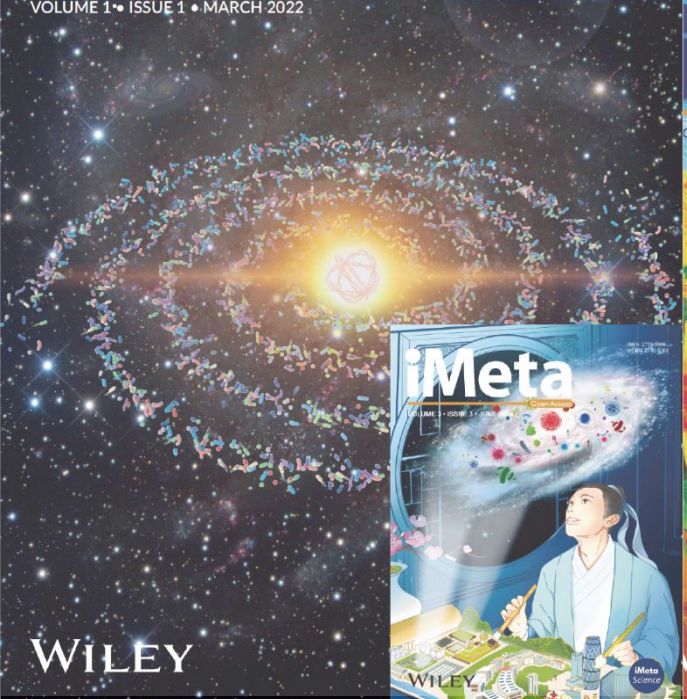


iMeta 大会 2024

构建创新型科研生态

会

议

手

册

主办单位： *iMeta* 编辑部

协办单位： 南方科技大学

湘湖实验室

承葛生物

海普洛斯

2024 年 10 月 11-13 日

深圳市南山区人民医院

iMeta WILEY

Publishers Since 1807

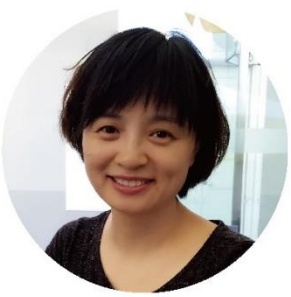
iMeta: 整合宏组学重新认识生命和环境科学

“iMeta” (影响因子23.7)由威立、宏科学组织和数千名华人科学家共同出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前5% (IF>20) 的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、60万用户的社交媒体宣传等。2022年2月起发行，相继被ESCI、PubMed、Google Scholar和Scopus等数据库收录。IF 23.7位列微生物学研究期刊全球第一。外审平均21天；投稿至发表中位数57天。截止2024年9月，发文220篇，全文下载70万次，被引近5000次，文章平均被引20+次!

主编团队

刘双江 研究员

中国科学院微生物研究所、山东大学



傅静远 教授

荷兰格罗宁根大学

执行主编

刘永鑫 研究员

中国农业科学院深圳基因组所

李丹宜 首席科学家

热心肠生物技术研究院

陈同 副研究员

中国中医科学院

iMeta

邮箱: office@imeta.science

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目录

会议信息

会议名称：*iMeta* 大会 2024—构建创新型科研生态

时间：2024 年 10 月 11 日–13 日

地点：深圳市南山区人民医院行政楼三层会议中心

主办单位：*iMeta* 编辑部

协办单位：南方科技大学、湘湖实验室、承葛生物、海普洛斯

承办单位：南山区人民医院

规模：<500 人

会议通知下载：http://www.imeta.science/meeting/2024/Annoucement.pdf

会议网站：http://www.imeta.science/meeting/2024 扫码访问会议官网查看更多信息

会议食宿：会议为参会人员提供 10 月 11 日晚餐，12-13 日午餐、晚餐。其他食宿费用需自理。所有参会人员请务必提前自行预定酒店：可参考会议网站推荐的协议酒店和价格。

交通：导航定位“深圳市南山区人民医院-西门”，行政楼三楼会议中心；地处深圳中心位置，距离宝安机场、深圳北站均小于 20 公里，打车 30 分钟约 60 元，地铁桃园站 C 口临近医院北门，出站后直走至红绿灯左转至行政楼(西门)，步行约 500 米。

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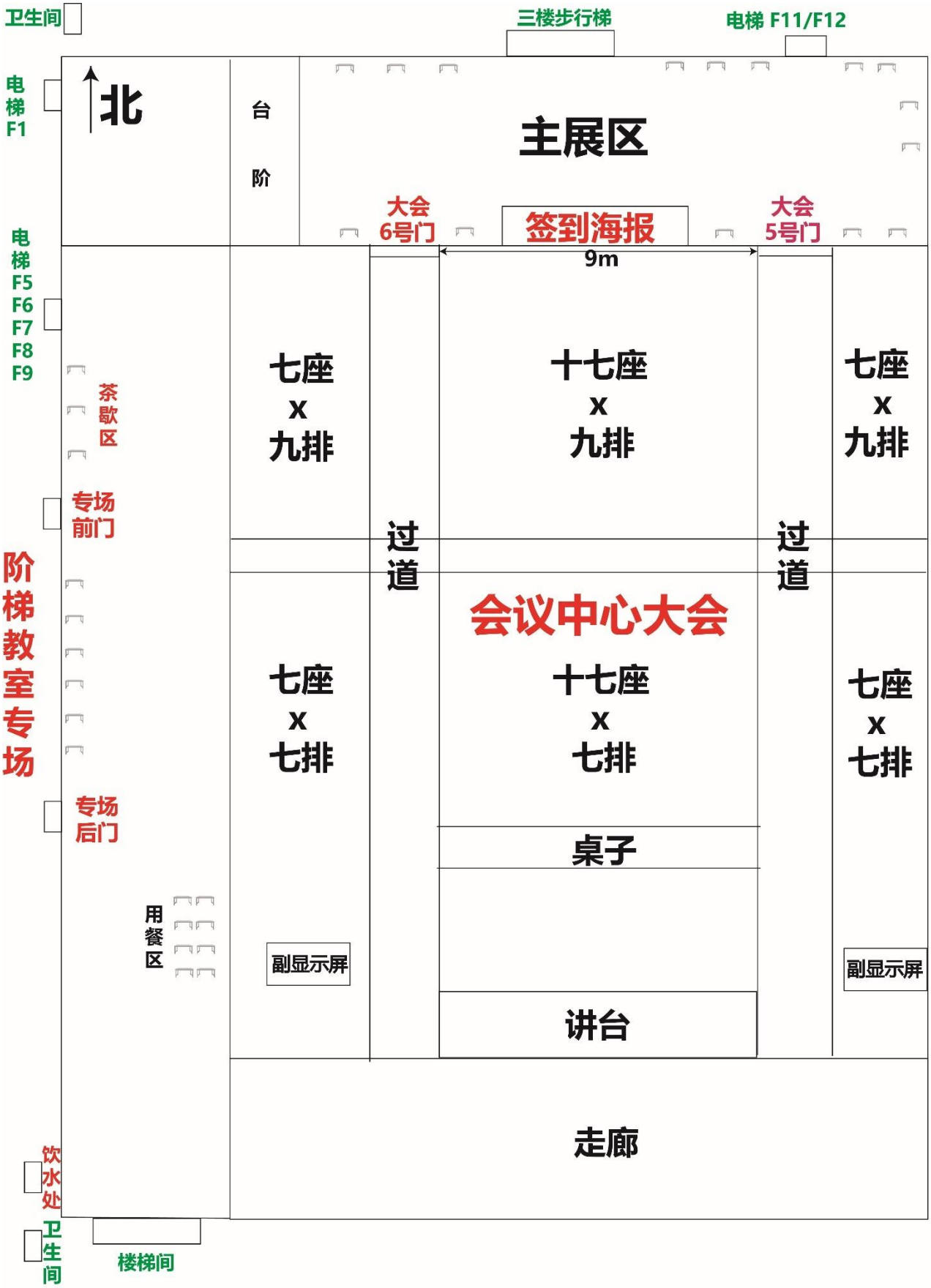
注册和发票	书泽	13624574695	会议日程	高云云	13717545179
报告 PPT	罗豪	15270962905	会议论文集	荀佳妮	15231572937

三层会议中心平台图


卫生间
三楼步行梯
电梯 F11/F12
电梯 F1
北
台阶
主展区
大会 6号门
签到海报
大会 5号门
9m
电梯 F5 F6 F7 F8 F9
茶歇区
七座 x 九排
十七座 x 九排
七座 x 九排
专场前门
过道
过道
阶梯教室专场
会议中心大会
七座 x 七排
十七座 x 七排
七座 x 七排
专场后门
桌子
用餐区
副显示屏
副显示屏
讲台
走廊
饮水处
卫生间
楼梯间

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会议日程

iMeta 大会 2024 详细日程				
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	浙江大学	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	刘志鹏 上海百趣代谢组学
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	
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				

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
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	唐啸宇 深圳湾实验室
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研究	
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用	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	中国农业科学院深圳基因组研究所	iMeta 系列期刊进展报告和未来规划	施春林 iMeta 执行编辑 /iMetaOmics 执行主编
19:20-19:40	各位主编颁奖		颁发执行副主编、青年编委聘书	
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	张学礼 广东省人民医院
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 安徽医科大学
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	
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
10:20-10:40	文涛	南京农业大学	系统微生物研究中的多组学应用与技术流程开发	

10:40-11:00	**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	
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	金双侠 华中农业大学
14:15-14:30	焦玉霞	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	全体	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	Atanas G. Atanasov	Ludwig Boltzmann Institute for Digital Health and Patient Safety (Austria)	The International Natural Product Sciences Taskforce (INPST), an open innovation platform to invigorate the research field of natural compounds in the era of digital communications (线上)	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			

前沿技术

三楼会议中心 10 月 11 日(周五)下午 14:00-18:30

主席：宁康、陈卫华、刘志鹏、苏晓泉

主持人
宁康 教授
华中科技大学

教授，博士生导师，生物信息与系统生物学系系主任。研究重点方向为生物大数据和微生物组的挖掘及其在健康与环境等领域的应用，尤其关注人工智能和微生物组交叉领域的知识发现和资源转化应用。近 5 年来作为通讯或共通讯作者，已在 *Nature Communications*、*PNAS*、*Gut*、*Genome Biology*、*Genome Medicine*、*Briefings in Bioinformatics* 等头部学术期刊发表学术论文 60 余篇。其中多篇入选 ESI 高被引论文。相关工作入选 2019 年度“中国生物信息学十大应用”。2021-2023 年连续全球前 2%顶尖科学家“年度科学影响力”榜单。2022 年当选中国计算机协会 CCF 杰出会员。担任中国生物信息学学会（筹）-基因组信息学分会副主任委员、湖北省生物信息学会秘书长等专业学会职务。担任全国生物信息大会等国内领域顶级会议委员。

14:00-14:20

报告题目：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

夏雨 教授（南方科技大学）

香港大学博士。现任南方科技大学，环境科学与工程学院副教授，博士生导师。研究兴趣集中于：利用 Nanopore 测序为代表的基因组学技术，解密复杂环境微生物群落中的种间互作关系以及耐药基因转移规律。近五年来在 *Environmental Science & Technology*, *Water Research*, *Genome Research* 等期刊发表一作/通讯论文 50 余篇，总引用次数 3900 余次(Google Scholar)。现任 *iMeta*, *Frontiers in Environmental Science* 期刊副主编，中国工程院院刊 *Engineering* 青年编委。主持国自然面上项目、青年项目各一项。获市“海外高层次人才”，校“研究生优秀导师”等荣誉。曾担任美国微生物协会香港地区青年大使。

报告简介： Rare species are vital members of a microbial community, but retrieving their genomes is difficult because of their low abundance. The ReadUntil (RU) approach allows nanopore devices to sequence specific DNA molecules selectively in real time, which provides an opportunity for enriching rare species. Despite the robustness of enriching rare species by reducing the sequencing depth of known host sequences, such as the human genome, there is still a gap in RU-based enriching of rare species in environmental samples whose community composition is unclear, and many rare species have poor or incomplete reference genomes in public databases. Therefore, here we present metaRUpore to overcome this challenge. When we applied metaRUpore to a thermophilic anaerobic digester (TAD) community and human gut microbial community, it reduced coverage of the high-abundance populations and modestly increased (~2×) the genome coverage of the rare taxa, facilitating successful recovery of near-finished metagenome-assembled genomes (nf-MAGs) of rare species. The simplicity and robustness of the approach make it accessible for laboratories with moderate computational resources, and hold the potential to become the standard practice in future metagenomic sequencing of complicated microbiomes.

14:20-14:40

报告题目：Using Metagenomic Approaches to Investigate Antibiotic Resistance in “One Health” Framework

李炳 副教授（清华大学）

博导，JCR1 区 SCI 期刊 AMB 副主编。长期从事环境微生物学研究，荣获教育部自然科学一等奖和广东省环境保护科学技术奖一等奖（排名第一），入选 2 项国家级重大人才计划青年项目（万人青拔、神农英才）、2 项省部级人才计划（国家环境保护技术青年拔尖人才、广东省杰青）、2023 年爱思唯尔“中国高被引学者”。在包括 *ISME J*、*Microbiome* 等在内期刊发表论文 130 余篇，H 指数 53，总引 12700 余次。

报告简介：抗生素耐药细菌(ARB)和抗生素耐药基因(ARGs)的传播及其对公众健康的威胁已经引起了广泛关注。抗生素耐药性不仅是临床医学问题，也是新兴的全球性环境污染问题。本研究应用宏基因组学方法，利用结构化数据库重构、生物信息学网络分析、组装与分箱等技术手段，基于“One Health”框架，系统研究了“人-动物-环境”各要素中抗生素耐药基因赋存状态、宿主定位及风险等级评估研究。

14:40-15:00

报告题目：腾讯医疗大模型助力医疗健康数智化升级

苏永超（腾讯健康南区架构师负责人）

苏永超，十余年医疗行业经验，深度参与政府、医院及大健康企业数字化建设，聚焦医疗战略咨询和系统规划，在健康城市、智慧医院等领域有丰富的设计、交付和管理经验，参与多项国家、省、市医疗信息化标准编写。

报告简介：腾讯医疗大模型通过深度学习与人工智能技术，为医疗健康领域带来智能化升级，医疗大模型能够精准分析海量医疗数据，辅助医生进行疾病诊断和治疗方案制定，提升诊疗效率与准确性；同时，还能为患者提供个性化健康管理建议，推动医疗资源配置优化，助力实现医疗健康服务的数智化转型。

主持人
陈卫华 教授
华中科技大学

华中卓越特聘教授、博士生导师。主要研究肠道菌群精细调控与人、动物健康。通过实验与生物信息学分析相结合，发现肠道微生态异常与疾病的关联；利用噬菌体或小分子物质对特定肠道细菌精准调控，以达到改善微生态、改善和治疗疾病之目的。近 5 年，以主要作者（通讯或第一）身份在 *Gut*、*Cell Host & Microbe*、*Cell Metabolism*、*Nature Communications*、*Genome Biology*、*Microbiome*、*Advanced Science* 等杂志发表文章 30 多篇。

15:00-15:20

报告题目：AI 语言模型与微生物组

方臻成 副教授（南方医科大学）

于 2020 年在北京大学取得整合生命科学（生物学）博士学位。研究方向为基于人工智能的微生物基因组分析算法设计。目前针对噬菌体、质粒、益生菌等研究对象，开发了系列基因组注释工具，以首位一作、末位通讯发表 SCI 文章 8 篇（IF>10 三篇），h 指数为 8，主持国家自然科学基金青年、面上各一项。其中 PPR-Meta 工具已被引百余次，被广泛用于未知噬菌体与质粒的挖掘。现任 *iMetaOmics* 执行副主编。

报告简介：语言（大）模型已成为解码生物序列的核心技术。微生物测序数据中存在大量“暗物质”序列，这些序列难以通过数据库搜索进行物种、功能等注释。近期，团队基于语言模型，分别开发了基于宏基因组的益生菌挖掘工具 metaProbiotics（*Brief Bioinform*, 2024）和质粒片段移动性识别工具 MOBFinder（*GigaScience*, 2024），推动新型益生菌的发现及质粒对宿主健康影响的研究。

15:20-15:40

报告题目：从微生物关联网络预测到相互作用验证

王玉琳 教授（山东大学）

山东大学微生物技术国家重点实验室研究员。主要围绕肠道微生物间及其与宿主间互作网络开展生物信息学和肠道微生物组相关研究。发表学术论文 40 余篇，以一作/通讯（含并列）发表于 *Nature Communications*、*Microbiome*、*Science China Life Science* 等（H-index 23）。

报告简介：微生物以群落的形式广泛分布在地球不同生境中，群落中的成员通过相互作用形成复杂的微生物网络。目前，微生物互作研究主要基于微生物共现或关联网络的预测，这导致该领域的研究仍处于描述性阶段，缺乏对微生物相互作用的实验验证和机理解析。因此，亟需建立相应的研究方法以准确解析微生物间互作关系及其作用机制。本研究针对不同环境样本，结合微生物关联网络预测、菌株定向分离培养和互作验证，开展微生物间互作研究。

15:40-16:00

报告题目：肠道微生物和代谢整合分析方法及策略

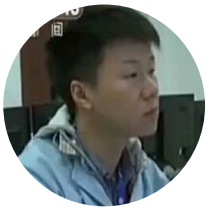
倪艳 教授（浙江大学）

浙江大学医学院附属儿童医院，国家儿童健康与疾病临床研究中心，特聘研究员，内分泌代谢病研究中心执行主任，浙江大学公共卫生学院流行病学和生物统计学，博士生导师。主要研究方向是肥胖相关代谢性疾病和消化道疾病的肠道菌群-宿主-代谢网络的调控机制。已发表领域内高影响的 SCI 论文共计 60+篇，相关研究结果发表在 *iMeta*, *Alimentary pharmacology & therapeutics*, *eBioMedicine*、*JCEM*、*Analytical Chemistry*、*Bioinformatics* 等杂志。主持或参与国内外研究课题 9 项、专利 6 项、参与论著编写 2 项， H 指数 45。

报告简介：菌群代谢产物是宿主-肠道菌群互作的关键媒介和信号分子，是预防和治疗代谢性疾病的潜在靶点。随着宏基因组测序技术和高通量质谱检测技术的发展，大量的肠道菌群和代谢组学数据产生，但是两者之间的相互作用分析面临巨大挑战。我们将从相关性分析、代谢功能分析、代谢溯源分析、肠菌代谢酶分析、菌-代谢中介效应分析等多个角度、多个维度，全面介绍肠道微生物和代谢整合分析方法及策略。

16:00-16:30

茶歇



主持人

刘志鹏 研究员

上海百趣 代谢组学

现任上海百趣代谢组学技术研究中心高级研究员，主要从事宏基因组、代谢组、转录组、蛋白质组等组学与复杂疾病的跨组学关联研究，挖掘“饮食干预或外部环境-肠道微生物-宿主代谢”之间关系在多种复杂疾病发生发展中起的作用，并尝试疾病“预防、诊断、监控、改善”的个体化医疗探索，致力于人体肠道微生态与临床代谢组相关的科学研究和应用转化研究。参与完成多项国家自然基金、国家科技部 973、载人航天工程等重大项目。在 *Nature Medicine*、*Nature Communications*、*Gut* 等期刊发表论文共 11 篇，研究成果被 *Nature Reviews Endocrinology*、*Nature Reviews Cardiology* 等期刊杂志评论，累计影响因子 IF：142，被引 2500 次。参编完成“十三五”规划教材《神经系统单基因病诊断学》(上中下)、《植物适应非生物胁迫的代谢组学研究》；“绿航星际”项目成果于 2018 年入选青少年读物《飞舟日记 - “太空 180 试验”》、于 2020 年入选《2020-2021 学年高一新教材地理必修第一册》“第一章：宇宙中的地球” 、于 2023 年入选中国国家博物馆：逐梦寰宇问苍穹—中国载人航天工程 30 年成就展。已申请受理国际 PCT 专利 5 项，已获授权国际 PCT 专利 4 项，已获授权国内专利 2 项，并曾获得 2 项国际基因工程机械大赛 IGEM 金奖。兼任国际学术杂志 *The Innovation*、*iMeta* 编委会成员，兼任 *Current Medicinal Chemistry*、*Current Microbiology*、*Applied Microbiology and Biotechnology*、*Scientific Reports* 等杂志审稿人。

16:30-16:50

报告题目：微生物大分子的表征和功能分析

王军 教授（中国科学院微生物研究所）

王军研究员关注微生物组研究领域的核心问题——微生物组深度的组成和功能差异以及在疾病中的作用，并在此基础上转化利用能够用于疾病治疗的微生物组成分；近五年，以最后或共同通讯作者身份在 *Nature Biotechnology* 等杂志发表 SCI 论文 45 篇，累计影响因子>600, H-index 41。2017 年获得国家项目资助，同时获得由德国马普学会任命的马普合作伙伴小组组长 (Max-Planck Partner Group Leader)，2022 年获得北京市杰出青年科学基金项目资助，主持国家“病原学与防疫技术体系研究”重点专项。获得 2023 年度中源协和生命医学“创新突破奖”，研究成果被英国三大报之一的卫报(Guardian)评选为“2022 年十大科学进展”之一。

报告简介：生命科学研究包括微生物组研究日益成为技术和数据驱动的学科领域，在微生物组研究领域，第二代测序技术是学科兴起的主要推动因素，肠道和其他部位微生物的组成和功能在多组学的研究框架内不断深入。在此基础上，我们的研究在新的测序技术尤其是第三代测序技术的使用，新的数据形式和更大数据量的收集和分析，以及更新的数据分析方法包括人工智能领域进行了一系列的研究。在这些技术和数据进步的基础上，我们解答微生物组的基础组成多样性（包括细菌组、真菌组和病毒组的组成和功能），阐述其在健康和疾病中的作用（免疫、代谢类疾病），以及在微生物组中进行挖掘和利用其中的抗菌肽和抗癌肽等。后续技术和数据分析的进一步发展，将更有力推动微生物组的整体，全面和闭环研究。

16:50-17:10

报告题目：高颜值在线数据分析绘图和论文组图

陈同 副研究员/主编（中国中医科学院中药资源中心）

2009 年本科毕业于东北林业大学，2015 年硕博毕业于中国科学院遗传与发育生物学研究所，研究方向是中药资源大数据+人工智能驱动的高质量中药材的鉴定、遗传改造、生态重塑、异源合成和中药新资源的发现等，在 *Cell Stem Cell* (封面文章)，*Nucleic Acids Research*，*Nature communications*、*Protein & Cell*、*iMeta* 等高水平杂志以第一或通讯作者发表文章十余篇，累积引用 3000 +次；开发在线绘图和分析平台 ImageGP、BIC、EVenn、植物整合基因组平台 IMP （获中华中医药学会 2023 年年度十大学术进展之一），使用超 70 万人次；运营有十四万人关注的微信公众号《生信宝典》，分享有 1400 多篇生物信息分析原创文章、教程和视频，阅读播放千万次。联合创办 iMeta 期刊，现为执行主编，致力于打造微生物和生物信息领域的国产高水平综合性杂志。

报告简介：有没有遇到过绘图的困扰？有没有羡慕过别人做出的美图？有没有想过如何组图？快来使用高颜值免费在线绘图工具 ImageGP 吧，集成数据分析、数据格式转换和数据可视化于一体，提供丰富的可定制参数，满足您的个性化需求；提供绘图代码，轻松在线和在本地重现绘制，简易进行二次开发；导出多种格式，便于后期处理。有了一张张的美图，轻松统一格式，删繁就简，组合成论文中的 Figure123456。

17:10-17:30

报告题目：微生物单细胞转录组研究进展与展望

孙会增 教授/优青（浙江大学）

浙江大学“百人计划”研究员，博导，动物科技系副系主任。国家优秀青年科学基金和浙江省杰出青年科学基金获得者，主要从事反刍动物营养和消化道微生物组研究。发表系列研究论文 50 余篇，其中最后通讯作者文章近 3 年发表在 *Nature Microbiology*、*Microbiome*、*Journal of Advanced Research* 等高影响期刊；担任 *Microbiome* 期刊编委，*iMeta* 期刊青年编委，*Animal Nutriomics* 期刊编辑部副主任，荣获第七届“井冈新秀”、“颐和”青年创新奖、杨胜营养科技创新奖等奖励荣誉。

报告简介：本报告将系统介绍微生物单细胞转录的研究进展，详细介绍基于随机引物微流控系统和微生物泛基因组图谱的菌群单细胞转录组技术原理及其在瘤胃微生物上的应用实践，展望该技术的未来发展趋势。

前沿技术

| 三楼会议中心-496 座(大会)
| 10 月 11 日（周五）下午 14:00-18:30

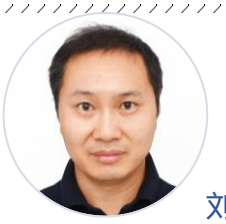
主席：宁康、陈卫华、刘志鹏、苏晓泉

主持人
苏晓泉 教授
青岛大学

博士，教授，博士生导师。泰山学者青年专家，山东省青创人才引育团队带头人，CCF 高级会员，青岛大学特聘教授。研究方向为生物信息学与大数据科学，已在该领域内 *iMeta*、*mBio*、*mSystems*、*Bioinformatics* 等高水平期刊发表学术论文 50 余篇，引用 2700 余次，H-index 26。主持国家自然科学基金项目 3 项、国家重点研发计划任务、山东省自然基金重大基础项目、中科院重点部署项目子课题等，相关成果获得 10 项软件著作权。担任 *iMeta*、*Medicine in Microecology* 等期刊编委。

17:30-17:50

报告题目：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



刘威 教授（安徽农业大学）

安徽农业大学，教授，博士生导师。利用传统的模式生物果蝇进行微生物组与宿主互作基础研究，同时利用资源昆虫黑水虻开发废弃物资源应用研究。以第一作者或通讯作者的研究论文发表在 *Nature Communications, eLife, Translational Neurodegeneration, Human Molecular Genetics*，*Journal of Genetics and Genomics*，*Insect Science* 等国际学术期刊上，获得国家发明专利 2 项。

报告简介：大多数研究集中于微生物组调控宿主表型，但宿主调控微生物组结构和功能未引起足够的重视。同种细菌个体间存在着表型异质性，现有常规的方法只能从群体角度研究，有可能掩盖了细胞间差异。以微生物组-果蝇作为模型，发现宿主调控微生物组数量、形态和致病性的表型。利用混池转录组，发现宿主对微生物组代谢和毒力调控。最后，利用细菌单细胞 RNA-seq 技术，解析出宿主对微生物组在单细胞分辨率上代谢和致病异质性的调控。因此，本研究将极大地深化我们对微生物组功能异质性的认知，为精准调控菌群提供重要的理论和科学借鉴。

17:50-18:10

报告题目：环境病毒组学工具和研究进展

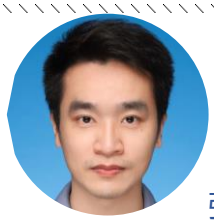
周之超 副研究员/主编（深圳大学）

周之超，深大“百人计划”副教授、博士生导师。2017 年获得香港大学博士学位，2019 年起在美国威斯康星大学细菌学系工作，担任研究助理教授职位，主要从事深海热液微生物组及病毒组研究，获得 Diversity 2023 Young Investigator Award。2024 年起入职深圳大学。在微生物/病毒组学分析方法、微生物/病毒碳和硫循环等取得了一系列成果，共发表 50+篇 SCI 论文（一作/共一 20+篇），包括发表在 *The ISME Journal*（4），*Nature Communications*（1 共一），*Microbiome*（1 共一，1 一作）等著名杂志。Google Citation 近 3500 次，H-index 为 28。

报告简介：环境病毒组学是研究病毒在环境中的多样性、功能和生态关系的重要研究方向。通过高通量测序技术，环境病毒组学可以直接从环境样本中捕获并分析病毒基因组，揭示传统方法无法检测的病毒种类和功能。这一领域的研究已经揭示了病毒在全球生态系统中的重要作用，如影响微生物群落结构、参与碳氮硫循环等。近年来，随着病毒组学分析工具的进步（如 VIBRANT，ViWrap 等），环境病毒组学的发展加速，为理解病毒生态学及其在环境中的潜在应用提供了新的视角。

18:10-18:25

报告题目：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



张智闵 （美格基因/中山大学）

生物信息学博士, 美格基因科服事业部总监, 深圳高层次人才, 哈工大（深圳）校外导师, 中山大学校外导师。参与国内外多项医学微生物组学研究项目，研究成果刊登在 *The Lancet Infectious Diseases*、*JENU* 等期刊，并授权 30+项生物信息方面专利与软著，也同时为美格云生态(http://cloud.magigene.com/)开发总负责人。

报告简介：本报告旨在对多种前沿二代测序平台在微生物组学领域（包括微生物多样性、宏基因组等）的数据表现进行全面客观解析与比较（包含数据质量及组学分析结果等方面）的差异，通过此报告，也有助于科研工作者根据自身研究需求，选择最合适的测序平台，从而提高研究效率和准确性。针对三代测序平台，在报告中针对华大智造自主研发的 CycloneSEQ-WT02 在实测数据上的表现与应用做展开介绍。

18:25-18:30

报告题目：华大智造 CycloneSEQ 纳米孔测序技术科研赋能计划华南区发布会

曾广怡（华大智造华南战区总监）

华大智造华南区总监，整体负责华大智造长短读长测序仪和时空组学业务。

报告简介：华大智造 CycloneSEQ 纳米孔测序技术科研赋能计划发布，征集人体微生态和农业微生态的研究课题，为入选的课题提供配套长读长的测序试剂支持。

19:00-21:00

欢迎晚宴

特邀报告

三楼会议中心 10 月 12 日(周六)上午 9:00-12:00

主席：刘永鑫、戴磊、唐啸宇

主持人

刘永鑫 研究员

深圳基因组所/大鹏湾实验室

中国农科院基因组所食品中心研究员，微生物组与营养健康团队首席，*iMeta* 执行主编，宏基因组公众号创始人。聚焦微生物组方法开发、功能挖掘和科学传播，在 *Nature Biotechnology*、*Nature Microbiology* 等发表论文 80 余篇，被引 21000 余次，连续入选全球前 2%顶尖科学家。兼任中国微生物组、计算合成生物学专委会委员。创办 17 万+同行关注的宏基因组公众号，主编《微生物组实验手册》专著，发起 iMeta 期刊(IF 23.7)，位列微生物学研究类全球第一。兼职为 *NC*、*NAR*、*Microbiome* 等 90 余种期刊审稿 260 余次。

9:00-9:25

开幕式：宣传片、主持人、特邀嘉宾致辞

9:25-9:30

大会合影

9:30-10:00

报告题目：肠道微生物群体反应调控与抗生素替代

印遇龙 教授/院士（中国科学院亚热带农业生态研究所）

中国工程院院士，全国人大代表，博士生和博士后导师。现任中国科学院亚热带农业生态研究所研究员，畜禽养殖污染控制与资源化技术国家工程实验室主任，中国农学会微量元素与食物链分会理事长，世界中医药学会联合会芳香产业分会名誉理事长，*Animal Nutrition* 杂志主编，*The Innovation Life* 副主编，*iMeta*、美国 *Journal of Animal Science* (2017-2020)，美国 *Domestic Animal Endocrinology*（2007-2009）和中国科学 生命科学中英文版的编委。长期从事猪健康养殖研究，先后主持完成院、省、国家、国际合作科研项目 30 多项。在 *PNAS*、*CNS* 子刊等刊物发表高质量论文 300 多篇，所有英文论文被引用 60000 多次， H-index in Google Scholar 108，以第一完成人获国家科技进步奖二等奖二项和国家自然科学奖二等奖一项， 曾获湖南省杰出贡献奖，何梁何利科技进步奖，2018 年在澳大利亚布里斯班举行的第 14 届国际猪消化生理学大会上获 Asia-Pacific Nutrition Award (杰出成就奖)。

报告简介：肠道中高密度菌群时时刻刻都在分泌特定的信号分子，从而适应复杂多变的肠道环境，发挥生理功能。植物提取物、有机酸、益生菌等替抗产品可通过群体感应抑制病原菌定植，改善上皮屏障功能，促进营养吸收。合成生物学等新型技术可创制工程益生菌，通过群体感应解除病原菌防御机制，推动饲料转化利用。

特邀报告

| 三楼会议中心-496 座(大会)
| 10 月 12 日（周六）上午 9:00-12:00

主席：刘永鑫、戴磊、唐啸宇

主持人

戴磊 研究员

中科院深圳先进院

中国科学院深圳先进技术研究院研究员、博士生导师，合成微生物组研究中心主任●国家重点研发计划青年项目负责人，入选《麻省理工科技评论》中国区“35 岁以下科技创新 35 人”。戴磊实验室在定量生物学、合成生物学与微生物组学的交叉领域进行原创性研究，致力于对宿主共生微生物组的结构和功能进行精准表征和调控，解决人体健康、农业生产等重大问题。

10:00-10:25

报告题目：微生态和肿瘤研究的历程和体会

于君 教授/院士（香港中文大学）

香港中文大学医学院助理院长；消化疾病研究国家重点实验室主任，消化疾病研究所所长，卓敏内科与药物治疗学讲座教授。任中国医学科学院学部委员，欧洲科学院院士，香港科学院院士，*Gut, Oncogene, Molecular Oncology* 副主编；*Cancer Cell* 顾问编辑。 从事微生态与肿瘤作用机制、诊断、预防和治疗等研究。发表 SCI 论文 610 篇(296 篇为通讯作者), 影响因子 10 以上论文 230 篇，ISI 总引用>47,000 次，ISI H 指数 110；Google scholar H 指数 127。高被引科学家；全球医学领域顶尖科学家(中国第八)。

报告简介：微生态和肿瘤研究的历程和体会。

10:25-10:50

报告题目：单细胞空间组学技术开发及数据挖掘

赵方庆 研究员/杰青（中国科学院北京生命科学研究院）

博士生导师，国家杰出青年基金获得者、中国科学院特聘研究员。主要致力于建立高效的算法模型和实验技术，探索人体微生物与非编码 RNA 的结构组成与变化规律，以期解析它们与健康和疾病的关系。近年来，在 *Cell*、*Gut*、*Nature Biotechnology*、*Nature Methods*、*Nature Computational Science*、*Nature Communications* 等刊物上发表通讯作者论文 100 余篇。

报告简介：单细胞空间组学技术开发及数据挖掘。

10:50-11:10

茶歇

主持人
唐啸宇 研究员
深圳湾实验室

深圳湾实验室特聘研究员，担任中国生物物理学会肠道菌群分会委员，美国微生物学会《*Microbiology Spectrum*》编辑，在 *National Science Review, Nature Chemical Biology, Angew Chem, PNAS, mBio* 等期刊合作发表论文 30 余篇。主要从事海洋和人体微生物天然活性小分子的基因组挖掘、生物合成机制、化学生态学功能等研究。

11:10-11:35

报告题目：科赫法则---从微生物到微生物组

刘双江 教授/杰青（中国科学院微生物研究所/山东大学）

中国科学院微生物研究所研究员、山东大学特聘教授。现任中国生物物理学会肠道菌群分会会长、中国微生物学会环境微生物专业委员会副主任、*iMeta* 主编、《微生物学报》执行主编、《生物工程学报》副主编。曾任中国科学院微生物研究所所长(2013-2019)。2010 年获得全国优秀科技工作者称号。作为项目负责人，主持科技部重点研发项目、国家自然科学基金重点项目、国家自然科学基金重大项目、国家自然科学基金杰出青年基金项目、中国科学院百人计划人才项目、中国科学院重大和重要研究项目。主要研究领域是环境微生物和人体肠道微生物组。

报告简介：科赫法则是判定因果关系的金标准。从微生物到微生物组，科赫法则的应用遇到了诸多困难，例如微生物菌株分离培养、功能冗余等。报告将从微生物组复杂性、与宿主互作关系的复杂性等，探讨如何应用科赫法则探究微生物组与宿主表型的因果关系。

11:35-12:00

报告题目：化学分子驱动的菌群与宿主互作机制研究

刘宏伟 研究员/微生物组专委会主席（中国科学院微生物研究所）

中科院微生物所微生物组与微生态研究室主任，二级研究员，入选百千万人才国家级人选，“中青年有突出贡献专家”，国务院政府特殊津贴专家；兼任中国科学院大学医学院 药学教研室主任、微生物与生化药学学科带头人、岗位教授；开展天然产物化学与肠道菌群交叉研究。在 *Nature Microbiology*，*Nature Metabolisms*，*Nat. Comm.*、*Cell Rep.*、*Angew. Chem. Int. Ed.*等发表论文 110 余篇，H index 44；两篇论文入选 ESI 高被引论文。

报告简介：化学分子驱动的菌群与宿主互作机制研究涵盖两个维度。其一，口服外源活性分子驱动肠道核心菌生长，调节菌群结构与宿主功能。如灵芝活性分子促进 Parabacteroides distasonis 增加，缓解宿主糖脂代谢紊乱。其二，基于代谢组研究筛选肠道中与健康和疾病相关的菌群代谢分子。成功鉴定出小克里斯滕森菌生成的新型次级胆汁酸，阐明了其改善宿主代谢的具体机制。以化学分子为基础的策略为微生物组与人体健康研究开辟了崭新思路。

大会报告

三楼会议中心 10 月 12 日(周六)下午 14:00-17:30

主席：陈实富、杜长征、冯桂海、蒋超

主持人

陈实富 创始人/CTO

海普洛斯

中科院博士，海普洛斯创始人兼首席技术官，中科院深圳先进技术研究院客座研究员。2019 年深圳市青年科技奖获得者，深圳市科技达人。主要研究生物信息学和肿瘤基因组学。是开源项目组 OpenGene 的发起人，多款热门生物信息学软件的作者。发表国际期刊和会议论文 90 余篇，其中一作兼通讯最高单篇引用 14500 余次，连续两年入选“全球前 2%顶尖科学家榜单”，拥有 20 余项发明专利和 30 多项软件著作权。是 iMeta 期刊执行副主编，中国抗癌协会肿瘤标志专委会青年委员，肿瘤测序及大数据分析专委会委员，深圳市生物信息云计算产业促进会理事。

14:00-14:25

报告题目：仔猪氨基酸代谢与免疫细胞命运

任文凯 教授/杰青（华南农业大学）

华南农业大学二级教授，博士生导师，*Animal Nutrition* 副 主编，*Fundamental Research* 编辑。长期从事仔猪营养代谢与免疫、 感染的研究, 文章发表在 *Molecular Cell* (2024)、*Science Bulletin* (2024)、*PNAS* (2022)、*Science Advances* (2021，2024)、*Cell Reports*(2022)等期刊上。曾获得广东省五四青年奖章（2023）、国家 杰出青年科学基金（2022）、广东省科学技术奖科技进步一等奖（排名 第二）（2022）、国家优秀青年科学基金（2019）、广东省“青年珠江 学者”（2018）等。

报告简介：本报告将介绍本组关于氨基酸代谢对免疫细胞命运决定机制的研究进展。

14:25-14:50

报告题目：Solutions for Sequencing-based pathogen and AMR identification and profiling.

Robert Schlaberg (Illumina, VP, Distringuished Scientist)

Robert Schlaberg is a medical director at ARUP Laboratories, an assistant professor of Pathology at the University of Utah. Illumina Distringuished Scientist, focus on solutions for Sequencing-based pathogen and AMR identification and profiling.

Robert Schlaberg 是来自犹他大学病理学系的助理教授，同时也为 ARUP 实验室的医学主任。他同时兼职因美纳测序公司的杰出科学家，从事基于测序技术的病原和耐药基因的新方法开发，已发表论文 84 篇，被引 2384 次，h 指数 22。

大会报告

| 三楼会议中心-496 座(大会)
| 10 月 12 日（周六）下午 14:00-17:30

主席：陈实富、杜长征、冯桂海、蒋超

主持人
杜长征 副教授
清华大学

医生科学家，专业从事消化道肿瘤标志物、转化医学及创新性临床疗法的研究，H-index 18，引用 985 次

14:50-15:15

报告题目：肠道菌源酶：代谢性疾病干预的新路径

姜长涛 教授/杰青（北京大学）

北京大学教授，基础医学院副院长，免疫学系主任，国家杰出青年科学基金获得者、科学探索奖获得者。从事肠道菌群及其菌源酶与代谢性疾病的研究。以通讯作者在 *Cell*、*Science*、*Nature* 等期刊发表论文 20 余篇，入选 *Cell Metabolism* 杂志编委。获授权发明专利 7 项，获中国生命科学十大进展、教育部“中国高等学校十大科技进展”、北京市自然科学一等奖（第一完成人）、科学探索奖、中国青年科技奖、谈家桢生命科学创新奖等奖励。主持基金委重大研究计划集成项目、重点项目、专项项目、国家重点研发计划等十余项基金。

报告简介：本报告将介绍肠道菌源酶：代谢性疾病干预的新路径。

15:15-15:40

报告题目：肿瘤转移过程中的免疫监控与逃逸机制

石虎兵 教授/青千（四川大学华西医院）

石虎兵，教授、博士生导师。国家重点研发计划“精准医学研究”项目负责人；国家高层次青年人才计划。主要利用多维交叉组学技术，从事以分子靶向和免疫检测点阻断的肿瘤精准个体化治疗机理研究。期间共发表研究论文 60 余篇，影响因子超过 1200，被引用 12000 余次，撰写专著 4 项，以第一作者或通讯作者发表论文 30 余篇，包括：*Nature*，*Cell*，*Cancer Cell*（2 篇，其一为封面文章），*Cancer Discovery*（3 篇），*Signal Transduction and Targeted Therapy*，*Cell Discovery*，*Nature Biomedical Engineering*，*Nature Communications*，*Blood*（封面文章），*Advanced Functional Materials*（封面文章），*Genome Research*（封面文章）等。主编《计算机辅助药物设计理论及应用》专著，担任 *Signal Transduction and Targeted Therapy*，*Medicine in novel technology and device* 等杂志编委。

报告简介：肿瘤转移过程中的免疫监控与逃逸机制。

15:40-16:10

茶歇

主持人
冯桂海 研究员
中科院动物所

冯桂海，博士，中国科学院动物研究所研究员，中国科学院青促会优秀会员。研究聚焦基因表达剂量控制机制及再生相关研究，参与发表文章 50 余篇，被引 4100 余次，H-index 26。以共同第一作者在 *Nature*、*Cell* 等杂志发表文章 10 余篇，作为主要作者的工作两次获评“中国生命科学十大进展”；荣获 2020 年中国科学院杰出科技成就奖（主要完成者）及 2019 年度“全国妇幼健康科学技术奖”自然科学奖一等奖。

16:10-16:30

报告题目：棉花基因编辑工具开发及分子育种应用

金双侠 教授/杰青（华中农业大学）

国家杰青、教育部青年长江学者。研究方向：棉花生物技术（遗传转化，合成生物学、基因编辑），棉花与害虫分子互作，高等植物基因组进化。在 *Nature Genetics, Nature Communications, Genome Biology , Advanced Science, Trends in Plant Science* 等杂志发表论文 100 多篇，12 篇论文入选高被引、热点论文，论文引用 7000 多次，H 指数 44.担任 *Plant Biotechnology Journal* (IF:10.1) 执行主编，*Genome Biology* (（IF:10.1) 编委，*Crop Journal*（IF:6.0) 副主编。

报告简介：主要介绍棉花系列基因编辑工具的研发：包括 CRISPR/Cas9, Cas12a, Cas12b, CBE, ABE 单碱基编辑器，dCas9-TV 转录激活系统，Cas13 敲低系统、基因敲入系统等；以及利用基因编辑工具开展棉花分子育种：创造除草剂抗性棉花、棕色棉花植株、新型抗虫材料、无棉酚、高油酸棉花新种质等。

16:30-16:50

报告题目：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

李亮 副教授（南方科技大学）

长期开发与应用自主知识产权的类器官及器官芯片模型系统，进行了包括人源气道、肺、肝、胆管、肠、血管、肾、脑等的类器官及其器官芯片系统的开发，进行多器官的联动，应用于临床来源病原与菌群组分微生物-宿主互作机制的研究与药物研发，发表 SCI 论文多篇，包括 *Cell Host & Microbe* (封面文章), *Nature Metabolism, American Journal of Respiratory and Critical Care Medicine, Gastroenterology, Cell Research, Cell Reports, mBio* 等。

报告简介：类器官是一类高度还原、代表体内器官结构和功能的三维“微器官”系统，具有高度类似于体内相应器官的细胞种类、形态分布与相应功能。具有操作简便、通量较高、没有物种差异、可实时监测、检测方法多样等优点，因此其在感染与免疫机制研究、生物医药转化应用研发等方面备受瞩目。本报告将围绕开发与应用类器官进行微生物与宿主互作的研究进展与经验，展示类器官这一新兴宿主模型在微生物相关研究中的探索性应用，展望其未来可能的医药研发与转化应用潜力。

主持人
蒋超 研究员
浙江大学

蒋超博士现任浙江大学生命科学研究院研究员、博导，兼聘浙江大学附属第一医院。博士毕业于 *Indiana University*，师从 Dr. Yves Brun，研究方向为微生物进化。博士后在 Stanford University 医学院遗传系个体医学中心进行研究，合作导师为精准医学先驱 Dr. Michael Snyder。长期致力于环境空气暴露组、人体与环境微生物组、微生物进化、精准医学研究以及相关的分子实验和生信分析方法开发及应用。以通讯或一作在国际知名期刊 *Cell*、*Nature*、*Nature Communications*、*Nature Protocols*、*Cell Reports*、*iMeta*、*ES&T*、*Journal of Hazardous Materials*、*Briefings in Bioinformatics*、*Cell Discovery*、*mSystems*、*STOTEN* 等杂志发表多篇研究论文，获得国内外专利若干。主持国自然专项等项目。任 *iMeta*、*iMetaomics*、*Scientific Reports*、*Current Microbiology*、*Bio-protocols* 副主编、*The Innovation Life* 编委。

16:50-17:10

报告题目：微生态医疗与研究转化平台

张帮周 首席技术官（承葛医药集团）

厦门大学-美国密歇根州立大学微生物生态学博士（师从“世界微生态之父”美国科学院 James Tiedje 院士），中南大学、福建中医药大学硕士生导师，厦门市留学人员创业专项资金获得者，厦门联合呼吸健康研究院微生态医疗技术创新中心主任。长期从事微生物生态学与人体健康的研究与转化工作，利用微生物学、宏基因组学等方法研究粪便微生态及菌群移植与消化、代谢、肿瘤等疾病间的关系，阐述微生态影响疾病发生发展的机制，开发精准菌群移植治疗平台、微生态活菌药物和基于粪便微生态的肿瘤早筛技术。

17:10-17:30

报告题目：细菌生物材料

郑迪威 研究员（中国科学院过程工程研究所）

郑迪威，中科院过程工程研究所研究员、博导，生化工程国家重点实验室/生物药制备与递送重点实验室主任助理。入选国家基金委优青、湖北省高层次人才计划、中科院过程所百人计划（过程杰青）。长期以来聚焦细菌生物材料研究，在 *Nature Biomedical Engineering* (3), *Nature Communications* (3), *Advanced Materials* (6)等期刊上发表一作/通讯 SCI 论文 27 篇，含 ESI 高被引论文 5 篇，累计被引 5900 次，H 因子 40，授权/受理专利 5 项。相关研究成果得到 *Nature, Science* 等期刊的正面引用。曾获得第十届中国青少年科技创新奖、中国生物材料学会科学技术二等奖、中国化学会化学化工与材料京博优秀博士论文奖铜奖、中国生物物理学会纳米生物学分会“优秀青年学者奖”、中国生物材料大会“青年学者奖”、湖北省“长江学子”、武汉大学十大杰出青年等奖项。连续三年入选斯坦福大学发布全球前 2%顶尖科学家榜单。

报告简介：共生菌群，如肠道菌群、口腔菌群等，在一系列重大疾病的发生、发展和治疗中有着重要的作用。利用细菌疗法调控共生菌群为治疗相关疾病提供了新的方向。本人和课题组提出了利用材料基元和化学方法来改造细菌的研究思路，在保留细菌自身活性的前提下赋予其特定的功能，发展了具有药物递送、荧光成像、光控药物合成功能的改造菌株，并进一步聚焦肿瘤和代谢性疾病。通过调控肿瘤中的促/抑癌菌，解决了在体内复杂菌群中调控特定细菌的技术难题。针对肾衰竭的毒素清除难题，构建了通过口服即可清除代谢毒素的人造菌群材料，为肾病提供了全新的治疗模式。系列研究为治疗菌群相关疾病提供了新思路，为开发功能强大、效果稳定的细菌疗法提供了重要指导。

生物技术专场

主席：李乐园、张俊亚

三楼阶梯教室(专场) 10 月 12 日(周六)下午 14:00-15:40

主持人

李乐园研究员

国家蛋白质科学中心（北京）

李乐园，国家蛋白质科学中心（北京）特聘研究员，北京市高端领军人才自然科学研究系列研究员，“北京项目”获得者、海外人才项目获得者。2016 年至 2022 年在加拿大渥太华大学先后担任博士后研究员和副研究员，2022 年 8 月加入国家蛋白质科学中心（北京）。主要从事人体微生物组的微生物系统生态学与宏蛋白质组研究，作为课题负责人承担国家自然科学基金面上项目等多项课题。在 *iMeta*、*Nature Communications*（两篇）、*Microbiome* 等著名学术期刊发表学术论文 40 余篇，含 4 篇封面文章。目前谷歌学术引用~2000 次、H-index 20，i10-index 32。兼任国际宏蛋白质组学组织首届和第二届执委会成员/国际通讯员、2024 HUPO 国际大会组委会成员、热心肠智库专家、iMeta 青年编委。

14:00-14:20

报告题目：高通量单细胞和单细菌 RNA 测序技术的开发与应用

王永成 教授（浙江大学）

哈佛大学化学与生物化学博士，浙江大学良渚实验室研究员和博士生导师。入选《麻省理工科技评论》中国“35 岁以下科技创新 35 人”。主要从事微流控单细胞和单菌测序技术的开发与应用，近 2 年以通讯作者在 *Nature Microbiology*、*Nature Communications* 等期刊发表十多篇论文。通过成果转化创立了单细胞测序技术公司 M20 Genomics，获得了启明创投、红杉中国等顶尖投资机构的投资，入选世界经济论坛“2023 年度技术先锋”和《财富》2023 中国最具社会影响力的创业公司。

报告简介：目前的商业化高通量单细胞 RNA 测序技术通常只能处理有较高活性的真核细胞样本。我们开发的新一代基于随机引物的高通量单细胞全转录组测序平台不仅能够处理新鲜细胞，同时在活性较差的冻存和 FFPE 样本上也取得了优异的结果，且实现了单细胞 RNA 全长序列检测和非编码 RNA 的检测，推动了单细胞测序技术走向临床应用。更重要的是，该平台不仅可以处理真核细胞，也实现了细菌等微生物的单细胞转录组测序，这为研究微生物耐药、微生物组和微生物宿主相互作用等提供了新的工具。

14:20-14:40

报告题目：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

陈迪俊 副教授（南京大学）

南京大学副教授、博士生导师，江苏省特聘教授。2003-2008 年在哈尔滨医科大学获得生物信息学学士学位，2017 年在德国哈雷-维滕贝格大学获得博士学位，先后在浙江大学、波茨坦大学和洪堡大学从事研究工作，主要研究方向是功能基因组学和人工智能生物学。共发表学术论文 70 余篇，其中以第一或者通讯（含共同）作者在 *Science Advance*、*Nature Communications*（6 篇）、*Nature Plants*、*Nature Neuroscience* 等主流期刊发表论文近 30 篇，Google H 指数为 36。

报告简介：癌症转移是导致癌症相关死亡的主要原因，而肿瘤微环境的演变在转移过程中起到了关键作用。我们利用配对样本，深入解析了胰腺癌肝转移中的肿瘤微环境，揭示了原发和转移部位肿瘤细胞的转录组差异，并鉴定出与免疫抑制微环境形成相关的基质和免疫细胞特定亚型。为进一步解析肿瘤转移过程中微环境的复杂空间结构，我们开发了统计学习框架 SpaTopic，提供了一种创新的分析方法，用于探索、比较和解读肿瘤的空间分辨转录组学数据。

生物技术专场 | 三楼阶梯教室-120 座(专场) | 10 月 12 日（周六）下午 14:00-15:40

主席：李乐园、张俊亚

主持人

张俊亚 副研究员

中国科学院生态环境研究中心

德国“洪堡学者”，中国科学院生态环境研究中心 副研究员，• 欧洲华人生态环境协会 (European Chinese Association for Eco-Environment)，副主席，北京生态修复协会理事，*iMeta* 青年编委，入选美国斯坦福大学发布的 2023 年度“全球前 2%顶尖科学家榜单”，中国科学院优秀“院长奖”获得者，研究方向为畜禽粪污/污泥资源化利用协同新污染控制。已在 *ES&T*，*Water Res. JHM* 等发表第一/通讯作者学术论文 40 余篇，Google 学术 H 指数为 43，主持/参与 10 余项国家及省部级项目。

14:40-15:00

报告题目：功能微生物的原位靶向分离技术

赵圣国 研究员（中国农业科学院）

博士生生导师，研究方向为反刍动物营养与瘤胃微生物。主持国家级项目 3 项，获得神农奖等省部级奖励 3 项、颐和青年创新奖等社会奖励 2 项，被评为农业农村部杰出青年农业科学家。在 *Microbiome*、*Applied and Environmental Microbiology*、*Animal Nutrition* 等 SCI 期刊发表 45 篇。出版著作 9 部，授权发明专利 7 项，获批国家新饲料添加剂 1 项。担任 *Animal*、生物技术通报等期刊编辑，担任中国农学会理事、中国饲料工业协会生物饲料技术委员会委员。

报告简介：分离培养微生物，不仅有助于菌群与表型因果关系机制验证，而且有利于益生菌产品开发。然而，分离培养技术尤其是功能微生物的靶向分离技术仍不成熟，限制了功能微生物的分离。本研究基于原位分离培养的思想，构建了磁性纳米颗粒和微球包裹两种功能微生物靶向分离技术，实现了纤维分解菌和尿素分解菌等功能微生物的靶向分离。研究合成了表面修饰纤维素的超顺磁性纳米颗粒，纤维分解菌结合效率达到 99%，特异性分离纤维降解菌的效率为 99.95%。通过微球包裹单细胞技术，在模拟环境中进行原位培养，实现靶向分离效率 54%，扩展现有菌种数量 34.38%。克服了培养组方法工作量大的困难，具有通量高、简便性强、易于厌氧操作等技术优势，为消化道微生物分离培养提供了新技术。

生物技术专场 | 三楼阶梯教室-120 座(专场) | 10 月 12 日（周六）下午 14:00-15:40

主席：李乐园、张俊亚

15:00-15:20

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关系

施琳 副教授（陕西师范大学）

陕西省高校科协青年人才，兼任西安交通大学全球健康研究院人类营养与代谢实验室共同主任，中国营养学会营养与代谢分会和基础营养学分会委员，陕西省饮食营养协会理事。研究领域为膳食营养与肠道菌群互作调控及其健康改善作用机制、多组学技术开发与应用等。主持参与国家级、省部级科学研究项目 10 余项，联合主持瑞典 FORMAS 基金一项。近五年，以第一作者或通讯作者在 *Nature Communications*、*Microbiome*、*Journal of Internal Medicine*、*Redox biology* 等具有国际影响力的营养学和医学领域期刊发表论文 40 余篇。与来自临床医学、公共卫生等相关领域 34 位专家合作发表我国首部《中国居民减重运动专家共识》。

报告简介： 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 explained by age, sex, body fat indices and habitual diet. Notably, we found associations between microbial CPs and cardiovascular phenotypes, i.e., hypertriglyceridemia, metabolic syndrome and obesity, with altitude serving as an effecting factor. Our findings offer new perspectives on the interplay between host-exogenous factors and gut microbiota, as well as their link to cardiometabolic health in high-altitude populations.

15:20-15:40

报告题目：法医土壤微生物研究进展及案例应用

苑美青 教授（公安部鉴定中心）

2008 年毕业于中国农业大学生物系微生物学专业，同年入公安部物证鉴定中心至今，主要从事全国范围内重特大及疑难刑事案件的 DNA 鉴定工作。并且致力于法医微生物研究及其实战化应用。在法医人体微生物、法医土壤微生物、法医环境微生物方向都有持续和深入研究，并且成功应用于实际办案。其中法医土壤微生物学研究达到国际先进水平。主持国家级课题 1 项，参与国家级课题 2 项，主持省部级课题 3 项，主持中心基本科研业务费课题 8 项

报告简介：许多刑事案件中，案发现场、抛尸现场以及死者或者作案人的鞋底、衣物或作案工具上都可能粘附泥土。土壤物证具有广泛性、分散性、隐蔽性强等特点，在一些疑难案件中显示出其良好的物证属性和证据价值。随着高通量测序技术的发展，法医土壤微生物的研究已经从传统的分离培养及鉴定特征微生物和序列多态性，发展到宏基因组测序，并通过生物信息学分析、人工智能分析进行土壤微生物群落组成及差异分析，实现嫌疑土壤样本的相似性比对和未知来源样本的地理溯源。公安部鉴定中心法医微生物实战化应用创新团队十余年来一直致力于将最新的土壤微生物研究技术应用到实际案件中来，采样范围遍及全国大部分地区，揭示城市土壤细菌群落分布的地理分布规律以及时空稳定性，科研成果获得公安部科技进步二等奖，并在多起实际案例中得到成功应用。

15:40-16:10

茶歇

医学专场

主席：龚文平、陆铖

三楼阶梯教室(专场) 10 月 12 日(周六)下午 16:10-17:30

主持人

龚文平 副研究员

解放军总医院第八医学中心

硕士研究生导师，解放军总医院第八医学中心结核病医学部研究所副所长，副研究员。长期从事结核病新型疫苗和结核潜伏感染鉴别诊断生物标志物研究。近五年主持国家、北京市、全军、总医院及中心各类课题 8 项，参加 2 项；获解放军总医院医疗成果二等奖 1 项、北京市科协北京青年优秀科技论文奖 1 项、北京防痨协会优秀科技论文一等奖 1 项、北京免疫学会青年学者奖。先后入选北京市科协“青年人才托举工程”，解放军总医院“3+1”新秀人才。相关研究成果获得国家发明专利 13 项，以第一/通讯作者在 *The Lancet Infectious Diseases, Military Medical Research, eClinicalMedicine* 等国际高水平期刊发表论文 60 余篇篇，参编专著 4 部。

目前担任中国防痨协会青年理事会常务委员、人兽共患结核病专业分会常务委员、中国研究型医院学会结核病学专业委员会委员、北京防痨协会基础专业分会委员。

16:10-16:30

报告题目：槲皮素诱导阿克曼菌调节宿主胆汁酸代谢以缓解肥胖

王新霞 教授（浙江大学）

浙江大学求是特聘教授，博导，国家生猪产业技术创新战略联盟常务理事，中国畜牧兽医学会动物营养分会理事，浙江省畜牧兽医学会副秘书长，研究方向：肠道微生物与猪肉品质和健康，主持国家自然基金重点、国家重点研发等项目 20 余项，以第一/通讯作者（含共同）在 *Autophagy*、*EMBO Reports* 等高影响力期刊发表论文 50 余篇，总被引 3088 次，指导学生获浙江大学优博论文，出版著作《动物脂肪沉积与 RNA 甲基化调控》，获浙江省自然科学一等奖，中华神农科技进步一等奖等，2022 年入选浙江省“万人计划”科技领军创新人才，全球前 2%顶尖科学家榜单，获浙江省产学研合作创新奖，多次应邀在国际国内学术会议做大会报告。H-index: 33。

报告简介：槲皮素是膳食中重要的天然黄酮类化合物，槲皮素会促进肠道 *A. muciniphila* 的相对丰度显著升高，产生更多的吲哚-3-乳酸（ILA）通过血液循环进入肝脏。ILA 上调 m6A 去甲基化酶 FTO 的表达降低 Cyp8b1 mRNA 的 m6A 水平，延长了 Cyp8b1 mRNA 的半衰期并显著提高了 CYP8B1 的蛋白表达，进而促进胆固醇转化为胆酸。胆酸通过激活脂肪组织中胆汁酸受体 FXR 调节炎症及脂代谢关键基因的转录，最终显著抑制脂肪沉积。我们的工作为解决肥胖问题提出了一个新的治疗靶点，扩展了关于 m6A 修饰在胆汁酸代谢途径中的关键调节作用的有限认识。

16:30-16:50

报告题目：肠道微生物群与孤独症：从“相关”到“因果”——从相关到因果?

王明帮 副研究员（深圳市龙岗区妇幼保健院）

关注围产-新生儿期风险因素与神经发育疾病发生；发表 58 篇 SCI 论文，被引超 6000 次，H 因子 23。主持国家自然科学基金 2 项、其他省部级等项目 4 项，累计经费 474 万元。获批国家发明专利 5 项，作为成果的主要完成人获福建省科技进步三等奖 1 项。中国生物物理学会肠道菌群分会理事，“热心肠智库”专家，担任 *Children*、*Journal of Genetics and Genomics*、*Brain-X* 和 *Neuroscience Bulletin* 等期刊的编委，是 *iMeta* 的执行副主编（医学方向）。

报告简介：孤独症（ASD）是一组伴随终身的神经发育障碍，肠道菌群与 ASD 的关系正从相关性过渡到因果性，阐明菌群-肠-脑轴机制是治疗 ASD 的新希望。此次报告我们将介绍肠道微生物群与孤独症从相关到因果的证据链。并介绍我们最近开展的前瞻性出生队列、粪菌移植术（FMT）干预 ASD 临床研究；以及通过多组学、机器学习-因果推断等方法发现驱动性的谷氨酸-GABA 途径细菌；采用培养组学技术分离驱动 ASD 改善的产 GABA 细菌的最新研究结果。

主持人
陆铖 研究员
广东省人民医院

陆铖，研究员，广东省医学影像智能分析与应用重点实验室副主任，博导。主要从事数字病理人工智能、模式识别、图像与视频分析等医工交叉研究。主持国家自然优青(海外)、面上项目各一项。以第一/通讯作者身份在 *Lancet Digital Health,j Clinical Investigation*、*Modern Pathology*、*Medical lmage Analysis*、 *IEEEReviews in Biomedical Engineering* 等发表 60 余篇论文，H-index 27，授权美国专利 7 项。

16:50-17:10

报告题目：循环肿瘤细胞（CTC）生物学研究以及临床应用

洪鑫 副教授（南方科技大学）

本科和博士毕业于新加坡国立大学，并在哈佛医学院接受多年博士后训练，在循环肿瘤细胞（CTC)生物学机制研究以及液体活检技术研发方面具有丰富的学术积累.曾以一作/通讯在 *Cancer Discovery* 、*PNAS*、*EMBO J*、*Aging & Disease* 等期刊发表 30 多篇 SCI 文章, 引用超过 1800 次，H-index = 21，拥有三项国际专利。曾获得新加坡 A*STAR JCO Early Career Development Award、美国 AACR Scholar-In-Training Award、广东省和深圳市引进高层次人才等多个奖项。近三年获批包括国自然外国优秀青年学者、国自然面上、国家重点研发计划等不同等级基金 10 多项，担任南方科技大学医学院-上医健联合实验室主任，是数个 SCI期刊的客座编辑或者编委，包括 *Theranostics, Aging and Disease* 以及 *BMC Cancer* 等。

报告简介：本次报告将通过 CTC 单细胞测序技术探索肿瘤远程的机制以及潜在的临床应用。

17:10-17:30

报告题目：精准菌群移植的临床应用

何剑全（上海承葛生物）

医学博士，副主任医师，研究代谢性疾病、认知障碍和肠道微生态综合干预机制。建立健康人源肠道菌群生物样本库，获批国家科技部人类遗传资源采集和保藏资质，CNAS 认可。对精准菌群移植的供体筛选、制备流程、质量控制、精准配型、临床应用等经验丰富。主持国家自然科学基金 1 项，省部级课题 4 项，发表高质量 SCI 论文 10 篇，获批发明专利 2 项。

报告简介：精准菌群移植的菌群库建设，体系建设，临床应用的专家共识和案例分享。

编委会

主席：施春林

三楼会议中心 10 月 12 日(周六)晚上 19:00-21:00

主持人

施春林 主编

iMeta 执行编辑/*iMetaOmics* 执行主编

硕士毕业于韩国庆尚大学，博士毕业于挪威奥斯陆大学，师从 Reidunn Aalen 院士；长期从事植物发育和植物小肽信号传导的研究，在 *Nature Plants*、*Plant Cell*、*Molecular Plant*、*PNAS*、*JXB* 等期刊发表论文 20 余篇。目前为 ANGONOVO 生物公司的研发科学家，*iMeta* 全职科学编辑，*MP* 编辑。

19:00-19:20

报告题目：*iMeta* 系列期刊进展报告和未来规划

刘永鑫 研究员（深圳基因组所/大鹏湾实验室）

中国农科院基因组所食品中心研究员，微生物组与营养健康团队首席，*iMeta* 执行主编，宏基因组公众号创始人。聚焦微生物组方法开发、功能挖掘和科学传播，在 *Nature Biotechnology*、*Nature Microbiology* 等发表论文 80 余篇，被引 21000 余次，连续入选全球前 2%顶尖科学家。兼任中国微生物组、计算合成生物学专委会委员。创办 17 万+同行关注的宏基因组公众号，主编《微生物组实验手册》专著，发起 *iMeta* 期刊(IF 23.7)，位列微生物学研究类全球第一。兼职为 *NC*、*NAR*、*Microbiome* 等 90 余种期刊审稿 260 余次。

报告简介：截止 2024 年 9 月，*iMeta* 创刊发行 2 年零 7 个月，发表 220 篇文章，来自全球 200 多个国家地区全文下载 70 余万次，被引用近 5000 次，篇均引用 21 次。期待先后被 Scopus、Web of Science、PubMed 等主流数据库收录。2024 年 6 月首个影响因子 23.7，位列微生物学科全球第二，研究类第一。预计明年 6 月第二个 IF 可达 33.7，将进一步增加其中相关领域中的影响力。姊妹刊 *iMetaOmics* 已经于 2024 年 6 月创刊发行，定位 IF>10 的交叉学科综合期刊，预计两年后获得影响因子。未来将陆续发起更多专业子刊 *iMetaGut/iMetaGenome/iMetaBioinfo* 等，打造创新型科研生态。

19:20-19:40

颁发执行副主编、青年编委聘书

19:40-20:40

编委发言讨论

20:40-21:00

主编总结发言

肠道菌群

主席：姜昆、李福勇、张学礼、李雪萌

三楼会议中心 10 月 13 日(周日)上午 9:00-12:00

主持人

姜昆 研究员

山东大学

山东大学微生物技术研究院研究员，山东省青年泰山学者。主要研究方向为肠道菌间以及肠道菌与宿主间互作的分子机制，并对具有应用潜力的相关蛋白或分子进行相关研发应用。相关研究在 *Nature Microbiology*，*Trends in Microbiology, J Biol Chem*， *Pest Manag Sci* 和 *PLOS Pathogens* 等期刊发表一作/通讯（含共同）文章 11 篇，授权发明专利 2 项，主持国家级科研项目 5 项。

9:00-9:20

报告题目：DPP4 调控肠道菌群和免疫对话

钟继新 研究员（华中科技大学）

华中科技大学教授、博士生导师，国家海外高层次人才，研究方向为免疫与菌群调控，研究受国家自然科学基金（4 项）、美国国立卫生研究院（3 项）、美国心脏协会（3 项）、美国免疫学会等十余项课题资助，以通讯作者在 *Lancet Rheumatol*、*Adv Sci*、*Pharm Rev* 等杂志发表 SCI 论文 60 余篇。H 指数 42。

报告简介：DPP4 在肠道菌群和免疫对话，以及炎症性肠病中的调控作用。

9:20-9:40

报告题目：“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

段屹 教授（中国科学技术大学）

教授，博士生导师。国家海外高层次人才计划入选者。多年来一直致力于人体共生菌群与健康和疾病的相关研究，学术成果以第一及通讯作者身份发表于 *Nature*，*Nature Communications*，*Nature Reviews Gastroenterology & Hepatology*，*Journal of Hepatology*，*Gut* 等高影响因子期刊，并被 *Nature*，*Science*，*Cell*，*Nature Reviews Drug Discovery*，*Nature Reviews Gastroenterology & Hepatology*，*Cell Host Microbes*，*Hepatology* 等国际著名刊物点评报道，获得 Faculty of 1000 收录并被两位独立推荐人分别给予最高等级评价。迄今共发表 SCI 论文 36 篇（其中 17 篇 IF>10），申请发明专利 1 项，相关成果被引用 2600 余次，h 指数 20，i10 指数 31。

报告简介：肠道菌群失调已被证实与多种疾病的发生发展显著相关。然而，对其致病机制的精准解析并据此开发相应的干预治疗手段的研究，还相对较少。我们于 Nature 杂志发表的论文，首次揭示了特定肠道菌株编码的细菌毒素，能够引起肝细胞死亡从而加剧酒精性肝炎，并据此开发了相应的噬菌体疗法来缓解酒精性肝炎。此研究获得 Nature 主编的高级评价，及 Nature、Science、Cell 三大主刊的推荐报道。通过“相关性—因果性—干预治疗”三步走的策略，实现“从临床中来，回临床中去”的临床型基础研究闭环。本报告还将介绍其它类似相关研究，从肠道菌群研究的角度，为听众解析此类研究范式。

主持人
李福勇 研究员
浙江大学

浙江大学百人计划研究员、博士生导师，国家高层次青年引进人才，国家自然科学基金优秀青年科学基金项目(海外)获得者。主要研究方向为消化道功能微生物组与宿主的交互作用，聚焦本领域热点，结合多组学技术、分子微生物学技术及经典微生物学技术，阐释了宿主与肠道微生物在营养和遗传层面的交互作用，取得一系列创新性学术成果。在 *Microbiome*、*BMC Biology*、*Cell Host and Microbe*、*ISME*、*Pharmacological Research* 等权威学术期刊发表 SCI 论文 30 篇；其中以第一或通讯作者在 *Microbiome*（3 篇）和 *Pharmacological research*（1 篇）等国际主流杂志发表 SCI 论文 10 篇。现担任国际权威期刊 *Microbiome* 杂志 Associate Editor。

9:40-10:00

报告题目：人类活动驱动微生物的中长期进化研究

周哲敏 教授（苏州大学）

苏州大学特聘教授，博士生导师，江苏省特聘教授。以生物信息学、细菌群体遗传学和微生物组学为主要研究方向，开展“同一健康”框架下病原体的群体结构和进化机制研究。近五年共发表通讯或一作 SCI 论文 13 篇，包括 *Nature Microbiology*、*Nature Food*、*Lancet Microbe*、*Nature Communications* 和 *Genome Research* 等知名刊物，单篇最高引用 688 次。迄今共发表 SCI 论文 84 篇，共被引用 8348 次，H 因子 44。

报告简介：人类与微生物的体内互作机制已经有较多研究，但尚缺乏中长期尺度的共进化模式研究。本报告基于本人此前建立的全球最大细菌基因组分型数据库 EnteroBase，并结合国内外的大量标志性样本，解析在百年至万年尺度上人类活动对细菌进化的影响。其中，耐碳青霉烯肺炎克雷伯（CRKP）的研究聚焦中国跨省医疗介导的 CRKP 地域流行趋势转变。大规模沙门氏菌研究解析了现代农业生产和全球贸易导致的细菌宿主跳转、耐药提高和全球传播。最后，基于全球合作采集的 300 份古代牙结石化石，并结合 2000 余份公共宏基因组样本，我们解析了口腔微生物从人科共同祖先、尼安德特人、农业革命至工业革命这漫长进化过程中的变化。

10:00-10:20

报告题目：肠道菌群与肠易激综合征

苏奇 副教授（香港中文大学）

香港中文大学医学院研究助理教授，香港中文大学深圳研究院副教授，博士生导师；利用机器学习，生物信息学和宏基因组等交叉技术手段从事新冠后遗症，自闭症和肠易激综合症等疾病的早期诊断，肠道微生态和益生菌等方面的基础和转化研究；主持竞争性研究经费多项；以第一/共一/通讯作者在 *Nature Microbiology*、*Cell Host & Microbe*、*Lancet Infectious Diseases*、*Nature Communications*、*Gut* 等国际期刊发表论文 37 篇；一作论文他引 1200 余次。

报告简介：肠易激综合征 (IBS) 是一种常见且异质性高的胃肠道疾病，其发病机制尚不明确。肠道菌群在 IBS 的发病过程中起到重要作用。本报告将重点探讨肠道菌群失调与 IBS 之间的关联，并解析粪菌移植 (FMT) 对 IBS 患者的影响及其分子机制。发现 IBS 亚型具有不同的肠道菌群特征，FMT 能通过降低产硫化氢细菌的丰度来有效缓解腹胀，并且阿克曼菌可能通过特定信号通路缓解腹泻。相关发现强调了针对不同 IBS 亚型进行个性化菌群调节的重要性。

主持人
张学礼 博士
广东省人民医院

广东省人民医院高层次人才，研究兴趣为基于多组学/多模态数据探究复杂疾病的共病关系并寻找新型组合生物标志物，以第一/通讯作者在重症医学顶刊 *Intensive Care Medicine*（IF:41.8），BMC 系列旗舰杂志 *BMC Medicine*（IF:11.8），生物信息学顶刊 *Bioinformatics* 及 *iMeta*（IF:23.7）等 SCI 期刊发表论文 10 余篇，被 *Nature Reviews Clinical Oncology*、*Nature Reviews Gastroenterology & Hepatology* 等高水平期刊引用，总引用量超过 700 次，h 指数 15，i10 指数 22。

10:20-10:40

报告题目：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

王进 教授（东南大学）

东南大学青年首席教授、公共卫生学院副院长。从事食物过敏、过敏性疾病与肠道微生态、重大疾病早期诊断与预警技术开发等研究。主持国家自然科学优秀青年基金（海外）、国家重点研发计划、国自然区域创新发展联合基金（子课题）、国家自然科学基金等国家省部级项目 10 余项。以第一或通讯作者在 *NAT COMMUN*，*CHEM ENG J*、*J HAZARD MATER*、*ALLERGY*、*TRENDS FOOD SCI TECH* 等发表论文 80 余篇, h 指数 24。

报告简介：世界卫生组织(WHO)报告指出，全球有 3%-10%的人口对食物过敏。随着环境和饮食结构的变化，及抗生素药物的滥用等，近年来食物过敏人群数量快速递增，已成为全球性的公共卫生难题。课题组通过细胞模型、动物模型、人群队列、以及代谢组学和微生物组学等多组学技术，探究了母乳益生菌 Probio-M9 和短链脂肪酸干预对肠道微生物结构的影响，阐明了其缓解食物过敏的免疫作用机制。本研究为新型过敏治疗技术的开发提供了支撑及临床研究提供了理论依据。

10:40-11:00 茶歇

11:00-11:20

报告题目：伏诺拉生二联方案根除幽门螺杆菌

胡奕 副教授（南昌大学）

现任南昌大学第一附属医院消化内科副主任医师、硕士生导师。香港中文大学博士后、副研究员。致力于幽门螺杆菌致癌机制、根除方案的优化及胰腺癌致病机制及转化研究。主持国家自然科学基金项目 2 项，省厅级课题 8 项。以第一作者/通讯作者发表 SCI 论文 37 篇，核心期刊论文 12 篇，H 指数 20（google）。

报告简介：一项多中心临床研究，旨在探讨伏诺拉生联合低剂量或高剂量阿莫西林 14 天根除幽门螺杆菌（Hp）的疗效及安全性，并评估其对肠道微生态及抗性基因的影响。研究成果投稿至 *Lancet Microbe*（in revision）。发现低剂量阿莫西林联合伏诺拉生二联方案组的疗效非劣效于高剂量组，两组对肠道微生态及总体抗性基因的影响小。低剂量组对β内酰胺类抗性基因的影响可短期恢复，但高剂量组尚未恢复。我们的研究优化了伏诺拉生联合阿莫西林二联方案，基于多中心、大样本、多角度的数据提出了在我国适用的高效、安全的根除方案。

主持人
李雪萌 副教授
广东医科大学

博/硕士生导师，博士后合作导师；东莞市特色人才（第二层次）；广东医科大学高层次（第三层次）引进人才；芬兰赫尔辛基大学联合培养博士。现任广东湛江海洋医药研究院双聘教授，主要研究方向具体包括（1）在长寿或衰老人群肠道菌群多组学分析；（2）细菌分离培养及功能鉴定；以第一作者或通讯作者在 *Advanced Material*、*iMeta*、*Sensors & Actuators: B Chemical* 等发表高水平 SCI 论文 8 篇.已主持国家、省市级项目 7 项，共计主持经费 615 万。

11:20-11:40

报告题目：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

简星星 副教授（中南大学）

中南大学湘雅医院特聘副研究员，硕士生导师。主要致力于高通量多组学数据的挖掘与整合分析，探究疾病发生发展的潜在机制，为疾病的早期诊断和临床治疗提供新思路。以第一作者/通讯作者（含并列）身份在 *Cell Metabolism*、*Microbiome*、*Nature Communications*、*Journal of Allergy and Clinical Immunology*、*British Journal of Dermatology* 等期刊发表研究论文 16 篇。综合影响力（Researchgate）总引用量 562，H 指数 12。

报告简介：多发性骨髓瘤（Multiple Myeloma）是一种常见于中老年人的血液系统恶性肿瘤，当前不可治愈，耐药复发是导致患者死亡的主要因素。宏基因组测序分析初诊和复发 MM 患者的粪便样本，我们发现“氮源循环肠道微生物”显著富集。体外和体内验证实验揭示：代表菌 *Citrobacter freundii* 会加速 MM 宿主肿瘤进程；且通过增加血铵水平、提高 MM 细胞对 NH4+的摄入和增强 NEK2 蛋白的稳定性，从而诱导 MM 对硼替佐米耐药。该研究发现肠道菌群与宿主代谢互作诱导 MM 肿瘤耐药新机制。

11:40-12:00

报告题目：益生菌与免疫细胞互作机制

王亮亮 研究员（中国科学院微生物所）

中国科学院微生物所研究员、研究组长。主要从事肿瘤免疫细胞中表观转录调控机制及与微生物组互作的研究工作，开发了多种潜在的肿瘤免疫治疗“增敏剂”。以通讯或第一作者在 *Cancer Cell*、*Gut*、*Science Translational Medicine*、*JCI* 等国际期刊发表论文多篇；H 指数 15。

报告简介：肿瘤条件下，一种特定益生菌能够特异性激活树突状细胞中 STING 相关 I 型干扰素信号通路，从而刺激杀伤性 T 细胞；炎症条件下，特异性激活单核细胞中的 STING 相关抗炎信号通路；为开发特定工程益生菌在癌症及炎症疾病治疗中的应用提供理论基础。

同一健康专场

三楼阶梯教室(专场) 10 月 13 日(周日)上午 9:00-12:00

主席：曹国栋、黄适、何建瑜

主持人

曹国栋 博士

安徽医科大学

2021 年浙江大学医学院博士毕业。现就职于安徽医科大学第一附属医院普外科，硕士研究生导师。主要研究方向为胃肠道肿瘤发病机制、胃肠道疾病的交叉医学研究。在 Advanced Functional Materials、Advanced Sciences、Nano Research 等期刊发表 30 余篇论文，h 指数 16。主持国家自然科学基金 1 项、安徽省省厅级基金 3 项。

9:00-9:20

报告题目：抗菌药物使用对养殖环境耐药组的影响

王少林 教授（中国农业大学）

主要从事药理基因组, 毒理基因组，微生物基因组、宏基因组和生物信息学方面的研究；在重要国际期刊上发表 SCI 论文 100 余篇，主要研究成果论文引用 9000 余次以上，H-Index,52, 参与出版英文著作 4 个章节，主持国家重点研发计划课题、自然科学基金、农业部细菌耐药性监测项目等 10 余项。

报告简介：由于抗菌药物的不合理使用，畜禽养殖场环境成为耐药基因的一个重要储库，耐药基因通过污水和堆肥处理不能被有效消除，从而使环境成为耐药基因或耐药菌传播的重要介质和储库，给人类健康和公共卫生安全带来巨大威胁。畜禽养殖过程复杂，抗菌药物的使用方式对畜禽肠道菌群及环境菌群的耐药组的产生、持留与传博的作用与调控机制尚不明确，因此研究畜禽养殖环境耐药组的动态变化规律，对于控制耐药性的产生与传播具有重要的意义。

9:20-9:40

报告题目：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

刘逸宸 副教授（中国科学院古脊椎动物与古人类研究所）

2019 年阿德莱德大学获博士学位，主要研究微生物与人群的协同演化与古 DNA 技术优化革新，迄今以第一作者或通讯作者在 *Science*、*Cell*、*Molecular Biology and Evolution*、*Current Biology* 等国内外知名学术期刊发表 SCI 论文 11 篇，总影响因子超过 300。

报告简介：尽管人类食用食用发酵乳制品的历史悠久，但目前对人类历史上对发酵微生物的应用以及其演化知之甚少。我们获得了首例古代奶制品 DNA，探索了青铜时期古代小河人群的生活方式和乳酸菌的演化。尽管之前认为开菲尔是从高加索地区传播到欧洲，重建的古代乳酸菌基因组显示还有另一条东亚内陆的传播路线。此外，我们还发现了乳酸菌中对环境压力以及宿主互作相关的水平基因转移，这很可能是适应性演化和人类驯化的结果。

9:40-10:00

报告题目：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

顾少华 博士（北京大学）

北京大学前沿交叉学科研究院定量生物学中心和北大-清华生命科学联合中心博士后，中国博士后创新人才支持计划获得者。主要从事铁载体介导的微生物生态与土壤健康、微生物次级代谢产物铁载体的演化规律、互作网络、生态功能等方面的研究。相关成果发表在 *Nature Microbiology*、*The ISME Journal*、*Environmental Science & Technology*、*mSystem*、*Soil Biology & Biochemistry*、*eLife* 等国际学术期刊，引用总计 982 次，h 指数 11。*iMeta* 青年编委，主持博后面上，国家自然科学基金青年基金项目。

报告简介：众所周知，从基因组序列预测细菌的社会相互作用非常困难。在这里，我们开发了生物信息学工具来预测微生物分泌的铁载体是否会促进或抑制群落成员的生长。我们开发了一种协同演化算法，根据实验验证将所有铁载体合成酶与相应的受体基因组进行匹配，准确率 >90%。我们推导出了微生物群落铁互作网络，以表明非致病和致病物种对铁载体介导相互作用的选择不同，通过这种从序列到生态的研究为基于铁互作网络筛选抗病物种提供了有效策略。

主持人

黄适 助理教授

香港大学

香港大学牙医学院助理教授，微生物组创新中心负责人， 国际知名学术期刊 mSystems，iMeta 等学术期刊编辑。 2016 年获中国科学院大学博士学位。2017 年至 2021 年在美国工程院院士 Rob Knight 团队进行博士后训练。在微生物组拉曼单细胞分选方法学研究、痕量样本微生物组分析、益生菌适应性进化等领域研究经验丰富。 发表高水平文章 60 余篇，其中以第一或通讯作者在 *Nature Methods*， *Cell Host Microbe* 等国际知名学术期刊发表论文 20 篇。h 指数 32。入选 2023 年科睿唯安世界 1%顶尖科学家。获发明专利 7 项，其中授权国际专利 2 项。 主持和参加包括国家青年自然基金、香港 HMRF、香港大学大型仪器项目等多项科研基金。

10:00-10:20 活体生物药的合理设计 (线上)

刘洋彧 副教授（哈佛医学院）

现任哈佛大学医学院副教授和布莱根女子医院副研究员，兼任伊利诺伊大学卡尔·伍斯基因组生物学研究所人工智能与建模中心客座研究员。他于 2009 年从伊利诺伊大学获得物理学博士学位。他于 2013 年加入哈佛大学医学院。他的实验室(https://yangyuliu.bwh.harvard.edu)目前的研究重点是从群落生态学，网络科学，控制论，和机器学习等多个角度研究复杂微生物群落，尤其关注人类微生物组的一系列根本性问题以及人类微生物组在疾病治疗和精准营养上的应用。迄今为止，刘洋彧博士已经发表学术论文 140 余篇（其中 *Cell/Nature/Science* 正刊及子刊近 40 篇），总引用超万次，并担任多个学术期刊的副编辑，近 70 个学术期刊的特约审稿人，以及 10 多个国际会议的组织或程序委员会成员。

报告简介：活体生物药 (LBP）是一类含有具有活性生物体（如细菌）并可用于预防、治疗或治愈人类疾病或适应证的生物制品。推进 LBP 开发的一个关键挑战是识别驱动疾病发病机制的特定微生物物种。我们开发了广义微生物表型三角测量 (GMPT) 方法。我们使用来自经典群落生态模型的合成数据对 GMPT 进行了系统验证，发现 GMPT 在识别致病物种方面优于现有方法（包括 DAA 和 MPT），并且准确度极高。我们将 GMPT 应用于一系列与微生物组相关的疾病，从艰难梭菌感染到创伤后应激障碍和 COVID-19。这些应用显示了 GMPT 在指导 LBP 合理设计方面的巨大潜力。

10:20-10:40

报告题目：系统微生物研究中的多组学应用与技术流程开发

文涛 青年研究员/博新计划（南京农业大学）

博士毕业于南京农业大学，目前在南京农业大学沈其荣院士课题组任钟山青年研究员。在 *Nature Communications, ISME J*，*Microbiome*， *Protein&Cell*，*New Phytologist*，*iMeta*，*Fundamental Research*，等期刊上发表了多篇文章。主持国家自然基金青年基金，中国博士后创新人才支持计划，江苏省青年基金等项目。开发了 ggClusterNet, EasyMultiOmics 等 R 包, Easyamplicon, EasymetaPro2 等组学分析流程。iMeta 期刊青年编委。总引用 1700 余次，H 指数 18。

报告简介：系统性微生物组学研究包括多个系统，例如肠道微生物与人体，土壤微生物与植物，植物微生物与动物等，关系的复杂性导致必须采用多组学共同探索微生物介导的系统性生物关联，由此开发多组学分析与网络分析技术，从而探索万物互联的过程。

10:40-11:00 茶歇

主持人
何建瑜 博士
浙江海洋大学

浙江海洋大学海洋科学与技术学院 C 类人才，讲师，硕士生导师。博士期间获国家留学基金委公派留学全额资助。研究方向为海洋微生物生态学，现主要负责厚壳贻贝微生物数据的发掘及其适应性进化分析。主持国家自然科学基金青年基金、浙江省基础公益研究计划项目等 4 项；参与国家自然科学基金国际（地区）合作与交流项目、面上项目、浙江省尖兵领燕研发计划项目等 4 项。研究成果在 *Science of The Total Environment*、*Aquaculture*、*Oikos*、水产学报等生态水产领域重要杂志发表论文 40 余篇，被引 420 余次，h 指数 11。目前为中国生态学学会会员、*iMeta* 期刊青年编委。

11:00-11:20

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

刘广宇 副教授（杭州师范大学）

从本科到博士后都在牛津大学完成。博士和博士后阶段师从著名细菌学家 Christoph Tang 教授，获牛津大学卓越博士后奖。2022 年入选杭州市海外高层次人才引进计划。主要研究领域为“膜蛋白大分子机器介导病原细菌致病与耐药的机制、以及人体菌群的基因编辑与靶向调控”，已在 *EMBO Journal*，*eLife* 等期刊发表 SCI 论文 9 篇，总引用 404 次，h 指数 8，主持国家自然科学基金一项。

报告简介：多组分的膜蛋白复合体在细菌的生理、毒力与耐药中发挥着至关重要的作用，但其组装的质量控制机制仍不明确。如何识别和清除膜中未正确组装入复合体的孤儿蛋白组分这一问题亟待探索。在膜内蛋白酶中，菱形（rhomboid）蛋白酶是分布最为广泛的蛋白超家族，在真核生物中，菱形蛋白酶介导细胞间通讯、炎症反应等关键作用。相比之下，原核生物中菱形蛋白的功能一直是个谜。在这个工作中，我们发现志贺菌的菱形蛋白酶 GlpG 和新鉴定的 Rhom7 参与了膜蛋白复合体的质量控制。菱形蛋白酶通过感知跨膜区的稳定性，特异性靶向切割不稳定的呼吸链复合体的孤儿组分，当组分被正确组装入功能复合体时，其不稳定跨膜区得到复合体其它组分保护，使其免疫菱形蛋白酶的切割。GlpG 或 Rhom7 的初步切割是孤儿底物后续进一步降解的关键步骤。考虑到这种策略在古老细菌中的存在，且菱形蛋白在所有生命领域中的广泛存在，这种质量控制范式很可能也在真核生物中调控重要事件，并保护细胞免受孤儿蛋白的损害影响。

11:20-11:40

报告题目：微塑料的环境地球化学行为及生态毒性效应研究

徐智敏 副教授（中国科学院亚热带农业生态研究所）

副研究员/博士生导师。任 *iMeta* 执行副主编、*Soil Sci & Environ* 科学编辑等学术兼职。以第一/通讯作者在 *Soil Boil Biochem*、*J. Hazard. Mater.*、*Environ Int* 等发表高水平 SCI 论文 25 篇，h 指数 19，主编/副主编教材专著 3 部，授权发明专利 5 项。主持国自然基金、广东省基金面上等 20 多项重要课题。从事水土关键元素(碳氮铁镉等)耦合循环及其微生物学机制。获 2024 地理信息科技进步二等奖、2023 年华夏建设科学技术奖三等奖、2021 年广东省环境保护科学技术一等奖等省部/市厅级奖 9 项。

报告简介：本报告探讨了微塑料在环境中对元素循环和重金属迁移转化的影响，以及微生物在这一过程中发挥的关键作用。总结了微塑料与微生物相互作用的复杂机制，并讨论了微生物如何影响微塑料的持久性和重金属的生物有效性。通过深入理解微塑料、重金属和微生物之间的相互作用，我们可以更好地评估微塑料污染的环境风险，并制定有效的污染控制策略。这对于保护生态系统和维护环境健康具有重要意义。

11:40-12:00

报告题目：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

黄俊卿 教授（暨南大学）

教授（青年破格）。美国 Rutger 大学访问学者（Chi-tang Ho 院士、黄庆荣教授），2018 年进入暨南大学，先后破格晋升副研究员、教授；主要关注复方证治机制及有效成分开发应用研究。现任国家中医药管理局重点学科后备学科带头人、省高新技术企业评审专家、省青科协会员、省中医药学会中医养生保健专业委员会常务委员、香港营康美集营养部一级研究员等职务。研究成果在国家级省级项目以及企业横向课题的支持下，以第一/通讯作者在 *Adv Sci*、*Microbiome* 等期刊发表论文 30 余篇，其中一区 TOP 论文比例超 70%，最高单篇引用 550 次，封面论文 3 篇，h-index 21。

报告简介：中医经典方逍遥散是疏肝健脾的代表方，组方契合抑郁症最常见的中医肝郁脾虚证病机，但其治疗机制尚未完全明确。现有研究证据显示，逍遥散对于胃肠道功能紊乱具有显著调节作用，且肝郁脾虚型抑郁症的发生发展过程中往往伴有胃肠道异常；这提示肝郁脾虚型抑郁症与胃肠功能紊乱可能具有高度相关性。 为确证上述理论，本研究着眼于肠道代谢调控下前额皮质 C3/CR3 补体级联机制，在前期多组学联合分析及分子实验的基础上，探讨逍遥散调控脑肠交互稳态干预抑郁症的作用机制及物质基础。

期刊论坛

主席：金双侠

三楼会议中心 10 月 13 日(周日)下午 14:00-15:30

主持人

金双侠 教授/杰青

华中农业大学

国家杰青、教育部青年长江学者。研究方向：棉花生物技术（遗传转化，合成生物学、基因编辑），棉花与害虫分子互作，高等植物基因组进化。在 *Nature Genetics, Nature Communications, Genome Biology , Advanced Science, Trends in Plant Science* 等杂志发表论文 100 多篇，12 篇论文入选高被引、热点论文，论文引用 7000 多次，H 指数 44。担任 *Plant Biotechnology Journal* (IF:10.1) 执行主编，*Genome Biology* （(IF:10.1) 编委，*Crop Journal* (IF:6.0) 副主编。

14:00-14:15

报告题目：*GigaScience* 期刊介绍与投审稿技巧

周红玲 主任（*GigaScience* 学术编辑）

GigaScience 出版社编辑部主任，同时担任 *GigaScience & GigaByte* 双刊学术编辑，*GigaScience* 出版社期刊发展负责人。负责日常稿件处理、国内期刊运营以及出版社运营等工作。担任中国科技期刊学会国际交流与合作工作委员会委员；广东省科技期刊编辑学会理事。主持广东省高质量科技期刊建设项目两项；作为主要译者出版译著《草木之形》，发表多篇科研和出版领域文章。获得 2023 年度深圳市盐田区“梧桐菁英”科技创新企业人才称号。

报告简介：*GigaScience* 于 2012 年创刊，主要发表生命科学和医学领域的大数据相关研究。数据类文章不仅包括基因组学和其他高通量生物学研究，还涵盖了影像学、神经科学、生态学和队列数据，以及系统生物学和其他新的大数据类型；方法类文章包括大数据处理相关的软件、工具和工作流等；同时还包括研究性论文、综述和评论类文章。本报告将着重介绍期刊的情况、特点，目前的收稿标准，以及投审稿过程中的注意事项。

14:15-14:30

To be a GPBee (线上)

焦玉霞 教授（国家生物信息中心 GPB 执行主编）

GPB 执行主编，博士毕业于新加坡国立大学生物系。2011 年加入中国科学院北京基因组研究所（国家生物信息中心），全面负责 GPB 期刊运行，主要负责稿件组约、初审和期刊活动策划。

报告简介：*Genomics、Proteomics & Bioinformatics*（简称 GPB)是由国家生物信息中心与中国遗传学会共同主办的英文学术期刊，由牛津大学出版社开放出版。刊载来自世界范围内组学、生物信息学及相关领域的优质稿件。期刊入选“中国科技期刊卓越行动计划”重点期刊项目(2019–2023)。报告将介绍期刊基本情况，投稿注意事项及特色活动等。

期刊论坛 | 三楼阶梯教室-120 座(专场)
| 10 月 13 日（周日）下午 14:00-15:30

主席：金双侠

14:30-14:45

报告题目：Advanced Science and Wiley Life & Health Sciences

雷蕾 教授（威立出版集团）

Wiley 出版集团，期刊发展部，高级编辑主任，常驻北京 北京大学生物科学和经济学双学士，宾夕法尼亚州立大学植物生物学博士、博士后，加入 Wiley 前担任 Nature Plants 期刊高级编辑（常驻纽约），拥有近十六年的科学研究和学术出版经验，先后在国际主流期刊上发表研究、综述和评论文章六十余篇。 雷蕾博士现在负责和支持 Wiley 部分生命科学期刊的定位规划，团队建设，内容审核，和可持续发展，包括 Advanced 期刊生命和医学系列（如 *Advanced Science*，*Advanced Biology* 等），*Global Change Biology*，*GCB Bioenergy*，*Land Degradation & Development*，*Journal of Agronomy and Crop Science*，*Grass and Forage Science, Modern Agriculture* 等，也协助国内机构开办有国际影响力的期刊，如 *Cell Proliferation*，*iMeta*，*iMetaOmics, mLife, Animal Research and One Health, New Plant Protection* 等。

报告简介：

14:45-15:00

iMeta 期刊介绍和高影响力文章特点

刘永鑫 研究员（深圳基因组所/大鹏湾实验室）

中国农科院基因组所食品中心研究员，微生物组与营养健康团队首席，*iMeta* 执行主编，宏基因组公众号创始人。聚焦微生物组方法开发、功能挖掘和科学传播，在 *Nature Biotechnology*、*Nature Microbiology* 等发表论文 80 余篇，被引 21000 余次，连续入选全球前 2%顶尖科学家。兼任中国微生物组、计算合成生物学专委会委员。创办 17 万+同行关注的宏基因组公众号，主编《微生物组实验手册》专著，发起 *iMeta* 期刊(IF 23.7)，位列微生物学研究类全球第一。兼职为 *NC*、*NAR*、*Microbiome* 等 90 余种期刊审稿 260 余次。

报告简介：高影响力文章主要分为研究、方法和综述 3 类进行分别介绍。研究需要有新的突破性创新，为其他研究提供研究思路的范式，比如你做的水稻菌群的研究，可以供其他植物如小麦、玉米、马铃薯等研究供参考。方法需要有通用性，尤其是分析方法的 GitHub、WebServer 需要边开发边宣传，需要用户不断的反馈测试和优化，积累用户基础，才能成为领域真正需要的好方法。综述需要有比较大的视角，为领域提供最新的教科书，即要系统总结前人结果，又要有新的思考，以及对未来方向的引领。

15:00-15:30

全体讨论：学术期刊的未来在中国

15:30-16:00

茶歇

组学专场

主席：安三奇、梁卓斌、李晓东

三楼阶梯教室(专场) 10 月 13 日(周日)下午 14:00-16:40

主持人

安三奇 教授

广西医科大学

教授，博导，获得八桂青年拔尖人才等省级重大人才称号，并主持国家自然科学基金在内基金 5 项。担任 *Oncogene*、*iMeta*、*Briefs in Bioinformatics* 等多个高水平期刊审稿人和青年编委，发表论文 30 余篇，并被 *Faculty Opinions*(原 F1000)列为推荐论文。研究方向为 RNA 与生物信息，在 *NAR*、*Oncogene*、*GPB* 等发表论文 30 余篇，h 指数 11。

14:00-14:20

报告题目：基于公共数据资源的基因功能演化方法的开发与应用

刘默洋 副教授（上海交通大学）

上海交通大学农业与生物学院副研究员，上海交通大学热带园艺植物研究中心副主任；上海青年扬帆科技英才，硕士生导师，碁政导师；中国燕麦荞麦专业委员会理事，上海植物生物技术专业委员会委员。主要运用系统生物学、分子生物学、人工智能技术等方法，解决基因功能演化相关的基础及生产问题。近四年在 *Cell Reports*、*Science Bulletin*、*Plant Communications*、*Horticulture Research* 等期刊发表 SCI 论文 30 余篇，h 指数 16；担任 *iMetaOmics* 执行副主编；主持多项国家级、省部级科研项目。

报告简介：随着高通量测序技术的快速发展和测序成本的持续下降，植物多组学数据呈现出爆炸式增长。然而，如何高效利用这些海量数据以解析基因功能的演化过程，成为当前亟待解决的科学问题。为此，本文提出将人工智能方法与系统发育分析相结合的策略，通过有效整合不同尺度数据，深入解析基因功能的演化机制。本研究不仅为揭示植物基因功能的复杂演化提供了全新视角，还为农业和生物技术的未来应用奠定了坚实基础。

14:20-14:40

报告题目：沙漠微生物暗物质挖掘及其代谢潜能勘探

董雷 副教授（中山大学）

从事极端或特殊生境（沙漠、丹霞地貌、沿海滩涂、航天育种、肠道等）微生物系统学、资源挖掘及应用基础研究。担任 *Advanced Biotechnology*、*iMeta*、生物多样性期刊青年编委。*Nature Communications*、*iMeta*、*IJSEM*、*ANTO*、*Current Microbiology* 等国内外期刊审稿人。以第一或通讯作者（含共同）在 *Sci Total Environ*（3 篇）、*npj Biofilms Microbiomes*、*Org Lett*、*Environ Microbiome*、*Int J Syst Evol Microbiol*（11 篇）等期刊发表 SCI 论文 30 余篇，授权专利 2 项，参编专著 4 部。先后承担了包括国家自然科学基金委青年，面上项目，第三次新疆综合科学考察子课题等多项课题。

报告简介：极端生境中蕴藏着大量微生物暗物质。本团队构建了极端干旱的沙漠生境微生物的选择性分离方法，提出了基于培养组学的宏基因组学研究新策略 CBM，以及针对沙漠链霉菌的高效分离新方法 SCP。近三年先后发现了原核生物 10 个新属和 22 个新种，分离并保藏了数万株沙漠微生物种质资源。我们还报道了一批具有抗菌、抗结核活性的新颖化合物（如 Atrovimycin 系列等），并不断拓展其应用场景（天然色素、生防菌剂等），揭示了沙漠极端生境微生物的巨大应用潜能。

主持人
梁卓斌 研究员
深圳湾实验室

深圳湾实验室特聘研究员 PI，兼任香港大学、西班牙巴塞罗那大学、首都医科大学校外博士生导师，西北农林科技大学，华南理工大学校外硕士生导师，南方科技大学附属光明凤凰学校科学校长，深圳市生物医药促进会细胞外囊泡技术专业委员会常务委员，担任 *Engineering Microbiology* 等期刊青年编委。研究方向聚焦基因组编辑与合成生物学平台的技术开发与基因组损伤修复在人类疾病中的机理研究，主持和参与多项国内外科研基金，在 *Nat Biotech.*、*Nat Comm.*等期刊发表论文 20 余篇，总被引近 1500 次。主要成果包括：阐明农杆菌 T-DNA 双链化、酵母 NHEJ DNA 修复通路及人类 FANCI-FANCD2 复合体修复 DNA 损伤的新机制；开发改良型 eMAGE、Prime Editing 等基因编辑工具，并应用于精准医疗；开发合成生物学平台技术，实现植物底盘青蒿素等天然产物合成、工程微生物降解废弃塑料及肿瘤治疗，相关专利已申请。

14:40-15:00

植物-有害生物-农药的数字化与智能化

王崎 特聘教授（贵州大学）

特聘教授，硕士生导师，目前就职于贵州大学公共大数据国家重点实验室，清华大学访问学者，获得贵州省高层次留学人才项目，贵阳贵安科技人才项目，贵州大学科研创新团队负责人，广东工业大学校外导师，贵州省大数据局专家库专家，贵州省人才发展研究所人工智能库专家，《贵州省劳动用工大数据综合服务平台》技术顾问。博士在读期间曾在京东人工智能研究院担任算法工程师，而后成为广东省和比利时林堡省在国际教育合作方面的第一位联合培养博士研究生，并于 2020 年 12 月获得国内工学博士学位，2021 年 2 月获得国外工程技术博士学位，是广东工业大学第一位获得双博士学位的毕业生。长期从事计算机视觉和智慧农业的相关研究，截至至今作为第一或者通讯作者发表 SCI 论文 26 篇，其中 CCF A 类和 SCI 1 区论文共计 16 篇，所发表的学术期刊论文累计影响因子（IF）>150，主持承担了 1 项国家自然科学基金，以及 3 项省部级课题，曾多次获得了国际国内的知名科研竞赛奖项，获 11 项中国发明专利授权。指导本科生发表 SCI 1 区论文并获国家级大学生创新创业项目 1 项，获得全国大学生挑战杯（大挑）全国特等奖以及若干省级校级竞赛奖励。此外，担任 *Plant Phenomics* 期刊青年编委，20 多个国际顶级会议和期刊的审稿人，如 *TCYB, TNNLS, TMM, TKDD, ACMMM, Plant Phenomics* 等等。主持并完成了一项比利时国际双边科学合作项目，为中比双方科研合作奠定了良好的基础。

报告简介：作物病害是作物减产的主要因素之一，而农药是治疗病害最有效最经济的手段。随着人工智能的快速发展，开展作物病害诊断-用药治疗的一整套数字化和智能化方案成为可能，具有巨大应用潜力，但当前的病害诊断研究缺乏系统性的研究，农药的数字化更未有人研究。汇报人从如何构建病害数字化、农药数字化、病害诊断智能化、精准用药智能化开展本次报告，为新一代人工智能赋能绿色植保提供参考和思考价值。

15:00-15:20

RNA 选择性剪接的鉴定及其功能解析

孙强 副教授（浙江大学）

浙江大学医学院附属第四医院/浙江大学“一带一路”国际医学院（筹）/浙江大学国际健康医学研究院特聘副研究员。主要研究方向为肿瘤泛基因组及肿瘤中复杂剪接事件研究。自博士阶段以来，主要取得了以下研究成果：1. 利用纳米孔测序技术系统性阐述结直肠癌中可变剪接变化情况； 2. 利用流式质谱成像技术系统性分析 RNA m6A 修饰在糖尿病肾病进展中的作用；3.开发 RNA 修饰相关检测及功能研究工具。至今，以第一或通讯作者（含共同）在 *Genome Medicine*，*Analytical Chemistry*，*Experimental & Molecular Medicine*，*Applied Materials Today* 及 *The FASEB Journal* 等知名国际期刊发表 20 余篇学术论文，总引 700 余次。

报告简介：选择性剪接是真核生物转录后调控重要机制之一，这一过程能够从单个基因产生多个 RNA 转录本，使蛋白质组多样化。异常选择性剪接被认为是癌症发展的一个标志，直接参与调控肿瘤发生、发展所涉及的多种生物学过程，如增殖、凋亡、肿瘤转移等，对选择性剪接进行系统性研究可能为恶性肿瘤提供潜在的生物标志物。由于系统分析的技术局限性，转录组的复杂性在很大程度上被削弱，系统地识别选择性剪接颇具挑战。本次报告将介绍基于选择性剪接相关研究现状与当前挑战，重点介绍报告人实验室近期在选择性剪接方面的工作。

15:20-15:40

报告题目：海洋被膜细菌生命特征研究与资源开发应用

张伟鹏 教授（中国海洋大学）

以“海洋生物被膜物种-功能多样性特点与资源开发”为研究方向，聚焦：1）海洋生物被膜物种多样性与核心功能；2）典型生物被膜细菌的物质与能量代谢机制；3）基于人工智能的生物被膜资源开发。以通讯或第一作者在 *iMeta*、*Nature Communications*（3 篇）、*Microbiome*（2 篇）等杂志发表论文 35 篇。共发表论文 100 篇，引用超 4000 次，H 指数 38。

报告简介：在海洋环境中，附生微生物（即生物被膜, biofilm）所蕴含的物种和功能被严重低估且存在大片未知。我们近几年的工作聚焦“海洋生物被膜物种-功能多样性特点与资源开发”：刻画了全球海洋生物被膜菌种多样性与核心功能；选择分离自海生物被膜的玫瑰杆菌建立了模式生物研究体系，揭示了海洋细菌能量代谢的新途径；建立了生物被膜可培养细菌种质库，并基于深度学习开发出 300 多个具有抑制病原细菌活性的多肽分子。

15:40-16:00

茶歇

主持人
李晓东
深圳市南山区人民医院

主任医师，新生儿科主任、儿科教研室及儿科规培基地主任。完成国家省市区级课题 20 余项，获省市级科技成果 3 项，撰写论文 100 余篇，参编学术专著 2 部。1984 年本科毕业于白求恩医科大学儿科系，广东医科大学硕士研究生导师、岭南名医中国医师协会儿科医师分会第四届委员会委员，中国医师协会新生儿医师分会第三届呼吸专业委员会委员，广东省临床医学学会第一届胎儿医学专业委员会副主任委员，广东省基层医药学会第一届新生儿专业委员会副主任委员，广东省医学会围产医学分会第六届委员会委员兼秘书、第七届委员会常务委员兼秘书，广东省医学会新生儿学分会第一、二届委员会委员广东省康复学会儿童发育与康复专业委员会委员，广东省医师协会儿科医师分会第二届委员会委员、第三届委员会常务委员，广东省医师协会新生儿科医师分会第一届委员会常务委员广东省医师协会围产医学分会第一、二届委员会委员，深圳市医学会第二届新生儿专业委员会副主任委员，深圳市医学会第七届儿科专业委员会常务委员，深圳市医学会第三届围产专业委员会委员，深圳市医师协会新生儿医师分会第一届理事会副理事长，深圳市医师协会儿科医师分会第二届理事会常务理事。

16:00-16:20

报告题目：DNA 甲基转移酶及其修饰模式影响细菌毒力表型的机制

刘洋 副教授（南方科技大学）

南方科技大学医院医学研究中心副主任，副研究员，硕士生导师。丹麦技术大学博士、南洋理工大学和新加坡国立大学博士后、深圳市海外引进高层次人才。主要通过微生物学、生化与分子生物学、生物信息学方法，进行细菌基因调控与耐药机理、微生物组与疾病健康方面的研究。在 *Journal of Clinical Microbiology*，*Antimicrobial agents and chemotherapy*，*mSystems* 等学术期刊发表 SCI 文章 30 余篇。SCI 的总影响因子>150，被引次数超 1500 次，H-Index 15。主持国家自然科学基金青年项目 1 项，广东省基础与应用基础研究基金面上项目 2 项，南山区卫健系统科技重大项目 1 项。

报告简介：DNA 甲基转移酶介导的甲基化修饰是细菌表观遗传调控的关键方式。我们开发了一种用户友好的生信工具，可以分析 DNA 甲基化特征和预测转录调控的影响。以铜绿假单胞菌临床菌株为模型，结合多种研究手段，我们系统研究了新型 DNA 甲基转移酶及甲基化模式通过关键基因影响多种细菌毒力（包括 NO 稳态、铁稳态和 T3SS）的机制。本项目旨在揭示细菌表观遗传学的新机制，并为病原菌精准诊治扩展方向。

16:20-16:40

报告题目：PPL 通过相分离和结合 HuR 促进骨形成的力生物学机制

印崇 副教授（川北医学院）

博士研究生，硕士生导师；川北医学院附属医院副研究员，华人骨矿物研究协会会员，中国细胞生物协会会员，中国抗癌协会会员，嘉陵江英才。主要从事骨骼系统相关疾病的遗传学和基因治疗研发。主持国家自然科学基金 1 项，省自然科学基金 1 项，申报国家发明专利 4 项。发表 SCI 论文 14 篇，研究成果发表在 *Cell Death & Differentiation*、*Pharmacological Research*、*Journal of Controlled Release* 等期刊，H 因子 19 分。

报告简介：力学刺激不足导致的成骨细胞分化水平降低，是骨质疏松发生的重要原因之一。细胞相分离可以响应力学刺激，调控成骨分化，但力学刺激调控相分离和成骨分化的机制尚不清楚。我们发现在 Plakin 蛋白家族成员 PPL 的相分离作用受到力学刺激的调控。PPL 通过其无序区（Intrinsically disordered region, IDR）发生相分离，并结合成骨细胞分化因子 HuR 来促进成骨分化。本研究为深入了解力学刺激影响骨形成的机制提供了新的实验基础，并为预防和治疗骨质疏松症提供了新的策略。

国际项目

主席：甘人友

三楼会议中心 10 月 13 日(周日)下午 16:00-17:30

主持人
甘人友 助理教授
香港理工大学

担任香港理工大学理学院食品科学与营养系助理教授&校长青年学者，曾担任新加坡 A*STAR 食品与生物技术创新研究院首席研究员。研究主要聚焦植物基食品、食品功能成分、益生菌、肠道菌群与人类营养/健康，相关工作发表了 200 多篇 SCIE 论文，被引用了 2 万余次，H 指数为 71（谷歌学术）；担任多个食品与营养相关国际期刊的编辑，入选 Clarivate“Highly Cited Researcher”（农业科学，2021-2023），以及斯坦福大学“World Top 2% Scientists”（食品科学/营养与膳食科学，2022-2023）。

16:00-16:15

报告题目：The International Natural Product Sciences Taskforce (INPST), an open innovation platform to invigorate the research field of natural compounds in the era of digital communications (线上)

Atanas G. Atanasov（Ludwig Boltzmann Institute for Digital Health and Patient Safety (Austria)

Atanas G. Atanasov is Principle Investigator of Ludwig Boltzmann Institute for Digital Health and Patient Safety (LBI-DHPS) at Medical University of Vienna (Austria), Professor of IGAB PAS (Poland), and Editor-in-Chief of Current Research in Biotechnology (#CRBIOTECH) and Exploration of Digital Health Technologies (#ExplorDHT). Dr Atanasov holds MSc in Biotechnology (from the University of Sofia, Bulgaria), PhD in Biochemistry (from the University of Bern, Switzerland), and Habilitation (Dr. habil. / PD) in Pharmaceutical Biology (from the University of Vienna, Austria). He has published >300 papers in the areas of Molecular Medicine, Digital Health, Open Innovation, Biotechnology, Natural Products, Nutrition, Science Communication, and Molecular Pharmacology. Moreover, Dr Atanas G. Atanasov is ranked as a Cross-Field Highly Cited Researcher (by Clarivate) since 2021, is included in the World’s Top 2% Scientists list (by Stanford University/Scopus/Elsevier 2023 data), and is a distinguished promoter of digital science communication (including use of social media, e.g., a >100 000-followers X (formerly Twitter)) and open innovation (e.g., through the executive leadership of open innovation platforms focused on Digital Health and Patient Safety (DHPSP) and on Natural Product Research (INPST).

Atanas G. Atanasov 是维也纳医科大学路德维希·玻尔兹曼数字健康与患者安全研究所 (LBI-DHPS) 的首席研究员、波兰 IGAB PAS 教授，以及 Current Research in Biotechnology 和 Exploration of Digital Health Technologies 的主编。Atanasov 博士拥有生物化学博士学位（瑞士伯尔尼大学）和药物生物学特许资格（奥地利维也纳大学）。他在分子医学、数字健康、开放式创新、生物技术、天然产物、营养、科学传播和分子药理学等领域发表了 300 多篇论文，文章被引用超 35000 余次。自 2021 年起被评为科睿维安全球高被引研究员，以及全球前 2% 顶尖科学家。致力于生物产物药物挖掘的研究。

报告简介：The International Natural Product Sciences Taskforce (INPST), an open innovation platform to invigorate the research field of natural compounds in the era of digital communications.

国际项目

| 三楼会议中心-496 座(大会)
| 10 月 13 日（周日）下午 16:00-17:30

主席：甘人友

16:15-16:30

报告题目：宏组学指南联盟（易扩增子/易宏基因组/微生物组手册）

高云云 博士（中国农科院基因组所/大鹏湾实验室）

毕业于北京林业大学，目前于中国农科院基因组所刘永鑫研究员团队，主攻生物信息学，近五年于 *iMeta*、*Protein & Cell* 等期刊，以第一作者或共一作者发表论文 7 篇，累计影响因子 76.5；先后获中国博士后科学基金第 75 批面上资助二等资助（2024 年）、国家自然科学基金区域联合基金重点项目子课题负责人(2024-2027 年)、中国农业科学院“优秀博士后”等荣誉。

报告简介：报告将详细介绍易扩增子/易宏基因组/微生物组手册等项目的进展，号召全球同行共同发起《宏组学指南联盟》。

16:30-16:45

报告题目：Fastplong: ultra-fast preprocessing for long reads

陈实富 创始人/CTO（海普洛斯）

中科院博士，海普洛斯创始人兼首席技术官，中科院深圳先进技术研究院客座研究员。2019 年深圳市青年科技奖获得者，深圳市科技达人。主要研究生物信息学和肿瘤基因组学。是开源项目组 OpenGene 的发起人，多款热门生物信息学软件的作者。发表国际期刊和会议论文 90 余篇，其中一作兼通讯最高单篇引用 14500 余次，连续两年入选“全球前 2%顶尖科学家榜单”，拥有 20 余项发明专利和 30 多项软件著作权。是 iMeta 期刊执行副主编，中国抗癌协会肿瘤标志专委会青年委员，肿瘤测序及大数据分析专委会委员，深圳市生物信息云计算产业促进会理事。

报告简介：报告将围绕三代长读长数据质控痛点，在二代宏基因组质控软件 fastp 的基础上，发起一个三代测序（比如 Nanopore, Pacbio 等平台）的数据的处理软件。

16:45-17:00

闭幕式

会议论文集

(按提交时间先后顺序排序)

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

Mengdi Xu(徐梦迪)[1, 3], Ehsan Hashemi [3], Hui Gao(高辉)[3], Qumar Zaman [3], Yi Ma(马毅)[1], Jufang Wang(王菊芳)[1], Wenjun Mao(毛文君) [2], Zhuobin Liang(梁卓斌)[3*]

[1]School of Biology and Biological Engineering, South China University of Technology, Guangzhou, Guangdong, 510006, China

[2]Department of Cardiothoracic Surgery, The Affiliated Wuxi People's Hospital of Nanjing Medical University, Wuxi, Jiangsu, 214023 China.

[3] Institute of Molecular Physiology, Shenzhen Bay Laboratory, Shenzhen, Guangdong, 518132, China.

* Correspondence to Zhuobin Liang (zbliang@szbl.ac.cn)

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

Running title: tRNA therapeutics

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*]

[1]MOE Key Laboratory of Gene Function and Regulation, State Key Laboratory for Biocontrol, School of Agriculture and Biotechnology, School of Life Science, Sun Yat-sen University, Guangzhou, 510275, P. R. China;

[#]These authors contributed equally: Yi-Feng Zhang, Ou-Yang Zhuo

*Correspondence: zhengll33@mail.sysu.edu.cn (Ling-Ling Zheng)

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

Running title: The bidirection of host-microbe interations

Sheng Zhang[1], Ziguang Wang[1], Wei Liu[1,*]
[1]School of Plant Protection, Anhui Agricultural University, Hefei, Anhui, China
*Correspondence: liuwei5@ahau.edu.cn (Wei Liu)

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

Running title: marine biofilm bioresources

Weipeng Zhang[1*]
[1]MOE Key Laboratory of Evolution & Marine Biodiversity and Institute of Evolution & Marine Biodiversity, Ocean University of China, Qingdao, China
*Correspondence: zhangweipeng@ouc.edu.cn (Weipeng Zhang)

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

Running title: Clinical and translational glycoproteomics

Yujia Wang[#], Kaixin Lei [#], Lijun Zhao*, Yong Zhang*
Department of General Practice Ward/International Medical Center Ward, General Practice Medical Center and Institutes for Systems Genetics, West China Hospital, Sichuan University, Chengdu 610041, China
[#]These authors contributed equally: Yujia Wang, Kaixin Lei
*Correspondence: nankai1989@foxmail.com (Yong Zhang); lijun709vip@gmail.com (Lijun Zhao)

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

Running title: PlantDRAW: Web Tool for Plant Disease Phenomics

Xue Wu[a,1], Zhihao Yuan[b,1], Xiaoyang Wan[b,1] , Xinyu Dong[b,1], Qi Wang[b,c,1,*], Qinglong Geb, Gefei Hao[a, b*]
[a]State Key Laboratory of Green Pesticide, Key Laboratory of Green Pesticide and Agricultural Bioengineering, Ministry of Education, Center for Research and Development of Fine Chemicals, Guizhou University, Guiyang 550025, P. R. China
[b]State Key Laboratory of Public Big Data, College of Computer Science and Technology, Guizhou University, Guiyang, 550025, Guizhou, China
[c]Department of Computer Science and Technology, Tsinghua University, Beijing, 100084, China

[1]These authors contributed equally: Xue Wu, Zhihao Yuan, Xiaoyang Wan, Xinyu Dong, Qi Wang
*Correspondence: qiwang@gzu.edu.cn (Qi Wang), gfhao@gzu.edu.cn

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

Running title: Microbiome and mycotoxins distribution patterns of wheat grains in China

Xin Zhou[1], Da Li[1], Qinni Yang[2], Minghao Liu[1], Zhihui Qi[3], Fang Tang[3], Lei Cai[1]*
[1]State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China
[2]College of Life Science, Northeast Forestry University, Harbin, China
[3]Academy of National Food and Strategic Reserves Administration, Beijing, China
*Correspondence: cail@im.ac.cn (Lei Cai)

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

Running title: Microbiome and metabolic health in Tibetans

Lin Shi [1,#], Tiemei Li [2,#], Tianqi Liu [1,#], Qingxia Huang [3], Ruijie Xu, Wenxiu Jian [2], Lanqi Zhou[1], Qi Wang[3], Lei Zhao, Xiaomin Sun[4], Bin Zhang [2], Haijing Wang [2], Huiru Tang [3,*], Youfa Wang, [4,*] Wen Peng [2,5,*]

1 School of Food Engineering and Nutritional Science, Shaanxi Normal University, Xi'an, China, No. 199 Chang'an South Rd, Shaanxi, 710062, China

2 Nutrition and Health Promotion Center, Department of Public Health Medical College, Qinghai University, No. 16 Kunlun Rd, Xining, 810008, China

3 State Key Laboratory of Genetic Engineering, School of Life Sciences, Human Phenome Institute, Zhangjiang Fudan International Innovation Center, Metabonomics and Systems Biology Laboratory at Shanghai International Centre for Molecular Phenomics, Zhongshan Hospital, Fudan University, Shanghai 200032, China

4 Global Health Institute, School of Public Health, Xi'an Jiaotong University, Room 3104, No. 21 Hongren Building, West China Science and Technology lnnovation Harbour (iHarbour), Xi'an, 710061, China

5 Qinghai Provincial Key Laboratory of Prevention and Control of Glucolipid Metabolic Diseases with Traditional Chinese Medicine, Medical College, Qinghai University, No. 16 Kunlun Rd, Xining, 810008, China

# These authors contributed equally to this work: Lin Shi, Tiemei Li, Tianqi Liu

*Corresponding authors: huiru_tang@fudan.edu.cn (Huiru Tang), youfawang@gmail.com (Youfa Wang), wen.peng2014@foxmail.com (Wen Peng)

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*

Wei Li[1,2], YuXiao Jiang[1,2], Xutong Sun[1,2], Sirui Xu[1,2], Lihong Li[1,2], Qingsong Shao[1,2]*, Ying Zheng[1,2]*
[1]State Key Laboratory of Subtropical Silviculture, Zhejiang A&F University, Hangzhou, 311300, China
[2]Zhejiang Provincial Key Laboratory of Resources Protection and Innovation of Traditional Chinese Medicine, Zhejiang A&F University, Hangzhou, 311300, China
*Correspondence:zhengying@zafu.edu.cn (Ying Zheng)

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

Running title: Batch Effect Explorer for image-based multi-center studies

Yuxin Wu[1,2,3,†], Xiongjun Xu[4,†], Yuan Cheng[1,2,3,†], Xiuming Zhang[5†], Fanxi Liu[6], Zhenhui Li[7], Lei Hu[1,2,3], Anant Madabhushi[8,9,10],, Peng Gao[11,12,*], Zaiyi Liu[1,3,*], Cheng Lu[1,2,3,*]

[1]Department of Radiology, Guangdong Provincial People's Hospital (Guangdong Academy of Medical Sciences), Southern Medical University, Guangzhou 510080, China.

[2] Medical Research Institute, Guangdong Provincial People's Hospital (Guangdong Academy of Medical Sciences), Southern Medical University, Guangzhou 510080, China.

[3] Guangdong Provincial Key Laboratory of Artificial Intelligence in Medical Image Analysis and Application， Guangzhou 510080, China.

[4] Department of Stomatology, The Third Affiliated Hospital of Sun Yat-Sen University, Guangzhou City, Guangdong Province, China.

[5] Department of Pathology, The First Affiliated Hospital, School of Medicine, Zhejiang University, Hangzhou, China.

[6] Department of Computer Science, School of Computing, National University of Singapore, Republic of Singapore.

[7] Department of Radiology, the Third Affiliated Hospital of Kunming Medical University, Yunnan Cancer Hospital, Yunnan Cancer Center, Kunming, Yunnan, China.

[8] Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology and Emory University, Atlanta, GA, USA

[9] Radiology and Imaging Sciences, Biomedical Informatics (BMI) and Pathology, Georgia Institute of Technology and Emory University, Atlanta, GA, USA

[10] Atlanta Veterans Administration Medical Center, Atlanta, GA, USA

[11] Key Laboratory for Experimental Teratology of Ministry of Education, Department of Pathology, School of Basic Medical Sciences, Shandong University, Jinan, China.

[12] Department of Pathology, Qilu Hospital, Shandong University, Jinan, China.

† These authors contributed equally to this work and should be considered co-first authors.

*Correspondence: lucheng@gdph.org.cn (Cheng Lu), liuzaiyi@gdph.org.cn (Zaiyi Liu), gaopeng@sdu.edu.cn (Peng Gao)

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

Running title: Bacterial communities under antibiotic stresses

Lixiao Wang[1, 2*], Hang Song[1, 2], Qibo Lv[1, 2], Qi Shao[1, 2]

[1]School of life sciences, Zhengzhou University, Zhenghzou, China

[2]Institute of Biodiversity and Ecology, Zhengzhou University, Zhengzhou, China

*Correspondence: wanglixiao@zzu.edu.cn (Lixiao Wang)

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

Running title: Gut Microbiota-Mediated Innovation of Food Functional Ingredients

Ren-You Gan[1*]

[1]Department of Food Science and Nutrition, Faculty of Science, The Hong Kong Polytechnic University, Hong Kong SAR, China

*Correspondence: renyou.gan@polyu.edu.hk (Ren-You Gan)

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

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

Qian Zhang[1#], Miao Yang[2#], Qian Zhang[1*]
[1]Department of Pharmacy, The Affiliated Bozhou Hospital of Anhui Medical University, Bozhou 236800, Anhui Province, China
[2]Department of Neurology, The Affiliated Bozhou Hospital of Anhui Medical University, Bozhou 236800, Anhui Province, China
#These authors contributed equally:Qian Zhang, Miao Yang
*Correspondence: zhangqian9428@163.com (Qian Zhang)

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.

Restricted intake of sulfur-containing amino acids reversed the hepatic injury induced by excess *Desulfovibrio* through gut-liver axis

Running title: Restricted sulfur amino acids intake reversed hepatic injury by excess *Desulfovibrio*

Lingxi Zhou[1], Gexue Lu[2], Yawen Nie[2], Yilin Ren[3], Jin-Song Shi[2], Yuzheng Xue[3], Zheng-Hong Xu[1,4], Yan Geng[2,3]*
[1]The Key Laboratory of Industrial Biotechnology, Ministry of Education; School of Biotechnology, Jiangnan University, Wuxi, China
[2]Key Laboratory of Carbohydrate Chemistry and Biotechnology, Ministry of Education, School of Life Sciences and Health Engineering, Jiangnan University, Wuxi, China
[3]Department of Gastroenterology, Affiliated Hospital of Jiangnan University, Wuxi, China
[4] College of Biomass Science and Engineering, Sichuan University, Chengdu, China
*Correspondence: School of Life Science and Health Engineering, Jiangnan University, Wuxi 214122, China gengyan@jiangnan.edu.cn (Yan Geng)

Abstract

Diet is a key player in gut–liver axis. However, the effect of different dietary patterns on gut microbiota and liver functions remains unclear. Here, we used rodent standard chow and purified diet to mimic two common human dietary patterns: grain and plant-based diet and refined-foodbased diet, respectively and explored their impacts on gut microbiota and liver. Gut microbiota experienced a great shift with notable increase in Desulfovibrio, gut bile acid (BA) levels elevated significantly, and liver inflammation was observed in mice fed with the purified diet. Liver inflammation and elevated gut BA levels also occurred in mice fed with the chow diet after receiving *Desulfovibrio desulfuricans* ATCC 29,577 (DSV). Restriction of sulfur-containing amino acids (SAAs) prevented liver injury mainly through higher hepatic antioxidant and detoxifying ability and reversed the elevated BA levels due to excess *Desulfovibrio*. Ex vivo fermentation of human fecal microbiota with primary BAs demonstrated that DSV enhanced production of secondary BAs. Higher concentration of both primary and secondary BAs were found in the gut of germ-free mice after receiving DSV. In conclusion, Restriction of SAAs in diet may become an effective dietary intervention to prevent liver injury associated with excess *Desulfovibrio* in the gut.

Keywords: gut microbiota, liver-gut axis, Desulfovibrio, purified diet, bile acid metabolism, sulfur-containing amino acids

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

Running title: Deciphering Mass Shifts from Proteomics-based Open Modification Searching

Jinfeng Chen[1,2,#], Lei Zhang[1,2,#], Xinhang Hou[3,#], Hongyi Li[4], Zhao Sun[5], Yunchao Wang[6], Jie Gao[5], Xinli Xue[1], Yang Yang[1], Kun Liu[1], Yibo Huang[1], Yuyuan Gao[1], Qian Zhao[1], Li Zhang[1], Xinchao Hu[1], Bowen Dong[1], Yuanyuan Wang[1], Jingyi Li[1], An Zhang[1], Yuxue Jiao[1], Xiaoxiao Zuo[7], Wen-zhi Guo[5], Shui-jun Zhang[5], Tongwen Sun[4], Yuming Xu6, Xiangnan Li[5], Zhong-Fa Yang[8], Chao Liu[3,*], Jing-Hua Yang[1,2,*]

[1] Clinical Systems Biology Key Laboratories of Henan, the First Affiliated Hospital of Zhengzhou University, Zhengzhou, 450052, Henan, China.

[2] Institute of Infection and Immunity, Henan Academy of Innovations in Medical Science, Zhengzhou, Henan, 450052, China

[3] School of Engineering Medicine & School of Biological Science and Medical Engineering, Beihang University, Beijing, 100191, China.

[4] General ICU, the First Affiliated Hospital of Zhengzhou University, Zhengzhou, Henan, 450052, China.

[5] Department of Surgery, the First Affiliated Hospital of Zhengzhou University, Zhengzhou, 450052, Henan, China.

[6] Department of Neurology, the First Affiliated Hospital of Zhengzhou University, Zhengzhou, Henan, 450052, China.

[7] Radiotherapy Department, the First Affiliated Hospital of Zhengzhou University, Zhengzhou, Henan, 450052, China.

[8] Weifang Key Laboratory of Collaborative Innovation of Intelligent Diagnosis and Treatment and Molecular Diseases, School of Basic Medical Sciences, Shandong Second Medical University, Weifang, China.

# These authors contribute equally to the work.

* Correspondence: Jing-Hua Yang, jhy@zzu.edu.cn; Chao Liu, liuchaobuaa@buaa.edu.cn.

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

Running title: Microbiome and AI Applications in Clinical Diagnostics

Weiwei Gao[1#], Xionggen Xiang[1#], Xianfu Yi[2]*,Yuchao Zhang[3,4]*
[1]Institute of Weishi Biotechnology Research, Hunan, China
[2]Department of Bioinformatics, School of Basic Medical Sciences, Tianjin Medical University, Tianjin, China
[3]Institute of Health Sciences, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, University of Chinese Academy of Sciences, Shanghai, China
[4]School of Life Science, Fudan University, Shanghai, China
[#]These authors contributed equally: Weiwei Gao,Xionggen Xiang
*Correspondence:yixianfu@tmu.edu.cn(Xianfu Yi); zhangyuchao@sibs.ac.cn(Yuchao Zhang)

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

Yibing Zhao[1,2,#], Tengyue Wang[1,2,#], Chuanhong Wang[1,2], Zhen Tao[1,2], Mengjie Zhao[1,2], Jiaxin Yu[1,2], Qingyang Zhang[1,2], XiaoDou Li[1,2], Jinghui Dong[1,2], Peijin Li[1,2,*]

[1]The National Key Engineering Lab of Crop Stress Resistance Breeding, The School of Life Sciences, Anhui Agricultural University, Hefei, China

[2]Center for Crop Pest Detection and Control, Anhui Agricultural University, Hefei, China

[#]These authors contributed equally: Tengyue Wang

*Correspondence: Peijin.li@ahau.edu.cn (Peijin Li)

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

Application of bacterial biomaterials in disease treatment

Di-Wei Zheng[1*], Wei Wei [1], Guang-Hui Ma[1,]
[1]Institute of Process Engineering, Chinese Academy of Sciences, Beijing, 100190
*Email: dwzheng@ipe.ac.cn

Abstract

Symbiotic microbial communities, such as gut microbiota and oral microbiota, play a crucial role in the occurrence, development, and treatment of various significant diseases. Utilizing bacteriotherapy to regulate symbiotic microbial communities has provided a novel direction for treating related diseases. Our research team proposed a study approach involving the modification of bacteria using material elements and chemical methods. This approach aims to impart specific functionalities to bacteria while preserving their inherent activities. We have developed modified bacterial strains capable of drug delivery, fluorescence imaging, and light-controlled drug synthesis. Moreover, our research has focused extensively on tumors and metabolic disorders.

By modulating both cancer-promoting and cancer-inhibiting bacteria within tumors, we have overcome the technical challenges associated with regulating specific bacteria within complex microbial communities in the human body. This strategy maximizes the therapeutic effects of chemotherapy and immunotherapy in colorectal cancer and oral squamous cell carcinoma, respectively[1,2]. Addressing the dilemma of toxin clearance in renal failure, we have engineered artificial microbial community materials that can orally eliminate metabolic toxins[3]. The designed bacterial/material hybrid demonstrates remarkable efficacy in mouse and pig animal models.

Our series of studies have provided innovative perspectives for treating diseases related to microbial communities and have offered essential guidance for developing a potent and stable bacteriotherapy.

Keywords: Engineered living materials; bacterial/material hybrid; symbiotic microbiota; cancer therapy; metabolic disease

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

Running title: Integrated metaproteomics/metagenomics reveals the mechanism of replant disease

Linkun Wu[1,2*], Qian Li[1,2], Wenxiong Lin[1,2]

[1]College of JunCao Science and Ecology, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China.

[2]Fujian Provincial Key Laboratory of Agroecological Processing and Safety Monitoring, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China.

*Correspondence: wulinkun619@163.com (Linkun Wu)

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

Running title: Glycerolipid Metabolism-Associated Prognostic Signatures in HCC

Fang Liu[1#], Hui Zhao[2#], Zhe Liu[3,4*]

[1]Rocgene (Beijing) Technology Co., Ltd., Beijing, China

[2]Westlake Laboratory of Life Sciences and Biomedicine, Hangzhou, China

[3]Department of Computer Science, City University of Hong Kong, Hong Kong, China

[4]Institute for Hepatology, National Clinical Research Center for Infectious Disease, Shenzhen Third People's Hospital; The Second Affiliated Hospital, School of Medicine, Southern University of Science and Technology, Shenzhen, China

[#]These authors contributed equally: Fang Liu, Hui Zhao

*Correspondence: zliu39-c@my.cityu.edu.hk (Zhe Liu)

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

Running title: Adaptive mechanisms of aerobic granular sludge by quantitative proteomic analysis

Yao Shen[1#], Qi-Xin Liu[1#], Shuo Wang[1,2]*, Ji Li[1,2]

[1]Jiangsu Key Laboratory of Anaerobic Biotechnology, School of Environment and Ecology, Jiangnan University, Wuxi, China

[2] Jiangsu College of Water Treatment Technology and Material Collaborative Innovation Center, Suzhou, China

[#]These authors contributed equally: Yao Shen, Qi-Xin Liu

*Correspondence: shuowang@jiangnan.edu.cn (Shuo Wang)

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

Running title: Antibiotic Resistance Genes in Cow Milk and Pasture

Jinyu Zhou[1], Xu Lin[1], Kairu He[1], Shuaiqi Ji[1], Junrui Wu[1*], Rina Wu[1*], Zhishen Mu[2*]

[1]College of Food Science, Shenyang Agricultural University, Liaoning Engineering Research Center of Food Fermentation Technology, Shenyang Key Laboratory of Microbial Fermentation Technology Innovation, Shenyang 110866, P.R. China.

[2]Inner Mongolia Enterprise Key Laboratory of Dairy Nutrition, Health & Safety, Inner Mongolia Mengniu Dairy (Group) Co., Ltd., Huhhot 011500, P.R. China.

*Correspondence: junruiwu@126.com (Junrui Wu); wrn6956@163.com (Rina Wu); Science20170101@163.com (Zhishen Mu)

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

Running title: Intervention of gut microbiota in ulcerative colitis using a probiotic colon-targeted delivery system enhanced by the antioxidant *Codonopsis pilosula* polysaccharides.

Henan Zhang[1,2], Jiayi Tang[1,3], Danli Yan[1,2],Ying Wang[1,2], Junrui Wu[1,3], Rina Wu[1,2 *]

[1] College of Food Science, Shenyang Agricultural University, Shenyang 110866, P. R. China;

[2]Key Laboratory of Microbial Fermentation Technology Innovation, Shenyang, Liaoning, 110866, P.R. China.

[3]Engineering Research Center of Food Fermentation Technology, Shenyang 110161, P. R. China.

*Correspondence: wrn6956@163.com, rinawu@syau.edu.cn (Rina Wu)

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

Running title: GISDD: an integrated sequence and genotyping database platform for dengue virus

Xiang Guo[1], Ziyao Li[1], Liqiang Li[1,2], Xiaohua Liu[1], Xiaoqing Zhang[1], Yuji Wang[1], Minling Hu[1], Wenwen Ren[1], Shu Zeng[1], Haiyang Chen[1], Liu Ge[1], Shihan Liu[1], Zhiqiang Peng[3], Jiufeng Sun[4], Xin Zhang[3], Lei Luo[5], Jie Peng[6], Benyun Shi[7], Rangke Wu[8], Jiming Liu[9], Fuchun Zhang[10], Xiao-Guang Chen[1], Tong Chen[11*], Xiaohong Zhou[1*]

[1]Institute of Tropical Medicine, Department of Pathogen Biology, School of Public Health, Southern Medical University; Guangdong Provincial Key Laboratory of Tropical Disease Research; Key Laboratory of Infectious Diseases Research in South China, Ministry of Education, Guangzhou 510515, Guangdong, China

[2]Department of Clinical Laboratory, The Third People's Hospital of Shenzhen, Southern University of Science and Technology, National Clinical Research Center for Infectious Diseases, Guangdong Provincial Clinical Research Center for Infectious Diseases (Tuberculosis), Shenzhen Clinical Research Research Center for Tuberculosis, Shenzhen 518112, China

[2]Guangdong Provincial Center for Disease Control and Prevention, Guangzhou 511430, China

[3]Guangdong Provincial Institute of Public Health, Guangdong Provincial Center for Disease Control and Prevention, Guangzhou 511430, China

[4]Guangdong Provincial Institute of Public Health, Guangdong Provincial Center for Disease Control and Prevention, Guangzhou 511430, China

[5]Guangzhou Center for Disease Control and Prevention, Guangzhou 510440, China

[6]Department of Infectious Disease, Nanfang Hospital, Southern Medical University, Guangzhou 510515, China

[7]College of Computer and Information Engineering, Nanjing Tech University, Nanjing 211816, China

[8]The School of Foreign Studies, Southern Medical University, Guangzhou 510515, China

[9]Department of Computer Science, Hong Kong Baptist University, Hong Kong 999077, China

[10]Guangzhou Medical Research Institute of Infectious Diseases, Infectious Disease Center, Guangzhou Eighth People's Hospital, Guangzhou Medical University, Guangzhou 510440, China

[11]State Key Laboratory for Quality Ensurance and Sustainable Use of Dao-di Herbs, National Resource Center for Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing 100000, China

*Correspondence: daizhouxh@163.com (Xiaohong Zhou), chent@nrc.ac.cn (Tong Chen)

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

Running title: The impact of Staphylococcus aureus and other bacteria colonizing the surface of pressure ulcers on wound healing should not be underestimated

Master's Student: Changyuan Guo, Supervisor: Dr. Heng Li and Prof. Zhemin Zhou
Suzhou Medical College of Soochow University

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

Running title:Anemoside B4 relieves neuropathic pain by inhibiting key inflammatory mediators

Zuchang Guo[1,2#], Minghong Zhao[1,3#], Tianming Lu[1, 4#], Chong Qiu[1], Tong Yang[1,3], Qixin Wang[1], Jigang Wang[1, 3, 4*], Qiuyan Guo[1*]

[1] Artemisinin Research Center and Institute of Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing, 100700, China;

[2] Postgraduate school, Jiangxi University of Chinese Medicine, Nanchang, 330009, China

[3] The First School of Clinical Medicine, Gannan Medical University, Ganzhou, 341000, China;

[4] School of Public Health of Guangxi Medical University, Nanning, 530021, China

[#]These authors contributed equally:Zuchang Guo,Minghong Zhao,Tianming Lu

*Correspondence: qyguo@icmm.ac.cn (Qiuyan Guo)

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

Running title: Practical experiences on the prevention of nosocomial infection

Wang Li[1, 2#], Xue Wang[1#], Xuelu Yu[1], Jingwen Chen[1,2], Jishun Yang[1]*, Mingke Wang[1]*

[1]Naval Medical Center of PLA, Naval Medical University, Shanghai, China

[2]School of Pharmacy, Bengbu Medical University, Bengbu, Anhui Province, China

[#]These authors contributed equally: Wang Li, Xue Wang

*Correspondence: wmke021@163.com (Mingke Wang); jasunyang@foxmail.com (Jishun Yang)

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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

Yongbin Xu[1], Yupeng Liu[1], Jie Chen[1], Yonglin, Zhao[1], Songshan Shi[1], Shunchun Wang[1],*, Huijun Wang[1],*
[1]The MOE Key Laboratory for Standardization of Chinese Medicines and the SATCM Key Laboratory for New Resources and Quality Evaluation of Chinese Medicines, Institute of Chinese Mate ria Medica, Shanghai University of Traditional Chinese Medicine, 1200 Cailun Road, Shanghai, 201203, PR China
*Correspondence: shunchunwang@126.com (Shunchun Wang), huijun.wang@outlook.com (Huijun Wang)

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

Running title: Fecal Microbiota Transplantation for IgA Nephropathy

Wenqiang Zhi[1,2], Huiwen Zhi[1,2], Xiaoli Yuan[2], Yafeng Li[1,2,3*]

[1]Academy of Microbial Ecology, Shanxi Medical University, Taiyuan, China

[2]The Nephrology Department of Shanxi Provincial People's Hospital, Shanxi Medical University; Taiyuan, 030001, China

[3]Core Laboratory, Shanxi Provincial People's Hospital (Fifth Hospital), Shanxi Medical University; Taiyuan, China

*Correspondence: dr.yafengli@gmail.com (Yafeng Li)

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

Physical barriers limit the activity of bacterial decomposers

Tingting Cao[a, b, #], Qing Zhang[b, #], Yunru Chen[a, d], Qiang Li[a], You Fang[a], Yunchao Luo[e], Chengjiao Duan[f], Qi chen[a], Xinzhang Song[b], Xingjun Tian[a,c *]

[a] School of Life Sciences, Nanjing University, Nanjing, Jiangsu 210023, China

[b] State Key Laboratory of Subtropical Silviculture, Zhejiang A&F University, Hangzhou 311300, China

[c] Co-Innovation Center for Sustainable Forestry in Southern China, Nanjing Forestry University

[d] Beijing Municipal Ecological and Environmental Monitoring Center, Beijing 100048, China

[e] School of Life Sciences, Shanxi Normal University, 339 Taiyu Road, Taiyuan 030031, China

[f] College of Resources and Environment, Shanxi Agricultural University, Taigu, Shanxi Province 030801, PR China

[#]These authors contributed equally: Tingting Cao, Qing Zhang

*Correspondence: tianxj@nju.edu.cn (Xingjun Tian)

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

Running title: Gut microbiota, diet and hyperuricemia

Jingwen Chen[1, 2#], Xuelu Yu[1, 2#], Qing Chang[3], Noora Barzkar[4], Xue Wang[1], Xiao Huang[1], Jishun Yang[1]*, Mingke Wang[1]*

[1]Naval Medical Center of PLA, Naval Medical University, Shanghai, China

[2]School of Pharmacy, Bengbu Medical University, Bengbu, Anhui Province, China

[3]The Third Department of Convalescence, Beidaihe Rehabilitation and Convalescence Center of People's Liberation Army, Qinhuangdao, Hebei Province, China

[4]Borneo Marine Research Institute, Higher Institution Centers of Excellence, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia

[#]These authors contributed equally: Jingwen Chen, Xuelu Yu

*Correspondence: wmke021@163.com (Mingke Wang); jasunyang@foxmail.com (Jishun Yang)

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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

Running title: Specific synbiotics preparations are alleviating the progression of IgAN

Huiwen Zhi[1], Wenqiang Zhi[1], Feng Wu[1], Lu Zhao[1], Xiaotong Li[1], Yafeng Li[1, 2, 3*]

[1]The department of Nephrology, Shanxi Provincial People's Hospital (Fifth Hospital) of Shanxi Medical University; Taiyuan, China

[2]Core Laboratory, Shanxi Provincial People's Hospital (Fifth Hospital), Shanxi Medical University; Taiyuan, China;

[3]Academy of Microbial Ecology, Shanxi Medical University, Taiyuan, China;

*Correspondence: dr.yafengli@gmail.com (Yafeng Li)

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

Running title: Intestinal microbiota and vasculitis

Wenqiang Zhi[1,2], Huiwen Zhi[1,2], Qian Wang[2], Yafeng Li[1,2,3*]

[1]Academy of Microbial Ecology, Shanxi Medical University, Taiyuan, China

[2]The Nephrology Department of Shanxi Provincial People's Hospital, Shanxi Medical University; Taiyuan, 030001, China

[3]Core Laboratory, Shanxi Provincial People's Hospital (Fifth Hospital), Shanxi Medical University; Taiyuan,China;

*Correspondence: dr.yafengli@gmail.com (Yafeng Li)

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

Running title: M-gene breeding innovate agriculture sustainability

Feiying Zhu[1], Pin Su[1], Qianze Peng[1], Deyong Zhang[1]*

[1] Hunan Academy of Agricultural Sciences, Changsha 410125, China

*Correspondence: zhangdeyong@hhrrc.ac.cn (Deyong Zhang)

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

Running title: Spatial metabolomics of *Fissistigma oldhamii*

Wenjuan Liu[1#], Runan Zhang[1#], Wenjuan Tian[1], Menghuan Zeng[1], Ye Liu[1], Xinyan Wu[1], Bin Hu[1], Xiangjian Zhong[1], Hao Huang[1*], Haibo Hu[1,2*]

[1]Jiangxi Province Key Laboratory of Pharmacology of Traditional Chinese Medicine, National Engineering Research Center for Modernization of Traditional Chinese Medicine – Hakka Medical Resources Branch, School of Pharmacy, Gannan Medical University, Ganzhou 341000, China.

[2]Department of Biology, Animal Physiology and Neurobiology Section, KU Leuven, Leuven 3000, Belgium.

[#]These authors contributed equally: Wenjuan Liu, Runan Zhang

*Correspondence: hhb2017@gmu.edu.cn (Haibo Hu)

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

Running title: Probiotic fermentation of herbs

Yongjun Wei[1,2,3*], Xiaoling Zhang[1,3], Leli Wang[4], Yulong Yin[4,*]

[1]School of Pharmaceutical Sciences, Zhengzhou University, Zhengzhou, Henan 450001, China
[2]Center for Lipid Engineering, Muyuan Laboratory, Zhengzhou, Henan 450016, China
[3]Zhengzhou Research Base, State Key Laboratory of Cotton Bio-breeding and Integrated Utilization, Laboratory of Synthetic Biology, Zhengzhou University, Zhengzhou, Henan 450001, China
[4]Engineering Technology Research Center for Fermented Veterinary Traditional Chinese Medicine of Henan Province, Henan Institute of Modern Fermentation Technology Co. Ltd., Kaifeng, Henan 475400, China

*Correspondence: yongjunwei@zzu.edu.cn (Yongjun Wei); yinyulong@isa.ac.cn (Yulong Yin)

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

Running title: Large language model ESMARG for characterizing antibiotic resistance genes in cyanobacterial aggregate

Congmin Zhu[1,2#], Haimeng Li[3#], Yuqing Yang[3]*

[1]School of Biomedical Engineering, Capital Medical University; Beijing, China

[2]Beijing Key Laboratory of Fundamental Research on Biomechanics in Clinical Application

[3]State Key Laboratory of Networking and Switching Technology, Beijing University of Posts and Telecommunications, Beijing, China

[#]These authors contributed equally: Congmin Zhu, Haimeng Li

*Correspondence: congminz@ccmu.edu.cn (Congmin Zhu); yangyuqing@bupt.edu.cn (Yuqing Yang)

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*

Running title: Genomic analysis of *Sogatella furcifera*

Ting Cui[1,#], Qing Bai [1,#], Weiqiang Yu[1], Dongyang Guo[1], Yawen Ban[1], Kun Chen[1], Ali Raza[1], Guohui Zhou[2], Qingfa Wu [1,2,*]

[1]Center for Advanced Interdisciplinary Science and Biomedicine of IHM, Division of Life Sciences and Medicine, University of Science and Technology of China, Hefei, Anhui 230027, China

[2]Guangdong Province Key Laboratory of Microbial Signals and Disease Control, College of Agriculture, South China Agricultural University, Guangzhou, Guangdong 510642, China

[3]Department of Pharmacy, The First Affiliated Hospital of USTC, Division of Life Sciences and Medicine, University of Science and Technology of China, Hefei, Anhui, 230001, China

[#]These authors contributed equally: Ting Cui, Qing Bai

*Correspondence: baiqing@ustc.edu.cn (Qing Bai), wuqf@ustc.edu.cn (Qingfa Wu)

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

Running title: Core bacteria enhance disease resistance in kiwifruit

Min Fu[1#], Yunhe Chen[1#], Yong-Xin Liu[2], Xiaoxi Chang[1], Lei Zhang[1], Xinyi Yang[1], Li Li[3], Lixin Zhang[1*]

[1]Anhui Province Key Laboratory of Integrated Pest Management on Crops, College of Plant Protection, Anhui Agricultural University, Hefei 230036, China

[2]Shenzhen Branch, Guangdong Laboratory of Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture and Rural Affairs, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, Guangdong 518120, China

[3]CAS Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, CAS Engineering Laboratory for Kiwifruit Industrial Technology, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China

[#]These authors contributed equally: Min Fu, Yunhe Chen

*Correspondence: lxzhang@ahau.edu.cn (Lixin Zhang)

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

Antibacterial effect and phytochemical components of the aerial parts from *Allium sativum*

Running title: Antibacterial ingredients of *Allium sativum*

Chuan Pu[1], Haoyue Hu[1], Ruihang Cao[1], Yunhui Ouyang[1], Liping Rao[1], Haibo Hu[1], Xiangjian Zhong[1], Hao Huang[1], Zheng Wei[2], Haixue Kuang[3], Bin Hu[1]*

[1]Jiangxi Province Key Laboratory of Pharmacology of Traditional Chinese Medicine, National Engineering Research Center for Modernization of Traditional Chinese Medicine - Hakka Medical Resources Branch, School of Pharmacy, Gannan Medical University, Ganzhou, China

[2]Ganzhou people's Hospital, Ganzhou, China

[3]Key Laboratory of Chinese Materia Medica, School of Pharmacy, Heilongjiang University of Chinese Medicine, Harbin, China

*Correspondence: hubin@gmu.edu.cn (Bin Hu)

Abstract

The bulbs of *Allium sativum* (garlic) are widely used as food or condiment, while they have also been used as a famous traditional medicine since ancient times for the treatment of diarrhea, dysentery, pertussis, tuberculosis and scabies, etc. However, most studies have focused on bulbs, and few studies have focused on the abundant aerial parts, which are usually discarded during the harvest season. In this paper, the inhibitory effects of 70% ethanol crude extract from the aerial parts and its extracts (petroleum ether, ethyl acetate, *n*-butanol, and residual water extracts) on *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* were studied for the first time. The results showed that the extracts had different degrees of inhibitory effects on the tested bacteria *in vitro*, and the ethyl acetate extract had the strongest antibacterial activity. The results of antibacterial mechanism showed that the ethyl acetate extract could significantly inhibit the formation of biofilm of *S. epidermidis* and *S. aureus*, and destroy the integrity of cell wall and cell membrane, thus exerting antibacterial effect. 12 compounds were isolated from the ethyl acetate extract, and their structures were identified by NMR and MS analysis. *In vitro* experiments showed that some compounds had good antibacterial activity. The above results support that the aerial parts of *A. sativum* are an interesting source of bioactive ingredients, which can be used to prevent and treat bacterial infectious diseases.

Keywords: *Allium sativum*, antibacterial effect, phytochemical components

Bacteria-Mediated Colorectal Cancer Immune Subtyping

Shuting Xia[1#], Likun Wang[2#], Yangzhuo Xu[2#], Fulin Yang[1], Yina Liu[1], Fuliang Qian[2], Xiaodong Yang[1], Zhemin Zhou[1*]

[1]Cancer Institute, Suzhou Medical College, Soochow University, Suzhou, China

[2]School of Public Health.Suzhou Medical College, Soochow University, Suzhou, China

[#]These authors contributed equally: Shuting Xia, Likun Wang, Yangzhuo Xu

*Correspondence: zmzhou@suda.edu.cn (Zhemin Zhou)

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

Runan Zhang[1#], Wenjuan Liu[1#], Wenjuan Tian[1], Menghuan Zeng[1], Ye Liu[1], Xinyan Wu[1], Bin Hu[1], Haibo Hu[1,2], Hao Huang[1*], Xiangjian Zhong[1*]

[1]Jiangxi Province Key Laboratory of Pharmacology of Traditional Chinese Medicine, National Engineering Research Center for Modernization of Traditional Chinese Medicine - Hakka Medical Resources Branch, School of Pharmacy, Gannan Medical University, Ganzhou 341000, China.

[2]Department of Biology, Animal Physiology and Neurobiology Section, KU Leuven, Leuven 3000, Belgium.

[#]These authors contributed equally: Runan Zhang, Wenjuan Liu

*Correspondence: xiangjzhong@163.com (Xiangjian Zhong)

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

Running title: Application study of sedimentary ancient DNA technology in archaeological sites

Zhengquan Gu[1], Yuanyang Cai[1,4], Xu Han[1,4], Zihao Huang[1,2,3,6], Zhe Xue6, Haoran Dong[1,7], Yu Gao[1], Fahu Chen[1,7], Yucheng Wang[1,3,5,6*]

[1]Group of Alpine Paleoecology and Human Adaptation (ALPHA), State Key Laboratory of Tibetan Plateau Earth System, Environment and Resources (TPESER), Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing 100101, China

[2]Shenzhen Branch, Guangdong Laboratory of Lingnan Modern Agriculture, Key Laboratory of Synthetic Biology, Ministry of Agriculture and Rural Affairs, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China

[3]Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, UK

[4]University of Chinese Academy of Science, Beijing, 100049, China

[5]Centre for Ancient Environmental Genomics, Globe Institute, University of Copenhagen, Copenhagen, Denmark

[6]Department of Zoology, University of Cambridge, Cambridge, CB2 3EJ, UK

[7]Key Laboratory of Western China's Environmental Science (Ministry of Education), College of Earth and Environmental Science, Lanzhou University, Lanzhou 730000, China

*Correspondence: yw502@cam.ac.uk (Yucheng Wang)

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

SIDERITE: Unveiling hidden siderophore diversity in the chemical space through digital exploration

Running title: Siderophore information database and application

Ruolin He[1#], Shaohua Gu[1,2#], Jiazheng Xu[3], Xuejian Li[4], Haoran Chen[4], Zhengying Shao[3], Fanhao Wang[1], Jiqi Shao[1], Wen-Bing Yin[5,6], Long Qian[1*], Zhong Wei[3*], Zhiyuan Li[1,2*]

[1]Center for Quantitative Biology, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, China

[2]Peking-Tsinghua Center for Life Sciences, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, China

[3]Jiangsu provincial key lab for solid organic waste utilization, Key lab of organic-based fertilizers of China，Jiangsu Collaborative Innovation Center for Solid Organic Wastes, Educational Ministry Engineering Center of Resource-saving fertilizers, Nanjing Agricultural University, Nanjing, China

[4]Beyond Flux Technology Co., Ltd., Beijing, China

[5]State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China

[6]Savaid Medical School, University of Chinese Academy of Sciences, Beijing, China

[#]These authors contributed equally: Ruolin He, Shaohua Gu

*Correspondence: zhiyuanli@pku.edu.cn (Zhiyuan Li), weizhong@njau.edu.cn (Zhong Wei), long.qian@pku.edu.cn (Long Qian)

Abstract

Siderophores, a highly diverse family of secondary metabolites, play a crucial role in facilitating the acquisition of the essential iron. However, the current discovery of siderophore relies largely on manual approaches. In this work, we introduced a siderophore information database (SIDERTE), a digitized siderophore information database containing 945 siderophore records with 707 unique structures (Updated in 2024 May). Leveraging this digitalized dataset, we gained a systematic overview of siderophores by their clustering patterns in the chemical space. Building upon this, we developed a ligand-based method for predicting new iron-binding molecules. Applying this method to 407,270 natural product molecules from the collection of open natural products (COCONUT) database, we predicted a staggering 3,199 siderophore candidates, showcasing remarkable siderophore structural diversity that are largely unexplored. 48 molecules of 3199 candidates are available in the commercial natural product library. We experimentally confirmed that 40 out of the 48 molecules possessed iron-binding abilities by chrome azurol S (CAS) assay. Our study provides a valuable resource for accelerating the discovery of novel iron-binding molecules and advancing our understanding towards siderophores.

Keywords: Siderophore, Database, Natural product

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

Running title: Bacteria LX to reduce PAEs accumulation in rice

Lihui Liu *, Liwan Feng, Ruihao Zhuang, Yue Zhang, Zitao Lu
School of Life Sciences and Biopharmaceutics, Guangdong Pharmaceutical University, Guangzhou, China
*Correspondence: lihuiliu@gdpu.edu.cn (Lihui Liu)

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

Running title: Enhancing BGC Functional Alignment via BGC Block Aligner

Jiqi Shao[1], Zhiyuan Li[1]*

[1]Center for Quantitative Biology, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, 100871, China

*Correspondence: zhiyuanli@pku.edu.cn (Zhiyuan Li)

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

Functional complementarity between the abundant and rare microbial populations of biological soil crusts drives intense regulation on the integrated networks of metal homeostasis mediating biogeochemical cycle

Yansong Wang, Zengru Wang, Yubing Liu

State Key Laboratory of Grassland Agro-ecosystems; Key Laboratory of Grassland Livestock Industry Innovation, Ministry of Agriculture and Rural Affairs; Engineering Research Center of Grassland Industry, Ministry of Education; College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou 730020, Gansu Province, PR China

Abstract

Biological soil crusts (BSCs) cover approximately 40% of arid and semi-arid lands, playing a pivotal role in biogeochemical cycling. Within BSC microbial communities, bacteria and fungi form the core active taxa, with abundant and rare populations that maintain biogeochemical cycles through distinct yet complementary roles, intricately connected via metal homeostasis. Here, we employed GeoChip 5.0 to analyze the functional genes associated with metal homeostasis and the metabolism of carbon (C), nitrogen (N), and sulfur (S) within these microbial populations, as well as the factors influencing BSC development in the Tengger Desert and the Loess Plateau. The results showed that in both regions, rare microbial populations predominantly drove the coupled networks of metal homeostasis and biogeochemical cycling, with metal homeostasis particularly dependent on these rare populations rather than abundant ones. In the Tengger Desert, rare populations primarily drove the C, N, and S cycles, while on the Loess Plateau, both abundant and rare populations jointly regulated these cycles using distinct gene sets. In the nutrient-limited soils of the Tengger Desert, available phosphorus, organic carbon, and total carbon contents were the primary limiting factors, especially for functional genes involved in metal homeostasis and the C and N cycles of both abundant and rare populations. On the Loess Plateau, available iron and calcium had a more substantial influence, with total nitrogen and total phosphorus also serving as important limiting factors. This study underscores the functional complementarity between abundant and rare microbial populations in BSCs, emphasizing their critical role in regulating integrated networks of metal homeostasis, which drive biogeochemical cycles in arid regions.

Keywords: Abundant populations, rare populations, functional genes, microbial metal homeostasis, biogeochemical cycle.

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

Running title: Punicalagin alleviates hyperuricemia in mice

Tong Jin[1,2], Ailin Wang[1], Jian Guo[1], Wenxiu Zhu[1], Yingying Zhang[2], Xiaodong Xia[1]*

[1]State Key Laboratory of Marine Food Processing and Safety Control, National Engineering Research Center of Seafood, School of Food Science and Technology, Dalian Polytechnic University, Dalian, China

[2]Department of Food Safety, College of Food Science and Engineering, Northwest A&F University, Xianyang, China

*Correspondence: foodscixiaodong@dlpu.edu.cn (Xiaodong Xia)

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

Running title: Identification of lactic acid bacteria in single cell level

Yan Ren[1,2], Yang Zheng[1], Xiaojing Wang[1], Shuang Qu[1], Lijun Sun[3], Chenyong Song[4], Jia Ding[4], Yuetong Ji[3,4], Guoze Wang[1,2], Pengfei Zhu[3,4]* and Likun Cheng[1,2]*
[1]School of Life Science and Technology, Inner Mongolia University of Science and Technology, Baotou, China
[2]Inner Mongolia Key Laboratory for Biomass-Energy Conversion, Baotou, China
[3]Single-Cell Center, CAS Key Laboratory of Biofuels, Shandong Key Laboratory of Energy Genetics, Qingdao Institute of BioEnergy and Bioprocess Technology, Chinese Academy of Sciences, Qingdao, Shandong, China
[4]Qingdao Single-Cell Biotechnology Co., Ltd., Qingdao, Shandong, China

*Correspondence: zhupf@singlecellbiotech.com (Pengfei Zhu); chlkun@qq.com (Likun Cheng)

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

Running title: A New Framework for Tracing Gene Function Evolution Using Public Genomic Data

Junjie Deng[1], Moyang Liu[1]*

[1]School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai 200240, China

*Correspondence: cooljeep@sjtu.edu.cn (Moyang Liu)

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

Running title: Coevolution of the microbiome and host genome in high-altitude adaptation

Jiaming Jin [1,2,#], Chaoliang Wen [1,2,#,*], Jing Feng[3], Junying Li[1,2], Xueying Ma[3], Ning Yang[1,2,*]

[1]State Key Laboratory of Animal Biotech Breeding and Frontier Science Center for Molecular Design Breeding, China Agricultural University, Beijing, 100193, China

[2]National Engineering Laboratory for Animal Breeding and Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing 100193, China

[3]Institute of Animal Husbandry and Veterinary Medicine, Tibet Academy of Agricultural and Animal Husbandry Science, Lhasa 850009, China

[#]These authors contributed equally: Jiaming Jin, Chaoliang Wen

*Correspondences: clwen@cau.edu.cn (Chaoliang Wen), nyang@cau.edu.cn (Ning Yang)

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

Shaohua Gu[1,2,3], Zhengying Shao[3], Zeyang Qu[1], Yuanzhe Shao[2], Ruolin He[1], Jiqi Shao[1], Guanyue Xiong[1], Alexandre Jousset[3], Ville-Petri Friman[5], Zhong Wei[3*], Rolf Kümmerli[4*], Zhiyuan Li1,[2*]

[1]Name of the Institution, city and country in font Arial 81 Center for Quantitative Biology, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, 100871, China.

[2]Peking-Tsinghua Center for Life Sciences, Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, 100871, China.

[3]Jiangsu Provincial Key Lab for Organic Solid Waste Utilization, Key lab of organic-based fertilizers of China, Nanjing Agricultural University, Nanjing, P R China.

[4]University of Zurich, Department of Quantitative Biomedicine, Winterthurerstr. 190, 8057 Zurich, Switzerland.

[5]University of Helsinki, Department of Microbiology, 00014, Helsinki, Finland.

Email: weizhong@njau.edu.cn; rolf.kuemmerli@uzh.ch; zhiyuanli@pku.edu.cn.

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

Running title: Bacterial rhomboid proteases mediate quality control of orphan membrane proteins

Guangyu Liu[1], Feng Chen[1], Stephen E Beaton[3], Adam G Grieve[1], Rhiannon Evans[3], Miranda Rogers[1], Kvido Strisovsky[4] , Fraser A Armstrong[3], Matthew Freeman[1] , Rachel M Exley[1],* & Christoph M Tang[1],**

[1]School of Basic Biomedical Sciences, Zhejiang Key Laboratory of Medical Epigenetics, Hangzhou Normal University, Hangzhou, China

[2]Sir William Dunn School of Pathology, University of Oxford, Oxford, UK

[3]Inorganic Chemistry Laboratory, University of Oxford, Oxford, UK

[4]Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, Praha 6, Czech Republic

*Correspondence: rachel.exley02@path.ox.ac.uk (Rachel M Exley)

*Correspondence: christoph.tang@path.ox.ac.uk (Christoph M Tang)

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

Tianyuan Song[1 2]*, Dingqi Zhang[3], Yonghong Hu[4], Zhenyu Gu[1 2], Qing Gu[1 2]

[1]School of Food Science and Biotechnology, Zhejiang Gongshang University, Hangzhou, Zhejiang, 310018, People's Republic of China

[2]Key Laboratory for Food Microbial Technology of Zhejiang Province, College of Food Science and Biotechnology, Zhejiang Gongshang University, Hangzhou Zhejiang, 310018, People's Republic of China

[3]School of Pharmaceutical Sciences, Tsinghua University, Beijing 100084, China

[4]Institute of Surgery of Integrated Traditional Chinese and Western Medicine, Shuguang Hospital Affiliated to Shanghai University ofTraditional Chinese Medicine, China

*Correspondence: songtianyuan@mail.zjgsu.edu.cn (Tianyuan Song)

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

Running title: Identification of Microbial Biomarkers for Inflammatory Bowel Disease

Shicheng Yu[1] *

[1] Guangzhou National Laboratory, Guangzhou, China

*Correspondence: shyu@whu.edu.cn (Shicheng Yu)

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

Running title: Effects of synbiotic supplementation on immune parameters and gut microbiota

Xiaoqin Li[1 2 3], Shan Hu[2 3], Jiawei Yin[2 3], Xiaobo Peng[2 3], Lei King[2 3], Linyan Li[2 3], Zihui Xu[2 3], Li Zhou[4], Zhao Peng[2 3], Xiaolei Ze[5], Xuguang Zhang[5], Qiangchuan Hou[6], Zhilei Shan[2 3], Liegang Liu[2 3]*

Tong Chen[2#], Yong-Xin Liu[3#], Luqi Huang[2]*

[1] School of Public Health, Lanzhou University, Lanzhou, China.

[2]Department of Nutrition and Food Hygiene, Hubei Key Laboratory of Food Nutrition and Safety, School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China.

[3]Ministry of Education Key Lab of Environment and Health, School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China.

[4]Academy of Nutrition and Health, Hubei Province Key Laboratory of Occupational, Hazard Identification and Control, School of Public Health, Wuhan University of Science and Technology, Wuhan, China.

[5]Microbiome Research and Application Center, BYHEALTH Institute of Nutrition & Health, Guangzhou, China.

[6]Hubei Provincial Engineering and Technology Research Center for Food Ingredients, Hubei University of Arts and Science, Xiangyang, Hubei province, China.

*Correspondence: lgliu@mails.tjmu.edu.cn (Liegang Liu)

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

Running title: Infection shaping microbial homeostasis improve disease resistance

Zhengben Wu[1], Changbai Hu[1], Qiulu He[1], Yujun zhang[1], Yongyao Yu[1 2*]

[1]College of Fisheries, Huazhong Agricultural University, Wuhan, China

[2]Hubei Hongshan Laboratory, Wuhan, China

*Correspondence: yuyy@mail.hzau.edu.cn (Yongyao Yu)

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

Efficacy of Ganwei Baihe Decoction in Alleviating Constipation Through Modulation of Gut Microbiota and Metabolism

Running title: GWBH on consitpation by modulating gut microbiota and metabolism.

Sumei LI*, Congcong YU, Chunchi FENG, Xinhua HU, Yousheng LI, Shouxia XIE*, Wenpeng YUAN*

Department of Pharmacology, Shenzhen People's Hospital (The Second Clinical Medical College, Jinan University, The First Affiliated Hospital, Southern University of Science and Technology), Shenzhen, 518020, China.

*Correspondence: lism81@163.com (SM LI); szshouxia@163.com (SX XIE); yuanwpsz@163.com (WP YUAN)

Abstract

Background and Purpose: Negative emotion related constipation have become increasingly prevalent in modern society. Ganwei Baihe Decoction (GWBH), a well-established prescription formulated by the renowned Traditional Chinese Medicine (TCM) physician Duheng Xia, has been used for several decades to treat liver-stomach disharmony, a condition marked by digestive disorders linked to negative emotions, including constipation. This study aims to explore the efficacy of GWBH in alleviating constipation by modulating gut microbiota and metabolic function through a self-experiment.

Methods: The self-experiment was conducted by the first author, who had experienced mild constipation related to negative emotions for several years. The decoction was administered for a period of 3 weeks, with a sampling period of 36 days. Multiple adjustments were made to the GWBH formula to customize it to the subject's individual needs. Liver and kidney function tests, as well as an annual physical examination, were conducted before and after the treatment period. Amplicon sequencing was employed to analyze gut microbiota composition, while untargeted liquid chromatography-mass spectrometry (LC-MS) was used to profile fecal metabolites.

Results: After administration of the decoction, defecation performance improved from type 2 to type 4, indicating normalized bowel movements. Liver and kidney function assessments, along with physical examination results, revealed reductions in bilirubin, triglycerides, and creatinine levels, alongside improvements in immune markers. 16S rRNA sequencing identified a sustained high abundance of *Faecalibacterium* during the treatment period. Untargeted fecal metabolomics analysis demonstrated a significant increase in indole levels and a decrease in 2-arachidonoylglycerol (2-AG) levels.

Discussion and Conclusion: The reductions in triglycerides, bilirubin, and creatinine suggest improvements in liver and kidney function, as well as lipid metabolism, as a result of GWBH treatment. *Faecalibacterium*, a key butyrate-producing bacterium in the gut, is associated with inflammatory conditions and is typically reduced in patients with constipation and obesity. The observed decrease in 2-AG may contribute to constipation relief, given its reported association with constipation. Interestingly, 2-AG has been linked to appetite stimulation, while indole has been reported to suppress appetite. The significant decrease in 2-AG and increase in indole following GWBH treatment suggest a potential role in weight management. This study highlights the therapeutic efficacy of GWBH in alleviating constipation associated with negative emotions and suggests its potential for promoting weight loss by modulating gut microbiota and metabolism, thereby enhancing immune function.

Keywords: obesity, cconstipation, *Faecalibacterium*, 2-arachidonoylglycerol, indole

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

Running title: Tissue-specific succession of gut microbiomes (< 80 character)

Xiaowei Song[1,2,3]*, Mengyang Zhang[3], Yuanyuan Zhai[3], Xiangzhen Li[2]

[1] College of Software Engineering, Chengdu University of Information and Technology, Chengdu, Sichuan, China

[2] CAS Key Laboratory of Environmental and Applied Microbiology, Environmental Microbiology Key Laboratory of Sichuan Province, Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, Sichuan, China

[3] Institute for Conservation and Utilization of Agro-bioresources in Dabie Mountains, College of Life Sciences, Xinyang Normal University, Xinyang, Henan, China

*Correspondence: sxw@cuit.edu.cn (Xiaowei Song)

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

Running title: Regional differences dominate the incidence, and severity in endophyte community of taso-ko

Jian-Wei Guo[1#], Rong-Chuan Tian[1,2#], Lei Yu[1*]

[1]College of Agronomy and Life Sciences/Yunnan Urban Agricultural Engineering and Technological Research Center, Kunming University, Kunming 650214, Yunnan, China

[2]Institute of Biomedical Research, Yunnan University, Kunming 650500, Yunnan, China

[#]These authors contributed equally: Jian-Wei Guo, Rong-Chuan Tian

*Correspondence: yulei0425@163.com (Lei Yu)

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

Running title: Fish intestinal microbiota could regulate mucosal vaccine-induced humoral immunity

Chen Zhang[1], Yun Sun[1,2,3,4,*], Yongcan Zhou[1,2,3,4,*]

[1]School of Breeding and Multiplication (Sanya Institute of Breeding and Multiplication), Hainan University, Sanya, Hainan 572022, China

[2]Collaborative Innovation Center of Marine Science and Technology, School of Marine Biology and Fisheries, Hainan University, Haikou 570228, China

[3]Engineering Research Center of Hainan Province for Blue Carbon and Coastal Wetland Conservation and Restoration, China

[4]International Joint Research Center of Hainan Province for Blue Carbon and Coastal Wetland, China

*Correspondence: syshui207@126.com (Yun Sun), zychnu@163.com (Yongcan Zhou)

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

Running title: *Parabacteroides distasonis* regulates the temperature sensitivity of SVCV

Yujun Zhang[1, 2], Yan Gao[1, 2], Yongyao Yu[1,2], Xueqin Liu[1, 2]*

[1]National Key Laboratory of Agricultural Microbiology, College of Fisheries, Huazhong Agricultural University, Wuhan, Hubei, China

[2]Hubei Engineering Technology Research Center for Aquatic Animal Diseases Control and Prevention, Wuhan, Hubei, China

*Correspondence: xueqinliu@mail.hzau.edu.cn (Xueqin Liu)

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

Running title: Nanomedicine effectively balances anti-tumor efficacy and maintains intestinal homeostasis

Qingya Liu[1], Yun Yang[1], Yan Yu[1], Meng Pan[1], Liping Yuan[1], Zhiyong Qian[1]*

[1]Department of Biotherapy, Cancer Center and State Key Laboratory of Biotherapy, West China Hospital, Sichuan University, Chengdu, China

*Correspondence: anderson-qian@163.com (Zhiyong Qian)

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

Running title: Microbial Contamination Threats to Medicine-Food Consumption

Mingxi Zhou[1#], Ruixin Wu[2#], Chongming Jiang[3], Yu-Shui Ma[1], DaFu[4], Hegen Li[5*], Chang-Sheng Dong[1,5*]

[1]Cancer Institute of Traditional Chinese Medicine, Longhua Hospital, Shanghai University of Traditional Chinese Medicine, Shanghai, 200032, China

[2]Preclinical Department, Shanghai Municipal Hospital of Traditional Chinese Medicine, Shanghai University of Traditional Chinese Medicine, Shanghai 200071, China; School of Traditional Chinese Medicine, Shanghai University of Traditional Chinese Medicine, Shanghai 201203, China

[3]Terasaki Institute for Biomedical Innovation, Los Angeles, CA, 90024, USA.

[4]GeneralSurgery, Institute of Pancreatic Diseases, Ruijin Hospital, Shanghai Jiaotong University School of Medicine, Shanghai 200025, China

[5]Department of Oncology, Longhua Hospital, Shanghai University of Traditional Chinese Medicine, Shanghai, 200032, China

[#]These authors contributed equally: Mingxi Zhou, Ruixin Wu

*Correspondence: csdong@shutcm.edu.cn (Chang-Sheng Dong), shlaogen@163.com (Hegen Li)

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

Running title: PPL promoting bone formation via phase separation

Chong. Yin[1,2,3*], Ye. Tian[3], Airong. Qian[3]

[1]Department of Clinical Laboratory, Lab of epigenetics and RNA therapy, Department of Rehabilitation Medicine, Affiliated Hospital of North Sichuan Medical College, Nanchong, Sichuan, 637000, P.R.China;

[2]Department of Laboratory Medicine, Translational Medicine Research Center, North Sichuan Medical College, Nanchong, Sichuan, 637000, P.R.China;

[3]Lab for Bone Metabolism, Xi'an Key Laboratory of Special Medicine and Health Engineering, Key Lab for Space Biosciences and Biotechnology, Research Center for Special Medicine and Health Systems Engineering, NPU-UAB Joint Laboratory for Bone Metabolism, School of Life Sciences, Northwestern Polytechnical University, Xi'an, Shaanxi, 710000, P.R.China.

*Correspondence: yinchong42@nsmc.edu.cn (Chong Yin)

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

Running title: Metabolites in AKI to CKD Transition

Jiaojiao Fan[1#], Hanyan Meng[2#], Danqing Hu[3#], Jiaxi Fang[4], Dongyang An[3], Xinyu Wang[5], Yugen Sha[6], Wei Zhou[2*]

[1]Department of Pediatrics, The First Affiliated Hospital of Zhengzhou University, Zhengzhou 450052, China.

[2]Department of Nephrology, The Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center for Child Health, National Children's Regional Medical Center, Hangzhou 310052, China.

[3]Zhejiang Chinese Medical University, Hangzhou 310009, China

[4]Department of Ultrasound, Taizhou Central Hospital, Taizhou 318000, China

[5]Department of Pediatrics, The First Affiliated Hospital of Nanjing Medical University, Nanjing 210029, China.

[6]Department of Nephrology, Children's Hospital of Nanjing Medical University, Nanjing 210008, China.

[#]These authors contributed equally: Jiaojiao Fan, Hanyan Meng, Danqing Hu

*Correspondence: dracozhou@zju.edu.cn (Wei Zhou)

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

Yin-Xing Niu[1], Fang Li[1,2*]

[1]College of Resources and Environment, Henan Agricultural University, Zhengzhou 450002, China

[2]College of Urban and Environmental Sciences, Peking University, Beijing 100871, China

*Correspondence: fangli0901@henau.edu.cn (Fang Li)

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

Hongliang Xue,[1,2] Xu Chen,[3] and Wenhua Ling[4,5]

1. Department of Nutrition, School of Public Health, Guangzhou Medical University, Guangzhou, China;

2. The Key Laboratory of Advanced Interdisciplinary Studies, The First Affiliated Hospital, Guangzhou Medical University, Guangzhou, China;

3. Department of Food Science and Nutrition, The Hong Kong Polytechnic University, Kowloon Hong Kong;

4. Guangdong Provincial Key Laboratory of Food, Nutrition and Health, Guangzhou, China;

5. Department of Nutrition, School of Public Health, Sun Yat-sen University, Guangzhou, China.

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

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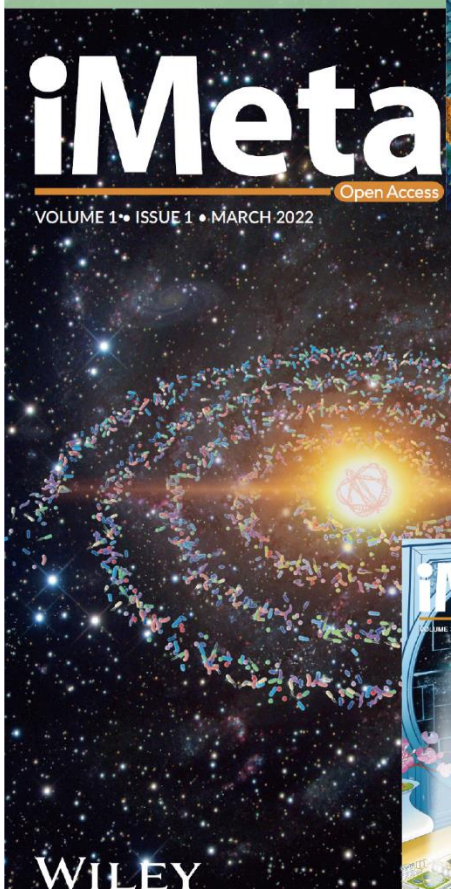

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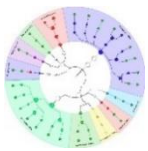

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