively determine whether batch effects exist among medical image datasets from different sites. BEEx incorporates a suite of tools that provide visualization and quantitative metrics based on intensity, gradient, and texture features to allow users to determine whether there are any image variables or combinations of variables that can distinguish datasets from different sites in an unsupervised manner. BEEx supports various medical imaging techniques, including microscopy and radiology. In this study, we present four use cases to investigate the presence of batch effects. The results of this study clearly demonstrate that BEEx can identify batch effects and validate the effectiveness of rectification methods for batch effect reduction. The source code for BEEx was implemented in Python and is available at https://github.com/wuusn/beex. The corresponding data are available at https://figshare.com/s/a58be7e45928df2dfcb2. A reproducible capsule of our work is also hosted on the CodeOcean platform with a provisional DOI of 10.24433/CO.1796644.v1.

Keywords: batch effect, digital pathology, radiology

Succession mechanisms of bacterial communities in the Yellow River under antibiotic stresses

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Abstract

The ecological risks and health safety problems caused by the abuse of antibiotics are increasingly prominent. Thus, the occurrence and distribution of antibiotics in the Yellow River and the response mechanism of bacterial communities need to be explored urgently. The amounts of seven quinolones and the related bacterial communities in the Yellow River through Henan Province was explored. Results showed that the contents of 7 quinolone antibiotics showed unique spatiotemporal heterogeneities, yet the clustering of community composition were inconsistent with those of environmental factors, suggesting that neutral processes played a certain role in the assembling of microbiota. The combined analysis of LEfSe and neutral community model (NCM) showed that distributions of 47.25% of marker species during spring flood and 46.04% in summer flood were greatly affected by environmental factors. The NCM was more suitable for non-marker species, among which 97.56% in spring flood and 97.86% in summer flood showed neutral distribution. All the community networks showed certain modularity except at site of XLD during spring flood. The modularities of networks during summer flood were significantly higher than spring flood ($P < 0.001$). Accordingly, the connectivity and aggregation coefficients of the former were significantly lower than those of the latter ($P < 0.001$). Combined analyses of key nodes and structural equational modelling indicated that multi-resistant *Acinetobacter lwoffii* and *Candidatus Planktophila* were key taxa of the comunities in spring flood, under the stresses of ofloxacin, lomefloxacin, pefloxacin and fluroxacin; while *Peredibacter starrii*, *Aquaspirillum serpens* and *Acinetobacter variabilis* played key roles in the assembling of communities affected by norfloxacin, pefloxacin and fluroxacin during summer flood. The correlations of "antibiotic stress - niche/neutrality dynamic equilibrium - community internal structure - key taxa in assembling" discussed in this study has deepened the understanding of the pattern and succession mechanisms of freshwater microbiota, and provided reference significance for the Yellow River harnessing.

Keywords: bacterial community, succession mechanisms, quinolone, the Yellow River, spring flood, summer flood.

Development of Novel Food Functional Ingredients via Gut Microbiota-Mediated Biotransformation of Dietary Phytochemicals: a Perspective

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Abstract

Dietary phytochemicals have been reported with diverse bioactivities based on in vitro and in vivo studies, while the health benefits of consuming phytochemical-rich foods (e.g., fruit and vegetables) and nutraceuticals in humans remain inconsistent. This discrepancy can be critically associated with the interindividual variability of human gut microbiota-mediated metabolism of phytochemical precursors, since many have poor oral bioavailability and can largely enter the colon to be metabolized by gut microbiota. Several studies indicate that some gut metabolites of phytochemicals can be bioactive and even more potent than respective precursors, like urolithins from ellagitannins, S-equol from soy isoflavones, and enterolignans from lignans. However, the fundamentals of gut microbiota-mediated metabolism of many phytochemicals, such as specific microorganisms, genes, enzymes, and bioactive metabolites remain largely unknown, limiting our ability to manipulate gut microbiota for human nutrition and health. Deciphering these fundamental issues by integrating multi-omics and classic biochemical techniques can support the development of novel food functional ingredients and next-generation nutraceuticals and probiotics via the strategy of gut microbiota-mediated biotransformation of dietary phytochemicals.

Keywords: Phytochemicals, Gut Bacteria, Bioactive Metabolites, Biotransformation Mechanism, Functional Food

The Construction of Electrically Neutral Nanoparticles and Research on Overcoming Tumor Resistance to Chemotherapy

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Abstract

The problem of tumor chemotherapy resistance is a critical clinical challenge, and high-charged polymer macromolecules, a new class of anti-tumor agents, can rapidly kill tumor cells and overcome chemotherapy resistance, attracting the attention of many researchers. However, high-charged macromolecular polymers usually exist as single polymer chains in solution, and when their positive charges are exposed, they may produce irreversible nonspecific toxicity when they accidentally bind to host cells. We synthesized a series of high-charged polyamino acid macromolecules and low-charged polymers with different functional groups through ring-opening polymerization reactions, and utilized electrostatic interactions to self-assemble into neutral Drug-Free nanoparticles, thus shielding and neutralizing the positive charges of high-charged polyamino acid macromolecules and reducing toxicity, providing a new research direction for overcoming chemotherapy resistance in tumors.

Keywords: data, drug delivery, biomaterials, nanotechnology, tumors, microenvironment.

OpenDecipher: Deciphering Mass Shifts in Proteomes via Side Chain Reactive Potentials

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Abstract

Proteomics-based open modification searching (OMS) have been a powerful tool for discovering novel post-translational modifications (PTMs). It remains challenging to decipher the chemistry and structure solely based on the mass shifts. Recognizing PTMs exhibit chemical and catalytic principles, we devised OpenDecipher, a workflow that deciphered mass shifts by enumerating their modification structures and the reactive potentials. Firstly, the sites of modification for each AA of the available 7229 modifications via 6 reaction rules were collectively reffered to as reactive-modification generation rulesets. Accordingly, OpenDecipher was trained to produce probabilistic predictions of modification structures, achieving over 88.88% test accuracy, using five-fold cross-validation. In an internal OMS dataset, OpenDecipher systematically revealed 1710 out of 2,357 mass shifts from 3,416,275 peptide-spectrum matches were potential novel PTMs. OpenDecipher also unveiled that 77.7% of hemoglobin's sites underwent 756 distinct modifications, and disclosed the trajectories of 485 potential novel PTMs stemming from its physiological functions. Furthermore, OpenDecipher revealed 34 novel and 41 known PTMs at 169 sites across 59 proteins collectively regulating non-small cell lung cancer progression, either cooperatively or antagonistically. A total of 9 divergent PTMs are confirmed to represent potential prognostic biomarkers. In summary, OpenDecipher effectively deciphers the structure and chemistry of novel PTMs.

Keywords: OpenDecipher, Reactive-modification Generation Rulesets, Novel PTMs, PTM Trajectories, Prognostic Biomarkers

Leveraging Artificial Intelligence and Microbiome Data for Enhanced Clinical Diagnosis and Treatment Assessment

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Abstract

With the rapid advancement of microbiome research and artificial intelligence (AI) technologies, their integration is increasingly demonstrating potential in clinical medicine. The microbiome plays a crucial role in the development of various diseases, including gastrointestinal disorders, metabolic diseases, immune dysregulation, and cancer. Traditional methods for analyzing microbiome data encounter significant challenges in managing complex, multidimensional datasets, which limits their applicability in disease diagnosis and treatment. The introduction of AI, particularly machine learning and deep learning, offers robust support for processing large-scale microbiome data, recognizing patterns, and developing personalized treatment plans. By integrating multi-omics data with clinical information, more accurate disease diagnosis and treatment evaluation can be achieved. Additionally, AI algorithms expedite the discovery of novel biomarkers, facilitting the implementation of precision medicine in clinical practice. In the future, the convergence of microbiome research and AI is expected to open new avenues for disease prevention, diagnosis, and treatment, thereby enhancing the quality and efficiency of healthcare services.

Keywords: Microbiome, Artificial Intelligence, Clinical Diagnosis, Multi-omics Analysis, Precision Medicine

Soybean Promoting Factor (SPF) Promotes Soybean Growth through Regulating Rhizosphere Microbes

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Abstract

The symbiotic system between rhizobia and leguminous plants is one of the primary mechanisms for biological nitrogen fixation. Increasing the number of rhizobia within a certain range enhances plant's nitrogen fixation capability. In recent studies, we identified a root-specifically expressing gene *RSG*, the metabolite catalyzed by RSG promotes soybean growth significantly, in agree with this, the soybeans growing in the soil that grew Arabidopsis plants overexpressing *RSG* grew much better than the control. Conversely, soil that had grown *rsg* mutants significantly inhibits soybean growth. We identified the differentially accumulated metabolites including a compound named SPF in Arabidopsis overexpressing *RSG* through a combined transcriptomic and metabolomic analysis. Further experiments revealed that exogenous application of SPF at a concentration of 1.5 μM significantly stimulated the formation of soybean root nodules and increased both dry and fresh root weight, suggesting that the RSG may regulate plant growth through SPF. To explore the mechanism by which SPF regulates soybean root nodule symbiosis, we plan to screen differential microorganisms (DEMs) using 16S high-throughput sequencing and evaluate the impact of SPF on DEMs, nodule symbiosis and soybean growth, which will enrich our understanding of SPF role on plant-microbe interactions.

Keywords: SPF, soil microorganisms, growth, soybeans

An integrated metaproteomics/metagenomics investigation of the underlying mechanism for formation of replant disease of *Rehmannia glutinosa*

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Abstract

Replant disease, also known as consecutive monoculture problems, is a typical plant-soil negative feedback phenomenon characterized by the repeated cultivation of the same plants on the same land over several years, despite standard field management practices, resulting in poor plant growth, increased disease issues, and declines in both yield and quality. The results of comparative metaproteomic analysis revealed the presence of soil proteins originating from plants, bacteria, and fungi in the rhizosphere of *Rehmannia glutinosa* under consecutive monoculture. Most plant-derived proteins related to carbon and nitrogen metabolism, stress response, and secondary metabolism (i.e. phenylalanine ammonia-lyase functioning in the phenylpropanoid metabolism) were up-regulated under consecutive monoculture. Most of microbial proteins related to protein metabolism, cell wall biosynthesis, and virulence factor synthesis were also up-regulated under consecutive monoculture. High-throughput pyrosequencing combined with metagenomics and culture-dependent approaches revealed that consecutive monoculture of this plant significantly affects both the structure and function of rhizosphere bacterial and fungal communities, resulting in a significant decrease in fungal community diversity indices and the relative abundances of Actinobacteria and its derivatives (e.g., *Streptomyces*, *Arthrobacter*, *Nocardioides*), *Bacillus*, *Pseudomonas* and Basidiomycota, but a significant increase in the abundances of pathogenic fungi such as *Fusarium* and *F. oxyporum*. In addition, the abundances of *Bacillus* and *Pseudomonas* strains with antagonistic activities against *F. oxysporum* were significantly lower in the rhizosphere under consecutive monoculture. Furthermore, it was found that the imbalance in the rhizosphere microbial community structure under consecutive monoculture was mediated by specific components of root exudates (such as phenolic acids and certain bioactive compounds) and microbe-microbe interactions (such as antagonism, quorum sensing, and quorum quenching). The findings of this study provide theoretical references and new insights for elucidating the mechanisms of replant disease in medicinal plants and for exploring scientifically effective measures to mitigate the issue.

Keywords: Replant disease, rhizosphere microbiome, omics analysis, root exudate, rhizosphere interaction

Identification of Glycerolipid Metabolism-Associated Prognostic Signatures in Liver Hepatocellular Carcinoma by A Multi-omics Framework

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Abstract

The incidence rate of liver hepatocellular carcinoma (LIHC) is rising. It's one of the most common cancers worldwide and accounts for substantial morbidity and mortality. Progress has been made in the treatment of LIHC. However, improved outcomes are much needed. The increased glycerolipid metabolism needs for cancer cells underscore the importance of metabolic pathways in survival time. Multi-omics data was collected and analyzed to visualize the alteration of glycerolipid metabolism-associated genes at the mRNA, methylation, CNV, and somatic mutation levels. ssGSEA was employed for calculating glycerolipid metabolism model score (GMMS). Univariate and multivariate Cox regression was used for calculating the prognostic values of GMMS. The molecular function and mechanism of GMMS were analyzed. We combined a scRNA-seq dataset for validating cell type distributions of GMMS. This research provided GMMS as a candidate prognostic factor for LIHC. GMMS is related to cancer hallmarks and tumor immune environment. We identified drugs with GMMS-dependent sensitivity. Glycerolipid metabolism disorders might appear in malignant cells.

Keywords: liver hepatocellular carcinoma (LIHC), glycerolipid metabolism, multi-omics, drug sensitivity, tumor immune microenvironment (TME)

Unravelling the adaptive mechanisms of aerobic granular sludge granulation under tetracycline stress by quantitative proteomic analysis

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Abstract

The presence of high concentrations of tetracycline (TC) in pharmaceutical and livestock wastewater threaten to human health and ecosystems. Although previous studies have explored the effects of TC antibiotics on microbial communities, the micro-responses of how these substances impact the formation and stability of aerobic granular sludge (AGS) are not well-documented. Thus, this study delved into the adaptive mechanism involved in AGS granulation with the continuous TC addition (1 mg/L) using proteomic approach. The results showed that TC accelerated AGS formation, achieving granulation within 20 days, with pollutant removal efficiency and settling performance significantly improving as granule size increased. Detailed analysis of extracellular polymeric substances (EPS), protein/polysaccharide (PN/PS) ratio, amino acid hydrophilic-hydrophobic properties, and protein secondary structure identified a critical size threshold of 3-4 mm for AGS stability under TC stress, with granules larger than 4 mm being prone to destabilization. Thus, it is advisable to take the size-effect into account when employing the TC fast-start AGS process. Additionally, label-free proteomic analysis further revealed that outer membrane protein A (OmpA) upregulation mediates biofilm formation, while TC-targeted ribosomes and bacterial chemotaxis were identified as key mechanisms driving AGS drug tolerance and stress responses, respectively. This study provides insights into proteins and mechanisms underlying AGS stability, resistance and stress responses under high-levels TC conditions, informing future AGS process optimization.

Keywords: Tetracycline; Proteomics; Adaptive mechanisms; Bacterial chemotaxis; Antibiotics resistance; Aerobic granular sludge

Antibiotic Resistome in Cow Milk and Environmental Sources in Pastures: A New Insight

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Abstract

Different microbial communities and antibiotic resistance (AR) in livestock environments threaten human and animal health due to the possible gene transfer to raw milk, impacting food quality and safety. The study focused on the dairy farms located in Liaoning Province, China, to assess the microbial content in their raw milk. In this study, key microbial indicators, including *Bacillus*, *Micrococcus luteus*, and *Psychrobacter*, were identified to evaluate the level of environmental contamination. Metagenomic analysis revealed abundant ARGs in raw milk, such as *macB*, *tetA(58)*, *bcrA*, *novA*, and *oleC*, associated with macrolides, MLS, bacitracin, tetracycline, β-lactam, and aminoglycosides. The findings indicate that pasteurization and proper storage procedures significantly diminish the abundance of ARGs in milk. The microbial resistance landscape in both milk and pasture environments was characterized, observing a positive correlation between ARGs and the resident bacterial communities. Furthermore, it was discovered that the pasture environments had a modulating effect on the gut microbiota of long-term workers, facilitating the proliferation of pathogens and AR genes. Specifically, microbial analysis of the feces of permanent workers revealed a dominance of *Weissella*, *Staphylococcus*, and *Escherichia coli*, whereas *Prevotella* was prevalent in short-term workers. This study is the first to explore the intricate connections between ARGs and bacterial communities in pasture environments, as well as their potential repercussions on human gut microbiota. This study also initially provides the analysis to verify the potential of horizontal gene transfer of *tetA* from the pasture environment to raw milk. In conclusion, the results offer valuable insights into the ARG profiles and their bacterial hosts within dairy farm environments. These findings not only enrich our understanding of the dissemination of antibiotic resistance genes but also serve as a foundation for further monitoring and mitigating the spread of antibiotic resistance in such settings.

Keywords: metagenomics; antibiotic resistance gene; cow milk; pasture environment; horizontal gene transfer; gut microbiota; SourceTracker analysis

Intervention of gut microbiota in ulcerative colitis using a probiotic colon targeted delivery system based on the antioxidant effect of *Codonopsis pilosula* polysaccharides

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Abstract

The occurrence of enteritis is closely related to the damage to the intestinal barrier and the imbalance of the microbiota caused by oxidative stress, forming a vicious cycle and jointly promoting the development of intestinal inflammation. As a dominant bacterium for intervening in enteritis, *Faecalibacterium prausnitzii* has great application prospects. Research has found that *Lactobacillus plantarum* WW is as effective as *F. prausnitzii* in repairing intestinal microbiota disorders, and has better antioxidant effects. In order to further enhance the ability of L. plantarum WW to treat ulcerative colitis (UC), the active ingredient CPP-2 in *Codonopsis pilosula* polysaccharides was isolated and found to have significant antioxidant activity and the ability to promote probiotic proliferation. Also, sulfhydryl CPP-2 (SC-CPP-2) generated through chemical modification significantly enhanced the interaction between probiotics and intestinal mucus. After co embedding SC-CPP-2 with probiotics in microcapsules, the targeted release and adhesion of probiotics in the intestine were achieved. The experimental results showed that microcapsules containing SC-CPP-2 significantly alleviated inflammatory symptoms in DSS induced mouse UC models, and enhanced the reparative effect of *F. prausnitzii*, especially *L. plantarum* WW. Microcapsules containing SC-CPP-2 can improve intestinal microbiota disorder caused by inflammation by increasing the abundance of beneficial bacteria such as *Akkermansia* and *Lactobacillus* in the gut of UC mice, and reducing the abundance of harmful bacteria such as *Lachnospiraceae*. At the same time, metagenomics suggests that the improvement of intestinal microbiota can regulate the metabolic processes of proteins, amino acids, and fatty acids. Further transcriptome analysis revealed that SC-CPP-2 may participate in the intervention process of colitis by regulating oxidative phosphorylation pathways and specific genes (such as *mt-Co1*, *mt-Nd3*, and *mt-Co3*). Therefore, intestinal oxidative stress may be a key pathway for enhancing probiotics to repair gut microbiota disorders and alleviate UC.

Keywords: Probiotics, oxidative phosphorylation, microbiota, *Codonopsis pilosula*, ulcerative colitis

GISDD: a comprehensive global integrated sequence and genotyping database platform for dengue virus, facilitating a stratified coordinated surveillance strategy

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Abstract

Dengue, the most rapidly spreading mosquito-borne infectious disease in the past three decades, poses a significant threat to human lives and health, while also presenting a formidable challenge to the global public health system. The precise identification of dengue virus (DENV) strains and their transmission patterns, coupled with the establishment of a comprehensive global collaborative monitoring and traceability strategy, holds immense significance for collective prevention and control efforts. Using phylogenetics, population genetics, phylogeography, and phylodynamics, we established a unified global high-resolution genotyping framework of DENV 1-4 serotypes wtih three hierarchical layers of genotype, subgenotype, and clade with respective mean pairwise distances 2-6%, 0.8-2%, and ≤0.8%. Then, we characterized their epidemic patterns representing stratified spatio-genetic epidemic pairs of Continent-Genotype, Region-Subgenotype, and Nation-Clade. The relentless spread of dengue and its increasing disease burden highlight the urgent need for a comprehensive and coordinated global response. A significant gap remains in the establishment of an efficient surveillance and risk prediction model for dengue. Bridging this gap, we developed GISDD (Global Integrated Sequence and Genotyping Database for DENV), leveraging our extensive research endeavors. GISDD features a suite of integrated online analysis tools, including GISDDrlearn and GISDDrRef, enabling rapid identification and tracking of well-established DENV genotypes, subgenotypes, and clades, thus facilitating insights into the molecular epidemiology, temporal

and geographical dissemination patterns of outbreak-associated DENV lineages. Accessible at http://www.bic.ac.cn/GISDD/, GISDD serves a valuable resource for researchers, public health authorities, and the general public. It lays a robust foundation for the implementing stratified coordinated surveillance strategies, crucial for blocking the rapid global dissemination of dengue.

Keywords: dengue virus; database; genotyping; surveillance strategy; online tools

Amplicon and whole-genome sequencing technologies reveal the microbial community composition, resistance genes, and evolutionary traits in chronic, non-healing wounds like pressure ulcers, offering insights into bacterial impact on wound healing

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Abstract

Chronic wounds that fail to heal have become one of the most significant global public health issues, and the presence of biofilms is increasingly recognized as a major barrier to wound healing. Compared to ordinary wounds, chronic wounds, such as pressure ulcers, are more prone to biofilm formation and exhibit significantly reduced microbial diversity. To investigate the dominant bacterial communities and their biological characteristics in pressure ulcers, we sampled wound surfaces from patients with pressure ulcers. Using amplicon sequencing technology, combined with pressure ulcer tissue staining, fluorescence in situ hybridization (FISH) detection, proteomics, and metabolomics analysis, we characterized the microbial composition of pressure ulcers, with a particular focus on *Staphylococcus aureus*. Our results showed that the *Staphylococcus* genus accounted for the highest proportion of isolates from pressure ulcer wounds and carried the largest number and variety of resistance genes, including *marR*, *bacA*, and *fosB*. Whole-genome sequencing of 29 isolated *S. aureus* strains revealed that the vast majority were resistant to penicillin and methicillin. In summary, our study elucidates the epidemiological characteristics of *S. aureus* in pressure ulcers and, for the first time, applies proteomic and metabolomic analyses to *S. aureus* isolated from pressure ulcers. This provides a scientific basis for studying microbial colonization patterns in chronic wounds and lays the foundation for further exploration of how *S. aureus* biofilms impact pressure ulcer healing.

Keywords: Chronic wounds; Pressure ulcers; *Staphylococcus aureus*; Sequencing; Antibiotic resistance genes

Anemoside B4 Alleviates Neuropathic Pain through Suppressing ALOX15, GNGT1, GNGT2, GNB3 and TPH1 mediated Inflammation

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Abstract

Neuropathic pain (NP)is defined as a type of pain that results fromdamage or disease affecting the somatosensory system. The prevalence rate is 6.9%to 10%. Calcium channel modulators, tricyclic antidepressants, and 5-hydroxytryptamine-norepinephrine reuptake inhibitors (duloxetine, venlafaxine) are currently the first-line therapeutic drug of choice for NP. However, these drugs are associated with undesirable side effects, including addiction, cardiovascular complications, respiratory depression and weight gain.

At present natural products cause close attention to NP treatment with advantages of precise efficacy, and safety charac-teristics. Anemoside B4 (AB4), the active component of triterpenoid saponins in the traditional Chinese medicine *Pulsatilla*, has significant anti-inflammatory and analgesic effects. However, its pharmacological mechanism of action on NP is not clear.

In this study, The spinal nerve ligation (SNL) rat model was constructed to evaluate the analgesia effects of AB4 by detecting the thresholds of mechanical pain and response times to cold stimulate, Then the hippocampal tissues of rats were selected for transcriptomic study to identify the key targets of AB4 action on NP and further verified by RT-qPCR. Based on the experimental results, AB4 was shown to produce analgesic effects in the rat SNL model and Alox15, Gngt1, Gngt2, Gnb3 and Tph1 were found to be closely associated with neuroinflammation and central pain sensitization. In addition, the binding sites of AB4 to these targets were predicted by molecular docking. AB4 was found to form tight binding hydrogen bonding forces with key target molecules of the synaptic pathway, Alox15, Gngt1, Gngt2, Gnb3 and Tph1. In addition, the inhibitory effect of AB4 on cytokines such as IL-1β, IL-6 and TNF-α in rat serum was detected by ELISA, and it was found that AB4 reduced the levels of inflammatory factors IL-1β, IL-6 and TNF-α in the serum of SNL rats. The anti-inflammatory effect of AB4 was verified. According to the above results AB4 could effectively ameliorate NP by inhibiting Alox15, Gngt1, Gngt2, Gnb3 and Tph1. Our findings suggested that AB4 can be regarded as a promising candidate for NP treatment.

Key words: Anemoside B4, neuropathic pain, inflammation

Impact of coronavirus disease 2019 (COVID-19) pandemic on nosocomial infection and our practical experiences

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Funding: Scientific Research Foundation of Shanghai Municipal Health Commission of Changning District, No. 20234Y038.

Abstract

Hospital infection prevention and control is a still major challenge for medical institutions in the post-COVID-19 era. Previous studies have shown that COVID-19 can affect the hospital infection related data including: hand hygiene compliance was improved, bacterial resistance rate and bloodstream infection was increased, the incidence of ventilator-associated pneumonia was decreased, the type of pathogenic bacteria was changed, while the catheter-associated urinary tract infections did not change significantly. With in-depth analysis of relevant influencing factors in published literature and based on our practice experiences on the prevention of hospital infection, we propose these strategies to prevent and control nosocomial infection as follows: Firstly, medical staff, supplies, and wards should be prepared in advance. we strengthened the training of emergency team members including supervisors for epidemiological investigation, disinfection and eagle-eyed observer, enhanced the awareness of prevention and control in medical staff, and provided sufficient emergency stockpile of protective materials; Secondly, combined prevention and treatment measures could be adopted to control nosocomial infections during the COVID-19 pandemic, such as advocating viral infection prevention through vaccination, disinfection, and the training of heathcare personnel, and exploring therapeutic strategies involving cellular inflammatory factors and novel medications tailored for COVID-19 patients; Thirdly, information technology should be strengthened to prevent and control nosocomial infection during the COVID-19 epidemic, such as usage of Ding Talk, online diagnosis and service system, etc; Additionally, new scientific research products were developed such as low-temperature plasma generator and wireless stethoscope. The implementation of these strategies will vigorously promote the development of hospital infection prevention and control work, reduce the incidence of hospital infection, and protect the health of patients in the post-COVID-19 era.

Keywords: COVID-19, nosocomial infection, practical experiences, prevention and control

Mechanistic Insights into the Role of RG-I Polysaccharide in Modulating Gut Microbiota for the Treatment of NAFLD

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Abstract

Polysaccharides are gaining prominence for their therapeutic potential in metabolic disorders, particularly due to their safety and efficacy. *Typha angustifolia* L. pollen has been traditionally used in China for lipid-lowering purposes. A pectic polysaccharide (PTPS22) was isolated from T. *angustifolia* pollen, composed of rhamnogalacturonan I (RG-I) and arabinogalactan II (AG-II) domains. In a high-fat diet (HFD)-induced non-alcoholic fatty liver disease (NAFLD) mouse model, PTPS22 significantly reduced total cholesterol (TC) and triglyceride (TG) levels in serum and liver tissues. It also ameliorated intestinal barrier damage induced by HFD and promoted the growth of beneficial gut bacteria, particularly Bacteroides.

To further investigate the role of gut microbiota in the therapeutic effects of PTPS22, we conducted experiments using pseudo-germ-free mice and fecal microbiota transplantation (FMT). In pseudo-germ-free mice subjected to antibiotic intervention, PTPS22 did not reduce body weight or liver fat, suggesting the necessity of gut microbiota for its lipid-lowering effects. In contrast, mice receiving fecal microbiota from PTPS22-treated mice exhibited significant reductions in body weight and liver fat, highlighting the transferable effects of gut microbiota. These results underscore the importance of gut microbiota in mediating the lipid-lowering effects of PTPS22, particularly through the modulation of Bacteroides, positioning RG-I pectin PTPS22 as a promising candidate for NAFLD therapy through gut microbiota modulation.

Keywords: *Typha angustifolia* L., RG-I pectin polysaccharide, NAFLD, Gut microbiota, Bacteroides

Safety and Efficacy Assessment of Fecal Microbiota Transplantation as an Adjunctive Treatment for IgA Nephropathy: An Exploratory Clinical Trial

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Abstract

Objective: To assess the safety and efficacy of fecal microbiota transplantation (FMT) as an adjunctive therapeutic intervention for IgA nephropathy (IgAN).

Methods: Fifteen patients with IgA nephropathy were recruited based on inclusion and exclusion criteria and underwent FMT using enteric microbial capsules. Clinical indicators, intestinal microbiota and metabolomic profiles, as well as changes in serum immune cells and cytokines, were monitored before and after FMT.

Results: No severe adverse reactions were observed in the subjects. After FMT, there was a reduction in the 24-hour urinary protein quantification in subjects. The relative abundances of *Phocaeicola_vulgatus*, *Bacteroides_uniformis*, *Prevotella_copri*, *Phocaeicola_dorei, Bacteroides_ovatus*, *Bacteroides_xylanisolvens*, *Parabacteroides_distasonis*, *Bifidobacterium_pseudocatenulatum*, *Bacteroides_sp._HF-162*, and *Bifidobacterium_longum* changed after FMT. In terms of intestinal metabolites, the levels of acylcarnitine18:0 (ACar.18:0), cotinine, N-arachidonoyl-L-serine, phosphatidylcholine (PC. (18:3e/22:6)), serotonin, and fumagillin showed significant changes. Flow cytometry analysis showed the absolute count of plasma B cells decreased in subjects, and this change correlated with alterations in the intestinal microbiota and metabolites.

Conclusion: This study preliminarily evaluates the safety and efficacy of FMT in patients with IgAN. No significant adverse reactions were observed, and the administration of FMT alongside ACEI/ARB therapy was effective in reducing urinary protein levels in patients with IgAN, a process that may be associated with B-cell immunity.

Keywords: IgA Nephropathy, Fecal microbiota transplantation, Immune Function, Gut Microbiota and Metabolites, Clinical Trial

Enlarging interface reverses the dominance of fungi over bacteria in litter decomposition

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Abstract

Soil microorganisms are primary decomposers driving carbon and nutrient cycling in terrestrial ecosystems. One prevailing view is that fungi, rather than bacteria, play a predominant role in litter decomposition. However, the distinct ecological roles of fungi and bacteria has focused mainly on the chemical quality of litter. We hypothesized that the limiting activity of bacterial decomposers is associated with litter size. We conducted a 180-d decomposition microcosm experiment to investigate the effect of fragment size (large, 1–2 mm; middle, 0.18–0.28 mm; small, <0.07 mm) of litters on bacterial or fungal decomposition. Bacterial and fungal decomposition were accelerated with fragment size decrease, suggesting that an interface effect existed between microbial decomposers and litter. The decomposition ability of bacteria was more sensitive to changes in fragment size compared to fungi. The contrasting decomposition dominances of bacteria versus fungi were likely attributed to filamentous fungi penetrating litter interiors and forming mycelial bridges between scattered litters. Bacteria resided on litter surfaces and even formed biofilms. Consequently, the dominance of fungi and bacteria during litter decomposition in the conventional view should be revisited considering the litter size.

Keywords: litter decomposition; particle size; microbial ecology; fungal and bacterial dominance; interface effect

Regulation of gut microbiota through diet in preventing hyperuricemia

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Funding: Scientific Research Foundation of Shanghai Municipal Health Commission of Changning District, No. 20234Y038.

Abstract

In recent decades, the prevalence of hyperuricemia (HUA) has surged, positioning it as the second most significant metabolic disease impacting public health. HUA adversely affects patients' quality of life, and early detection, prevention, and treatment are challenging due to the lack of obvious clinical symptoms in the disease's early stages. Gut microbiota plays a crucial role in body metabolism, and while several studies have investigated its influence on HUA, the specific role of different bacterial genera and their mechanisms remain underexplored. Probiotics can enhance the breakdown of uria acid (UA), whereas harmful bacteria may inhibit this process. The gut microbiota influences both UA production and excretion, while elevated circulating UA can alter the intestinal environment, further impacting the gut microbiota. This creates a bidirectional relationship where UA levels and gut microbiota interact and influence each other. Regulating gut ecology through dietary changes may help prevent HUA. Diets high in protein and fat may reduce gut microbiota diversity, potentially affecting UA excretion. Patients with HUA are advised to reduce high-purine foods, increase their intake of vegetables, fruits, and whole grains. We also recommend the DASH dietary pattern as the first choice for patients with HUA. Additionally, supplementing with specific probiotics to regulate gut microbiota and maintain intestinal homeostasis is an effective strategy for preventing and treating diet-induced HUA.

Key Words: hyperuricemia, gut microbiota, interaction, dietary patterns

Specific supplementation of probiotics combined with meta-biotics, prebiotics, and high dietary fiber may alleviate the progression of IgAN

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Abstract

Background: IgAN is a kidney disease that seriously threatens human health, but its exact pathogenesis has not been elucidated. However, the current treatment of IgAN in China mainly aims to delay the progression of kidney disease, and it is difficult to intervene in the inflammation-immune response. Studies have shown that intestinal flora imbalance can induce intestinal mucosal barrier damage and participate in the pathogenesis of IgAN. The research on the intervention of intestinal flora imbalance to alleviate the progression of IgAN needs to be further explored.

Methods: In this study, the IgAN mice model induced by micro-23b gene knockout were specifically supplemented with intestinal probiotics and their derivatives (including probiotics, prebiotics, metabiotics, metabolites, etc.) and interfered with dietary structure (high dietary fiber). The changes in intestinal permeability, renal function, and inflammation-immune response in IgAN mice before and after treatment were compared.

Results: The results showed that compared with the control group, the experimental group showed remission trends in connexin, intestinal pathology, and intestinal sIgA. In addition, renal pathology, renal function (such as 24-hour urine microalbumin, serum creatinine, urea nitrogen) pathological results, and inflammatory factors showed a downward trend ($p < 0.05$). More interestingly, the experimental group's body weight, serum triglyceride, cholesterol, low-density lipoprotein, and other indicators also showed a significant downward trend ($p < 0.05$).

Conclusion: The specific synbiotics mixture selected in this study can alleviate the intestinal stress state to a certain extent by alleviating the imbalance of intestinal flora, reversing and delaying the occurrence and development of IgAN, and has a certain lipid-lowering effect to accelerate the basal metabolism of the body, to achieve the purpose of weight loss.

Our team provides a new idea for the prevention and adjuvant treatment of IgAN with probiotics by improving intestinal flora disorder, reducing the kidney's immune-inflammatory response, and delaying kidney disease.

Keywords: Gut Microbiota, Probiotics, Metabiotics, Prebiotics, Fucose, IgAN, Treatment

Landscape of intestinal microbiota in patients with vasculitis

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Abstract

Objective: This study explores the differential intestinal bacteria in patients with different types of vasculitis by analyzing the 16s sequencing data of intestinal bacteria in vasculitis patients and healthy controls.

Methods: By searching for vasculitis 16srRNA sequencing related intestinal bacteria papers in databases, systematically organizing and analyzing the literature, downloading the original data from related databases, screening the intestinal bacteria of vasculitis patients with Alpha Diversity Analysis and Beta Diversity Analysis, and finally comparing the intestinal differential bacteria of vasculitis patients with the control group.

Results: Compared with healthy controls, intestinal bacteria Alpha diversity and Beta diversity were reduced in vasculitis patients, and machine learning analysis showed that among the bacterial genera with the greatest importance of differences between patients with different types of vasculitis and healthy controls, the relative abundance of Prevotella was decreased in the centers of patients with IgAV, True/Euthyrobacterium was more abundant in patients with EGPA, Clostridium in patients with SLE elevated, and Enterococcus had higher relative abundance in KD patients. Fusobacterium were more abundant in UV patients and Uruburuella were more abundant in AAV patients.

Conclusions: Patients with vasculitis suffer from intestinal microecological dysregulation and have decreased abundance of several beneficial bacteria and increased abundance of potentially pathogenic bacteria, and this study may provide new ideas for the study of pathogenesis and diagnostic markers of vasculitis.

Keywords: Vasculitis, Intestinal microbiota, Intestinal microbiome, Machine Learning

The Rice M gene recruit its microbiome to mitigate diseases

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Abstract

Rice (*Oryza sativa L.*) is the prime staple food source for half of the global population. However, the rice blast restricts the healthy development of rice industry. Lately, a large number of studies have found that plants can recruit specific microorganisms to utilize specific host genetic traits to shape and maintain microbial communities with desired functions. Our previous work had revealed the mechanism of rice leaf microbiome assembly is regulated by host genetics, for the first time. And we defined these genes that can enrich beneficial microbial populations and inhibit pathogenic microbial populations in plants as M genes (Microbiome-shaping genes). The results indicate that specific M gene haplotypes in rice plants can significantly recruit specific microbiome resulting in plant healthy. Therefore, we focus on screening for specific M gene haplotypes connected with desirable microbiome structures can be implemented as part of pre-breeding strategies with germplasm collections. Meanwhile, we work on exploring essential signal molecules (such as phytohormones) which participate in communicating with M genes, to provide theoretical support for their roles in improving rice disease resistance traits. All in all, implementation of M gene breeding, advancing in line with R gene and S gene strategy, reinforce agriculture sustainability in a novel way.

Keywords: Rice, M gene, Plant microbiome, Phytohormones

Spatial Metabolomics of *Fissistigma oldhamii* using UPLC-HRMS-MS and Laser Microdissection: Insights into Toxic Aristololactam Distribution

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Abstract

The medicinal plant *Fissistigma oldhamii* is recognized for its properties in wind dispelling, damp removal, blood activation, and pain relief, utilizing both roots and aerial parts for medicinal purposes. However, its nephrotoxic aristololactam components necessitate a clear understanding of their distribution within the plant to guide safe medicinal use. This study employed laser microdissection technology to isolate various tissue cells from the primary medicinal parts (roots, stems, leaves) of *F. oldhamii*, followed by qualitative and quantitative spatial metabolomics analysis using high-resolution mass spectrometry. A total of 99 components were identified and localized within the tissue cells, with 5 shared across all cells: haplotubinone, norannuradhapurine, 1,2-dihydrotanshinquinone, xylopine, and oxoxylopine. Other components showed distinct distribution patterns; for instance, the specific components 5,6,7-trimethoxyflavone and norcepharadione B were found in the xylem cells of the roots, while norfissilandione was located in the root pericycle. The unique component fissicesine was present solely in the stem pericycle, and isoquercitrin was restricted to the palisade and non-glandular hair cells in the leaves. Notably, 10 toxic aristololactams were identified, showing the highest diversity in the roots and stems. Most of these toxic alkaloids exceeded 50% relative contents in the stems, especially for enterocarpam I, aristolactam BII, G I, and piperolactam C, which surpassed 80%. Additionally, these aristololactams are primarily concentrated in the periderm cells. These findings suggest that all plant parts should be carefully evaluated for oral administration, especially the stems. Overall, this research clarifies the in vivo distribution of key effective components and aristololactam compounds in *Fissistigma oldhamii*, assessing the medicinal value of different parts and providing a scientific basis for safe clinical application.

Keywords: *Fissistigma oldhamii*, Xiangteng, Laser microdissection, Aristololactam, Spatial metabolics.

Enhancing the functional properties of traditional Chinese herbs through probiotic fermentation

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Abstract

Traditional Chinese herbs contain hundreds of different components, including flavonoids, saponins, and polysaccharides, which are knowned for their diverse biological activities and pharmacological effects. However, the contents of these bioactive ingredients are often relatively low. Isolated microbes from traditional fermented foods can be utilized to ferment herbs, thereby enhancing herb bioactivites. We have isolated over 1,000 different microbial strains (most are probiotics) from various fermented foods, and investigated the characteristics and genomes of these strains. Based on this information and previous studies on probiotic fermented herbs, we screened out and synthesized several distinct functional probiotic microbiota. Fermenting herbs with some isolated probiotics and synthetic microbiota significantly increase the contents of bioactive compounds in *Astragali Radix*, *Epimedii Folium*, and several other herbs. This work lays a foundation for the future development and application of isolated probiotics derived from traditional fermented foods to enhance herb pharmacological activities.

Keywords: Probiotics; Fermenation; Herbs; Synthetic microbiota; Traditional fermented foods

Large language model helps mining the role of resistomes in cyanobacterial blooms

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Abstract

Eutrophication has threatened freshwater lakes worldwide, leading to the ecological problem of cyanobacterial blooms, whose basic unit is the cyanobacterial aggregate (CA). CA-attached bacteria, as carriers of antibiotic resistance genes (ARGs), play significant roles in cyanobacterial blooms. However, the mechanism underlying the mutual influence between CA and ARGs host remains poorly known. Metagenomics allows the identification of ARGs by aligning against databases, but unfortunately leading to high false negatives. To address this limitation and investigate the relationship between cyanobacterial blooms and ARGs, we propose a deep learning approach, ESMARG, based on a transformer-based large language model. Evaluation across 40 ARG categories demonstrates that ESMARG can predict and classify ARGs with high F1 score of 95.7% and 97.83%, and it is tens of times faster than alignment-based methods. Applying ESMARG to 26 CA metagenomes from Lake Taihu revealed that 20 ARG categories are broadly represented, with aminoglycoside, multidrug and tetracycline being the major categories. The total ARG abundance showed significant difference across sampling sites and seasons, and the ARG compositions were strongly aligned with cyanobacterial compositions, with Bacteroidetes and Alphaproteobacteria being the main carriers. The ARG abundance was positively correlated with the mobile genetic elements (MGEs) at the community level, and 46 out of the 110 recovered high-quality MAGs (42%) carried ARGs, with 19 of them (17%) carrying both AGR and MGEs. Furthermore, null model analyses indicated that the CA resistome variations were mainly controlled by stochastic assembly mechanisms. These results demonstrate that cyanobacterial blooms are a crucial driver of ARG diffusion and enrichment in freshwater, thus providing a reference for the ecology and evolution of ARGs for better assessing and managing water quality in lakes.

Keywords: cyanobacterial aggregate, metagenomics, antibiotic resistance genes, large language model

Chromosome-level genome assembly and population genomic analysis provide novel insights into the immunity and evolution of *Sogatella furcifera*

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Abstract

Sogatella furcifera is an agricultural pest of great concern in China and Southeast Asian countries. However, the lack of accurate and complete reference genome resources has hindered the understanding of immunity and evolution of *S. furcifera*. Here, we utilized Nanopore sequencing to generate a chromosome-level assembly and annotation of the *S. furcifera* genome (0.64 Gb), with a GC content of 34.25%. This genome comprised 15 chromosomes covering 95.04% of the estimated genome size, together with an additional 624 small scaffolds making up the remaining 4.96% of the genome of *S. furcifera*. A total of 24,669 protein-coding genes as well as 1211 long noncoding RNA and 7595 circular RNA transcripts were well annotated and predicted. Comparative genomic analysis revealed the rapidly evolved genes associated with multiple immune-related pathways in *S. furcifera*, which may be responsible for its rapid evolutionary adaptation. Genome resequencing of 44 individuals from 12 geographic populations revealed an absence of population structures and frequent gene flow among all populations. Sweep analysis indicated that 2926 genes were under natural selection and significantly enriched in several biological processes of morphogenesis and immunity. In addition, 14 immune genes in the classic immune pathways were selected for functional validation through RNA interference experiments, demonstrating the antiviral effects of *Dorsal* and *Dif* genes in *S. furcifera*. The first systematic identification of immune genes and noncoding RNAs from chromosome-level genome assembly plus the comparative and population genomic analysis will provide more insights into the understanding of the immunity and evolutionary adaptation of *S. furcifera*.

Keywords: chromosome-level genome assembly, *Sogatella furcifera*, comparative genomics, immune genes, population genomics

Genotype-associated core bacteria enhance host resistance to kiwifruit bacterial canker

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Abstract

The plant microbiome is closely related to host disease resistance or susceptibility, and revealing how microbes and their host plants respond to diseases is important for advancing coevolutionary theories of plant-microbiome interactions. Here, we integrated amplicon sequencing, machine learning, and culture-dependent methods to investigate the impact of plant compartment, host genotype, field location, and *Pseudomonas syringae* pv. *actinidiae* (*Psa*) invasion on the kiwifruit microbiome and to compare changes in the microbiome between the aboveground and belowground compartments of *Psa*-infected resistant and susceptible kiwifruit cultivars under natural field conditions. Compared to the susceptible cultivar 'Donghong', the resistant cultivar 'Wanjin' exhibited higher abundance of *Pseudomonas* spp. and *Sphingomonas* spp. in the phyllosphere, and a wide range of potential biocontrol bacteria, including *Bacillus* spp., *Streptomyces* spp., and *Lysobacter* spp., in the rhizosphere. The key bacterial taxa in belowground compartment of 'Wanjin' is largely independent of geography. *Psa* infection significantly affected the microbiome of the phyllosphere of kiwifruit plants, especially that of 'Donghong'. Resistant and susceptible kiwifruit cultivars exhibit distinct beneficial microbial recruitment strategies under *Psa* challenge. The phyllosphere of 'Donghong' in Jinzhai County was enriched with *Sphingomonas* spp. and *Pantoea* spp. under *Psa* infection, while the rhizosphere of 'Wanjin' was enriched with *Sphingomonas* spp. and *Novosphingobium* spp. We further identified five key biomarkers within the microbial community associated with *Psa* infection. Detached-branch inoculation experiments showed that *Pseudomonas* sp. RS54, *Stenotrophomonas* sp. R31 and *Lysobacter* sp. R34, which were isolated from the root endosphere or rhizosphere of 'Wanjin', could positively affect plant performance under *Psa* challenge. The combination use of *Pseudomonas* sp. R10 and *Stenotrophomonas* sp. R31 significantly improve the control of kiwifruit canker. The findings provided novel insights into soil–microbe–plant interactions and the role of microbes in plant disease resistance and susceptibility.

Keywords: Kiwifruit bacterial canker, *Pseudomonas syringae* pv. *actinidiae*, amplicon sequencing, microbiome assembly, beneficial microbes

Bacteria-Mediated Colorectal Cancer Immune Subtyping

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Abstract

For colorectal cancer, the benefits of immunotherapy are limited to a minority of patients with deficient mismatch repair (dMMR) and high microsatellite instability (MSI-H). Understanding the complexity and heterogeneity of the tumor immune microenvironment (TIME) and identifying immune-related colorectal cancer subtypes will improve antitumor immunotherapy. Currently, typing for colorectal cancer patients is mostly based on the genomic or transcriptomic changes of the patients themselves. This study, based on the combined analysis of transcriptomes and intra-tumor microbiomes from tumor and adjacent tissues of 31 colorectal cancer patients, found 1) Compared to the transcriptome, the differences in microbes between tumor and adjacent tissues are less than the differences between individuals, indicating that the impact of microbes on patients is systemic. 2) Based on the heterogeneity network analysis of the transcriptome and microbiome of tumor tissues, we identified a module 95(M95) which is highly related to immune response. Patients can be subclassified into two subtypes(CA1 and CA2) based on the genes of M95. CA1, showing significantly stronger immune infiltration than CA2, accompanied by overexpression of genes related to interferon-gamma response, PD-1, and MHC-II. 3) In the CA1 group, it is highly enriched of Bacteroides fragilis, Peptostreptococcus stomatis, Porphyromonas gingivalis, which is also confirmed the enrichment of Bacteroides fragilis and Porphyromonas gingivalis in the tissues of CA1 by immunohistochemistry. 4) Combining with the TCGA database, we found that the survival rate of the CA1 group was lower than that of the CA2 group. 5) Although the CA1 group had a poor prognosis, its immune activation status suggests that CA1 may be more sensitive to immunotherapy, the gene set of M95 combine 3 bacteria can serve as a potential biomarker for PD-1 treatment.

Keywords: colorectal cancer, immunotherapy, subtyping, microbiome, transcriptome

Research Progress on the Role of Gut Microbiota in the Pathogenesis of Alcoholic Liver Disease

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Abstract

Alcoholic liver disease (ALD) is a liver condition resulting from long-term excessive alcohol consumption. In recent years, research on the relationship between gut microbiota and ALD has been proliferating, uncovering the ubiquitous presence of gut microbiota dysbiosis in the course of ALD. This review aims to thoroughly explore the potential role of gut microbiota in the pathogenesis of ALD, emphasizing the intimate structural and functional connection between the gut and liver, along with their frequent material exchange. The gut plays a pivotal role in the progression of ALD, and alterations in gut microbiota metabolites such as bile acids, long-chain fatty acids, β-glucans, and moniliformin are closely linked to the occurrence and development of ALD. The mechanisms involved encompass gut-derived factors like impaired intestinal barrier function, microbial imbalance, and intensified gut-liver axis activity. Despite the progress made in current research, there are still numerous unknowns in the field of gut-derived mechanisms of ALD. Continuous exploration in this area will enhance our understanding of the pathological process of ALD and pave the way for the development of prevention and treatment strategies, as well as drugs targeting the gut for ALD intervention.

Keywords: Gut microbiota; Alcoholic liver disease; Mechanism of action; Drug development

Application study of sedimentary ancient DNA technology in archaeological sites and its potential in open-air sites on the Tibetan Plateau

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Abstract

Unveiling the species information preserved in archaeological sites and reconstructing the subsistence patterns of people across different periods are essential for understanding the prehistoric human-land relationship and investigating the emergence and evolution of civilization. In recent years, the advent of sedimentary ancient DNA technology has revolutionized archaeological research. This innovative technique enables the simultaneous identification of species—including humans, animals, plants, and microorganisms—by analyzing ancient DNA found in site deposits. It offers a systematic approach to reconstructing the living resources of ancient populations, presenting a novel avenue for archaeological exploration. However, this technology remains underutilized in certain types of archaeological sites, particularly open-air site. As a primary category of archaeological location, open-air site may suffering a high leaching risk and significant stratigraphic disturbance, which raise concerns about the reliability of ancient DNA studies in these contexts. The Tibetan Plateau, known as the "third pole" of the world, offers dry, cold, and anoxic conditions that are excellent for the preservation of ancient DNA in sediments. The open-air archaeological sites on the Tibetan Plateau provide a wealth of resources for ancient DNA studying. While the concerns about the open-air sites hinders the sedimentary ancient DNA application. In this paper, we summarize sedimentary ancient DNA studies within archaeological contexts and propose several methods to mitigate the effects of leaching: 1) Conduct systematic sampling and multi-parameter analyses to identify criteria for ancient DNA leaching and disturbance in open-air site sediments; 2) Utilize a combination of laboratory experiments and field simulations to assess the impact of leaching and disturbance under various sedimentary conditions on the distribution of sedimentary ancient DNA; 3) Develop systematic analysis methods for sedimentary ancient DNA, incorporating macro damage models and molecular dating to clarify the age of identified species. Therefore, we urge sedaDNA researchers to focus on establishing a study system for sedimentary ancient DNA that is tailored to open-air sites, providing crucial support for its effective application in this unique region.

Keywords: Tibetan Plateau; Environmental Archaeology; Neolithic Period; Sedimentary ancient DNA; Paleoecology

Bacterial consortium LX interaction with rice change phthalate environmental behavior and plant physiological characteristics in soil-crop system to reduce PAEs accumulation

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Abstract

The phthalatic esters (PAEs) poses a serious challenge to ecosystem and human health. This study aimed to evaluate the potential of plant growth promoting and PAE degrading consortium LX for reduce soil-crop accumulation of PAEs. The consortium LX consisted of three bacterial strains and exhibited DBP and DEHP degradation ability, which shortened the half-lives for DBP and DEHP in soils respectively by 20.0 d ~ 23.1 d and 36.6 d ~ 75.1 d. The inoculation of the consortium LX improved the activity of antioxidant enzymes in rice plant, alleviated PAE stress in rice cells and promoted rice growth, including promoting root development, photosynthesis, and nutrient absorption. The rice assisted by the bacterial consortium LX improved the availability of PAE in rhizosphere soil to enhance the biodegradation of DBP and DEHP (25%~113% increase, 30 d). Thus consortium LX inoculation effectively prevents the migration and transport of PAE in soil-plant, and reduced 46.1%~57.7% DBP and 30.2%~40.5% DEHP accumulation in rice grains. Moreover, the presence of the consortium LX regulated bacterial community structure of soil and plant to drive biodegradation and plant growth promoting functions. This study revealed the mechanism of bacterial bioaugmentation to reduce the accumulation of organic pollutants in crops, and provided new insights and technologies for the development and application of microbial agents.

Keywords: Food crop; Organic pollutant; Bioaccumulation; Biodegradation; Microbial community

BGC Block Aligner：A Protein Functional Site-Based Tool for Improved Alignment of Biosynthetic Gene Clusters

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Abstract

The diversity and widespread distribution of natural product biosynthetic gene clusters (BGCs) present significant challenges for data mining. Siderophore BGCs in microorganisms exemplify this issue due to their ubiquity and high diversity. This diversity manifests not only in the distribution of different siderophore BGCs across species but also in the extensive cross-species occurrence of functionally identical siderophore BGCs. Accurate identification and differentiation of these BGCs are crucial for natural product discovery and functional studies.

Traditional BGC alignment methods, which primarily rely on sequence similarity, face two major limitations: (1) difficulty in precisely distinguishing substrate recognition within the same protein family or domain based on sequence alone; (2) sequence similarity in cross-species analyses is heavily influenced by phylogenetic relationships, leading to inaccurate functional predictions. These limitations hinder the precise identification of natural product functional groups and limit the depth of data mining.

To address these challenges, we developed **BGC Block Aligner**, a BGC alignment algorithm based on protein functional sites. This approach leverages an in-depth understanding of core synthetic protein recognition mechanisms and protein structure predictions from tools like AlphaFold. The algorithm benchmarks core synthetic protein functions, focuses on recognition sites, and establishes a new standard for measuring BGC similarity, applicable to comparisons of BGCs from NRPS (Non-Ribosomal Peptide Synthetase) and NIS (NRPS-Independent Siderophore) pathways.

BGC Block Aligner significantly outperforms the current mainstream algorithm, BiG-SCAPE, in functional resolution, providing a powerful tool and a new research paradigm for natural product data mining. Utilizing this tool, we systematically clustered and classified microbial siderophore families. This method will facilitate deeper exploration of natural product diversity and promote the discovery and utilization of novel bioactive molecules.

Keywords: BGC, Natural Products, Siderophore

Punicalagin alleviates hyperuricemia in mice via modulating gut microbiota and branched-chain amino acid metabolism

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Abstract

Hyperuricemia is a metabolic disorder characterized by the high level of uric acid (UA) in serum. The incidence of HUA has been increasing in China in recent years. Punicalagin (PU) has been reported to improve hyperuricemia, but the underlying mechanisms remains largely unexplored. In this study, a hyperuricemia mice model was used to determine the protective effects of PU on hyperuricemia. PU decreased the levels of uric acid (UA), creatinine and urea nitrogen in murine serum, inhibited the activities of xanthine oxidase (XOD) and superoxide dismutase (SOD) in both liver and serum, and alleviated the pathological damage of liver and kidney. Meanwhile, PU decreased the expression levels of purine metabolism related proteins and genes in the liver and increased the expression levels of UA excretion related genes and proteins in the kidney of hyperuricemia mice. PU also effectively remodulated the composition of gut microbiota in mice, including the increased abundance of *Akkermansia* and *Lactobacillus* and the reduced abundance of harmful microorganisms including *Clostridiales* and *Streptococcus*. Fecal microbiota transplantation and antibiotic interference experiments also confirmed the important role of gut microbiota in the protective effects of PU on the hyperuricemia mice. Meanwhlie, PU stimulated the branched chain amino acids (BCAA) metabolism in the gut, and BCAA recapitulated the benefical effects of UA on hyperuricemia. In conclusion, punicalagin effectively relieved hyperuricemia in mice by modulating UA synthesis and excretion, which is at least partly mediated by gut microbiota and BCAA.

Keywords: Hyperuricemia; Punicalagin; Uric acid; Gut microbiota; Branched chain amino acids

Rapid identification of lactic acid bacteria at species/subspecies level via ensemble learning of Ramanomes

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Abstract

Rapid and accurate identification of lactic acid bacteria (LAB) species would greatly improve the screening rate for functional LAB. Although many conventional and molecular methods have proven efficient and reliable, LAB identification using these methods has generally been slow and tedious. Singlecell Raman spectroscopy (SCRS) provides the phenotypic profile of a single cell and can be performed by Raman spectroscopy (which directly detects vibrations of chemical bonds through inelastic scattering by a laser light) using an individual live cell. Recently, owing to its affordability, non-invasiveness, and label-free features, the Ramanome has emerged as a potential technique for fast bacterial detection. Here, we established a reference Ramanome database consisting of SCRS data from 1,650 cells from nine LAB species/subspecies and conducted further analysis using machine learning approaches, which have high efficiency and accuracy. We chose the ensemble meta-classifier (EMC), which is suitable for solving multi-classification problems, to perform in-depth mining and analysis of the Ramanome data. To optimize the accuracy and efficiency of the machine learning algorithm, we compared nine classifiers: LDA, SVM, RF, XGBoost, KNN, PLS-DA, CNN, LSTM, and EMC. EMC achieved the highest average prediction accuracy of 97.3% for recognizing LAB at the species/subspecies level. In summary, Ramanomes, with the integration of EMC, have promising potential for fast LAB species/subspecies identification in laboratories and may thus be further developed and sharpened for the direct identification and prediction of LAB species from fermented food.

Keywords: Ramanome, rapid classification, deep learning, LAB species/subspecies, fermented food

Development and application of gene function evolution methods based on public data resources

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Abstract

Gene function evolution is a fundamental aspect of molecular biology, crucial for understanding species adaptation and trait development. Despite the availability of vast genomic datasets, existing methods often fail to fully leverage public data resources to trace gene function evolution efficiently and systematically. The lack of integrative tools capable of addressing these challenges hampers progress in identifying evolutionary trends in gene function across species. Here, we present a novel framework that combines advanced computational methods and public genomic databases to investigate gene function evolution. Our approach integrates phylogenetic analysis, functional genomics, and machine learning techniques to create a comprehensive platform for tracing gene function across evolutionary timelines. We applied this framework to several gene families involved in key biological processes, revealing significant evolutionary shifts in function that were previously unrecognized. These results offer insights into gene regulatory mechanisms and how they have adapted across different species. In conclusion, our findings not only enhance our understanding of gene regulation and adaptation but also provide a powerful tool for future studies in evolutionary biology. The broader significance lies in the potential application of this approach to a wide range of species, facilitating advances in both basic research and applied biosciences.

Keywords: Gene function evolution, public genomic data, phylogenetic analysis, functional genomics, machine learning

Coevolution of the Symbiotic Microbiome and Host Genome During the High-Altitude Acclimatization of Chickens

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Abstract

The harsh environments of high-altitude habitats impose significant challenges for animal survival and reproduction. The adaptation of plateau endotherms has been studied for over a century. However, most investigations have focused on physiological responses and genetic mechanisms, with limited attention to the role of symbiotic microbiota. Here, we conducted an integrated analysis of gut and respiratory microbiomes in Tibetan chickens reared at high-altitude Lhasa and those preserved for 20 years at low-altitude Beijing, along with other breeds, to explore the coevolution of microbiota and host genetics in high-altitude adaptation. Our results demonstrated that the respiratory system is not sterile, and its microbial composition differs markedly from that of the gut. The cecal microbiota was more enriched in metabolic pathways, whereas the lung microbiota was more enriched in environmental information processing pathways. Higher microbial diversity was observed in the ceca of chickens housed in Lhasa, whereas lower diversity was observed in the lungs. Notably, consistent with the varying altitudes, the cecal and lung microbial communities could be classified into two distinct enterotypes and pulmotypes, respectively. Compared with the cecal microbiome, the lung microbiome exhibited a more rapid response to a high-altitude environment. Specifically, compared with 7 differentially represented genera in the ceca, 88 differentially represented genera were identified as microbial signatures of high-altitude acclimatization in the lung. Moreover, cecal *Acetobacteroides* is jointly regulated by both environmental conditions and host genetics. Specifically, the detection and abundance of cecal *Acetobacteroides* in the chickens from high altitudes were significantly greater than those in the chickens from low altitudes. By combining FST analysis and mbQTL mapping, we identified *NAT8L* as a key gene under natural selection that regulates the colonization of *Acetobacteroides*. These findings illuminate the synergistic role of the symbiotic microbiota and host genes in high-altitude adaptation and offer new perspectives for coevolution.

Keywords: high-altitude adaptation, cecal microbiota, pulmonary microbiota, genetic regulation, chickens

Siderophore synthetase-receptor gene coevolution reveals habitat- and pathogen-specific bacterial iron interaction networks

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Abstract

Bacterial social interactions play crucial roles in various ecological, medical, and biotechnological contexts. However, predicting these interactions from genome sequences is notoriously difficult Here, we developed bioinformatic tools to predict whether secreted iron-scavenging siderophores stimulate or inhibit the growth of community members. Siderophores are chemically diverse and can be stimulatory or inhibitory depending on whether bacteria possess or lack corresponding uptake receptors. We focused on 1928 representative *Pseudomonas* genomes and developed a co-evolution algorithm to match all encoded siderophore synthetases to corresponding receptor gene groups with >90% accuracy based on experimental validation. We derived community-level iron interaction networks to show that selection for siderophore-mediated interactions differs across habitats and lifestyles. Specifically, dense networks of siderophore sharing and competition were observed among environmental (soil/water/plant) strains and non-pathogenic species, while only fragmented networks occurred among human-derived strains and pathogenic species. Altogether, our sequence-to-ecology approach empowers the analyses of social interactions among thousands of bacterial strains and uncovers ways for targeted intervention to microbial communities.

Shigella sonnei rhomboid proteases mediate quality control of orphan components of respiratory complexes

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Abstract

Although multiprotein membrane complexes play crucial roles in bacterial physiology and virulence, the mechanisms governing their quality control remain incompletely understood. In particular, it is not known how unincorporated, orphan components of protein complexes are recognised and eliminated from membranes. Rhomboids, the most widespread and largest superfamily of intramembrane proteases, are known to play key roles in eukaryotes. In contrast, the function of prokaryotic rhomboids has remained enigmatic. Here, we show that the Shigella sonnei rhomboid
proteases GlpG and the newly identified Rhom7 are involved in membrane protein quality control by specifically targeting components of respiratory complexes, with the metastable transmembrane
domains (TMDs) of rhomboid substrates protected when they are incorporated into a functional complex. Initial cleavage by GlpG or Rhom7 allows subsequent degradation of the orphan substrate. Given the occurrence of this strategy in an evolutionary ancient organism and the presence of rhomboids in all domains of life, it is likely that this form of quality control also mediates critical events in eukaryotes and protects cells from the damaging effects of orphan proteins.

Keywords:
intramembrane proteolysis; membrane protein complexes; quality control; rhomboid; *Shigella*

Soybean Protein-derived Antihypertensive Peptides Attenuated Vascular Microenvironment Homeostasis in SHR Through Regulating Vascular Calcified Exosomes Formation and microRNA-150/VEGF Signaling Pathway

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Abstract

Hypertension is a growing global public health issue, leading to target organ damage such as cardiac hypertrophy, vascular remodeling, and renal impairment. These conditions eventually cause irreversible damage. Bioactive peptides offer promising therapeutic alternatives to traditional drugs, showing fewer side effects and better antihypertensive effects. Persistent high blood pressure exacerbates arterial damage by promoting cellular and matrix remodeling, contributing to calcium deposition. Studies on ACE inhibitors, angiotensin II type 1 receptor blockers, and aldosterone antagonists suggest potential for preventing calcification in vitro and in vivo. In previous research, we purified an antihypertensive peptide (SAP) from soybean protease hydrolysate, which improved vascular remodeling and altered exosomal miRNA composition in hypertensive rats. However, its impact on vascular calcification remains unclear. In this study, we isolated serum exosomes from SHR (SHR-Exo) and SAP-treated SHR (SAP-Exo), characterizing their size, shape, and markers. SHR-Exo enhanced VSMC proliferation, migration, and inflammation, inducing osteogenic marker expression. Loss-of-function tests revealed exosomal miRNAs as key factors in VSMC phenotypic switching. miR-143, miR-233, miR-712, miR-19b, and miR-150 were elevated in SHR-Exo compared to SAP-Exo. In aged SHR and WKY rats, SHR-Exo significantly increased systolic blood pressure and promoted vascular wall thickening, vessel narrowing, and inflammatory infiltration. This was linked to upregulation of MEK1, Erk1/2, Nox1, SOD2, and increased intracellular calcium. Conversely, SAP-Exo reduced blood pressure, improved vascular remodeling, and mitigated calcification. Proteomic analysis revealed activation of the miRNA-150-targeted VEGF pathway in SHR-Exo, which was inhibited by SAP treatment. Our findings highlight a novel mechanism by which SAP improves hypertension-induced vascular calcification.

Keywords: antihypertensive peptides; vascular smooth muscle cells; exosomes; vascular calcification; spontaneously hypertensive rat.

Identification of Microbial Biomarkers for Inflammatory Bowel Disease

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Abstract

Inflammatory bowel disease (IBD), including ulcerative colitis (UC) and Crohn's disease (CD), is a multifactorial chronic condition. IBD shares similar symptoms with other gastrointestinal diseases, such as irritable bowel syndrome (IBS), posing challenges for current diagnostic methods. Commonly used indicators for IBD, such as C-reactive protein (CRP) and fecal calprotectin, have limitations in aiding diagnosis. Changes in the microbiome are associated with disease activity, risk of relapse, and response to treatment, indicating a dynamic correlation between the gut microbiome and IBD. By analyzing 8 metagenomic datasets from 3 different regions/countries, we identified 20 differential microbial species as potential diagnostic markers for IBD. We constructed a classification model using a random forest algorithm, utilizing 5 datasets for model training and validation, while the remaining 3 datasets were used for validation. The model demonstrated a good classification performance for IBD. However, the exact roles of these species in IBD remain unclear and require further validation. Our study enhances the understanding of microbial composition in IBD, offering numerous potential diagnostic and therapeutic targets.

Keywords: Inflammatory bowel disease, microbial species, biomarkers

Effect of synbiotic supplementation on immune parameters and gut microbiota in healthy adults: a double-blind randomized controlled trial

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Abstract

Synbiotics are increasingly used by the general population to boost immunity. However, there is limited evidence concerning the immunomodulatory effects of synbiotics in healthy individuals. Therefore, we conducted a double-blind, randomized, placebo-controlled study in 106 healthy adults. Participants were randomly assigned to receive either synbiotics (containing *Bifidobacterium lactis* HN019 1.5 × 10^8 CFU/d, *Lactobacillus rhamnosus* HN001 7.5 × 10^7 CFU/d, and fructooligosaccharide 500 mg/d) or placebo for 8 weeks. Immune parameters and gut microbiota composition were measured at baseline, mid, and end of the study. Compared to the placebo group, participants receiving synbiotic supplementation exhibited greater reductions in plasma C-reactive protein (P = 0.088) and interferon-gamma (P = 0.008), along with larger increases in plasma interleukin (IL)-10 (P = 0.008) and stool secretory IgA (sIgA) (P = 0.014). Additionally, synbiotic supplementation led to an enrichment of beneficial bacteria (*Clostridium_sensu_stricto_1*, *Lactobacillus*, *Bifidobacterium*, and *Collinsella*) and several functional pathways related to amino acids and short-chain fatty acids biosynthesis, whereas reduced potential pro-inflammatory *Parabacteroides* compared to baseline. Importantly, alternations in anti-inflammatory markers (IL-10 and sIgA) were significantly correlated with microbial variations triggered by synbiotic supplementation. Stratification of participants into two enterotypes based on pre-treatment *Prevotella*-to-*Bacteroides* (*P*/*B*) ratio revealed a more favorable effect of synbiotic supplements in individuals with a higher *P*/*B* ratio. In conclusion, this study suggested the beneficial effects of synbiotic supplementation on immune parameters, which were correlated with synbiotics-induced microbial changes and modified by microbial enterotypes. These findings provided direct evidence supporting the personalized supplementation of synbiotics for immunomodulation.

Keywords: Synbiotics, immune parameters, gut microbiota, enterotypes

Infection-induced microbial dysbiosis: triggering secondary infection and training microbiota for enhanced resistance to pathogens

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Abstract

Mucosal tissues, as the direct interface between the host and the external environment, harbor a diverse array of microbes that collectively maintain a complex microbial homeostasis. However, this delicate balance can be easily disrupted upon pathogen invasion, posing an intriguing question: do the alterations in microbiota in response to pathogen infection facilitate further invasion or, conversely, protect the mucosal surface from primary or recurrent infections? To delve into this pivotal issue, we infected the gill mucosa of rainbow trout with *Ichthyophthirius multifiliis* (Ich), a widely prevalent mucosal pathogen, and investigated the modifications and functionalities of the microbiota during the onset and progression of the disease. Here our results revealed that the microbiota acts as a crucial barrier against parasites during the initial encounter with the host. Upon infection, the microbiome becomes dysbiosis and undergoes translocation, eliciting an inflammatory response. Concurrently, opportunistic pathogens such as *Microbacterium* and *Mycobacterium* infiltrate the visceral tissues, causing damage and effectively becoming accomplices of Ich, thereby inducing secondary bacterial infections. Nevertheless, surviving trout established a novel microbiome homeostasis, characterized by increased diversity and the proliferation of beneficial bacteria, such as *Bacillus thuringiensis*. More interestingly, by utilizing antimicrobial-treated trout and microbial transfer experiments, we found that the microbiome of the surviving fish had developed a remarkable capacity to defend against parasites. Consequently, our findings suggest that the role of the mucosal microbiota in response to pathogen infection is dual-edged. Following infection, the host's microbiota may undergo a reorganization process that potentially establishes a "training memory," enabling it to withstand more potent infections. This not only lays the foundation for exploring the functions of microbiota but also offers a promising avenue for disease biocontrol from a microbial perspective.

Keywords: microbiome, parasitic infections, dual-face, secondary infection, training memory

The discrepant succession of small and large gut microbiomes in amphibians across seasons

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Abstract

Gut microbiota and amphibian host functionalize as a relatively stable holobiont. However, the symbiosis in the holobiont can be disturbed by internal and external factors of intestines. The succession pattern and assembly mechanism of amphibian gut microbiota remain unresolved. It is difficult to explore the question by using a wild amphibian species, due to uncontrollable effects from living conditions and host genetic background. In this study, we utilized 16S rRNA gene amplicon sequencing to profile gut microbiomes for a cultivated amphibian species (i.e., Black-spotted frog) across cultivation seasons. The gut microbiome structure exhibited a highly variable succession pattern, which was significantly discrepant between small and large gut microbiomes. Specifically, small gut microbiomes possessed a smaller alpha diversity, and it was more stable than large gut microbiomes. The gut microbiomes were dramatically remodelled during metamorphosis and hibernation. Furthermore, the predicted functional traits also showed discrepant succession pattern in small and large gut microbiomes. Finally, we demonstrated that the assembly of small and large gut microbiomes was driven by different ecological processes. However, stochastic processes played a dominant role in both microbiomes, and a temporal-decay phenomenon occurred during succession of gut microbiomes. The study will enhance our understanding of tissue-specific remodeling of amphibian gut microbiotas across seasons.

Keywords: amphibian, bacteriome, ecological process, intestine, succession

Regional differences dominate the incidence, and severity in endophytic microbe community of *Amomum taso-ko* in Yunnan, China

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Abstract

Amomum tsao-ko within the family of Zingiberaceae, is a perennial herb mainly distributed in southwest China including Yunnan, Guangxi, Guizhou and northern Vietnam. Its dried fruits are popularly consumed as foods and medicines with digestion-promoting, antidiabetic, antimicrobial, antiobesitic, antiinflammatory, and neuroprotective effects. However, most plantation was suffering the threaten of fruit rot mainly caused by *Fusarium* spp. Growing evidence suggests that disease occurrence in plants is often accompanied by changes in the associated microbiome. This study investigated the diversity and community structure of endophytic fungi and bacteria associated with diseased and healthy fruits of *Amomum tsao-ko* from Wenshan Prefecture, Honghe Prefecture, Nujiang Prefecture, Yunnan, China by high-throughput sequencing. From the analysis of CAP, the presence or absence of disease, disease severity, and regional differences all have a significant impact on the similarity of microbial community structure and species composition (beta diversity), but the measured variables of disease and disease severity on microbial community changes is less than 10%. Regional differences not only have a significant impact on fungal community composition, but could explain over 20%. From the PCoA results, it can be seen that samples from the same region tend to cluster together, and regional differences are the dominant factor affecting the composition of the microbiota. However, healthy and diseased samples from the same region are clearly separated, indicating that the low explanatory power of disease status and severity on microbiota changes is likely due to the greater influence of regional differences. For bacteria, illness and its severity are the biggest influencing factors, which can explain 60-80% of changes in the microbiota; However, although the impact on fungi is also significant, the explanatory power is small, mainly due to the significant regional differences in fungal community composition, which are the main factors affecting fungal community composition.

Keywords: *Amomum tsao-ko*, fruit rot, disease severity, regional differences, microbial community structure

Multiomics revealed the mechanism of fish vaccine-induced humoral immunity regulated by intestinal microorganism

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Abstract

Vaccination, as an effective means of preventing infectious diseases, has been playing a vital role in the prevention and control of human and animal diseases. The intestinal microbiome affect the immune effect of mammalian mucosal vaccines, but whether the microbiome in fish gut has a similar regulatory function remains unclear. Here we reported the effect of an immersion subunit nervous necrosis virus (NNV) vaccine on the symbiotic microbiota and its correlation with the intestinal microbiome of pearl gentian grouper by metagenome and metabolome. Results showed that vaccination significantly changed the structure and composition of intestinal mucosal microbiota. After immunization, the proportion of *Streptococcus gallylyticus* and *Bifidobacterium longum* in intestinal were significantly increased, which is corresponding with the upregulated immunoglobulins, including IgT and IgM, in fish gill and gut. In addition, the metabolite differential analysis showed that immersion vaccination significantly increased the concentrations of short chain fatty acids including acetic acid and butyric acid but significantly decreased the concentrations of multiple lipid-related metabolites in grouper gut. Furthermore, the correlation analyses showed that most of the intestinal differential microorganisms were significantly correlated with intestinal differential metabolites after vaccination, confirming that intestinal microbiome could regulate fish vaccine-induced humoral immunity. This study provids significant implications for the possible impact of vaccination on human and animal intestinal microbiota and metabolism by expanding our novel understanding of vaccine protective mechanisms from microbial and metabolic perspectives.

Keywords: intestinal microorganism, metagenome, metabolome, nervous necrosis virus, oral vaccine, grouper

Parabacteroides distasonis regulates the infectivity and pathogenicity of SVCV at different water temperatures

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Abstract

Spring viremia of carp virus (SVCV) infects a wide range of fish species and causes high mortality rates in aquaculture. This viral infection is characterized by seasonal outbreaks that are temperature-dependent. However, the specific mechanism behind temperature-dependent SVCV infectivity and pathogenicity remains unclear. Given the high sensitivity of the composition of intestinal microbiota to temperature changes, it would be interesting to investigate if the intestinal microbiota of fish could play a role in modulating the infectivity of SVCV at different temperatures. Our study found that significantly higher infectivity and pathogenicity of SVCV infection in zebrafish occurred at relatively lower temperature. Comparative analysis of the intestinal microbiota in zebrafish exposed to high- and low-temperature conditions revealed that temperature influenced the abundance and diversity of the intestinal microbiota in zebrafish. A significantly higher abundance of *Parabacteroides distasonis* and its metabolite secondary bile acid (deoxycholic acid, DCA) was detected in the intestine of zebrafish exposed to high temperature. Both colonization of *Parabacteroides distasonis* and feeding of DCA to zebrafish at low temperature significantly reduced the mortality caused by SVCV. An in vitro assay demonstrated that DCA could inhibit the assembly and release of SVCV through TGR5 receptor. Notably, DCA also showed inhibitory effect on infectious hematopoietic necrosis virus, another *Rhabdoviridae* member known to be more infectious at low temperature. This study provides evidence that temperature can be an important factor to influence the composition of intestinal microbiota in zebrafish, consequently impacting the infectivity and pathogenicity of SVCV. The findings highlight the enrichment of *Parabacteroides distasonis* and its derivative, DCA, in the intestines of zebrafish raised at high temperature, and they possess an important role in preventing the infection of SVCV and other *Rhabdoviridae* members in host fish.

Keywords: Spring viremia of carp virus, Temperature, *Parabacteroides distasonis*, Deoxycholic acid, Zebrafish

Novel nanomedicine delivery systems effectively achieve a balance between chemotherapy efficacy and the preservation of intestinal homeostasis

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Abstract

There is a positive correlation between the dosage of chemotherapy administered and its efficacy in suppressing tumor cells; however, it should be noted that higher dosages may lead to off-target effects such as gastrointestinal toxicity, mainly manifested as vomiting, diarrhea, stomatitis, and colitis, etc. The gastrointestinal toxicity induced by chemotherapy is associated with modifications in the gastrointestinal microenvironment, where the intestinal barrier and microbiota play crucial roles. Chemotherapy drugs achieve anti-tumor effects by inhibiting the rapid proliferation of tumor cells, but their non-target distribution leads to vulnerability and damage to intestinal epithelial cells due to the shorter proliferation cycle and faster growth rate of these cells. The process primarily leads to an increase in intestinal permeability and apoptosis of intestinal epithelial cells, accompanied by a decrease in levels of intestinal tight junction proteins, thereby resulting in chemotherapy-induced diarrhea. The impairment of the intestinal barrier often leads to changes in the composition of the intestinal microbiota. Moreover, chemotherapy agents have the potential to directly influence the composition of the intestinal microbiota, leading to dysbiosis. This encompasses a decrease in both the diversity and abundance of intestinal microbes, accompanied by a shift in microbial composition from predominantly “beneficial” symbiotic microbes to predominantly “pathogenic” microbes. The dysbiosis of the intestinal microbiota may contribute to the development of mucositis, thereby exacerbating the clinical course of cancer. How can we achieve a balance between the anti-tumor therapeutic effect and intestinal homeostasis? Novel nanomedicine delivery systems utilize the properties of nanomaterials to achieve excellent dispersibility of water-insoluble drugs in water, prolonged circulation time, and tumor-targeting capability. These advancements effectively enhance the efficacy of anti-tumor treatments and preserve intestinal homeostasis, thereby reduce gastrointestinal toxicity.

Keywords: Chemotherapy, Anti-tumor, Intestinal homeostasis, Intestinal barrier, Intestinal microbiota

Microbial Contamination - an Increasing Threat to the Consumption of Medicine Food Homology

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Abstract

Food-borne diseases caused by microorganisms (bacteria, fungi, viruses) or toxins are a significant health problem worldwide. Increased public awareness and the shift toward preventive health fosters an increasing demand for functional foods with health benefits, such as medicinal and food homology (MFH) products derived from ancient Chinese medicine, which are rich in bioactive compounds and provide various health benefits. However, as a functional food with extensive application prospects in both the food and pharmaceutical sectors, MFH faces significant challenges related to microbial contamination throughout its distribution process. Such contamination not only jeopardizes product quality and safety but also potentially impacts its competitiveness in the global market. This review aims to systematically overview to explore the applications and health benefits of MFH and the health risks associated with microbial contamination in MFH. And also highlights the microbial challenges related to MFH and the future direction for advancements in microbial detection technologies.

Keywords: Foodborne diseases; microbial contamination; Medicine Food Homology; Quality control and detection; Food safety

Biomechanical mechanism of PPL promoting bone formation via phase separation and sequestering HuR

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Abstract

As an emerging threat to human health, osteoporosis may partially cause by impaired osteoblast differentiation through insufficient mechanical stimulation. Cell phase separation response to mechanical stimulation, and play an important role in regulating osteogenic differentiation and bone formation. However, the mechanism of mechanical stimulation regulating phase separation and osteogenic differentiation remains unclear. The Plakin family is ubiquitous in osteoblast and may mediate phase separation. While limited reports exist regarding the involvement of Plakin family phase separation and osteoblast differentiation.

In this study, the phase separation of PPL, a member of the Plakin family was identified. Relationship between PPL phase separation and osteogenic differentiation were also investigated. We also screened the downstream osteogenic regulator of PPL via phase separation. Further therapeutic potential of PPL on osteoporosis mice were also studied.

We found that PPL promoted osteoblast differentiation and bone formation through phase separation of its intrinsically disordered region (IDR). PLEC IDR modulated osteoblast differentiation by sequestering HuR, an osteoblast differentiation promoter, via phase separation. Moreover, the essential functional region of PPL IDR demonstrated therapeutic effect on osteoporosis mice.

This study discovered novel experimental basis for further understanding the mechanisms of mechanical stimulation affecting bone formation, and provided new strategies for the prevention and treatment of osteoporosis.

Keywords: osteoporosis, mechanical stimulation, phase separation, the Plakin family, HuR

Identification of Key Metabolites in the Transition from Acute Kidney Injury to Chronic Kidney Disease Using Two Animal Models

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Abstract

Background: Insufficient energy supply is considered a critical factor in the progression of acute kidney injury (AKI) to chronic kidney disease (CKD). This energy deficit can lead to cellular dysfunction, impaired repair mechanisms, and eventual fibrosis, which all contribute to the deterioration of kidney function. Therefore, the early identification of key metabolites involved in this process is urgently needed, as it could pave the way for timely therapeutic interventions.

Method: In this study, we performed metabolomic sequencing of kidney samples from two well-established animal models: the unilateral ischemia-reperfusion injury (uIRI) model and the unilateral ureteral obstruction (UUO) model. Samples were collected at multiple time points to capture the dynamic changes in metabolite levels. Specifically, for the uIRI model, samples were collected at 0, 1, 3, 14, and 21 days, while for the UUO model, samples were collected at 0, 1, 3, 7, and 14 days. By combining our unique mathematical computation methods and stringent screening strategies, we aimed to identify potential target metabolites that could serve as biomarkers or therapeutic targets.

Results: Our analysis revealed a complex pattern of metabolic changes over time. In the uIRI model, 14 metabolites showed a time-dependent increase, and 4 metabolites showed a time-dependent decrease. In the UUO model, 10 metabolites exhibited a time-dependent increase, whereas 17 metabolites exhibited a time-dependent decrease. Notably, one metabolite, 4-(Aminomethyl)-1-methylpiperidin-4-ol, showed a time-dependent increase in both models, suggesting its potential role in the common pathways driving the progression from AKI to CKD.

Conclusion: Our results provide a theoretical basis for the clinical identification and prevention of the transition from AKI to CKD. Early intervention strategies targeting these key metabolites could potentially halt or even reverse the progression of kidney disease, thereby improving patient outcomes.

Keywords: AKI to CKD; Metabolomics; Metabolites; Biomarker;

Inoculation with fungi enhances soil aggregation and salt discharge capacity of saline-alkali soils

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Abstract

Salinization of arable land constitutes a significant issue that currently hampers food production, resulting in the breakdown of soil structure and the degradation of the soil microbial community, thereby intensifying the salt stress experienced by crops. Soil microorganisms, especially fungi, serve as crucial biological agents in the remediation of saline-alkali soils, with the restoration effects of fungi on soil structure attracting particular attention. This study was conducted in the typical saline-alkali agricultural region of the Songnen Plain in Northeast China, where the focus was on investigating the fungal community structure and soil physicochemical properties to elucidate the detrimental impacts of salinization on soil aggregates and the driving forces behind fungal community succession. The results revealed a significant negative correlation between alkalinity and both the soil aggregate indexes and the fungal diversity indexes. Additionally, as alkalinity increased, notable alterations occurred in the composition and network structure of fungi, with the network structure tending towards simplification, resulting in a significant reduction in the stability of fungal biological networks. The abundance of beneficial fungi *Cladosporium* and *Mortierella* demonstrated a linear relationship with changes in the exchangeable sodium proportion. Inoculation experiment utilizing isolated pure strains *Cladosporium colombiae* and *Linnemannia amoeboidea* established that these fungal strains possess exceptional capabilities in promoting soil aggregation within saline-alkali environments, thereby enhancing the soil's salt excretion capacity. This research proposes a novel strategy for the amelioration of saline-alkali soils by harnessing indigenous microbial strains.

Keywords: soil aggregation, soil improvement, fungal community, microbial agents, exchangeable sodium

Anthocyanin alleviates Metabolic Disorders Induced by a High Fat/High Sugar Diet via Regulation of Gut Microbial Lipopolysaccharide and Short-Chain Fatty Acids Production

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Abstract

Anthocyanin (ACN) is known to improve metabolic disorders (MD), but its low bioavailability makes it hard to fully explain its pharmacological mechanisms. This study aimed to investigate whether the ACN induced beneficial effects were mediated through the regulation of gut microbiota. Firstly, Male C57BL/6N mice were fed a normal chow diet or high fat/high sugar (HFHS) diet co-administered with or without ACN for 10 weeks. Our results revealed that ACN supplementation significantly diminished HFHS-induced body weight gain, alleviated metabolic disorders like insulin resistance, systemic inflammation and endotoxemia. These effects were linked to suppressed oxidative stress and improved barrier function in intestine. Metagenomics analysis showed that ACN treatment greatly attenuated HFHS-induced gut microbiota alterations, regulated the lipopolysaccharides and short-chain fatty acids (SCFAs) production of gut microbiome. To validate the role of the gut microbiota in ACN induced beneficial effects, we performed fecal microbiota transplantation (FMT) and sterile fecal filtrate (SFF) to inoculate HFHS-fed mice. Microbiota from ACN-treated mice alleviated the obesity-associated metabolic disorders over microbiota from control mice and SFF shown by superiorly anti-inflammatory effect and gut barrier function, and also enhanced SCFAs production and inhibited fecal LPS production. Collectively, these observations demonstrated that the “gut microbiota-barrier axis” was an alternative target for the anti-MD effect of ACN. This study has also provided an explanation for the high efficacy of ACN despite the low bioavailability, and ACN holds great potential to be developed as a functional prebiotic.

Keywords: Anthocyanin; Intestinal microbiota; Epithelial barrier function