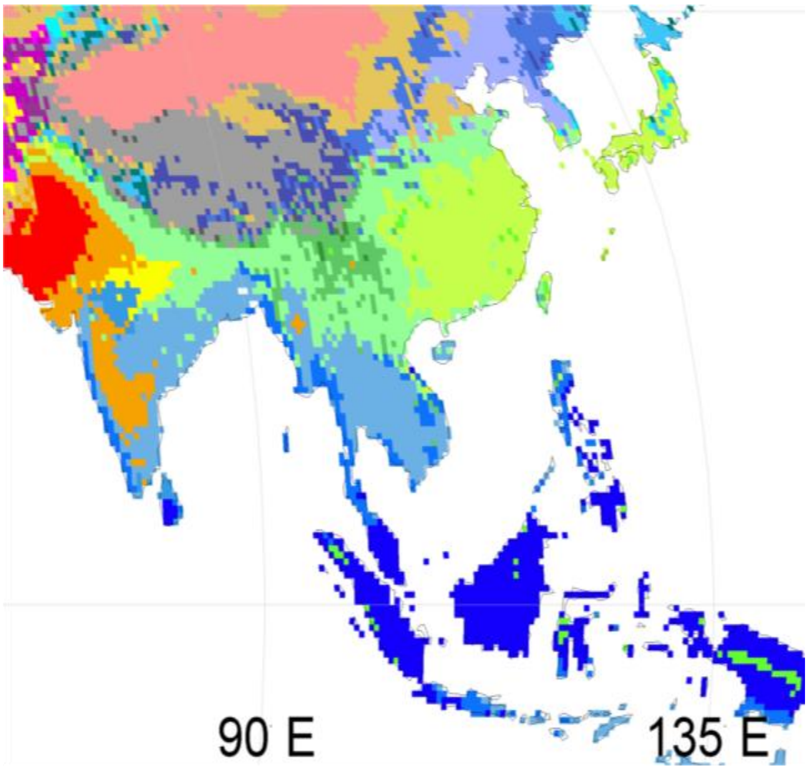
中国科协海智计划海南(海南大学)工作基地
海南省环南海陆域生物多样性国际联合研究中心

2024 年报

Annual Report 2024



海南大学
HAINAN UNIVERSITY

商务部 2024 年《全球发展倡议下拉美国家环境治理研修班》

2024 年 10 月 22 日-11 月 4 日，工作基地/研究中心参与承担了中国商务部主办、海南省商务厅和海南大学承办的《全球发展倡议下拉美国家环境治理研修班》。

本次援外培训班是中国商务部援外人力资源合作来华项目，学员共 24 名，来自拉丁美洲秘鲁、巴拿马、哥伦比亚、多米尼加、乌拉圭、哥斯达黎加、尼加拉瓜等 7 个国家。开班仪式有海南大学副校长陈骏、海南大学国际合作交流处（港澳台办公室）副处长（国际教育学院院长）肖艳玲、海南大学生态学院党总支书记林豪燕、海南大学国际教育学院副院长张钊等参加。工作基地负责人任明迅教授主持了开班仪式和闭幕仪式，并参与了全程授课与福建省三明市和厦门市的实地教学活动。

本次研修班由海南大学精心组织，海南大学生态学院以工作基地骨干成员为主策划了授课方向与课程设置、野外实践教学地点与形式等。一共邀请了 11 名经验丰富的专任教师，安排了 10 次课堂教学、5 场实地考察以及互动讨论等其他类型的实践活动，分享了污染防治、生态修复、国家公园与保护地规划、城市生态与乡村环境治理、生物多样性保护等领域的中国经验、中国智慧与中国方案。

自 2019 年起，工作基地骨干成员先后参与了 4 期商务部援外培训项目，面向老挝等东南亚国家、非洲热带国家以及拉丁美洲开展了国际合作与交流，促进了海南大学积极融入国家“一带一路”倡议、海南自由贸易港建设以及人类命运共同体发展大局。

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封面图片：环南海区域的气候类型和海南岛山地雨林（右上）、泰国洞穴植被（右中）和海南黎族船形屋（右下）。

第一届全国植物生态学大会暨《植物生态学报》编委会会议成功举办

2024 年 11 月 8 日-11 日，由《植物生态学报》、中国植物学会植物生态学专业委员会、河北大学主办，河北大学承办的“第一届全国植物生态学大会暨《植物生态学报》编委会会议”在河北保定顺利举办。

大会聚焦“生态系统结构与功能及对环境变化的响应”，设置了全球变化生态学、生态系统生态学、生理生态学、土壤和微生物生态学、生物多样性、生态遥感、群落与植被生态学、植物功能性状等 8 个专题分会场，邀请相关领域具有学术影响力的专家学者和优秀青年科学家开展学术报告，共同探讨植物生态学的前沿进展和发展趋势。

任明迅教授在 “生物多样性” 主题会场作了题为《植物中的“岛屿法则”—来自风筝果（*Hiptage benghalensis*）的证据》的口头报告，提出了植物与传粉者协同进化的“岛屿法则”，引起了与会专家的兴趣和热烈讨论。会议期间，任明迅教授还参加了《植物生态学报》编委会会议，同与会专家一起讨论了《植物生态学报》期刊建设与发展规划。

此次会议为植物生态学领域的专家学者和优秀青年科学家提供了一个高水平的交流平台。通过聚焦 “生态系统结构与功能及对环境变化的响应”，设置多个专题分会场，促进了不同研究方向的融合与碰撞。同时，编委会会议为《植物生态学报》的发展规划出谋划策，提升期刊的学术影响力，为植物生态学的发展提供更坚实的学术支撑。

一、背景与概况

工作基地/研究中心前身为 2017 年 7 月正式成立的海南大学环南海陆域生物多样性研究中心，同年 11 月受海南省科学技术协会资助，成为海南大学首个“海外智力为国服务行动计划”工作站。2020 年 6 月，在整合海南大学生态学、生物学等学科引进的海智专家与骨干教师的基础上，成立中国科学技术协会海智计划海南（海南大学）工作基地。2023 年 12 月，经海南省科技厅批准，启动建设海南省环南海陆域生物多样性国际联合研究中心。

现任学术委员会主任和首席海智专家：李百炼教授（美国加利福尼亚大学河滨分校）；工作基地/研究中心负责人：任明迅教授（海南大学生态学院）。

中国科学技术协会海智计划海南（海南大学）工作基地和海南省环南海陆域生物多样性国际联合研究中心实行“两位一体”的建设模式，聚焦海南岛、粤港澳大湾区、台湾地区以及环南海区域，集中开展海外智力引进、科技合作与交流、人才培养等工作，参与建设南海海洋资源利用国家重点实验室、热带特色林木花卉遗传与种质创新教育部重点实验室、海南省热带生态环境修复工程研究中心等，积极担当起海南大学在践行“一带一路”国家战略和国家生态文明试验区（海南）建设中的作用，力争成为环南海区域生物多样性与生态文化研究中心、合作与交流中心。

目前共设置三个研究方向：（1）生物多样性与生态保育；（2）环南海区域生态安全；（3）传统生态文化与当代生态文明建设。

国际合作方面，与美国加州大学河滨分校、美国佛罗里达国际大学、日本东京大学、荷兰瓦赫宁根大学、德国莱布尼兹热带海洋研究中心、德国亚琛工业大学以及环南海地区的新加坡国立大学、南洋理工大学、新加坡植物园、柬

埔寨皇家农业大学、菲律宾大学内湖省分校、越南 Ton Duc Thang 大学、马来西亚沙巴大学、中国台湾与香港地区多家机构签订了合作协议或开展过实质合作。

目前积累了大量的野外调查、科学实验和理论研究数据，从环南海区域收集了战略植物资源（热带作物野生近缘种、药用植物、油料植物、观赏植物等）近 3000 份（含植物活体、腊叶标本、DNA、种子等）。

目前，已引进海外智力专家有：

专家	国籍（是否华裔）	工作单位	研究领域
李百炼 Larry Bai-Lian Li	美国（华裔）	加利福尼亚大学河滨分校	人类生态学、生态规划
刘虹 Hong Liu	美国（华裔）	佛罗里达国际大学	生物多样性保护
邹乐明 Chou Loke Ming	新加坡（华裔）	新加坡国立大学	珊瑚礁生态
任添荣 Yam Wing Tim	新加坡（华裔）	新加坡植物园	兰花保育与新品种选育
练春兰 Chunlan Lian	日本（华裔）	日本东京大学	森林资源与生态学
张金龙 Jinlong Zhang	中国（华裔）	中国香港嘉道理农场暨植物园	植物分类与资源收集
谢宗宇	中国台湾（华裔）	中国台湾民享生态调查公司	生物多样性、 自然教育
张浩	中国香港（华裔）	中国香港高等教育研究院	生态规划
Mui-How PHUA	马来西亚（华裔）	马来西亚沙巴大学	森林生态学
Pastor L. Malabrigo	菲律宾（非华裔）	菲律宾大学内湖省分校	植物多样性与生态文化
Sandra Yap	菲律宾（非华裔）	菲律宾远东大学	热带植物多样性
Van The Pham	越南（非华裔）	越南 Ton Duc Thang 大学	植物多样性
Fabio Pinheiro	巴西(非华裔)	巴西 Campinas 大学	植物保育遗传学
Jordi Lopez-Puyol	西班牙(非华裔)	西班牙巴塞罗那植物所	岛屿植物 生态与保育
Salvotore Cozzolino	意大利(非华裔)	意大利那不勒斯大学	植物分子生态与保育遗传学

二、定位与研究方向

中国科学技术协会海智计划海南(海南大学)工作基地和海南省环南海陆域生物多样性国际联合研究中心以海南大学、中国热带农业科学院等机构的生态学、环境科学与工程、生物学专业青年人才为骨干，引进海内外高端智力，聚焦海南省与环南海区域生物多样性与生物资源、生态安全、传统生态文化与当代生态文明建设研究，主要服务国家“一带一路”战略、海南省“三区一中心”、海南热带雨林国家公园以及中国特色自由贸易港建设。

（一）生物多样性与生态保育

针对海南省和环南海区域(海南岛、台湾岛、菲律宾群岛、婆罗洲、马来半岛、中南半岛等)，开展重要战略植物资源如重要作物野生近缘种、特色林木花卉等的发掘、引种与基础生物学研究；利用基因组学相关技术挖掘重要、特色性状基因资源，阐释生物多样性的基因组学基础，开发有害动植物分子检测技术。针对海南岛热带雨林、淡水湿地、珊瑚礁、红树林与海岸带等，揭示生物多样性形成与维持机制、解析关键生态过程、开展退化生态系统恢复研究，优化与提升重要生态系统的生态服务功能等，保障和提升海南省生态安全。

（二）环南海区域生态安全

基于海南省地处中国大陆与东南亚的中间地带、位于中国南方生态屏障前沿及“一带一路”关键节点等，利用集中引进环南海区域海智专家的基础，从海南岛、南海岛礁、粤港澳大湾区、环南海区域等不同尺度开展海南岛生态安全及关键生态系统生态服务功能优化与提升、区域环境安全与生态文明建设等合作研究与交流，为中国-东盟人类命运共同体建设等保驾护航。

（三）传统生态文化与当代生态文明建设

在习近平生态文明思想、习近平文化思想的指导下，积极践行中华优秀传统生态文化的传承与创新利用，发掘海南省及环南海区域代表性非物质文化遗产为主的传统农耕技艺等优秀生态文化。近期聚焦已入选国家级非物质文化遗产和国家工业遗产的“洋浦千年古盐田晒盐技艺”和申报中的中国重要农业文化遗产“木棉稻田农林复合系统”，利用现代科学理论与技术揭示传统生态文化的科学原理与生态学基础，实现“把论文写在海南大地上”，促进中华优秀传统生态文化的创造性转化、创新性发展。同时，探索传统生态文化的现存价值及其在当代社会中的传承与利用途径，助力农民增收和乡村全面振兴，提升海南地方民族及中华民族的文化自信、民族自信，从生态文化维度丰富生态文明建设和中国式现代化内涵，打造国家生态文明试验区的“海南样板”。

三、大事记

➢ 海南省科学技术协会调研工作基地和海南省“海智计划”海南大学工作站

2024 年 1 月 16 日，海南省科协党组成员、副主席徐伟一行五人调研工作基地和海南省“海智计划”海南大学（环南海陆域生物多样性研究中心）工作站，并进行座谈。海南大学党委常委、副校长邹勇华，工作站首席海智专家李百炼院士及骨干成员出席。生态学院党委副书记林豪燕主持调研座谈会。

邹勇华介绍了海南大学自习近平总书记指示以来在各方面的巨大进展，强调海智平台在链接海外高层次人才的重要性，期望与海南省科协和中国科协加强合作。向文倩博士汇报了工作基地的基础建设、人才引进等工作及后续规划。李百炼院士肯定了目前取得的成绩，期望契合绿色发展开展进一步深入研究。徐伟指出，要紧密契合国家和省委省政府生态环境政策，利用生态资源深入开展科学研究，助力海南自贸港建设。

➢ 新增 2 项省部级项目

工作基地/研究中心 2024 年承担两项海南省项目：海南昌江黎族自治县生物多样性调查和评估项目（负责人：任明迅，项目经费：104.31 万元），海南琼中黎族苗族自治县生物多样性调查和评估项目（负责人：任明迅，项目经费：115.75 万元）。

本团队负责的昌江、琼中两县生物多样性相关知识调查与评估子项目，该项目隶属于海南省昌江黎族自治县和琼中黎族苗族自治县生物多样性调查与评估项目，主要针对县域内农业遗传资源、药用植物、传统技术与生产生活方式、传统文化和生物地理标志产品五大类与生物多样性相关的传统知识展开全面调

查和评估，本项目统计分析了各类传统知识条目以及涉及的物种，并针对性的给出受威胁原因和未来保护和持续利用的具体措施。

➢ 新增 3 项国家自然科学基金项目

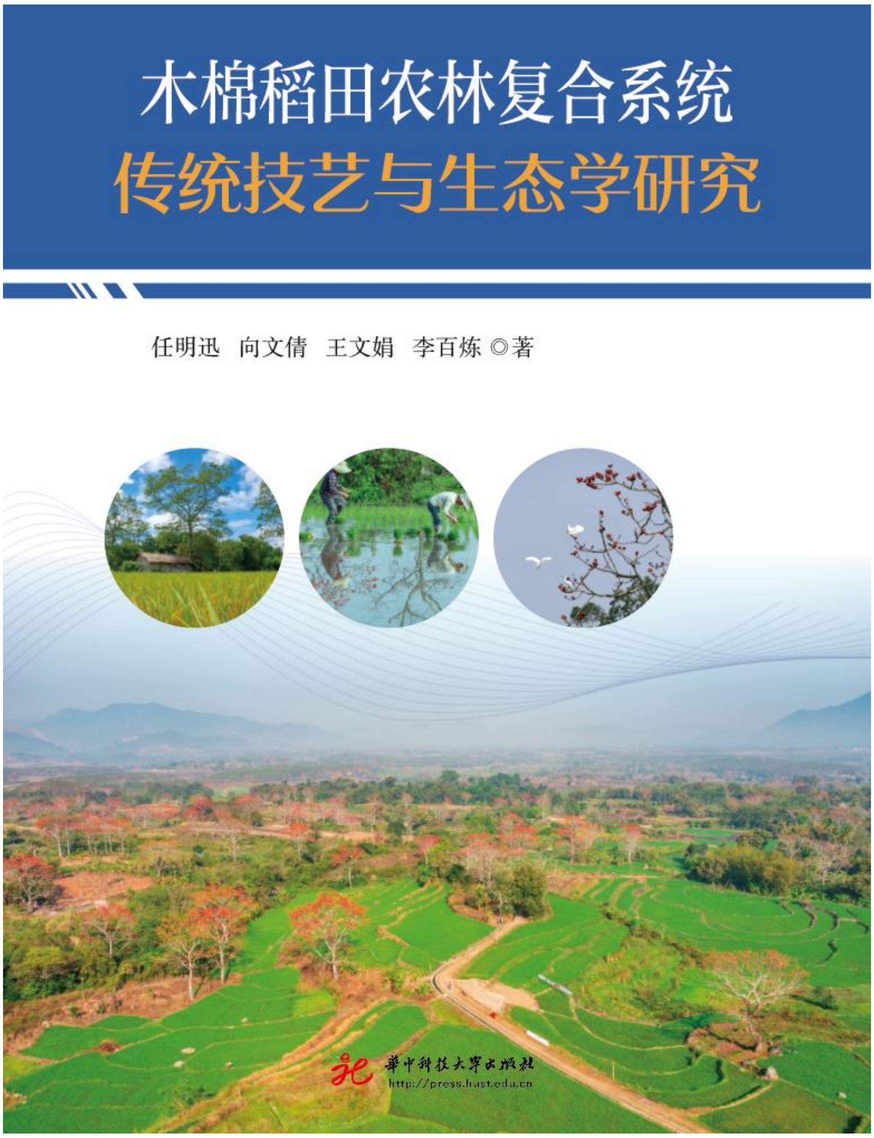
工作基地骨干成员在 2024 年国家自然科学基金集中申请项目申报中，获批资助 3 项，包括 2 项地区科学基金：木棉对稻田土壤微生物群落时空分布格局的影响及机制研究 (负责人：王文娟，执行期：2025.01-2028.12，总经费：32 万)；滨海盐沼湿地先锋植物盐地碱蓬谱系地理与适应性进化研究 (负责人：唐亮，执行期：2025.01-2028.12，总经费：32 万)，以及 1 项青年科学基金：离斑棉红蝽取食策略转换及亲子冲突对木棉种子扩散与幼苗更新的影响（负责人：向文倩，执行期：2025.01-2027.12，总经费：30 万元）。

➢ 《木棉稻田农林复合系统的传统技艺与生态学研究》专著出版

由任明迅、向文倩、王文娟、李百炼编著的《木棉稻田农林复合系统的传统技艺与生态学研究》于 2024 年 12 月正式出版，该书系统介绍了木棉稻田农林复合系统的定义与价值、种质资源与文化内涵、生物多样性与生态过程、优质高产技术及综合利用途径等，为海南省昌江县以“木棉稻田农林复合系统”申报 2025 年中国重要农业文化遗产奠定了基础。

木棉稻田农林复合系统集中分布在中国海南、广西、云南等地以及越南、印度等亚洲热带地区，是亚洲特有的一种传统立体种植模式。木棉稻田农林复合系统尚未受到关注和深入的研究，但其历史悠久的农耕技艺和传统文化、古老丰富的种质资源、独具特色的生物多样性传统知识，对于当代热带特色高效农业、生物多样性保护、文化自信及生态文明建设等具有积极作用。《木棉稻

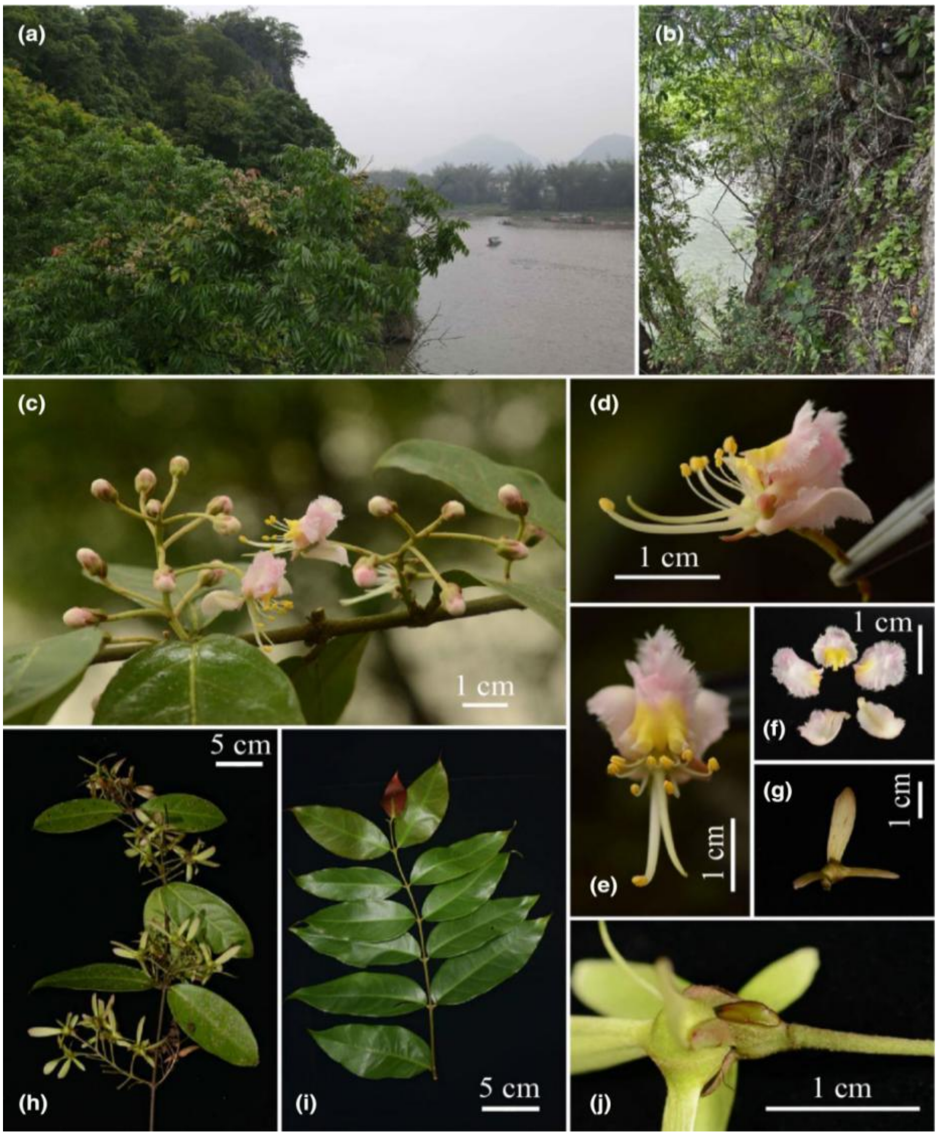
田农林复合系统的传统技艺与生态学研究》一书重点阐述了木棉稻田农林复合系统的定义与价值、传统文化内涵、资源循环利用与生物防治过程、物种多样性与生态系统稳定性、生产力与优质高产技术等，对比研究了木棉稻田农林复合系统和临近地区主要农业文化遗产的区别，探讨了木棉稻田农林复合系统的独特价值及其传承与创新利用策略与途径，针对申报中国重要农业文化遗产、打造“木棉稻米”地理标志产品、探索传统农业文化保护的“文化补偿”机制等提出了建议。


木棉稻田农林复合系统
传统技艺与生态学研究
任明迅　向文倩　王文娟　李百炼◎著
華中科技大學出版社
http://press.hust.edu.cn

四、代表性成果

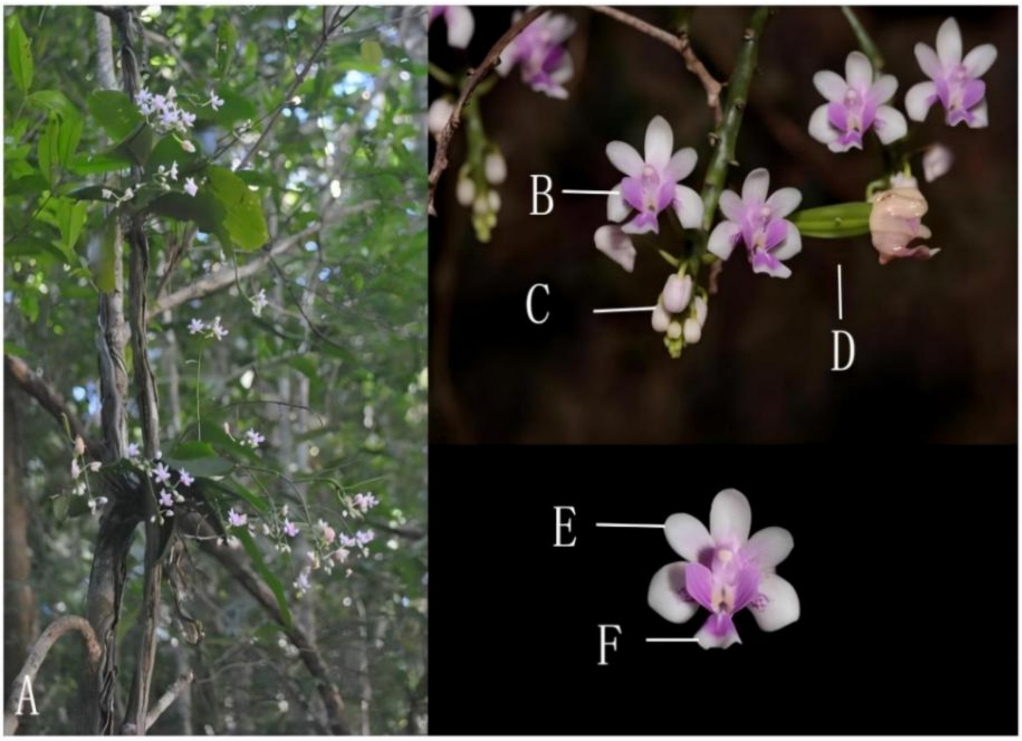
➢ 研究方向一：生物多样性与生态保育

任明迅团队联合广西壮族自治区中国科学院广西植物研究所谭珂、温放等专家，在广西阳朔发现新种阳朔风筝果（*Hiptage yangshuoensis*），并揭示其与相近种的形态差异及系统进化关系。该研究结合形态学及分子数据证实该新种的独立性，为喀斯特地区植物多样性保护提供了理论依据。相关成果已发表在《Ecology and Evolution》（2024, 14(8): e70099）。



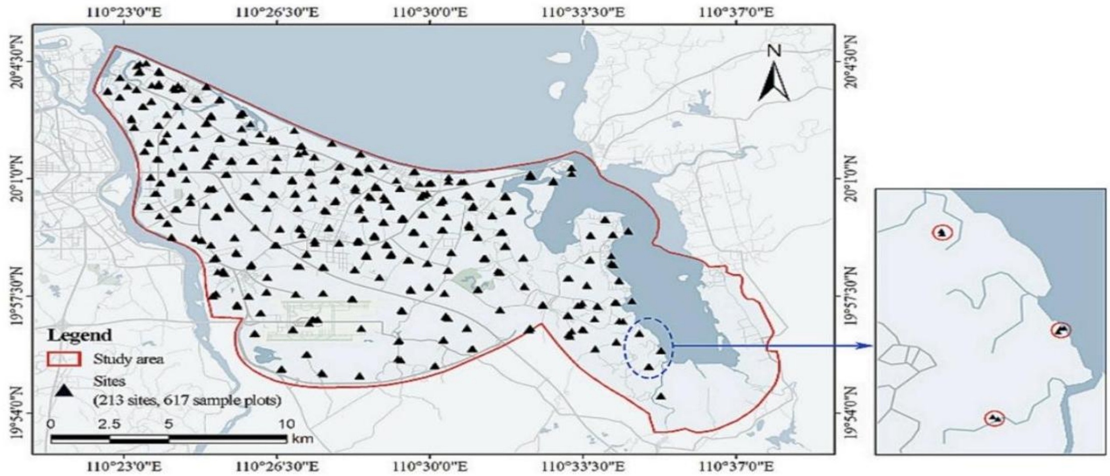
新发表物种：阳朔风筝果 (*Hiptage yangshuoensis*)

张哲博士探究了蝴蝶兰（*Phalaenopsis deliciosa*）叶绿体基因组，通过对其叶绿体基因组的测序与系统发育分析，确定其分类地位并揭示光合适应的遗传特性，该研究为兰花分子育种和栽培优化提供了数据支持。相关成果已发表在《Mitochondrial DNA Part B: Resources》（2024, 9(11): 1483-1486）。



蝴蝶兰（*Phalaenopsis deliciosa*）

杨帆团队聚焦于热带沿海城市非正式绿地（Informal Green Spaces, IGS）的植物多样性价值，特别是在物种多样性、功能多样性和系统发育多样性方面。通过对海口市江东新区的详细植被调查，建立了 213 个样地，考察了 343 个非正式绿地样本和 274 个正式绿地（Formal Green Spaces, FGS）样本。研究发现，IGS 比 FGS 拥有更高的物种丰富度和功能丰富度，研究强调了 IGS 在增强热带沿海城市生物多样性和韧性中的关键作用，并强调了将 IGS 纳入城市规划策略以支持可持续城市生态系统的必要性。相关成果已发表在《Science of The Total Environment》（2024, 955: 176741）。



研究区域和样地分布

为了了解不同潮位下海莲（*Bruguiera sexangula*）的群落特征和种群动态变化，以合理利用和保护现有的红树资源。杨帆团队在海南东寨港国家级自然保护区进行，比较了不同潮位下海莲的群落特征、年龄结构、分布格局、静态生命表和生存函数。结果显示，海莲是群落中的优势树种，群落的物种多样性指数和均匀度指数随潮位升高而增加，而海莲的重要值、胸径、树高和冠幅随潮位升高而降低。海莲种群在空间上呈现聚集分布格局，不同潮位的龄级结构分布不同。研究结果为该区域红树植物的保护和优化管理提供了重要的基础数据，揭示了不同潮位下海莲群落特征和种群动态的明显差异。相关成果已发表在《植物科学学报》（2024, 14: 32）。

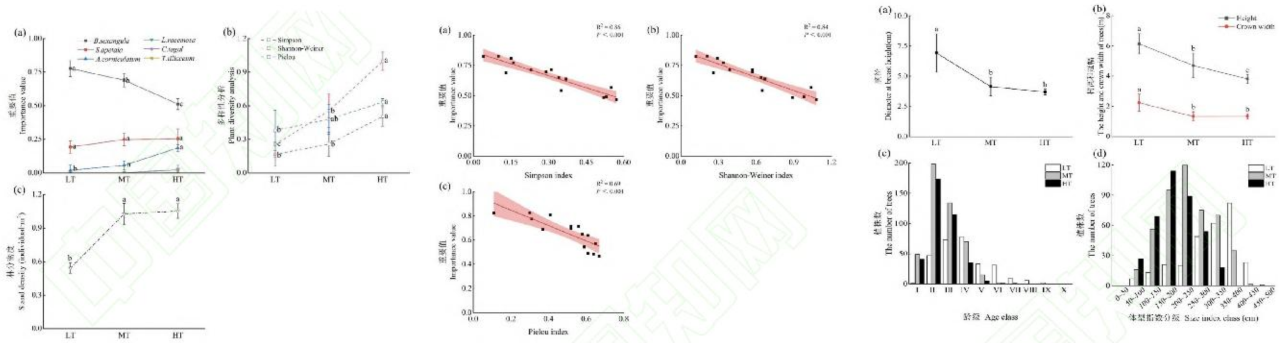


图 1 不同潮位生境海莲群落的特征及林分密度

Fig.1 Community characteristics and stand density of *Bruguiera sexangula* at different intertidal elevations

图 2 海莲重要值与群落多样性指数间的相关性分析

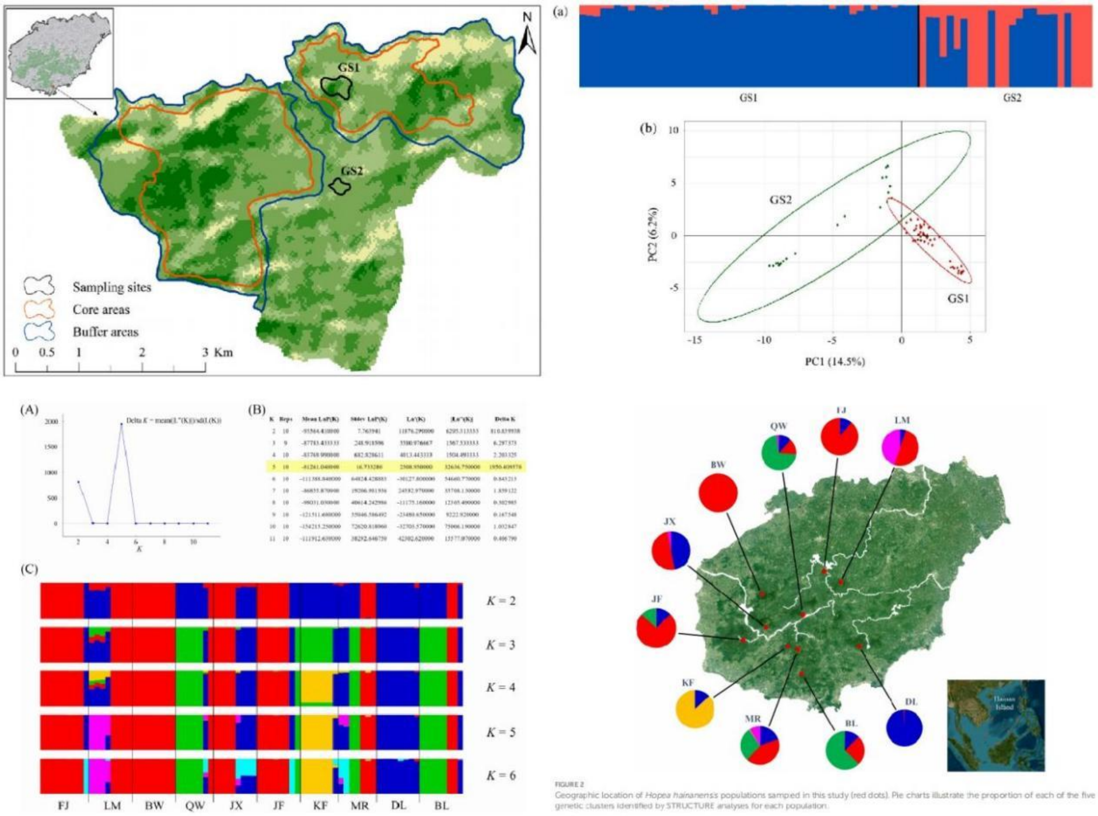
Fig.2 Correlation analysis between importance value and community diversity index of *B. sexangula*

图 3 不同潮位生境海莲种群的基本特征

Fig.3 Population characteristics of *B. sexangula* at different intertidal elevations

不同潮位下海莲的群落特征和种群动态变化

唐亮团队开展了针对海南岛龙脑香科 (Dipterocarpaceae) 坡垒属 (*Hopea*) 物种——坡垒 (*H. hainanensis*) 和铁凌 (*H. reticulata*) 的保护基因组学研究，揭示了这两个物种有效种群大小的严重缩减导致其核苷酸多样性极低的现象。研究结果为龙脑香科濒危物种的可持续管理与恢复策略提供了宝贵的基因组学依据，相关成果已发表在《Frontiers in Plant Science》（2024, 15: 1442807）、《Global Ecology and Conservation》（2024, 50: e02846）。

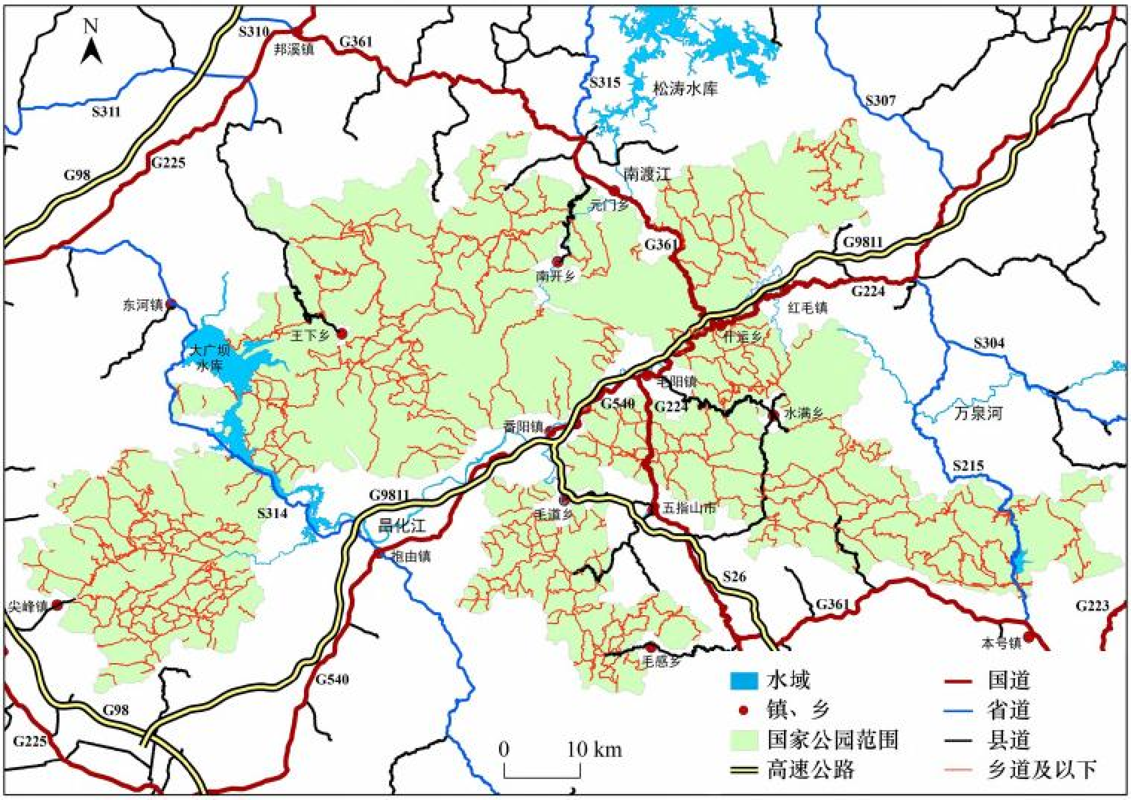


龙脑香科基因组学研究

此外，唐亮团队基于广泛的样本采集与高多态性 SSR 分子标记，探究了亚洲栽培稻 (*Oryza sativa*) 的两个野生祖先——野生稻 (*O. rufipogon*) 与 *O. nivara* 的交配系统，揭示了 *O. rufipogon* 与 *O. nivara* 遗传变异模式的差异源于两个物种不同的交配策略，混合交配系统向自交的转变加剧了种群间的遗传分化。研究结果为优良种质资源的保护提供启示，相关成果已发表在《Genetic Resources and Crop Evolution》（2024，doi: 10.1007/s10722-024-02043-x）。

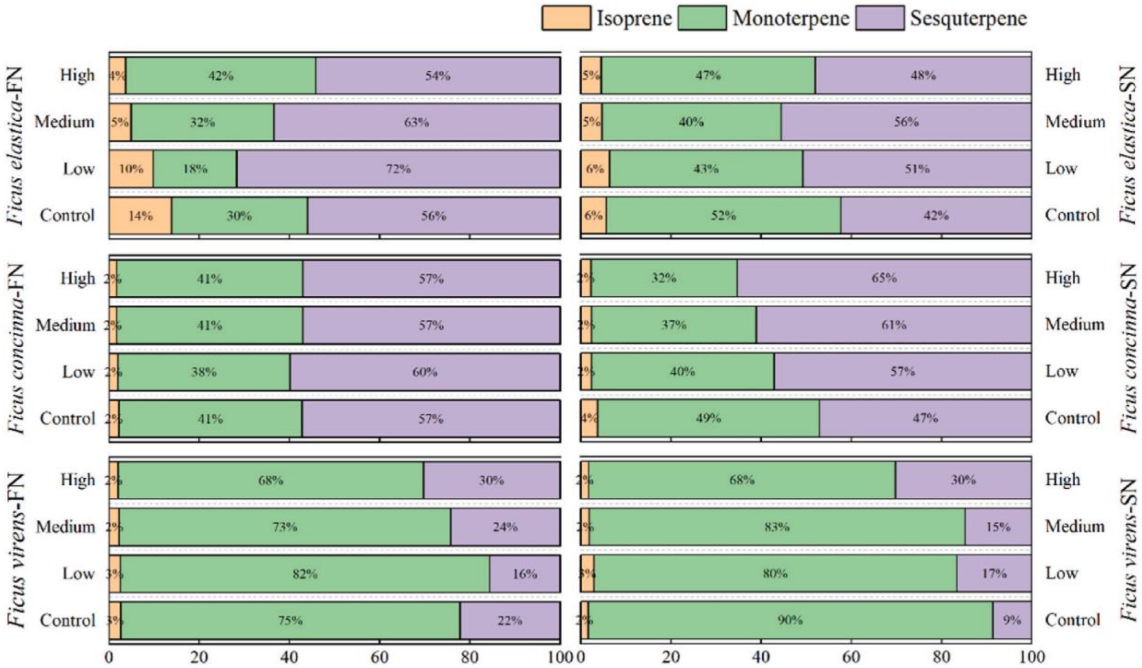
➢ 研究方向二：环南海区域生态安全

海南热带雨林国家公园是我国首批设立的国家公园之一，科学合理的交通规划是国家公园生态旅游、环境教育及社区发展的有力保障。任明迅团队以海口和三亚到海南热带雨林国家公园各乡镇或区域的公路交通线路为研究对象，采用 ArcGIS10.8 对其公路交通可达性进行量化研究。结果表明，尖峰岭区域、吊罗山区域和霸王岭区域具有更好的对外与对内交通可达性，为海南热带雨林国家公园公路乡村振兴产业和入口社区规划提供了依据。同时，穿越海南热带雨林国家公园的高速公路和国道等大型道路及其带来的人类干扰，可能存在长期的生态风险，提出了在关键节点增设高架林地和下穿隧道等生态廊道的建议。相关研究成果发表在《国家公园》（2024, 2(07): 447-455）。



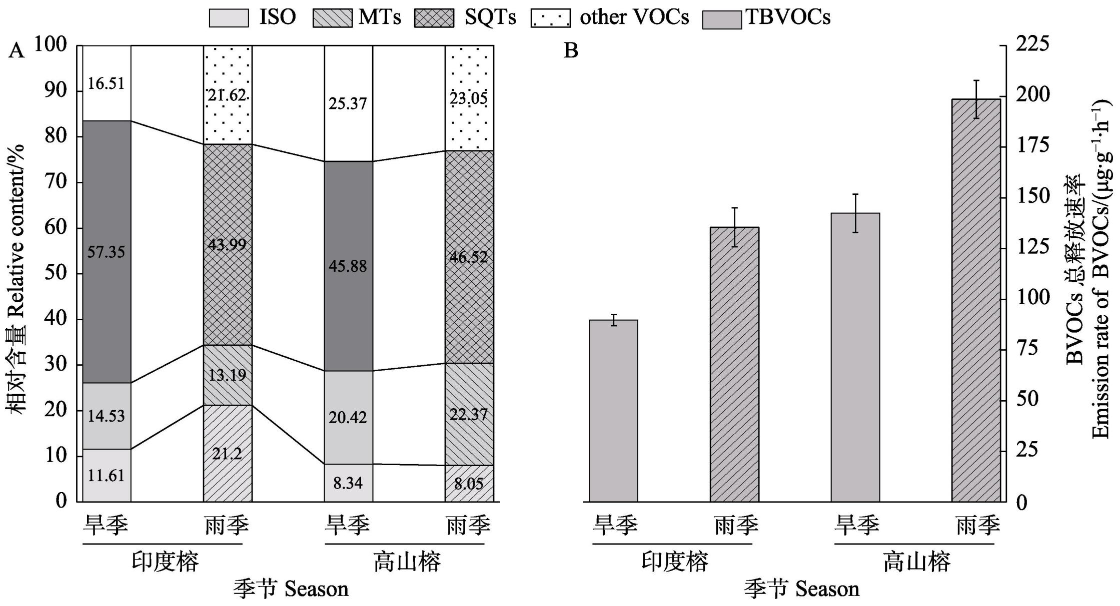
海南热带雨林国家公园道路交通分布图

何禾副教授和任明迅教授在榕属植物挥发性有机物研究领域取得研究进展。研究发现，不同浓度与施加方式的氮沉降影响了三种榕属植物幼苗生物挥发性有机物（BVOCs）排放及其对臭氧和二次有机气溶胶形成的潜力。氮浓度与BVOCs 排放速率正相关，叶面施氮影响大于根部施氮，异戊二烯主导了臭氧、单萜和倍半萜主导二次有机气溶胶（SOA）生成。相关成果发表在《Atmospheric Pollution Research》（2024, 15(9): 1309-1042）。



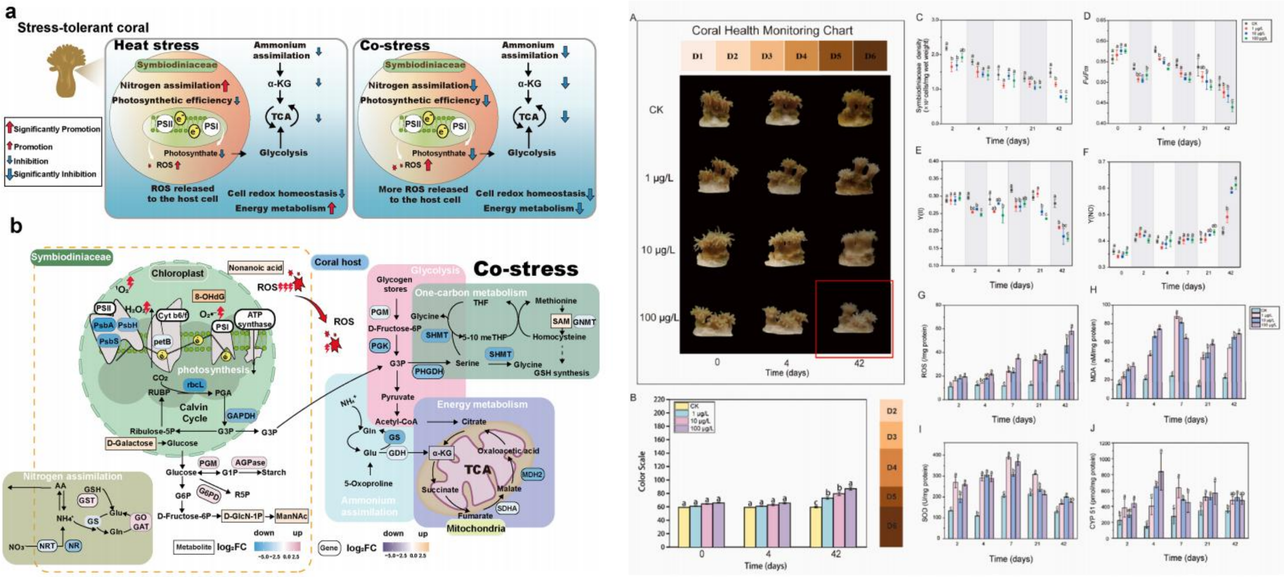
桑科榕属主要物种 BVOCs 的 SOA 生成潜力

何禾副教授和任明迅教授还研究了海口市两种常见榕属植物（印度榕和高山榕）BVOCs 排放特性，发现其 BVOCs 以异戊二烯和萜类为主，雨季排放量高于旱季，印度榕异戊二烯在雨季较旱季增加 1.82 倍。BVOCs 呈“早晚低、中午高”单峰排放模式，且与环境因素及植物生理参数相关。这些研究为热带和亚热带植物 BVOCs 排放数据库及空气质量评估提供了基础数据支持。相关成果已发表在《热带作物学报》（2024，45(11): 2448-2460）。



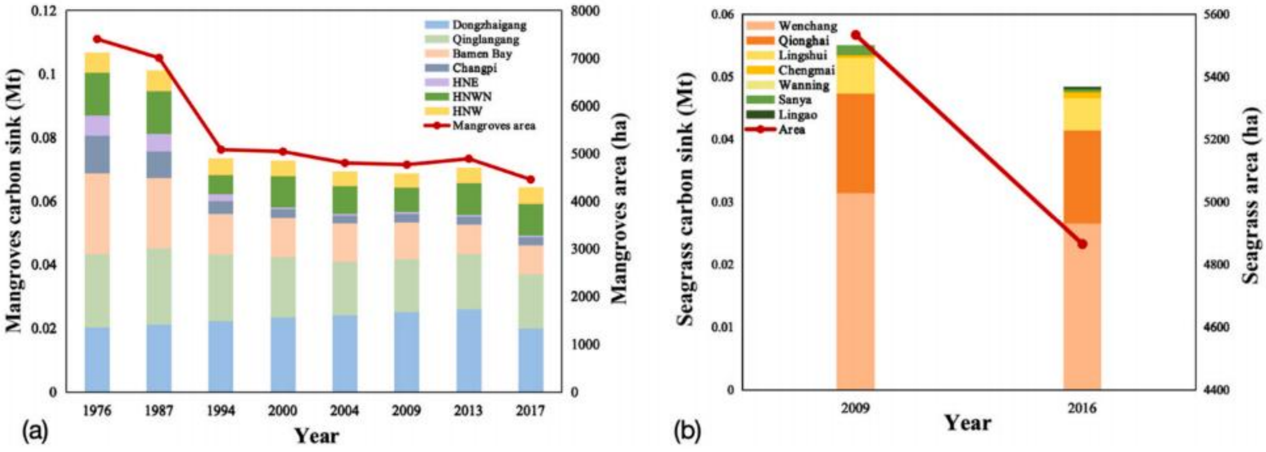
榕属植物排放 BVOCs 的相对含量和排放总量

随着海洋环境面临越来越多的挑战，珊瑚的生存状况也日益受到关注。目前，除草剂和海洋变暖以及药品和个人护理产品中的抗菌剂等因素都可能对珊瑚产生重大影响。赵洪伟团队研究发现，在除草剂和海洋变暖的综合影响中，PSII 抑制剂类除草剂（Prometryn）加剧了热应激对丛生盔形珊瑚 (*Galaxea fascicularis*)光合效率的抑制，可能破坏光系统修复机制，削弱热适应能力，放大热应激对关键能量和营养代谢途径的不利影响，引起更强的氧化应激反应。而在克雷巴唑（Climbazole）方面，高浓度（100 μ g/L）克雷巴唑使珊瑚颜色变浅，降低光合作用能力，增加氧化应激，还降低了微生物多样性并影响微生物群落功能。这些研究对于保护和管理近海珊瑚礁具有重要意义，并为保护策略提供新方向。相关成果已发表在《Environmental Science & Technology》（2024, 58(10): 4545-4557）、《Marine Environmental Research》（2024, 201: 106679）。



海洋变暖条件下扑草净暴露对珊瑚的影响示意图；珊瑚在不同浓度克雷巴唑下的应激反应

蓝碳生态系统因高效碳固存能力备受关注，海南岛以其红树林物种丰富度高成为研究蓝碳的理想之地。赵洪伟团队研究通过构建数据集计算红树林和海草床的蓝碳固存，包括生态系统面积和海草床覆盖度以估算总蓝碳固存，并识别了影响蓝碳固存的主要驱动因素，有直接因素如水产养殖、渔业活动和旅游人口等，间接因素如 GDP、农业氮肥使用和总人口等。结果显示，1976 年到 2017 年海南岛红树林碳固存下降 40%，2009 年到 2016 年海草床碳固存下降 13%，且碳固存空间分布有变化，文昌市下降最显著。渔业活动对红树林影响最大，GDP 增长和旅游人口对海草床覆盖有积极影响，人口增长则有最大负面影响。论文强调保护海南岛蓝碳生态系统需有效减少人为干扰，并提出增加蓝碳固存的管理建议，为保护和恢复蓝碳生态系统提供了科学依据和政策建议，同时也提供了海南岛蓝碳固存的详细分析。相关成果已发表在《Marine Environmental Research》（2024, 197: 106476）。



海南岛蓝碳总碳汇和红树林面积

杨帆团队聚焦红树植物水翁（*Syzygium nervosum*）和乌墨（*Syzygium cumini*）这两种耐淹树种，对比它们对不同胁迫在生长、生理生化以及盐胁迫相关离子积累方面的响应情况。该研究不仅为理解耐淹植物适应复杂环境压力提供了理论支撑，也在实践层面，对环南海区域红树林的保护与恢复有着重要的指导意义，有助于推动该区域生态环境的良好维护与发展。

➢ 研究方向三：传统生态文化与当代生态文明建设

为贯彻落实习近平总书记“希望广大科技工作者以提高全民科学素质为己任，把普及科学知识、弘扬科学精神、传播科学思想、倡导科学方法作为义不容辞的责任”的指示，工作基地/研究中心任明迅教授带领张哲博士、向文倩博士以及多名研究生积极参与海南各项科普活动及社区志愿者活动，向大众科普海南热带雨林国家公园中特殊的雨林奇观和独特的传统文化，以及洋浦盐田晒盐技艺、木棉稻田农林复合系统、滨海红树林生态与保护等，将科研成果用通俗易懂的方式走进大众，积极推动形成讲科学、爱科学、学科学、用科学的良好氛围。

1. 木棉稻田农林复合系统与木棉文化的研究与科普

在木棉繁殖适应与分子遗传研究的基础上，任明迅团队首次系统总结并提出了热带地区传统的农林复合种植模式“木棉稻田农林复合系统”，并利用分子生物学和景观生态学研究方法解析了这一传统立体种植模式的生态学基础，对服务热带特色高效农业和生态文明建设具有积极意义。研究发现，木棉发达的根系可以调节稻田土壤微生物群落、木棉花吸引鸟并控制田间害虫、凋落木棉花分解释放养分。相关成果发表在《热带生物学报》（2024,15(6): 800-811）、《生物多样性》（2023, 31(03):190-201）、《Plant and Soil》（2022, 479: 543-558）。

不同地区的木棉稻田农林复合系统景观

任明迅团队受邀参加“观箭逐梦 • 礼赞中华”火箭发射观礼嘉年华及研学活动，向前来的观礼嘉宾介绍了“木棉稻田农林复合系统”传统技艺与相关生

态文化。该活动由文昌航天科普中心和海南无字教育服务管理有限公司（海南无字教育科普基地）联合在文昌市航天科普中心举办。

木棉稻田农林复合系统及木棉稻米亮相文昌科普中心

2024 年春季，受昌江黎族自治县人民政府的邀请，任明迅团队成立木棉稻田农林复合系统申报中国重要农业文化遗产的专家组，在昌江黎族自治县政府会议室举行了申遗座谈会。

任明迅教授通过播放宣传视频和讲解申遗材料等方式，向参会专家及领导汇报了木棉稻田农林复合系统的重要价值和申遗准备工作，参会人员进行讨论并补充了木棉稻田农林复合系统的相关情况。专家一致认为，海南昌江木棉稻田农林复合系统历史悠久、文化底蕴深厚、群众积极性高，应该积极申报中国

重要农业文化遗产，服务海南省乡村振兴、现代特色高效农业和生态文明建设。

木棉稻田农林复合系统申遗座谈会

2024 年 2 月，昌江黎族自治县人民政府先后在七叉镇宝山村、叉河镇排岸村举办了“遇稻美好 • 木棉之恋”木棉稻田实景音乐秀。工作基地/研究中心博士后向文倩受邀向广大群众科学普及了中国源远流长的木棉文化与木棉稻田农林复合系统，极大的丰富了游客们对木棉的深入认识，提高了海南人民的文化自信和文化自觉，推动昌江“农文旅”融合发展，助力乡村振兴。

在海南省院士平台科研专项、昌江县政府委托项目、海南大学协同创新中心科研项目等资助下，在昌江排岸村租赁 100 亩高标准农田作为木棉稻田农林复合系统的优质高产技术研发与示范基地。带动当地村民打造“木棉稻米”品牌，其优质高产技术及相关产品（木棉稻米、木棉米酒、木棉枕头等）陆续亮相 2024 年海南冬季交易会、2024 年海南国际知识产权交易大会。相关工作对于促进当地的农业、生态、文化和旅游的融合发展具有积极意义，体现了海南大学服务地方经济发展和创建热带特色高效农业新模式的有益尝试。

木棉文化和木棉稻田农林复合系统系列科普活动

木棉稻田农林复合系统优质高产技术及相关产品亮相海南冬季交易会

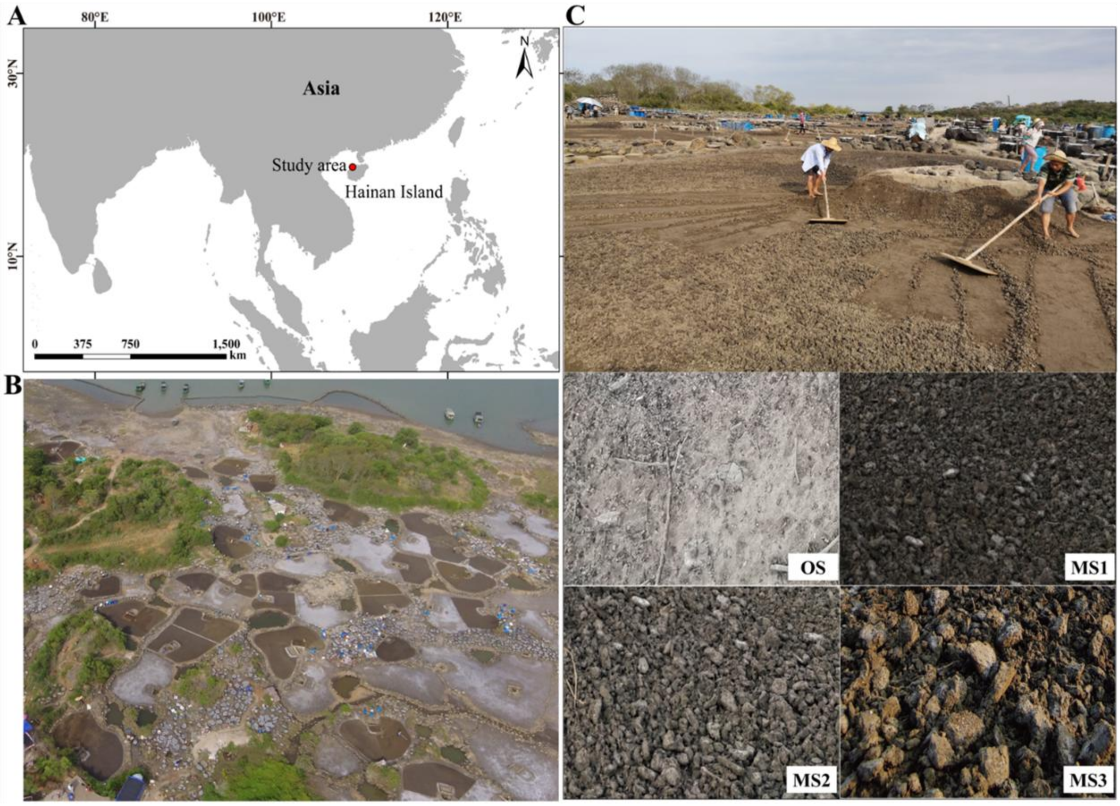
出版了专著《木棉稻田农林复合系统的传统技艺与生态学研究》，重点阐述了木棉稻田农林复合系统的定义与价值、传统文化内涵、资源循环利用与生物防治过程、物种多样性与生态系统稳定性、生产力与优质高产技术等，对比研究了木棉稻田农林复合系统和临近地区主要农业文化遗产的区别，探讨了木棉稻田农林复合系统的独特价值及其传承与创新利用策略与途径，针对申报中国重要农业文化遗产、打造“木棉稻米”地理标志产品、探索传统农业文化保护的“文化补偿”机制等提出了建议。

2. 洋浦千年古盐田耐盐微生物与“火山石盐”优质高产技术

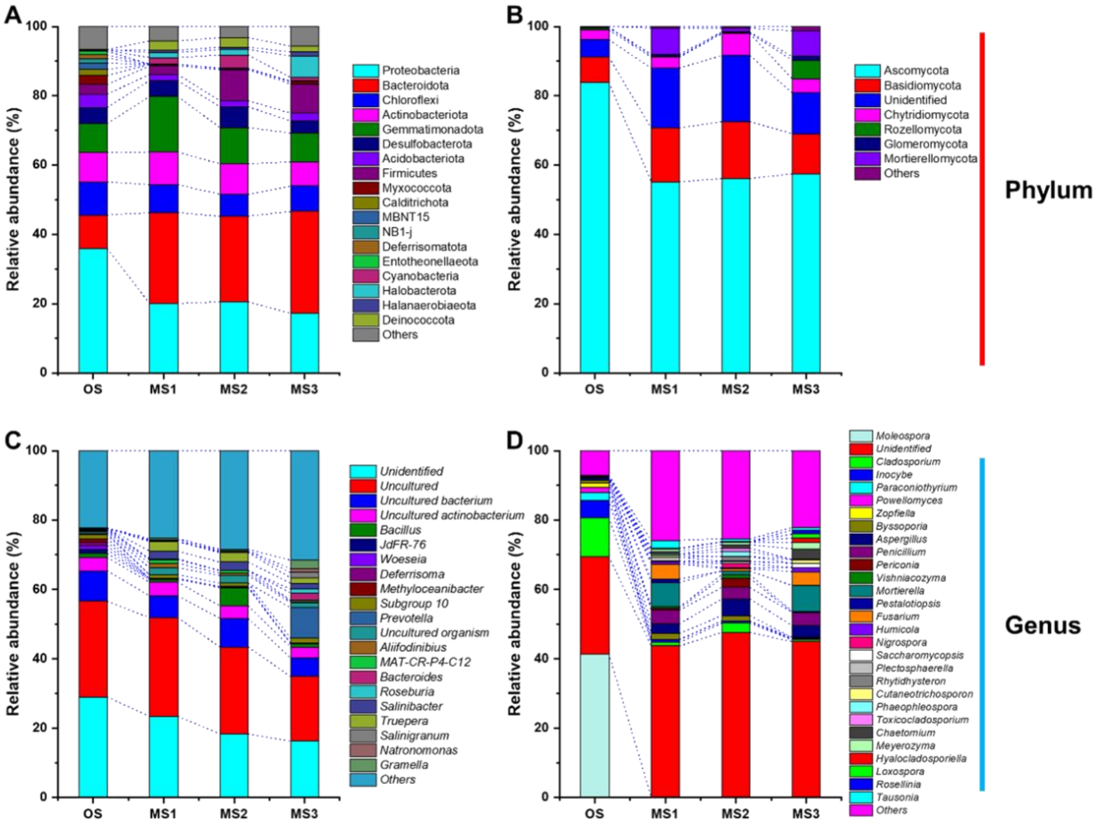
针对海南儋州的洋浦千年古盐田，研究了晒盐过程中的细菌和真菌多样性与群落结构时空变化，从现代科技角度解析了洋浦盐田晒盐技艺（2008 年入选了第二批国家级非物质文化遗产、2024 年入选国家工业遗产）的生物多样性基础与生态学原理，确定了关键微生物类群及其生态功能，证实了千年古盐田长期的高盐环境和火山岩石槽的卤水暴晒，可能选择和保留了特殊的耐盐微生物资源。

海南大学任明迅教授团队在揭示洋浦千年古盐田的传统文化和全过程微生物群落动态基础上，进一步深入研究了海泥在为期三天的日晒过程中的细菌和真菌群落演替及其对主要代谢物的影响。结果表明，真菌群落结构和动态受到 Na^+、Mg^{2+}和总氮的影响，而细菌群落主要由 Ca^{2+}、总钾和总磷决定《Applied Soil Ecology》（2024, 198: 105392）。

洋浦千年古盐田的研究有助于传统晒盐技艺的传承与创新利用，促进现代食品业和化工业耐盐微生物种质资源的挖掘与利用以及传统文化的“创造性转化、创新性发展”。



洋浦千年古盐田盐泥富集传统技艺



洋浦千年古盐田晒盐技艺中土壤细菌和真菌群落的相对丰度

3. 海南热带雨林国家公园科普视频系列

受海南省林业局（海南热带雨林国家公园管理局）资助，团队博士后张哲担任总导演兼制片人的海南热带雨林国家公园科普视频系列受到多方好评。该视频系列共 130 多集，包括动物篇、植物篇、风景名胜篇、民俗文化篇、人与雨林篇和雨林生态篇。目前，已在海南热带雨林国家公园官方哔哩哔哩、海南林业微信公众号等公众平台发布，累计播放上千万次，播放、点赞、微博相关话题讨论超 5000 万次。

其中，我团队博士后向文倩博士主讲的《木棉》入选中国生态环境部科技与财务司组织评选的优秀科普短视频、“典赞•2023 科普中国”提名奖两项奖励。2024 年 3 月，由海南大学张哲博士导演的《海南热带雨林国家公园科普视频系列》获得“作品类”梁希科普二等奖。

梁 希 科 普 奖

证 书

为表彰科普创作中所做出的突出贡献，特颁发此证书。

类　　别：科普作品类
作品名称：海南热带雨林国家公园科普视频系列
奖励等级：二等
获 奖 者：张哲
申报单位：海南大学

中国林学会
2024 年 3 月 28 日

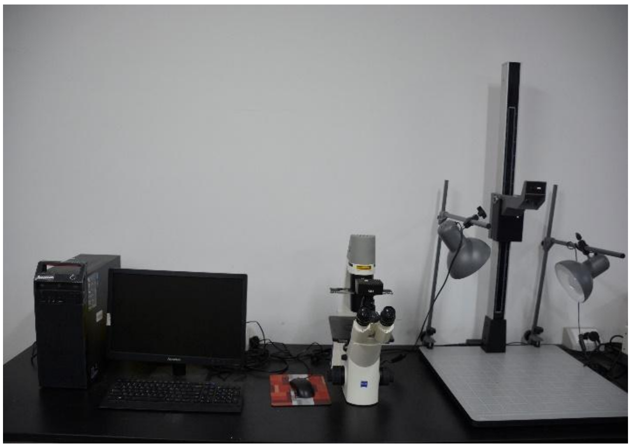
证书号：2023-KP-ZP-2-04-R01

梁希科普奖二等奖

五、平台建设

1. 分子生态学实验室

2. 植物形态分析实验室

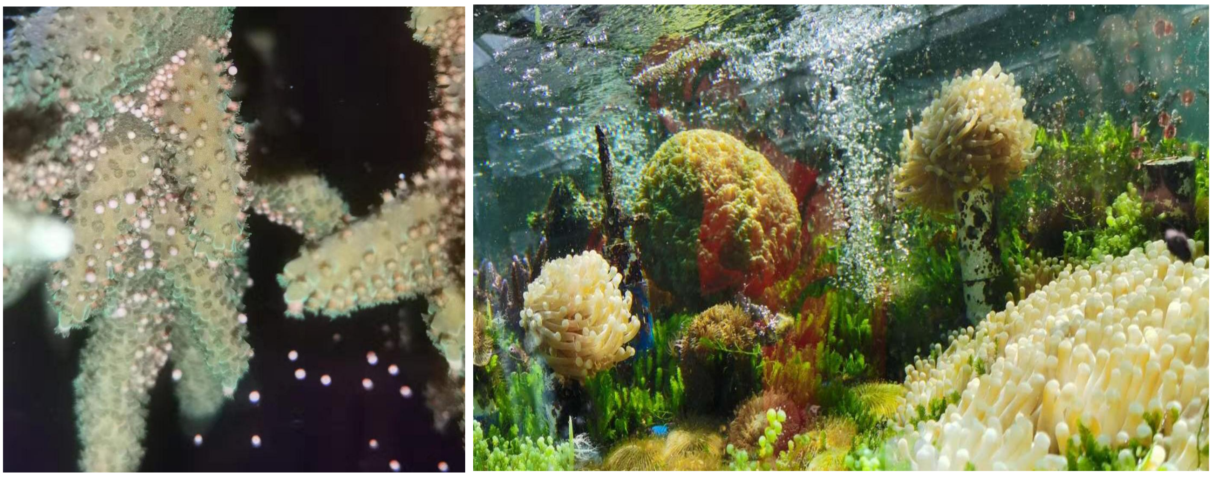


3. 植物化学分析室

4. 陆基珊瑚养殖基地

万宁市山根镇的繁育区与养殖区（30 亩）

珊瑚幼体生长情况



珊瑚排卵与受精生长

5. 木棉稻田农林复合系统优质高产技术研发与示范基地

海南昌江排岸村的木棉稻田农林复合系统优质高产技术研发与示范基地

6. 资源收集与保存

➢ 植物昆虫标本库

➢ 真菌标本库

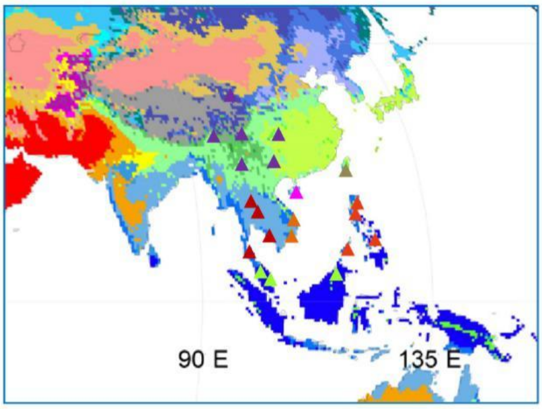
➢ 引种资源圃

➢ 野外重点采集与研究区域

▲ 广西和云南(横断山区)

▲ 台湾(恒春半岛、兰屿)

▲ 海南(霸王岭、尖峰岭)



▲ 菲律宾(吕宋岛、巴拉旺岛)

▲ 泰国(清迈、清莱)

▲ 越南(芽庄、巴拿山)

▲ 泰国(巴蜀、芭提雅)

▲ 马来西亚(沙巴、森美兰)

马来西亚（Kaki Bukit Tabur）

肯尼亚（Kilifi）

菲律宾（Arayat）

六、合作与交流

- 1 月 16 日，海南省科协党组成员、副主席徐伟一行五人调研海南省“海智计划”海南大学工作站，与工作站首席海智专家李百炼院士就工作开展国际交流合作与发展规划进行座谈。

- 2 月 18 日，昌江黎族自治县举办了“遇稻美好·木棉之恋”梯田实景音乐秀。任明迅教授和向文倩博士受邀参加活动，向广大群众宣传了源远流长的木棉文化与木棉稻田农林复合系统。

- 2 月 23-24 日，木棉文化和木棉稻田农林复合系统申遗座谈会在昌江黎族自治县政府会议室举行。 任明迅教授汇报了木棉稻田农林复合系统的申遗准备工作。

- 5 月 10 日，中国环境报对任明迅教授进行了独家专访和野外联合拍摄。在专访中，任明迅教授就海南热带雨林和海南坡鹿保护等问题发表了见解。

- 5 月 27 日，任明迅教授参加了在湖北神农架举行的 2024 “一带一路”生态保障人类命运共同体国际学术研讨会，与来自 46 个国家的专家学者、国际友人共话“一带一路”生态保障人类命运共同体建设。

- 6 月 9 日-15 日，任明迅教授陪同海南大学符宣国书记等出访巴西坎皮纳斯大学、巴伊亚大学、圣保罗大学以及美国亚利桑那州立大学，推动校际合作协议。

- 7 月 14-15 日，任明迅教授和向文倩博士参加了 2024 年生物多样性学术会议。任明迅教授受邀在“农业与生物多样性”分会场作了口头报告。

- 7 月 16 日-19 日，任明迅教授、唐亮教授和相关研究生参加了海南热带雨林保护研究基金 2024 年项目野外实践培训会。

- 8 月 18-22 日，向文倩博士参加了第六届生物多样性前沿论坛暨《生物多样性》编委会会议，作了题为《木棉风水林的微生物群落结构与碳氮磷循环功能基因分布》的报告。

- 8 月 19 日，任明迅教授受邀在海南省农业农村厅 2024 年度省农业农村（乡村振兴）系统干部能力提升培训班上作了《乡村振兴的关键：产业生态化和生态产业化》的培训课。

- 8 月 22 日，海南大学任明迅教授团队参加文昌航天科普中心科普活动，以中国科协海智计划海南(海南大学)工作基地名义开展了木棉文化科普活动。

- 9 月 28 日，任明迅教授和张哲副研究员参加 2024 年五指山市“全国科普日”暨中小学校园科技节活动，并受邀聘为五指山市部分中小学的科学副校长。

- 9 月 28 日，任明迅教授和张哲副研究员组织举行了由五指山市教育局主办的《海南热带雨林自然教育进校园》系列活动。

- 9 月 29 日，任明迅教授受邀参加 2024 年海南省自然教育协会成立大会 暨第一届第一次会员大会，并受邀代表会员发言。

- 10 月 14 日，任明迅教授在海南热带雨林国家公园自然教育进校园启动仪式上作了《海南热带雨林生物多样性》科普报告。

- 10 月 19-21 日，任明迅教授团队张清凤博士研究生等人前往琼海参加了 2024 世界生命科学大会。

- 10 月 20 日，工作基地魏雅丽博士研究生参加海南大学首届研究生科技节，并获优秀学术报告二等奖。

- 10 月 22 日-11 月 4 日，商务部资助的《全球发展倡议下拉美国家环境治理研修班》在海南大学顺利举办。任明迅教授主持了开班仪式和闭幕式，并和张乐博士并全程参与了授课与实践教学活动。

- 10 月 31 日，海南省环南海陆域生物多样性国际联合研究中心揭牌仪式暨首届环南海生物多样性与生态文化国际研讨会在海南大学国际学术交流中心顺利举行。

- 11 月 8-11 日，第一届全国植物生态学大会暨《植物生态学报》编委会会议在河北大学举行，任明迅教授团队参加会议。

- 12 月 5-8 日和 20-22 日，木棉稻田农林复合系统研究成果和相关产品亮相 2024 年第 27 届中国（海南）国际热带农产品冬季交易会、2024 年海南国际知识产权交易大会。

- 12 月 9-11 日，第二届(2024)“一带一路”高校联盟生态分盟学术会议在山东大学青岛校区举行，任明迅教授受邀参加了会议。

- 12 月 14-19 日，第七届国际生态峰会在河南郑州举行，向文倩博士及两位在读博士生马光辉、张清凤参加了会议。向文倩主持了分会场，马光辉和张清凤做了口头报告。

- 12 月 16 日，任明迅教授团队和海南省农业农村厅农村社会事业促进处阴若珂、副处长严立舰等赴昌江县与潘志勇副县长等讨论了木棉稻田农林复合系统申遗准备工作。

➢ 主办或参与主办的学术会议

会议名称	会议类别	会议时间	参加人数
全球发展倡议下拉美国家环境治理研修班	国际会议	2024 年 10 月	100
海南省环南海陆域生物多样性国际联合研究中心揭牌仪式暨首届环南海生物多样性与生态文化国际研讨会	国际会议	2024 年 10 月	30
生态环境可持续发展（海南）国际学术研讨会	国际会议	2024 年 12 月	300

➢ 学术报告情况

报告名称	报告人	会议名称	地点	时间
木棉稻田农林复合系统的生物多样性	任明迅	2024 年生物多样性学术会议	河北	2024.07
木棉文化的生物多样性传统知识	向文倩	2024 年生物多样性学术会议	河北	2024.07
木棉风水林的微生物群落结构与碳氮磷循环功能基因分布	向文倩	第六届生物多样性前沿论坛暨《生物多样性》编委会会议	兰州	2024.08
乡村振兴的关键：产业生态化和生态产业化	任明迅	海南省农业农村厅 2024 年度省农业农村（乡村振兴）系统干部能力提升培训班	海口	2024.08
洋浦千年古盐田的生态学基础及其传承发展	魏雅丽	海南大学首届研究生科技节	海口	2024.10
植物中的“岛屿法则”—来自风筝果（*Hiptage benghalensis*）的证据	任明迅	第一届全国植物生态学大会暨《植物生态学报》编委会会议	保定	2024.11
ecological adaptation of boat-house and traditional settlements of Li	马光辉	第七届国际生态峰会	郑州	2024.12

people in Hainan Island, China				
Freshwater Fish Diversity and Genetic Resources in Hainan Island of South China	张清凤	第七届国际生态峰会	郑州	2024.12

➢ 参加学术会议情况

会议名称	类别	时间	参会人员
2024 神农架“一带一路”生态保障人类命运共同体国际学术研讨会	国际会议（神农架）	2024.05	任明迅
海南热带雨林保护研究基金 2024 年项目野外实践培训会	全国会议（海口）	2024.07	任明迅、何倩倩、符国玉、熊恒煜
第六届生物多样性前沿论坛暨《生物多样性》编委会会议	全国会议（兰州）	2024.08	任明迅、向文倩、张钟文
第六届高等学校生态学本科专业建设与人才培养研讨会	全国会议（合肥）	2024.10	胡中民、王永健、任明迅
2024 世界生命科学大会	国际会议（琼海）	2024.10	张清凤、Gul Sumaira、张钟文、巫惠玲、何倩倩、符国玉
第一届全国植物生态学大会暨《植物生态学报》编委会会议	全国会议（保定）	2024.11	任明迅、张清凤、张钟文
生态环境可持续发展（海南）国际学术研讨会	国际会议（琼海）	2024.12	任明迅
第二届（2024）“一带一路”高校联盟生态分盟 学术会议	全国会议（青岛）	2024.12	任明迅
第七届国际生态峰会	国际会议（郑州）	2024.12	李百炼、向文倩、张清凤、马光辉

七、社会兼职

姓名	学术组织或科研机构	职务	任职时间
杨小波	国际生物多样性计划中国委员会	委员	2012-
	海南省生态学学会	理事长	2010-
	中国生态学会	常务理事	2012-
	海南省植物学会	副理事长	2011-
	海南省环境学会	副理事长	2008-
	海南省环境教育协会	常务副会长	2008-
任明迅	《Collectanea Botanica》	编委	2014-
	《植物生态学报》	编委	2024-
	《热带生物学报》	编委、专栏主持人	2020-
	中国科协海智计划海南（海南大学）工作基地	负责人	2020-
	热带特色林木花卉遗传与种质创新教育部重点实验室验室	副主任	2019-
	中国植物学会	理事	2023-
	中国林学会热带雨林分会	常务委员	2022-
	中国农学会农业文化遗产会分	理事	2024-
	海南省林学会	副秘书长	2018-
	海南省植物学会	副理事长	2023-
赵洪伟	中国环境科学学会污染源排放与管控专业委员会	委员	2022
	中国环境科学学会海洋生态安全专业委员会	委员	2023-
	Carbon Research	青年编委	2023-
	Marine Environmental Research	编委	2022
	海南省热带生态环境修复工程研究中心	主任	2023-
黄青	《亚热带植物科学》	编委	2020-
	海南省贺泓院士创新团队	负责人	2020-
	Frontiers in Microbiology	编委	2020

王鹏	Tropical Plants	编委	2022-
	《热带生物学报》	编委	2023-
	海南省人大	人大代表	2023-
	儋州市政协	政协委员	2022-
	农工党海南省委人口资源环境工作委员会	副主任	2022-
徐诗涛	海南省林学会	副理事长	2018
	海南省花卉协会	副理事长	2019
	海南省儋州市儋洋党旗红，博士村长行动油文村	博士村长	2023
向文倩	《生物多样性》	青年编委	2024-

八、在研项目

国家重点研发项目子课题

- 海洋牧场生态系统演变过程与固碳增汇途径（负责人：赵洪伟，执行期：2023－2026，总经费：41 万）

国家自然科学基金面上项目

- 飘还是漂？探究风筝果翅果的扩散机制及其对局域和区域种群遗传结构与基因流的影响(负责人：任明迅，执行期：2024－2027，直接经费：46 万)

国家自然科学基金地区科学基金

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- 海南热带雨林破碎化和面积减少对青梅、坡垒种群发育的影响研究(负责人：李东海，执行期：2023－2026，33 万)

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- 海南国家公园研究院科研专项：海南热带雨林国家公园人工生态系统未来演变方向研究与规划建议(负责人：杨小波，执行期 2021－2024，经费 180.5 万元)
- 海南省院士创新平台绩效奖励科研经费：海南省传统农耕文化的生态学基础及其对现代高效农业与生态文明建设的作用(负责人：任明迅，执行期：2022－2024，经费：100 万)
- 海南省院士创新平台运营与建设经费 (负责人：任明迅，执行期：2022－2024，经费：50 万)
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- 海南省院士创新平台专项：城市化建设对海南岛珊瑚礁的影响及其可恢复性评价(负责人：赵洪伟，执行期：2021－2024，经费：31 万)
- 海南国家公园研究院科研项目：海南热带雨林国家公园 40 种优先保护植物资源调查收集与保护研究 (负责人：唐亮，执行期：2024－2025，总经费：80 万)
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- 海南省自然科学基金高层次人才项目：五唇兰（兰科）的适宜生存区预测与谱系地理格局(负责人：张哲，执行期：2022－2025，经费：10 万)
- 海南省自然科学基金高层次人才项目：第四纪气候变化对海南岛及周边地区风筝果种群遗传结构和动态的影响(负责人：谭珂，执行期：2022－2025，经费：10 万)。
- 海南省自然科学基金面上项目：氮沉降驱动下海南霸王岭不同海拔森林土壤挥发性有机物排放动态及其影响因素研究(负责人：何禾，执行期：2022－2025，经费：8 万)
- 海南省自然科学基金，海南岛两种特有姜科植物的保护遗传学研究 (负责人：唐亮，执行期：2023.03－2025.12，总经费：8 万)
- 海南省自然科学基金青年基金：木棉-稻田体系中木棉花分解的养分动态及微生物机制(负责人：王文娟，执行期：2022－2025，经费：6 万)
- 海南省自然科学基金青年基金：海南岛山地雨林优势树种陆均松和鸡毛松对不同水热条件的分子适应机制(负责人：凌少军，执行期：2022－2025，经费：6 万)
- 海南省科学技术厅青年科学基金项目：海南三种同域分布蝴蝶兰属植物的生殖隔离与适应性进化(负责人：张哲，执行期：2021－2024，经费：5 万)

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➢ 学术著作

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十、代表性论著首页

木棉稻田农林复合系统
传统技艺与生态学研究

任明迅　向文倩　王文娟　李百炼 ◎著

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Article

Environmental Concentrations of Herbicide Prometryn Render Stress-Tolerant Corals Susceptible to Ocean Warming

Yanyu Zhou,[#] Qiuli Li,[#] Quan Zhang, Meile Yuan, Xiaoshan Zhu, Yuanchao Li, Qipei Li, Craig A. Downs, Danwei Huang, Loke-Ming Chou, and Hongwei Zhao*

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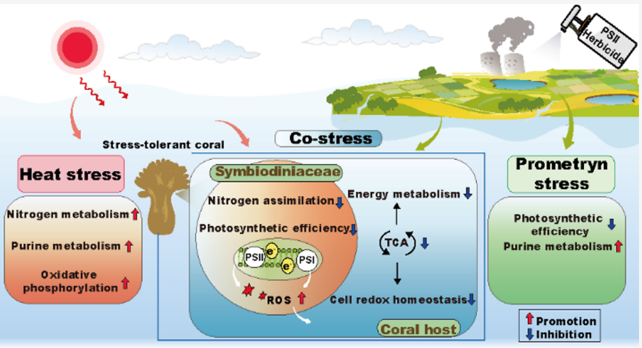
ABSTRACT: Global warming has caused the degradation of coral reefs around the world. While stress-tolerant corals have demonstrated the ability to acclimatize to ocean warming, it remains unclear whether they can sustain their thermal resilience when superimposed with other coastal environmental stressors. We report the combined impacts of a photosystem II (PSII) herbicide, prometryn, and ocean warming on the stress-tolerant coral *Galaxea fascicularis* through physiological and omics analyses. The results demonstrate that the heat-stress-induced inhibition of photosynthetic efficiency in *G. fascicularis* is exacerbated in the presence of prometryn. Transcriptomics and metabolomics analyses indicate that the prometryn exposure may overwhelm the photosystem repair mechanism in stress-tolerant corals, thereby compromising their capacity for thermal acclimation. Moreover, prometryn might amplify the adverse effects of heat stress on key energy and nutrient metabolism pathways and induce a stronger response to oxidative stress in stress-tolerant corals. The findings indicate that the presence of prometryn at environmentally relevant concentrations would render corals more susceptible to heat stress and exacerbate the breakdown of coral Symbiodiniaceae symbiosis. The present study provides valuable insights into the necessity of prioritizing PSII herbicide pollution reduction in coral reef protection efforts while mitigating the effects of climate change.



KEYWORDS: *Ocean warming, PSII herbicide, Prometryn, Omics, Stress-tolerant coral*

1. INTRODUCTION

Ocean warming poses a global threat to marine ecosystems.[1] The symbiotic relationship between corals and Symbiodiniaceae serves as the foundation for the health of coral reef ecosystems.[2] The increasing frequency and severity of coral bleaching events due to marine heatwaves endanger the structural integrity and functionality of these reefs.[3] Heat stress destabilizes photosystem II (PSII), reducing photosynthetic efficiency and increasing the generation of reactive oxygen species (ROS).[4] The vulnerability of PSII to heat and the resulting oxidative stress consistently characterize heat-induced coral bleaching. Factors that exacerbate these metabolic dysfunctions compromise the corals' ability to maintain homeostasis, making them more susceptible to bleaching. Despite the current dire situation, research has indicated that many surviving reef corals possess potential ecological resilience to ocean warming and may gradually increase their thermal thresholds over time.[5−7]

Co-occurring pollution exacerbates the challenges faced by coral reefs.[8−11] Herbicides, accounting for 47.5% of the global pesticide market, dominate in terms of usage statistics.[12] PSII herbicides, such as triazine herbicides, urea derivatives, and uracil, collectively account for approximately 5.7% of the global herbicide usage.[13] Furthermore, alongside atrazine, which ranks as the second most widely used herbicide worldwide, other PSII herbicides such as prometryn are progressively gaining market share in specific countries.[14,15] The PSII herbicides, widely employed in global agriculture and aquaculture, exhibit notable mobility and persistence, making them recurrently identified in both coastal seawater and coral samples.[16−19] This detection raises significant concerns regarding their potential impact on coral reef ecosystems. Notably, diuron and atrazine were measured within the Great Barrier Reef (GBR) around 1.2 μg L^{-1} during the period of 2017−2018.[20] Similarly, triazine herbicides, prometryn, simetryn and ametryn, were detected near the reef transect of Hainan Island, among which prometryn concentrations reached up to 0.4 μg L^{-1}.[21] The presence of Irgarol 1051 in coral reefs in Bermuda, Eastern Africa, Hawaii, the Florida

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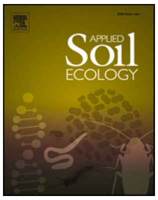

Succession of bacterial and fungal communities during the mud solarization of salt-making processing in a 1000-year-old marine solar saltern

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Keywords:
Solar salt
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Microbial succession

ABSTRACT

A 1000-year-old marine solar saltern in Hainan Island, South China, is in the continuation of traditional skills involving mud soak and solarization for three days to accumulate salt, which is a unique process contributing to the selection of highly halophilic microbes related to salt quality and flavor. Herein, the successions of physicochemical properties and bacterial and fungal communities of muds from the saltern were investigated during the processing of mud solarization. The results showed that Na^+, Cl^-, Mg^{2+} and total nitrogen were the main factors in explaining the fluctuation of the fungal community, whereas the bacterial community was predominantly determined by Ca^{2+}, total kalium and total phosphorus. During three days of mud solarization, the soil bacterial alpha diversity in the saltern was significantly lower than that of the surroundings, whereas the fungal alpha diversity showed an opposite trend. The bacterial functional groups with the same survival and adaptation strategies remained relatively stable, while the dominant functional type in fungi changed from monotropic to complex trophic mode. Additionally, some unidentified fungi species were increasingly found in mud. The abundances of *Saitozyma*, *Solicoccozyma* and *Wallemia* (Basidiomycota) increased and may contribute to the salt flavor through decomposing cellulose molecules into glucose due to their higher β-glucosidase activity, while the harmful fungal genera including *Inocybe* and *Paraconiothyrium* decreased obviously due to the stresses of salinity and solar exposure. These results showed that the traditional salt-making skills associated with mud solarization have selected a high abundance of beneficial halophilic microbes to increase the salt quality and flavor. Our findings not only reveal the underlying mechanisms for the long-history salt-making skills of this 1000-year-old unusual cultural heritage but also are highly valuable for bioprospecting to develop novel halophilic bacteria and fungi for modern chemistry industries.

1. Introduction

Solar salterns represent the earliest ways for humans to obtain salt, involving the processes of brine concentrating and NaCl crystallization by natural evaporation (Mani et al., 2012; Wei et al., 2022). Solar salterns as the hypersaline extreme environments for salt-making were generally characterized by unique physicochemical properties, for example, salinity gradient and intense ultraviolet radiation, which are usually distributed globally along tropical and subtropical coasts for the convenience of seawater aggregation, such as salterns at the Tuticorin salterns in India (Paul et al., 2020), salterns close to Ars-en-R'e Island (France) (Maziere et al., 2021) and salterns in Yongyudo (South Korea) (Heo et al., 2019). Microorganisms habited in these harsh environments have raised increasing attention as promising resources for novel bioactive compounds and tracing life's origin and adaptive evolution (Duarte et al., 2012; Ren et al., 2019; Ren et al., 2022; Wang et al., 2022).

Salterns are hypersaline extreme environments, and the microbial community in these places affects both the saltern physicochemical properties and the salt flavor and quality, such as the red pigmentation caused by halobacteria and β-carotene-rich unicellular alga *Dunaliella salina* (Chung et al., 2019), the phosphate-related available nutrients related to the growth of *D. salina* (Dolapsakis et al., 2005), the changes of oxygen concentrations caused by the photosynthesis of microbes (Wieland and Kuhl, 2006), etc. It is well-known that different geographical locations and traditional salt-making techniques of salterns all over the

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BMC Plant Biology

RESEARCH **Open Access**

Physio-biochemical and metabolomic responses of the woody plant Dalbergia odorifera to salinity and waterlogging

El- Hadji Malick Cisse[1,2,3], Bai-Hui Jiang, Li-Yan Yin[2], Ling-Feng Miao[1,4], Da-Dong Li[1,2,3], Jing-Jing Zhou[1] and Fan Yang[1,3*]

Background Trees have developed a broad spectrum of molecular mechanisms to counteract oxidative stress. Secondary metabolites via phenolic compounds emblematized the hidden bridge among plant kingdom, human health, and oxidative stress. Although studies have demonstrated that abiotic stresses can increase the production of medicinal compounds in plants, research comparing the efficiency of these stresses still needs to be explored. Thus, the present research paper provided an exhaustive comparative metabolomic study in *Dalbergia odorifera* under salinity (ST) and waterlogging (WL).

Results High ST reduced *D. odorifera*'s fresh biomass compared to WL. While WL only slightly affected leaf and vein size, ST had a significant negative impact. ST also caused more significant damage to water status and leaflet anatomy than WL. As a result, WL-treated seedlings exhibited better photosynthesis and an up-regulation of nonenzymatic pathways involved in scavenging reactive oxygen species. The metabolomic and physiological responses of *D. odorifera* under WL and salinity ST stress revealed an accumulation of secondary metabolites by the less aggressive stress (WL) to counterbalance the oxidative stress. Under WL, more metabolites were more regulated compared to ST. ST significantly altered the metabolite profile in *D. odorifera* leaflets, indicating its sensitivity to salinity. WL synthesized more metabolites involved in phenylpropanoid, flavone, flavonol, flavonoid, and isoflavonoid pathways than ST. Moreover, the down-regulation of L-phenylalanine correlated with increased p-coumarate, caffeate, and ferulate associated with better cell homeostasis and leaf anatomical indexes under WL.

Conclusions From a pharmacological and medicinal perspective, WL improved larger phenolics with therapeutic values compared to ST. Therefore, the data showed evidence of the crucial role of medical tree species' adaptability on ROS detoxification under environmental stresses that led to a significant accumulation of secondary metabolites with therapeutic value.

Keywords Abiotic stresses, Adaptability, Antioxidant, Medicinal tree, Metabolomic, Phenylpropanoids

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Research paper

Ecological stoichiometry and adaptations to drought and nitrogen in *Hevea brasiliensis* and *Dalbergia odorifera* in different planting patterns

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A R T I C L E I N F O

Keywords:
Drought stress
Growth performance
Nutrient availability
Plant interactions
Stoichiometric characteristics

A B S T R A C T

Two tropical forest trees (*Dalbergia odorifera* T. Chen and *Hevea brasiliensis* Muell. Arg), cultivated both in pure or mixed planting systems under drought and nitrogen-applied conditions, were selected at seedling stages as experimental materials to investigate their eco-physiological responses, interactions with neighboring trees, and the stoichiometry of carbon (C), nitrogen (N), and phosphorus (P). The results highlighted significant differences in biomass allocation between *D. odorifera*, which allocates more to root growth, and *H. brasiliensis*, favoring stem growth. It demonstrates that mixed planting enhances tree growth under well-watered conditions, while nitrogen application promotes growth across different moisture levels, with species-specific responses. Water and nitrogen interaction notably affects *H. brasiliensis* growth but less so for *D. odorifera*, revealing complex effects on their biochemical responses to oxidative stress. The mixed planting benefits both species, influencing nutrient dynamics and stoichiometry in *D. odorifera*. The study also shows that nitrogen application under well-watered conditions alters nutrient ratios, particularly affecting nutrient availability and competition between species in mixed planting setups. In conclusion, this research emphasizes the complex interplay between planting patterns, water, and nitrogen, which significantly impacts tree growth, nutrient dynamics, and stress responses, suggesting that specific management strategies could optimize forestry practices.

1. Introduction

Soil water and nitrogen (N) play a pivotal role in shaping the growth and development of plants, particularly during the crucial seedling growth phase of trees, as acknowledged by Geng et al. (2017). However, the escalating frequency and severity of drought events, driven by global warming and human interference, as highlighted by Hammond et al. (2022) and Müller and Bahn (2022), have thrown a shadow over this delicate equilibrium. Indeed, severe drought conditions exert a negative impact on plant growth and metabolic processes. Notably changes in plant morphological characteristics and also alter the allocation of biomass between aboveground and underground components as observed by Zhang et al. (2020) and Yu et al. (2022). Moreover, it can provoke the over-accumulation of reactive oxygen species, leading to greater peroxidation of plant cell membranes (Cisse et al., 2021; Li et al., 2023), and disrupting carbon and N metabolism (Peltier et al., 2023; Ru et al., 2023). Meanwhile, the recent proliferation in fossil fuel combustion and the widespread application of N-based agricultural fertilizers have fuelled a global increase in atmospheric N deposition, a trend anticipated to double from levels in the 1950s, as projected by Schlesinger (2009) and corroborated by Ren et al. (2017). Nonetheless, a definitive consensus remains elusive regarding how this N deposition phenomenon influences the adverse effects wrought by drought. N deposition which refers to the process by which atmospheric N compounds, primarily in the form of N oxides and ammonia are deposited onto the soil surface through various natural and human-induced activities can have both direct and indirect impacts on the health and resilience of the forest ecosystem (Braun et al., 2022). Indeed, N application has been used and studied for its potential benefits in plant growth under drought conditions. Some of these studies have reported several positive effects, including enhancements in plant osmolytes, the regulation of nutrient and biomass distribution patterns, increased

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Short Communication

Low genetic diversity and small effective population size in the endangered *Hopea reticulata* (Dipterocarpaceae) on Hainan Island, China

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ARTICLE INFO

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Genetic diversity
Population decline
Hopea reticulata Tardieu
Lowland rainforest

ABSTRACT

Hopea reticulata Tardieu (Dipterocarpaceae) represents a critically endangered tree species primarily confined to the Ganza Ridge of Hainan Island, China, with a couple of additional records of populations in Thailand and Vietnam. Neither the species' genetic diversity, which is essential for a species' long-term survival in the face of changing climate and various biotic stresses, nor the demographic history, which directly affects genetic diversity, has been examined. In this study, we employed double-digest restriction site-associated sequencing to investigate the population structure and evolutionary history of *H. reticulata* on Hainan Island. Our analysis revealed that *H. reticulata* exhibits the lowest nucleotide diversity ($\pi = 0.00091$) when compared to other well-known endangered tree species in China that have been assessed using high-throughput sequencing data. Utilizing the software Stairway Plot 2 for demographic history inference, we identified a significant reduction in effective population size of *H. reticulata*, a result concordant with the species' restricted geographic range and likely responsible for its low genetic diversity. Additionally, our research unveiled a weak genetic structure within geographically close *H. reticulata* populations, probably resulted from limited seed dispersal. These findings offer valuable insights into the conservation and management strategies required for the protection of *H. reticulata* on Hainan Island.

1. Introduction

The dominant tree species of lowland tropical rainforests in Asia belong to the family Dipterocarpaceae, which is well-known for the production of high-quality timber (Ghazoul, 2016). Long-term extensive logging activities on trees within this family have resulted

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Spatio-temporal variation and drivers of blue carbon sequestration in Hainan Island, China

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Blue carbon sequestration
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ABSTRACT

Blue carbon ecosystems, such as mangrove, seagrass bed and salt marsh, have attracted increasing attention due to their remarkable capacity for efficient carbon sequestration. However, the current threat posed by human activities to these ecosystems necessitates the characterization of their changes and identification of the primary driving factors in order to facilitate the gradual restoration of blue carbon ecosystems. In this study, we present an analysis of the spatio-temporal characteristics and primary influencing factors governing carbon sequestration in mangrove and seagrass beds located in Hainan Island. The findings revealed a 40% decline in carbon sequestration by mangroves from 1976 to 2017, while seagrass beds exhibited a 13% decrease in carbon sequestering between 2009 and 2016. The decline in carbon sequestration was primarily concentrated in Wenchang city, with aquaculture and population growth identified as the primary driving factors. Despite the implementation of measures aimed at reducing aquaculture in Hainan Island to promote blue carbon sequestration over the past two decades, the resulting recovery remains insufficient in achieving macro-level goals for carbon sequestration. This study emphasizes the necessity of safeguarding blue carbon ecosystems in Hainan Island by effectively mitigating anthropogenic disturbances.

The emission of greenhouse gases (GHGs) has led to a variety of environmental concerns, such as heightened surface and ocean temperatures, necessitating an urgent reduction in GHG emissions (Chmura et al., 2003). Coastal blue carbon ecosystems, such as mangroves, seagrass beds and salt marshes (Duarte et al., 2013), are globally acknowledged for their exceptional biological productivity. Despite occupying a mere 0.2% of the ocean's surface area, these ecosystems contribute approximately 50% of the annual carbon sequestration in the ocean (Gallo et al., 2017). However, the degradation of mangroves and seagrass beds has progressively intensified as a result of the combined impact of climate change and anthropogenic activities (Lovelock et al., 2015).

Mangroves and seagrass beds are the highest carbon sequestration ecosystems on Earth (Alongi, 2012). However, the process of ongoing land-use change in coastal regions has led to extensive degradation and transformation of these ecosystems, primarily for the purposes of aquaculture, agriculture, and urban expansion (Jia et al., 2014). Between 2000 and 2016, approximately 62% of the global mangrove coverage underwent conversion for aquaculture and agriculture purposes (Yu et al., 2013). Anthropogenic activities, such as urban development and the expansion of tourism, have also significantly contributed to the severe degradation of blue carbon sequestration (Alana et al., 2012), resulting in a decline in marine biodiversity and impacting the economic benefits derived from marine resources (Wang et al., 2020; Danovaro et al., 2020).

Although previous researches have successfully raised awareness of the crucial importance of mangroves and seagrass beds (Lee et al., 2019), it remains insufficient in effectively mitigating the ongoing decline in blue carbon sequestration. Furthermore, coastal wetland restoration has encountered significant challenges in recent years due to the impact of extreme weather events and other factors (Goldberg et al., 2020). Therefore, it is imperative to quantify historical changes in blue carbon sequestrations and assess the influence of different drivers on these changes. This will facilitate more efficient restoration of blue

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Effects of simulated nitrogen deposition on BVOCs emission dynamics and O_3 and SOA production potentials in seedlings of three *Ficus* species

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Nitrogen deposition
BVOCs
O_3
SOA

ABSTRACT

Nitrogen deposition affects the emission of biogenic volatile organic compounds (BVOCs) and thus their formation of ozone (O_3) and secondary organic aerosols (SOA). The present study employed four nitrogen concentrations (6, 10, 15, and 30 kg ha^{-1} yr^{-1}) and two nitrogen application methods (foliar surface and root application) to investigate the short-term effects of nitrogen deposition on BVOC emissions in seedlings of *Ficus virens*, *Ficus concinna* and *Ficus elastica* through controlled indoor pot experiments. The results demonstrated a positive correlation between the nitrogen concentration and the emission rate of BVOCs, with leaf nitrogen application exhibiting a significantly greater impact than root nitrogen application. The net photosynthetic rate and stomatal conductance emerged as pivotal factors influencing the emission of BVOCs. The maximum incremental reactivity (MIR) and fractional aerosol coefficient (FAC) methods were employed to assess the contribution of BVOCs to O_3 formation and SOA production. Our findings indicate that isoprene emitted by seedlings from the three plant species emerged as the predominant driver for O_3 formation, while monoterpenes and sesquiterpenes played a pivotal role in SOA production.

1. Introduction

Biogenic volatile organic compounds (BVOCs) are a diverse range of organic compounds synthesized by organisms in various ecosystems through metabolic and other physiological processes, encompassing isoprene, monoterpenes, sesquiterpenes, and more (Carslaw et al., 2010; Guo et al., 2014). BVOCs exhibit robust chemical reactivity and exert a significant influence on climate change, atmospheric environmental quality, radiation transfer, and energy distribution, as well as playing a pivotal role in the carbon cycle within ecosystems (Liu et al., 2022a,b). BVOCs and other atmospheric constituents participate in chemical and photochemical reactions, resulting in the formation of ozone (O_3), $PM_{2.5}$ (particles with aerodynamic diameters $\leq$2.5 μm), secondary organic aerosols (SOA), formaldehyde, and various other pollutants (Bai et al., 2018).

Although China has made significant improvements in overall ambient air quality (Zhao et al., 2013), there is a persistent upward trend in O_3 concentration across many regions, accompanied by an increasing prominence of SOA pollution (Zhang et al., 2021). When the near-surface O_3 concentration reaches a certain threshold, it exerts significant impacts on climate change, human health, the ecological environment, crops, and socioeconomic production (Feng et al., 2018). Additionally, it enhances atmospheric oxidation and facilitates the formation of SOA, thereby exacerbating air pollution (Li et al., 2020). Many VOCs in the atmosphere exhibit high photochemical reactivity and serve as crucial precursors to near-surface O_3 and SOA, which are significant atmospheric pollutants that currently impact urban and regional air quality in China. Globally, emissions of BVOCs contribute 20% and 76% to the formation of O_3 and SOA, respectively, as reported by Wang et al. (2019). Recent studies have demonstrated that BVOC emissions contribute 16.8% of the maximum daily O_3 concentration in China (Cao et al., 2022), while approximately 70% of the SOA formed over China originate from BVOCs (Wu et al., 2020). Therefore, accurately characterizing the effect of BVOC emissions on O_3 and SOA formation is crucial

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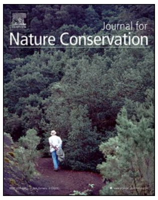

Ecosystem services in National Park of Hainan Tropical Rainforest of China: Spatiotemporal dynamics and conservation implications

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ARTICLE INFO

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Conservation priorities
Importance hierarchy
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ABSTRACT

Hainan island in south China harbours vast areas of virgin forests, with rich biodiversity and is included in the globally important Indo-Burma biodiversity hotspot. In 2018, a national park covering an area of 4269 km^2 of the island was proposed to conserve its rainforest ecosystem integrity and authenticity. In this study, using an integrated valuation of ecosystem services and tradeoffs (InVEST) model, a revised universal soil loss equation (RUSLE), a net primary productivity transformation formula, and the maximum entropy (MaxEnt) model, we quantified five ecosystem services, i.e. water conservation, soil retention, carbon storage, oxygen release and biodiversity maintenance. The data of five ecosystem services was recorded in the year 2000, 2010 and 2019, for seven regions of the national park including Mt. Jianfeng (JFL), Mt. Bawang (BWL), Mt. Diaoluo (DLS), Mt. Limu (LMS), Mt. Yingge (YGL), Mt. Wuzhi (WZS), and Maorui Forest Farm (MR). Then, we determined the importance of each of the ecosystem services for each region. Finally, we determined conservation priority sites of every regions respectively for each ecosystem service by comparing conservation efficiencies with the help of ordered weighted averaging. We found that total and mean amounts of five ecosystem services in the national park had declined in 2010 but increased in 2019, indicating the establishment of the national park effectively improved ecosystem services. Over 65 % areas of the national park exhibited dominant ecosystem services of water conservation, carbon storage and oxygen release. Soil retention was relatively uniform in seven regions, whereas the water conservation was concentrated in the eastern part of the national park, i.e. YGL, LMS, WZS and DLS. Carbon storage and oxygen release were highest at the central part of the national park including WZS, DLS, YGL, BWL, and MR, while biodiversity maintenance was the top ecosystem service for WZS, DLS, BWL and MR. Conservation priorities were assigned to natural forests in high-altitude areas in WZS, DLS, YGL, BWL, and MR, mostly in central parts of the national park. These results revealed the spatiotemporal pattern of ecosystem services and conservation priorities. It is helpful to facilitate precise management of this newly established national park. The innovative approach identifies key ecosystem services and their trade-offs to pinpoint conservation areas, offering valuable insights for the management of other national parks and protected areas.

1. Introduction

Ecosystem services are the benefits that humans obtain directly or indirectly from natural ecosystems (Daily, 1997; Costanza et al., 2014; Jiang et al., 2021), including provisioning, supporting, regulating and cultural services (Millennium Ecosystem Assessment, 2005). These form an important basis for maintenance and sustainable development of human society (Bai et al., 2020). Ecosystem services are central to conservation strategies(Lin et al., 2017). The management and optimization of ecosystem services are conducive to regional environmental sustainability, especially in mountain ecosystems (Gao et al., 2018). Traditionally, conservation planning has focused on the species, habitat and single ecosystem service, without consideration to spatio-temporal heterogeneity and trade-offs among various ecosystem services (Cao et al., 2019; Ma et al., 2021). Thus, functional zoning and conservation priorities identification that unifies multiple services, is the key to conservation policies(Costanza et al., 2017; Peng et al., 2017; Mao et al., 2019).

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RESEARCH ARTICLE

Exploring the mating systems of wild rice *Oryza rufipogon* and *O. nivara*: implications for population genetic variation

Jinqing Yang · Xinxia Liang · Yinping Wang · Jiyu Duan · Liang Tang · Xiaoming Zheng

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Abstract *Oryza rufipogon* Griff. and *O. nivara* Sharma et Shastry are wild ancestors of Asian cultivated rice, harboring a wealth of genetic variation valuable for rice breeding. Mating systems play an important role in shaping genetic variation within species, and could shed light on germplasm conservation. Despite the importance, previous research on the mating systems of *O. rufipogon* and *O. nivara* has been hindered by limited sample sizes and the use of unsuitable genetic markers. In this study, by collecting a large number of maternal plants and seeds from representative populations of both species, we estimated their outcrossing rates using an extended mixed-mating model along with 12 simple sequence repeats markers. Our results revealed distinct mating strategies between the two species. *Oryza rufipogon* exhibited a mixed mating system with an average outcrossing rate of 0.478, while *O. nivara* was predominantly selfing, with an average outcrossing rate of 0.256. In addition, compared to *O. nivara*, *O. rufipogon* has a higher genetic diversity within populations and lower differentiation among populations. The contrasting genetic variation patterns between the two wild rice species could result from demographic bottlenecks and a shift from mixed mating to primarily selfing in *O. nivara*. Overall, through our geographically widespread sampling, we have obtained reliable outcrossing rate estimates for *O. rufipogon* and *O. nivara*, thus facilitating both in situ and ex situ conservation of their germplasm.

Keywords Rice · *Oryza rufipogon* · *O. nivara* · Genetic variation · SSR marker · Outcrossing rate

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Jinqing Yang, Xinxia Liang have contributed equally to this work.

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NATURE NOTES

Hiptage yangshuoensis (Malpighiaceae), a new species on karst hills close to Lijiang River, Guangxi, China, based on molecular and morphological data

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Abstract

Hiptage yangshuoensis K.Tan & K.S.Nguyen, a new species of *Hiptage* collected from a karst cliff close to the Lijiang River, Northeast of Guangxi Zhuang Autonomous Region, China, is described and illustrated based on molecular and morphological data. *Hiptage yangshuoensis* shares some morphological similarities with the *H. multiflora* F.N.Wei, but easily distinguished by its long pedicels with articulate at top, one large calyx gland, oblanceolate middle wing and lanceolate lateral wings of samara, and young branch covered rusty sericeous. The new species status is also supported by molecular phylogenetic analyses based on nuclear ribosome internal transcribed spacer (nrITS), which showed distinct systematic distinctiveness from the most morphologically similar species, *H. multiflora*.

KEYWORDS

flora of Guangxi, karst landform, taxonomy, the Lijiang River

TAXONOMY CLASSIFICATION

Botany, Taxonomy

Ren-Fen Wang and Yao Ning contributed equally to this study.

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Molecular pathways of osmoregulation in response to salinity stress in the gills of the scalloped spiny lobster (*Panulirus homarus*) within survival salinity

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Panulirus homarus
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ABSTRACT

Scalloped spiny lobster (*Panulirus homarus*) aquaculture is the preferred strategy to resolve the conflict between supply and demand for lobster. Environmental conditions, such as salinity, are key to the success of lobster aquaculture. However, physiological responses of *P. homarus* to salinity stress have not been well studied. This study investigated the gill histology, osmoregulation and gill transcriptome of the early juvenile *P. homarus* (weight 19.04 ± 3.95 g) cultured at salinity 28 (control), 18, and 38 for 6 weeks. The results showed that the gill filaments of *P. homarus* exposed to low salinity showed severe separation of the cuticle and epithelial cells due to water absorption and swelling, as well as the dissolution and thinning of the cuticle and the rupture of the septum that separates the afferent and efferent channels. The serum osmolarity of *P. homarus* varied proportionately with external medium salinity and remained consistently above ambient osmolarity. The serum Na^+, Cl^-, K^+, and Mg^{2+} concentrations *P. homarus* exhibited a pattern similar to that of serum osmolality, while the concentration of Ca^{2+} remained unaffected at salinity 18 but significantly increased at salinity 38. Gill Na^+/K^+-ATPase activity of *P. homarus* increased ($p < 0.05$) under the both salinity stress. Salinity 18 significantly increased Glutamate dehydrogenase (GDH) and Glutamicpyruvic transaminase (GPT) activity in the hepatopancreas of *P. homarus* ($p < 0.05$). According to transcriptome analysis, versus control group (salinity 28), 929 and 1095 differentially expressed genes (DEGs) were obtained in the gills of *P. homarus* at salinity 18 and 38, respectively, with these DEGs were mainly involved in energy metabolism, transmembrane transport and oxidative stress and substance metabolism. In addition, the expression patterns of 8 key DEGs mainly related to amino acid metabolism, transmembrane transport and oxidative stress were verified by quantitative real-time PCR (RT-qPCR). The present study suggests that salinity 18 has a greater impact on *P. homarus* than salinity 38, and *P. homarus* demonstrates effective osmoregulation and handle with salinity fluctuations (18 to 38) through physiological and functional adaptations. This study provides an improved understanding of the physiological response strategies of *P. homarus* facing salinity stress, which is crucial for optimizing aquaculture practices for this species.

1. Introduction

The spiny lobster is a highly valued seafood product available to artisanal and commercial fisheries around the world, with a total land value of over $10 billion per year (Wang et al., 2018; Farhadi et al., 2022a). The high demand and pricing of the spiny lobster has led to the overfishing of almost all lobsters with economic value in the world (Cox and Johnston, 2003; Santos et al., 2022). To prevent the depletion of natural resources, many countries adopted various lobster catch restrictions, such as Indonesia blocking the export of lobster seedlings (Rahiel, 2023), and *Panulirus ornatus* was classified as a national second-grade protected animal in China. However, the above strategy has further exacerbated the market shortage of lobster. To break the vicious cycle of demand-overfishing-demand, lobster aquaculture is necessary (Jeffs, 2010). Successful examples in Vietnam and Indonesia demonstrate that lobster aquaculture is an effective way to solve supply

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Article

Differences in Metabolic Characteristics of Rhizosphere Fungal Community of Typical Arboreal, Shrubby and Herbaceous Species in Oasis of Arid Region

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Abstract: *Populus euphratica*, *Tamarix ramosissima*, and *Sophora alopecuroides* are, respectively, typical arboreal, shrubby, and herbaceous species in oases of arid regions. It is important to study the difference in metabolic characteristics of the rhizosphere fungal community of these plant species and their relationships with soil factors for the preservation of delicate arid oasis ecosystems with future environmental changes. In this study, we, respectively, collected 18 rhizosphere soil samples of *P. euphratica*, *T. ramosissima*, and *S. alopecuroides* to explore the difference in rhizosphere fungal metabolic characteristics of different plant life forms and their underlying driving factors. The results showed that (1) soil physicochemical properties (including soil water content, pH, etc.) were significantly different among different plant species ($p < 0.05$). (2) Rhizosphere fungal metabolic characteristics were significantly different between *S. alopecuroides* and *T. ramosissima* (ANOSIM, $p < 0.05$), which was mainly caused by the different utilization of carboxylic carbon. (3) The RDA showed that the main driving factors of the variations in rhizosphere fungal metabolic characteristics were different among different plant species. The main explanatory variables of the variations in the metabolic characteristics of the rhizosphere fungal community were carbon to nitrogen ratio (23%) and available potassium (17.4%) for *P. euphratica*, while soil organic carbon (23.1%), pH (8.6%), and total nitrogen (8.2%) for *T. ramosissima*, and soil clay content (36.6%) and soil organic carbon (12.6%) for *S. alopecuroides*. In conclusion, the variations in rhizosphere fungal metabolic characteristics in arid oases are dominantly affected by soil factors rather than plant life forms.

Keywords: arid oasis; life form; rhizosphere fungal community; metabolic characteristics; soil property

check for updates

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1. Introduction

As an important part of soil microorganisms, soil fungi participate in nutrient cycling, form symbioses with plants, and play key roles in promoting plant growth and regulating ecosystem processes [1]. The characteristics of fungal carbon metabolism serve as important indicators of fungal function [2], which not only reveals the use of carbon sources by fungi for growth and reproduction but also reflects the trophic role and ecological function of fungi in ecosystems [3,4]. Biolog-FF Microplate is a straightforward and rapid method to measure the diversity of fungal metabolism in the environment based on fungal metabolic response patterns induced by different substrates [5]. Previous studies showed that fungal growth and reproduction and their diversity were influenced by plant, soil, and other factors [6,7]. Therefore, the metabolism of the rhizosphere fungal community could be varied among plant life forms and their relationships with soil properties could be different among plant life forms as well.

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Long-term exposure to climbazole may affect the health of stress-tolerant coral *Galaxea fascicularis*

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ABSTRACT

The persistence of coral reefs globally is threatened by various forms of chemical pollution. Climbazole, an azole antibacterial agent extensively utilized in pharmaceuticals and personal care products (PPCPs) in everyday life, has been detected in various environment media and proved to have significant adverse effects on aquatic organism. However, the effects of climbazole on coral remain largely unknown. Therefore, in this study, we conducted a 42-day investigation to examine the effects of varying concentrations of climbazole on *Galaxea fascicularis* (*G. fascicularis*), a stress-tolerant coral species. Our investigations included coral color observations, physiological experiments, and assessments of microbial diversity. The results showed that, after 42 days of exposure, the coral color in the treatment group exposed to 100 μg/L climbazole significantly decreased by one color category on the reference chart (D6 shifted to D5), while there was no change in the control group. This was accompanied by an increase in oxidative stress and a decrease in photosynthetic capacity in coral specimens. Additionally, there was a notable alteration in microbial diversity, resulting in reduced community stability. Elevated levels of climbazole (100 μg/L) stress led to an increased abundance of potentially pathogenic bacteria such as *unclassified Erysipelotrichaceae*. However, at an environmentally relevant concentration of 1 μg/L, climbazole decreased the photosynthetic efficiency and induced oxidative stress in the stress-tolerant coral *G. fascicularis*, while not significantly impacting the microbial community diversity of the coral. The findings of our study have important implications for the protection and management of nearshore coral reefs and offer essential data for ecological risk assessment of climbazole.

1. Introduction

Coral reefs are highly diverse ecosystems that play crucial roles in maintaining marine biodiversity and productivity, coastal protection, as well as serving as a source of food and recreation. They play a pivotal role in socio-ecological processes within tropical coastal areas and significantly impact the livelihoods of local inhabitants (Fezzi et al., 2023; Sangaji et al., 2024). However, the persistence of coral reefs globally is threatened by localized land-based pollution, overfishing, climate change, and other factors, except for certain remote "wilderness" areas (Hughes et al., 2017). Among these threats, land-based pollution's impact on coral reefs is rapidly escalating (Kroon et al., 2016). Currently, extensive research has been conducted to investigate the impacts of eutrophication (Zhang et al., 2023), microplastics (Lei et al., 2021), heavy metals (Cheng et al., 2024; Islam et al., 2023), pesticides (Zhou et al., 2024), and other chemical pollution (Li et al., 2023b; Zhang et al., 2024) on coral reefs. The presence of these pollutants have exacerbated the vulnerability of coral reefs by causing oxidative stress, impairing photosynthetic systems, altering microbial communities, and disrupting other molecular biochemical processes of coral symbionts.

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Conservation genomic study of *Hopea hainanensis* (Dipterocarpaceae), an endangered tree with extremely small populations on Hainan Island, China

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Introduction: *Hopea hainanensis* Merrill & Chun is considered a keystone and indicator species in the tropical lowland rainforests of Hainan Island. Owing to its high-quality timber, *H. hainanensis* has been heavily exploited, leading to its classification as a first-class national protected plant in China and a plant species with extremely small populations (PSESPs).

Methods: This study analyzed genome-wide single nucleotide polymorphisms obtained through restriction site-associated DNA sequencing from 78 adult trees across 10 *H. hainanensis* populations on Hainan Island.

Results and discussion: The nucleotide diversity of the sampled populations ranged from 0.00096 to 0.00138, which is lower than that observed in several other PSESPs and endangered tree species. Bayesian unsupervised clustering, principal component analysis, and neighbor-joining tree reconstruction identified three to five genetic clusters in *H. hainanensis*, most of which were geographically widespread and shared by multiple populations. Demographic history analysis based on pooled samples indicated that the decline in the *H. hainanensis* population began approximately 20,000 years ago, starting from an ancestral population size of approximately 10,000 individuals. The reduction in population size accelerated approximately 4,000 years ago and has continued to the present, resulting in a severely reduced population on Hainan Island. Intensified genetic drift in small and isolated *H. hainanensis* populations may contribute to moderate differentiation between some of them, as revealed by pairwise F_{st}. In conclusion, our conservation genomic

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REVIEW

Physiologia Plantarum

Tree species and drought: Two mysterious long-standing counterparts

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Abstract

Around 252 million years ago (Late Permian), Earth experienced one of its most significant drought periods, coinciding with a global climate crisis, resulting in a devastating loss of forest trees with no hope of recovery. In the current epoch (Anthropocene), the worsening of drought stress is expected to significantly affect forest communities. Despite extensive efforts, there is significantly less research at the molecular level on forest trees than on annual crop species. Would it not be wise to allocate equal efforts to woody species, regardless of their importance in providing essential furniture and sustaining most terrestrial ecosystems? For instance, the poplar genome is roughly quadruple the size of the *Arabidopsis* genome and has 1.6 times the number of genes. Thus, a massive effort in genomic studies focusing on forest trees has become inevitable to understand their adaptation to harsh conditions. Nevertheless, with the emerging role and development of high-throughput DNA sequencing systems, there is a growing body of literature about the responses of trees under drought at the molecular and eco-physiological levels. Therefore, synthesizing these findings through contextualizing drought history and concepts is essential to understanding how woody species adapt to water-limited conditions. Comprehensive genomic research on trees is critical for preserving biodiversity and ecosystem function. Integrating molecular insights with eco-physiological analysis will enhance forest management under climate change.

1 | INTRODUCTION

The scientific community has faced challenges in reaching a consensus on the precise definitions of drought and beyond broad interpretations, such as "a deviation from typical water availability" (Slette et al., 2019). Although the terms used to describe drought can differ and be inconsistent, researchers strive to define tree species' and ecosystems' responses and adaptations during the post-drought period (Vilonen et al., 2022). A recent study defined drought as an insidious natural hazard that proceeds gradually and subtly, causing harmful effects (Wlostowski et al., 2022). The World Health Organization (WHO) defines drought as a prolonged period of dryness within the natural climate cycle, which can occur in any location worldwide (WHO, 2023). In an early chapter named Encyclopedia of World Climatology, drought was described as an insidious natural hazard that arises from a lack of precipitation compared to what is expected or deemed "normal." When this occurs over a season or an extended period, the amount of water available is inadequate to fulfil the demands of human activities (Wilhite, 2005). From the perspective of a plant biologist, drought in plants results from a water deficit in the soil, which prevents a specific plant or canopy from receiving the necessary amount of water to sustain its water requirements at a given time. This can significantly alter the plant's water status (Tardieu et al., 2018). A plant physiologist can fundamentally define drought as

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Plant diversity value of informal green spaces in tropical coastal urban areas: An empirical study of species, functional, and phylogenetic diversity

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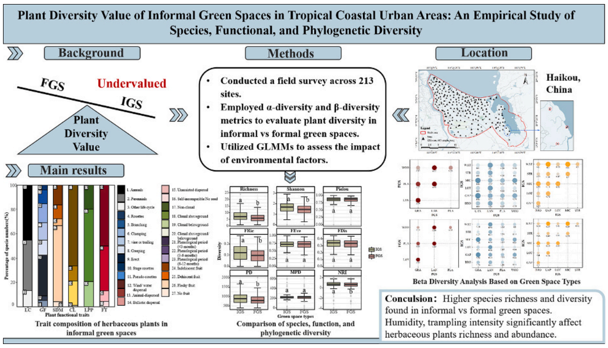
HIGHLIGHTS

- 235 herbaceous species from 179 genera in informal green spaces recorded.
- Informal green spaces show higher species and functional richness than formal spaces.
- Differences in phylogenetic diversity between informal and formal spaces were minor.
- Environmental factors like humidity and trampling impact plant diversity.
- Informal green spaces have diverse plants, notably in microsites and waterside.

GRAPHICAL ABSTRACT



- Conducted a field survey across 213 sites.
- Employed α-diversity and β-diversity metrics to evaluate plant diversity in informal vs formal green spaces.
- Utilized GLMMs to assess the impact of environmental factors.

Conculsion: Higher species richness and diversity found in informal vs formal green spaces. Humidity, trampling intensity significantly affect herbaceous plants richness and abundance.

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ABSTRACT

Informal green spaces (IGS) are a hot topic in urban biodiversity studies, but overlooked in urban biodiversity conservation or management, especially in tropical coastal cities, where comprehensive assessments remain scarce. Most existing research has been limited to species diversity (α-diversity), with few studies addressing functional and phylogenetic diversity as aspects of α-diversity, and species turnover (β-diversity) across multiple IGS types. This study bridges these gap by conducting a detailed vegetation survey in Jiangdong New Area of Haikou City, establishing 213 sites. Within these sites, we examined 343 IGS sample plots and 274 formal green spaces (FGS) sample plots. We assessed species, functional, and phylogenetic diversity using α and β diversity metrics and analyzed the influence of environmental factors with generalized linear mixed models (GLMMs). The results recorded 235 species of herbaceous plants from 179 genera and 54 families in IGS, including 215 spontaneous species, compared to 154 spontaneous species in FGS. Our findings indicate that IGS exhibited higher species richness and functional richness compared to FGS, though differences in phylogenetic diversity were less pronounced. Key environmental factors like relative humidity, trampling intensity, and proximity to urban areas significantly influenced species richness and abundance in IGS. These findings underscore the critical

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PLASTOME REPORT

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Characterization and phylogenetic analysis of the complete chloroplast genome sequence of *Phalaenopsis deliciosa* (Rchb. f. 1854)

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ABSTRACT

Phalaenopsis deliciosa (Rchb. f.), an ornamental orchid known for vibrant flowers, has a 148,090 bp chloroplast genome with 36.78% GC content. It includes an 85,241 bp large single-copy (LSC) region, an 11,649 bp small single-copy (SSC) region, and two 13,800 bp inverted repeats (IRs), encoding 122 genes (76 protein-coding, 38 tRNA, and 8 rRNA). This genome data refines the *Phalaenopsis* gene database and supports research on phylogeny and molecular breeding.

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Phalaenopsis; chloroplast; genome assembly; phylogenetic analysis

Introduction

Phalaenopsis (Vandeae, Orchidaceae) comprises more than 70 species worldwide, distributed in East Asia, South Asia, Southeast Asia, and North Oceania (Chen et al. 2009). Morphological and genetic evidence suggests that *Phalaenopsis* can be divided into four subgenera: *Phalaenopsis*, *Parishianae*, *Hygrouchilus*, and *Ornithochilus* (Li et al. 2016). Among them, the classification of the subgenus *Parishianae* is more complicated, containing four sections: *Parishianae*, *Esmeralda*, *Aphyllae*, and *Deliciosae* (Liu et al. 2020). More sample material is needed to refine the classification of subgenus *Parishianae*. *Phalaenopsis deliciosa* (Rchb. f. 1854) is distributed in South Asia and Southeast Asia, growing on tree trunks or valley rocks in mountain forests at altitudes of 450–1100 m. *P. deliciosa* was once considered a separate genus, *Kingidium*, but molecular evidence suggested that it should be assigned to the subgenus *Parishianae* of *Phalaenopsis* (Padolina et al. 2005). The habitat and basic characteristics of *P. deliciosa* are shown in Figure 1.

The chloroplast genome is crucial as it plays a key role in photosynthesis, which directly affects plant growth and development. Moreover, chloroplast genomes are often used in phylogenetic studies due to their relatively conserved nature (Jansen et al. 2007). This study aims to sequence and annotate the chloroplast genome of *P. deliciosa*, to explore the differences between its genes and other species within the genus *Phalaenopsis*, and to provide data support for clarifying the phylogenetic relationships under the genus *Phalaenopsis*, as well as the influence of geological history on species differentiation.

Materials and methods

With the approval of the Hainan Tropical Rainforest National Park Authority, Bawangling Branch Office, the fresh leaves of *P. deliciosa* were collected from Bawangling region of the Hainan Tropical Rainforest National Park, China (19°4′35″N, 109°13′12″E). A voucher specimen was kept at the Teaching Herbarium of the College of Forestry, Hainan University (Zhang Zhe, 107189517@qq.com, number: HUFB2022717). The annotated chloroplast genome was deposited to GenBank under the accession number: OM792977.

Second-generation sequencing technology was utilized for library construction and sequencing of total DNA extracted from plant leaves. The acquired data were subjected to quality filtering to obtain clean data. The total chloroplast genome was extracted from dry leaves using a modified CTAB protocol and sequenced using next-generation sequencing with the Illumina NovaSeq 6000 (San Diego, CA). The genome sequences were screened and assembled with GetOrganelle. The raw data have been submitted to the NCBI Sequence Read Archive (SRA) database under the accession number SRR18136583.

To evaluate the evolutionary relationships, 13 chloroplast genome sequences including four complete chloroplast genomes of Orchidaceae were used. A maximum-likelihood (ML) tree was constructed using MEGA 11 with 1000

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Suspended soils enrich local forest floor soils during the rainy season in a tropical monsoon rainforest of Hainan Island, South China

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Introduction: Epiphytic plants are abundant in rainforests and often serve as traps for litter and dust falling from the canopy. As it accumulates, this material can form nutrient rich soils, which are likely involved in local nutrient cycling and ecological processes.

Methods: To explore spatial and temporal variation in the influence of suspended soils on local nutrient cycles, we compared the physical, chemical and biological properties of suspended soils from the locally-dominant epiphytic Bird's nest fern (*Asplenium nidus* L.) to those of three types of forest floor soils (soil collected from upslope, downslope, and underneath the host tree) in a tropical monsoon rainforest in Bawangling National Nature Reserve on Hainan Island, China.

Results: Suspended and forest floor soils were all acidic, with suspended soils having much higher organic matter (66.84%) and water content (~ 300%) than forest floor soils. Suspended soils contained significantly more available nitrogen, phosphorous, and potassium and had much higher urease, cellulase, and catalase activities, indicating that they harbored diverse microbial communities with higher decomposition and biomineralization activity.

Discussion: Physicochemical traits of suspended soil and soil collected from under the host tree were significantly more similar in the rainy season than in the dry season, suggesting that suspended soils may contribute to local nutrient cycling as they are flushed out of epiphytic plants and enrich stemflow and forest floor soils.

Conclusion: Thus, suspended soils play a role in local nutrient cycling, especially during the rainy season. This study provides empirical support for the seasonality and heterogeneity of forest floor soil enrichment by suspended soils in tropical monsoon rainforests.

KEYWORDS

Asplenium nidus **L., suspended soil, canopy, monsoon rainforest, epiphytes**

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海南岛红树林生态系统总初级生产力分布格局及形成机制

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摘　要: 红树林具有较高的光合速率和较低的光补偿点,表现出较高的总初级生产力(gross primary production,GPP),是“蓝碳”的重要组成。准确估算区域红树林生态系统 GPP,并量化其限制因素贡献对于我国实现“双碳”目标具有重要意义。该文以海南岛红树林生态系统为研究对象,利用哨兵-2(Sentinel-2)影像和环境因子数据,基于红树植被光合作用-光能利用效率(MVP-LUE)模型估算了 2016—2020 年期间海南岛红树林生态系统 GPP,并探究其时空分布格局及形成机制。结果表明:(1)在研究期间,海南岛红树林生态系统年 GPP 呈现出增长趋势,在空间上呈现出东部高于西部、北部高于南部的分布格局。(2)在形成机制上,海南岛红树林生态系统月均 GPP 时空分布格局受到多气象因素的综合影响,年内季节性上 GPP 在“旱→雨”过渡期随着空气温度(air temperature,T_{air})的限制降低和光合有效辐射(photosynthetically active radiation,PAR)与海水温度的促进作用,展现出较高的 GPP;旱季中期 T_{air} 低,对 GPP 限制严重,但随着纬度的降低,红树林生态系统 GPP 受 T_{air} 限制的程度被减弱;雨季则因较高的云覆盖而使 PAR 成为 GPP 的限制因素。该研究结果为评估区域红树林对全球碳循环的贡献提供了基础数据,为揭示影响红树林生态系统碳动态的关键环境因素提供了理论支撑。

关键词: MVP-LUE 模型, 哨兵-2 影像, 时空分布格局, 限制因子, 红树林生态系统, 海南岛

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Distribution patterns of gross primary production of mangrove ecosystems in Hainan Island and their driving mechanisms

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水淹-盐胁迫对两耐淹树种生理生态及 Na^+、K^+和 Cl^-离子积累的影响

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摘　要：滨海河口河岸带植物易受到水淹和盐复合胁迫的影响。前期研究表明水翁（*Syzygium nervosum* A. Cunn. ex DC.）和乌墨（*Syzygium cumini* (L.) Skeels）具有较强的耐水淹能力，然而两种植物对水淹-盐复合胁迫的耐受性尚不清楚。本研究设置水淹、盐（350 mmol/L）及水淹-盐（175 mmol/L）复合胁迫 3 种胁迫处理，比较两物种对不同胁迫的生长、生理生化和盐胁迫相关离子积累的响应。结果显示，经过 24 d 处理，3 种胁迫处理均低了两物种的生物量，提高了还原型谷胱甘肽（GSH）含量、抗坏血酸过氧化物酶（APX）和谷胱甘肽还原酶（GR）的活性。水淹胁迫下两物种的超氧阴离子（$O_2^{\cdot -}$）和过氧化氢（H_2O_2）含量下降，根系 K^+含量上升，K^+/Na^+下降；盐胁迫下乌墨幼苗 $O_2^{\cdot -}$含量下降，水翁幼苗 $O_2^{\cdot -}$含量上升，两物种幼苗的脯氨酸含量、H_2O_2 含量、Na^+、Cl^-含量上升，K^+/Na^+下降；水淹-盐复合胁迫下两物种的 $O_2^{\cdot -}$、Na^+、Cl^-含量上升，K^+/Na^+下降。此外，与水淹相比，水淹-盐复合胁迫降低了两物种的生物量，提升了两物种的 $O_2^{\cdot -}$、Na^+、Cl^-含量。与水翁相比，乌墨幼苗在盐、水淹-盐复合胁迫下有较高的生物量、脯氨酸含量、GR 活性和 K^+/Na^+，以及较低的 H_2O_2、Na^+和 Cl^-含量，具有更强的盐、水淹-盐复合胁迫耐受能力。

关键词：水淹-盐复合胁迫；水翁；水淹；乌墨；盐胁迫
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Effects of waterlogging and salinity stresses on eco-physiology and accumulation of Na^+, K^+, and Cl^- in two waterlogging-tolerant arbor species

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Abstract: Plant growth in coastal estuarine riparian zones is vulnerable to combined waterlogging and salt stresses. Previous studies have shown that *Syzygium nervosum* A. Cunn. ex DC. and *Syzygium cumini* (L.) Skeels possess strong waterlogging tolerance. However, their tolerance to combined salinity and waterlogging stress is still unclear. In this study, three treatments, including waterlogging, salinity treatment (350 mmol/L), and combined salinity-waterlogging treatment (175 mmol/L), were used to compare the effects of different stresses on plant growth, physiological and biochemical traits, and ion accumulation in both species. After 24 d of treatment, the three stress treatments resulted in a decrease in the biomass of both species, as well as

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万泉河流域表层水体和沉积物中微塑料的污染特征

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摘　要: 新污染物微塑料（microplastics, MPs）已对全球水生生态系统的稳定性构成潜在的威胁。本研究基于海南岛万泉河流域的 10 份表层水体样品和 9 份沉积物样品，分析了万泉河流域不同环境介质中微塑料污染特征。结果表明：万泉河表层水体中微塑料丰度为 0～1.7 个/L，而沉积物中微塑料丰度为 0～14.8 个/kg。万泉河微塑料丰度分布总体趋势是从上游到下游乃至河口地区逐步升高，在支流汇合处突然增高。水体中小粒径微塑料（0.005～0.5 mm）的占比要高于沉积物中的占比，水体中微塑料以绿色为主，而沉积物样品以蓝色为主。水体及沉积物微塑料形状均以纤维状占比最高。赛璐玢（cellophane）是水体和沉积物中鉴定出的微塑料样品的最主要塑料聚合物类型。另外，水体中检测出了少量聚丙烯腈（PAN）以及聚对苯二甲酸乙二醇酯（PET）等塑料聚合物，而沉积物中检测出了聚丙烯（PP）、聚乙烯（PE）、聚苯乙烯（PS）、聚酰胺（PA）等塑料聚合物。研究表明，万泉河流域内的微塑料来源主要以农村生活污水、生活垃圾及渔业废弃物为主。万泉河的微塑料丰度相较于其他主要外河流水域总体偏低，但仍受到不同程度人类活动的影响。本研究可为热区外河流环境微塑料等新污染物监测和风险评估提供科学依据。

关键词: 微塑料；外河流；表层水体；沉积物；新污染物监测

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Microplastic pollution in surface water and sediments of Wanquan river basin

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Abstract: Microplastics (MPs) are a type of emerging contaminants that pose potential threats to the stability of global aquatic ecosystem. This study aimed to analyze the distribution characteristics and composition differences of microplastics in the Wanquan river basin of Hainan Island, using 10 water samples and 9 sediment samples. The results revealed that the abundance of microplastics in the surface water of the Wanquan

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旱-盐复合胁迫对降香黄檀幼苗生长和生理生化特性的影响

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摘要：为探究干旱-盐复合胁迫对陆生木本植物生长发育及生理生化特性的影响，通过盆栽试验在旱-盐复合胁迫(SD，25%~30%田间持水量+150 mmol/L NaCl)下对 3 种种植密度[每盆种植 1 株(DI)、2 株(DII)、3 株(DIII)]的降香黄檀(*Dalbergia odorifera*)幼苗的生长、光合色素含量和生理生化指标进行了研究。结果表明，DI 密度下 SD 处理显著抑制了株高增长量、基径增长量、总叶面积、主根长、总叶绿素含量和相对含水量，但过氧化氢酶和谷胱甘肽还原酶(GR)活性、可溶性蛋白和可溶性糖含量提高。与 DI 密度相比，DIII 密度进一步降低了 GR 活性和还原性谷胱甘肽含量，导致幼苗生长受到抑制。因此，在旱-盐复合胁迫的环境下，种植密度会对降香黄檀的生长产生影响，在海岸带栽植降香黄檀幼苗的过程中，应考虑低密度栽植模式进行栽培。

关键词：干旱胁迫；盐胁迫；种植密度；生长性状

Effects of Combined Drought and Salt Stress on Growth, Physio-chemical Characteristics of *Dalbergia odorifera* Seedlings

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Abstract: In order to explore the effects of drought-salt combined stress on the growth, physio-chemical characteristics of terrestrial woody plants, pot experiments were conducted in drought-salt combined stress (SD), the growth, photosynthetic pigment content and physiological and biochemical indexes of *Dalbergia odorifera* seedlings with three planting densities [1 plant (DI), 2 plants (DII) and 3 plants (DIII) per pot, respectively] were studied under 25%~30% field water capacity +150 mmol/L NaCl. The results showed that SD treatment significantly inhibited the growth of plant height, basal diameter, total leaf area, taproot length, total chlorophyll content and relative water content at DI density, but increased the activities of catalase and glutathione reductase (GR), soluble protein and soluble sugar content. Compared with DI density, DIII density further reduced GR activity and reduced glutathione content, resulting in inhibition of seedling growth. Therefore, under the combined drought and salt stress environment, planting density would affect the growth of *D. odorifera*, and low density planting mode should be considered in the coastal zone.

Key words: Drought stress; Salt stress; Planting density; Growth trait

干旱和盐是影响植物生长发育的两个最重要和最常见的环境胁迫因子[1]。生长在海岸带的植物常遭受海浪、海风、潮汐等因子带来的盐胁迫影响，同时由于滩涂沙地保水能力较差，干旱胁迫在海岸带也十分常见。从而导致此区域植物经常面临水分亏缺和盐分的双重胁迫[2]。干旱不仅影响植物的形态发育、还会扰乱其生理过程，如影响水分吸收、叶绿素合成以及抗氧化酶活性等，严重时还会阻碍植物生长甚至危及其生存[3–4]。同样，盐胁迫也会引起植物气孔关闭、叶绿素含量降低、光合作用减弱、水分利用效率降低、离子失衡和细胞毒性增加等使植物生长受到抑制[5–6]。但有研究表明，一些植物在旱盐复合胁迫下还具备一定的交叉适应性[6]。适量添加盐能够改善干旱胁迫下冬小麦(*Triticum aestivum*)的渗透调节能力和体内供水状况[7]；桔梗(*Platycodon grandiflorum*)叶绿素含量及抗氧化酶活力在旱-盐复合胁迫下显著提高，丙二醛含量显著降低[8]。以往研究主要集中在农作物和草本植物，热带陆生木本植物对旱-盐复合胁迫是否具备一定的交叉适应性目前仍不清楚。另外，种植密度是调节植物生物量的常见方法，通常高密度种植不利于增加木本植物生物量和产量[9]。而环境胁迫梯度假说认为，当环境胁迫程度较大时，物种之间的竞争会逐渐减弱甚至转变为互利关系[10–11]。随水淹程度增加，空心莲子草(*Alternanthera philoxeroides*)个体之间的竞争强度逐渐减弱，促进作用逐渐增强[12]；低水分条件下车桑子(*Dodonaea viscosa*)茎生物量和总生物随种植密度的增加逐渐增加[13]；干旱条件下高密度栽培更有利于延缓棉花叶片衰老，提高生长速率和物质生产能力[14]。因此，为了弥补海岸带生态脆弱性和缓解沿海地区生态环境恶化，有必要开展旱-盐复合胁迫与种植密

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东寨港自然保护区不同潮位下海莲群落特征及种群动态的比较研究

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摘 要：为了解不同生境下海莲（*Bruguiera sexangula* (Loureiro) Poiret）的群落特征和种群动态变化，合理利用与保护现有红树资源，对海南东寨港国家级自然保护区不同潮位下海莲的群落特征、年龄结构、分布格局、静态生命表以及生存函数等进行了研究。结果表明：（1）海莲为群落的优势树种，群落的物种多样性指数、均匀度指数以及林分密度随潮位升高逐渐增加，而海莲的重要值、胸径、树高以及冠幅随潮位升高逐渐降低；（2）海莲种群在空间上呈现聚集分布格局，不同潮位的龄级结构分布不同，低潮位种群为“凸”型而中高潮位种群为倒“J”型；（3）海莲种群的存活曲线在不同潮位上存在差异，低潮位植株死亡率在各龄级中相近为 Deevey-Ⅱ型，中高潮位植株死亡率在低龄级阶段高，在高龄级阶段相对稳定为 Deevey-Ⅲ型；（4）不同潮位海莲种群的生存率和累计死亡率函数平衡点均在幼苗阶段，第Ⅴ龄级后各潮位生存函数曲线的变化幅度变小。因此，不同潮位下海莲的群落特征和种群动态有明显差异。研究结果为该区域红树植物的保护及优化管理提供了重要的基础数据。

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海南岛珠溪河流域农业系统氮素流动特征及其环境效应

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摘　要：本研究基于NUFER（食物链养分流动）模型，量化了珠溪河流域1990—2020年农业系统的氮素流动特征及其环境排放强度。结果显示，与1990年相比，2020年环境氮排放增加了1.9倍，其中化肥和饲料是农业系统氮素的最大来源；1990年以来，水产养殖氮素排放对水环境污染的贡献由0.84×10^{-3} Gg增加至0.35 Gg，作物种植系统对水体总氮素的贡献最大，气体和淋溶是其氮排放的主要方式，畜禽养殖系统是向水体排放氮素的第二贡献者；从空间看，淋溶损失主要集中在流域下游与西部区域。因此，做好有机肥替代化肥和畜禽粪便处理，规范水产养殖方式和提高尾水处理技术，这是珠溪河流域减少氮素排放的关键。本研究有助于量化小流域农业系统氮素流动特征与来源，指导农业管理及水环境治理。

关键词：氮素流动；珠溪河流域；模型；农业系统；环境效应

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氮素投入是保障农业系统产量的基本手段[1]，自上世纪60年代以来，全球氮素化肥投入翻了两番[2]。我国作为农业大国，随着不断增长的粮食需求，化肥投入量也是长年居高不下[3]。然而，农业生产过程中较低的氮素利用效率，导致过量的氮素被排放到环境中，引发一系列农业面源污染问题，严重威胁当地生态环境安全，制约农业生产的可持续发展[4]。与此同时，随着公众生活水平的不断提高，膳食结构发生了巨大的变化，对肉蛋奶等的需求量激增[5]。我国畜牧业和水产养殖业得到迅速发展，规模化比例日益增加，畜禽粪污[6]及水产养殖废水直排[7]等农业活动引发的环境污染问题不容小觑。

小流域作为重要的生态子系统，主要受到具有随机性、复杂性、污染范围难以确定等特点的农业面源污染的影响[8]。目前，许多小流域氮污染严重，水体富营养化问题突出[9-12]。

其污染的发生不仅受到降雨、地质条件、气候变化等因素影响，还受到人类活动的干扰，包括：过度施肥、污水直排等[13]。海南岛作为具有数十个入海小流域且地理独立的岛屿，陆地生态系统的缓冲能力颇为有限，人类活动造成的氮素过量排放容易对其近海环境及生态系统造成不利影响。

NUFER模型作为定量国家和区域尺度食物链和农牧系统的氮磷流量、利用效率及环境损失的工具，在分析国家和市县尺度氮磷损失热点[13-14]、中国粮食生产氮素利用效率[15]、中国食品氮足迹[16]、京津冀地区农牧生产[17]、洱海作物种植及畜牧业氮磷流失定量分析[18]及海南岛食物链及水产养殖系统的氮素流动特征[19]等方面发挥了重要作用。但由于缺乏可靠的历史数据及定量工具，多数研究主要聚焦于区域及国

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海口市常见榕属植物 BVOCs 排放特征及与环境因素相关性

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摘　要：植物挥发性有机化合物（biogenic volatile organic compounds，BVOCs）是生物圈与大气之间的重要纽带，对大气化学、臭氧形成和二次有机气溶胶形成起着至关重要的作用。城市森林公园和绿化植物产生的挥发性排放物会对当地和区域空气质量产生重大影响。本研究选取了海口种植率较高的 2 种常见榕属植物，采用动态顶空套袋采集法和气质联用仪的鉴定分析，测量印度榕和高山榕的 BVOCs 排放量，并探讨其 BVOCs 的化学组分和排放特征。同时，试验持续监测环境因子[温度（T）、光合有效辐射（PAR）]和生理参数[气孔导度（G_s）、胞间二氧化碳浓度（C_i）、蒸腾速率（T_r）]，进一步分析榕属 BVOCs 排放的驱动因素。结果表明：印度榕和高山榕分别鉴定出 19 种和 12 种化合物，榕属植物 BVOCs 的排放以异戊二烯和萜类化合物为主，其中印度榕异戊二烯在雨季排放相对含量比旱季增大 1.82 倍，可见印度榕具有较大的异戊二烯排放潜力。萜烯化合物中的α-蒎烯、石竹烯贡献度较大。榕属 BVOCs 日变化呈现“早晚低、中午高”的单峰排放模式，BVOCs 排放量最大出现在中午 12：00 或 14：00 温度的或光合有效辐射最高的时刻。在雨季榕属 BVOCs 排放量显著高于旱季排放量。此外，榕属 BVOCs 排放量与环境因素的相关性具有一致性，与温度、光合有效辐射呈正相关，与其自身的生理参数蒸腾速率、气孔导度均呈正相关，与胞间 CO_2 浓度呈负相关。本研究拓展了热带榕属植物 BVOCs 排放特征的研究领域，为丰富热带和亚热带区域植物 BVOCs 排放清单数据库及其环境效应评估提供基础数据。

关键词：植物挥发性有机物；异戊二烯；单萜；环境因素；生理参数

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Characteristics of BVOCs Emissions from Common *Ficus* spp. in Haikou City and Correlation with Environmental Factor

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Abstract: Biogenic volatile organic compounds (BVOCs) serve as a critical link between the biosphere and the atmosphere, playing a vital role in atmospheric chemistry, ozone formation, and the creation of secondary organic aerosols. Volatile emissions from urban forest parks and greenery can have a significant impact on local and regional air quality. In this study, two common *Ficus* spp. plants with a high planting rate in Haikou were selected, and the BVOCs emissions of *F. elastica* and *F. altissima* were measured using the dynamic headspace bagging collection method and identification and analysis by gas chromatograph. The chemical components and emission characteristics of the BVOCs were also investigated. Meanwhile, the experiment continuously monitored environmental factors [temperature (T), photosynthetically active radiation (PAR)] and physiological parameters [stomatal conductance (G_s), intercellular CO_2 con-

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Zhang Z,Li Y Q, Li K Y,Ren M X.Highway traffic accessibility analysis for National Park of Hainan Tropical Rainforest.National Park,2024,2(7):447-455.

海南热带雨林国家公园公路交通可达性

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摘要:海南热带雨林国家公园是我国首批设立的国家公园之一,科学合理的交通规划是国家公园生态旅游、环境教育及社区发展的有力保障。以海口和三亚到海南热带雨林国家公园各乡镇或区域的公路交通线路为研究对象,采用 ArcGIS 10.8 对其公路交通可达性进行量化。主要结果如下:三亚与海南热带雨林国家公园各主要乡镇及各区域的公路交通平均旅行时间均显著低于海口;国家公园内公路交通可达性系数较高的乡镇主要分布在高速公路两侧,交通平均旅游时间及可达性系数较低,交通便利性较好;国家公园内不同区域公路交通可达性系数上,鹦哥岭区域、五指山区域、毛瑞区域、黎母山区域可达性系数小于 1,表明这些区域较尖峰岭区域、吊罗山区域和霸王岭区域具有更好的交通可达性。研究结果可以为海南热带雨林国家公园公路道路规划提供参考和本底资料。

关键词:海南热带雨林国家公园;交通可达性;交通规划

Highway traffic accessibility analysis for National Park of Hainan Tropical Rainforest

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Abstract: National Park of Hainan Tropical Rainforest is one of the first national parks established in China. Scientific and rational transportation planning is a powerful guarantee for ecotourism, environmental education and community development in national parks. Focusing on the highway transportation routes from Haikou and Sanya cities to the main towns or areas within National Park of Hainan Tropical Rainforest, this study quantifies the transportation accessibility of the main towns or areas within the park using ArcGIS 10.8. The main results are as follows: The average travel times from Sanya to the main towns and areas within National Park of Hainan Tropical Rainforest are all significantly shorter than those from Haikou; the towns with higher highway transportation accessibility coefficients within the park are primarily distributed on both sides of the highways; shorter average travel times and lower accessibility coefficients indicate more convenient transportation. The highway transportation accessibility coefficient varies among areas within the national park. Yinggeling, Wuzhishan, Maorui, and Limushan areas exhibit accessibility coefficients less than 1, indicating better transportation accessibility compared to Jianfengling, Diaoluoshan, and Bawangling areas. The results of this study can provide reference and basic data for road planning in National Park of Hainan Tropical Rainforest.

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加拿大省域林业入侵物种管理策略与经验启示*

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摘要: 随着全球环境变化和人类活动的加剧,入侵物种的传播速度快速提高,对森林健康和林业可持续发展造成严重影响。加拿大作为全球森林覆盖率最高的国家之一,在林业入侵生物管理方面积累了丰富的经验。文中以加拿大不列颠哥伦比亚省为例,梳理该省林业生物入侵现状,总结其政策法规、管理架构、决策框架以及投入保障等方面的实践与成效,提出了利益相关方的有效参与、数据共享的机制建立、受损生境的及时修复、气候变化的战略应对等启示,以期为我国的林业入侵物种管理提供有益的借鉴和参考。

关键词: 外来入侵物种,森林健康,防控措施,加拿大

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Provincial Management Strategies of Forestry-related Invasive Species in Canada and Their Insights

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Abstract: With the changing global environment and increasing human activities, invasive species take increasingly rapid pace in spreading, which has caused a serious impact on forest health and sustainable forest development. As one of the countries with the highest forest coverage in the world, Canada has accumulated rich experience in managing forestry-related invasive organisms. Taking British Columbia as an example, this paper examines the current situation of forestry biological invasion in the province and summarizes the practices and effectiveness of its policies and regulations, management structure, decision-making framework and resource allocation. Additionally, it offers insights over the effective participation of stakeholders, the establishment of data-sharing mechanisms, the timely restoration of damaged habitats, and strategic responses to climate change. These insights aim to provide valuable references for managing forestry-related invasive species in China.

Keywords: invasive alien species, forest health, prevention and control measure, Canada

随着全球化进程,入侵物种的扩散速度明显加快,导致生态系统退化、生物多样性丧失以及经济损失加剧。联合国生物多样性和生态系统服务政府间科学政策平台(Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, IPBES)发布的报告显示,目前已有超过 3.7 万种外来物种通过人类活动被引入到世界各地的生物群落中,其中外来入侵物种约 3 500 种[1]。全球入侵物种经济成本数据库(Invasive Species Global Economic Cost Database, InvaCost)显示,1970—2017 年生物入侵给全球带来的经济损失累计约 1.288 万亿美元(约合 9.27 万亿元人民币)[2]。我国林业生物入侵成本合计金额高达 981.2 亿美元(约合 6 627.71 亿元人民币),占全球支出的 54.05%,在数据库中排名第 1[3]。由此可见,我国已成为遭受外来入侵物种影响最为严重的国家之一。

加拿大拥有约 3.67 亿 hm^2 森林,占全球森林面积

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木棉稻田农林复合系统传统技艺对当代热带特色高效农业创新模式的启示

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摘　要：热带特色高效农业是海南省的重点主导产业。结合海南省特色种质资源和传统农业文化，打造具有海南特色和优势的特色高效农业创新模式对于发展海南省热带特色高效农业具有积极意义。本研究针对广泛分布在海南省的“木棉稻田农林复合系统”，系统总结了木棉稻田农林复合系统的传统农业文化与农耕技艺、种质资源、稻米与木棉产品品质与产量等，探讨了木棉稻田农林复合系统传统技艺的传承与利用、优质高产技术研发及其对发展当代热带特色高效农业的路径与模式，提出4个建议：（1）深入研究木棉农田生态系统资源循环过程与生态学基础；（2）充分利用传统稻种等不可替代的种质资源，打造“木棉稻米”等品牌；（3）挖掘和宣传传统农耕技艺及其科技原理，通过申报中国重要农业文化遗产等途径提高稻米和木棉花等农产品的文化与经济附加值；（4）系统打造农业、文化、生态、旅游及自然教育融合发展模式。

关键词：木棉文化；传统农耕技艺；生态农业；乡村振兴
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巫惠玲，向文倩，陈元君，等. 木棉稻田农林复合系统传统技艺对当代热带特色高效农业创新模式的启示 [J]. 热带生物学报，2024，15(6)：801-812. doi：10.15886/j.cnki.rdswxb.20240107

木棉（*Bombax ceiba* Linn.）是全球热带与亚热带地区常见高大乔木，树姿挺拔、花大可食、果实纤维可织，很早就为人们所认识和利用，在全球范围形成了丰富的资源利用方式与文化[1]，并成为中国岭南和西南干热山区以及越南、印度、缅甸等地的“文化关键种”[2-3]。在中国海南岛、广西西南部以及云南南部等地，越南、印度东北部、缅甸、孟加拉国等传统水稻种植区，木棉常被保留和补充栽种在稻田间，或在田边形成了“风水林”（图1）。木棉和稻田形成的这种“木棉稻田农林复合系统”立体种植模式，既能在收获稻米的同时收获用于纺织的木棉棉絮和可以食用的木棉花，又可能通过木棉树或“风水林”提高农田生态系统的稳定性和资源循环利用效率[1,4]。

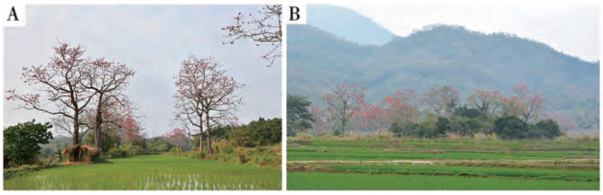

图1　典型的木棉稻田农林复合系统（A）和木棉“风水林”（B）

Fig. 1　Typical kapok-rice agroforestry system（A）and "Fengshui forest" dominated by kapok trees（B）

木棉稻田农林复合系统主要分布区靠近人类驯化栽培稻的早期起源中心，即珠江流域、长江中下游平原及印度东北部等[5-6]。因此，木棉稻田农林复合系统可能是一种较早出现的传统农耕模式，保存着很多古老珍稀的地方稻种[1]。木棉稻田

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木棉稻田农林复合系统中丰富类和稀有类微生物的分布特征及影响因素

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摘　要： 土壤微生物在农田生态系统功能方面发挥重要作用。然而，土壤微生物，特别是丰富类和稀有类微生物在农林复合系统中的分布规律还知之甚少。木棉稻田农林复合系统是长期保留在热带地区的一种传统农耕系统。本研究以海南省昌江县木棉（*Bombax Ceiba*）稻田农林复合系统为研究体系，分析与木棉树不同距离梯度上的稻田土壤中丰富类、稀有类细菌和真菌群落的分布特征及其与土壤因子的关系。结果表明：1）稀有类细菌的丰富度在靠近木棉的地方显著较高，而丰富类细菌和真菌的Shannon指数在靠近木棉的地方显著较低（$P<0.05$）；2）稀有类和丰富类细菌和真菌的群落组成在与木棉树的不同距离梯度上均存在显著差异（ANOSIM：$P=0.0001$）；3）丰富类细菌α多样性与速效钾呈显著负相关，而稀有类细菌α多样性与总磷和有机质呈显著正相关；丰富类真菌α多样性与土壤因子无显著相关性，但稀有类真菌α多样性与土壤速效氮、速效磷和有机质呈显著正相关；土壤速效养分是丰富类细菌和真菌群落结构变异的关键驱动因子，而稀有类细菌和真菌群落结构变异的关键驱动因子不仅包括土壤速效养分，还包括有机质；总体而言，速效钾是影响丰富类和稀有类微生物空间分布的最重要因素。本研究揭示了木棉对稻田各土壤微生物类群分布特征及其主要驱动因子的影响，为木棉稻田农林复合系统在农业可持续发展中的应用提供理论支撑。

关键词： 丰富和稀有类微生物；空间分布；农林复合系统；土壤理化

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土壤微生物作为生态系统中的重要分解者，在全球生物地球化学循环中发挥着不可替代的作用[1-3]。微生物群落通常由少量高丰度分类群，即丰富类（abundant taxa）和大量低丰度分类群，即稀有类（rare taxa）组成，二者在生态系统功能作用的发挥中均起着关键性作用[4-6]。丰富类微生物在生态系统碳循环、土壤有机物质分解和养分固定等方面都发挥着重要作用，并具有更广泛的环境适应性[7-9]。而稀有类可以快速响应环境变化，有着维持菌群和生态系统功能稳定性的作用，并且是微生物α和β多样性的重要贡献者[4, 6, 10]。研究丰富类和稀有类微生物的分布特征和影响因素对认识生态系统功能具有重要意义。目前，对丰富类和稀有类微生物分布格局的研究多集中在水生生态系统等自然生态系统中[11-12]，而对农田特别是农林复合系统中的丰富类和稀有类微生物空间分布和影响因素知之甚少。

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