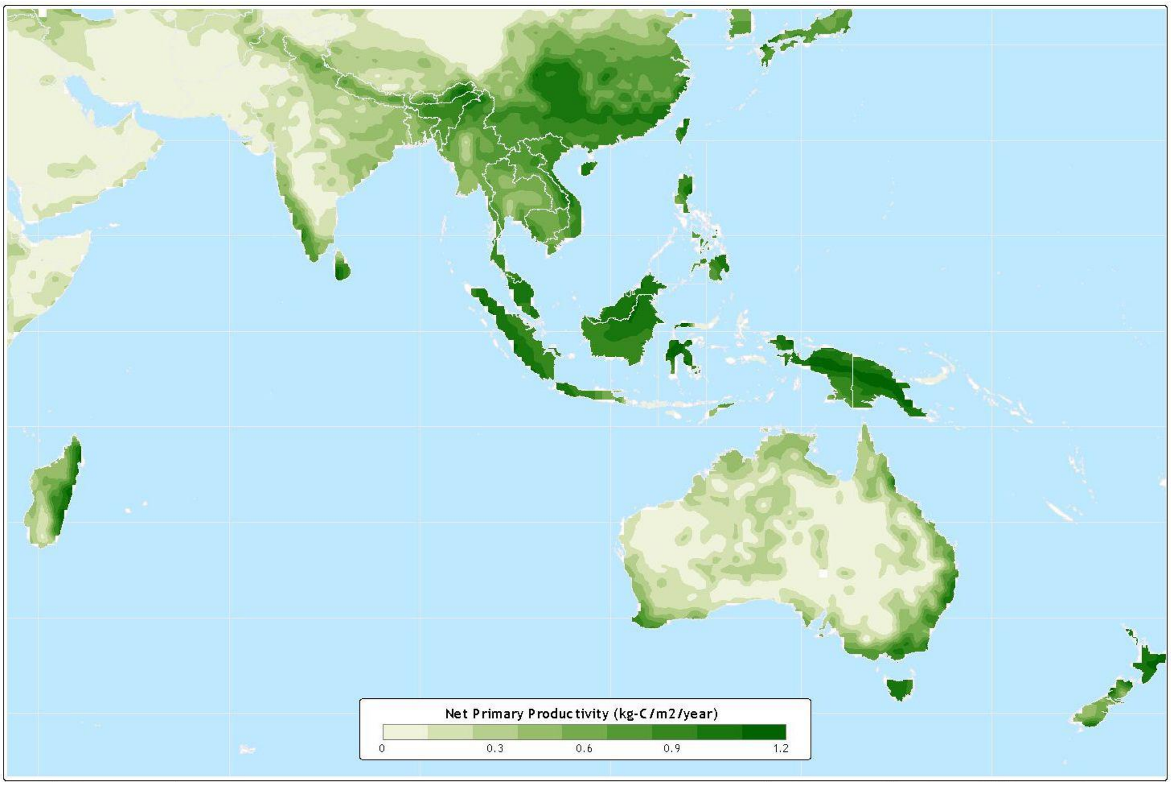
中国科协海智计划海南(海南大学)工作基地

海南大学环南海陆域生物多样性研究中心

2020 年报

Annual Report 2020



海南大学
HAINAN UNIVERSITY

第三届中国生态文明大讲坛在海南大学召开

2020 年 11 月 26 日，由中国生态学学会和海南大学主办、工作基地协助承办的“第三届中国生态文明大讲坛”在海南大学顺利举行。

本届生态文明大讲坛以海南大学为主会场，同时还在海南三亚、广西、云南、浙江、重庆等地开设了分会场，多方参与、多地联动，讲坛活动形式多样。

主会场在海南大学副校长陈险峰教授主持下举行了隆重的开幕式，中国生态学学会钟林生秘书长、海南大学骆清铭校长代表主办方致辞。随后，三位特邀专家发表了特邀报告：中国林业科学研究院刘世荣院长做了“基于自然的气候变化解决方案：森林减缓与适应”的报告，对气候变化的影响与基于自然的气候变化解决方案进行了清晰的讲解。海南大学杨小波教授的“我们与保护地的生态环境——以海南人与热带雨林国家公园为例”报告风趣幽默地详细介绍了海南热带雨林的物种多样性及保育现状。中国科学院动物研究所魏辅文院士在线分享了“生态文明与生物多样性保护”报告，从宏观的角度阐述了生态文明的内涵与生物多样性保护的关系。大讲坛开幕式及科普报告还首次通过中国生态学学会直播间对公众进行直播。

工作基地负责人任明迅教授全程参与了大讲坛，并曾参加了前两届大讲坛，积极争取和参与组织第三届中国生态文明大讲坛主会场在海南大学召开。本届大讲坛期间，任明迅教授还与全国大学生绿色营创始人唐锡阳先生(国家环保总局特聘环境使者) 、中国生态学学会理事兼科普工作委员会常务副主任唐建军教授、中国生态学学会常务理事/全国大学生绿色营理事长李振基教授等专家一起，专程奔赴三亚七加自然学校，举办了三亚分会场；并为海南大学生态与环境学院生态科普教育基地、绿色营海南小组举行了揭牌暨成立仪式。

目录

封面图片：环南海区域及周边地区的净初级生产力（制图：美国威斯康辛大学麦迪逊分校可持续与全球环境研究中心）。

《海南自贸区（港）背景下热带雨林保护与国家公园建设》国际交流会在海南海口隆重召开

2019 年 12 月 27 日至 28 日，海南省科协主办、工作基地/研究中心承办的“海南自贸区（港）背景下热带雨林保护与国家公园建设国际交流会”在海口召开。来自美国、日本、菲律宾、老挝、中国台湾、中国香港及内地学者共约 20 人参加了本次研讨会。

美国加利福尼亚大学河滨分校的李百炼教授（美国人类生态研究院院士、美国科学促进会会士、俄罗斯科学院外籍院士、中国科协海智专家）、菲律宾大学 Pastor L. Malabrigo 副教授、老挝国立大学 Soulichan 博士、日本东京大学陈元君博士、中国台湾地区陈健民教授和谢宗宇总经理、北京师范大学国家公园研究院院长张希武研究员（原国家林业局野生动植物保护司长）、中国科学院生态环境研究中心徐卫华研究员等人参会并作了精彩报告。

海南省科学技术协会党组书记胡月明副主席、海南省林业局党委书记夏斐局长、周亚东总工程师、海南省发展和改革委员会高佃恭处长、海南大学叶光亮副校长、生态与环境学院王旭副院长（主持工作）、海南大学林学院院长宋希强教授等人参加了开幕式和交流会。

谭正洪教授和任明迅教授分别在会上报告了工作基地在海南热带雨林国家公园的生态系统生产力、中线高速公路的可能影响与对策等方面的研究进展，并提出了生态服务功能优化与提升策略、生态廊道建设与长期监测的建议。

与会专家就体制机制创新促进海南热带雨林国家公园建设方面提出了建议书。

一、中心概况

海南大学环南海陆域生物多样性研究中心于 2017 年 7 月正式成立，同年 11 月受海南省科学技术协会资助，成为海南大学首家“海外智力为国服务行动计划”工作站。2020 年 6 月，在整合海南大学相关学科引进的海智专家与骨干教师的基础上，成为中国科学技术协会海智计划海南（海南大学）工作基地。现任学术委员会主任李百炼教授（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（海南大学生态与环境学院）。

中国科学技术协会海智计划海南（海南大学）工作基地和海南大学环南海陆域生物多样性研究中心实行“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，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，力争成为环南海生物多样性与生态文化研究中心、区域合作与交流中心。

目前设置三个研究方向：（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。

已与美国加州大学河滨分校、美国佛罗里达国际大学、日本东京大学以及环南海地区的新加坡南洋理工大学、新加坡国立大学、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、菲律宾邦板牙国立农业大学、越南 Ton Duc Thang 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。

3 年以来，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 2500 份（含植物活体、腊叶标本、DNA、种子等）。

在中国科协、海南省科协和海南大学的指导与支持下，工作基地/研究中心大力开展海外智力为国服务行动计划，积极引进美国、日本、新加坡等地知名华裔学者与当地专家，开展聚焦海南省和环南海区域生态环境、生物多样性领域的合作研究与人才培养。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
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
邹乐明 Chou Loke Ming	新加坡（华裔）	新加坡国立大学	珊瑚礁生态
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
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
Vu Van Lien	越南（非华裔）	越南国家自然博物馆	生态环境
Wattana Tanming	泰国（非华裔）	泰国清迈诗丽皇后植物园	热带植物多样性护
Erizal Sodikin	印尼（非华裔）	印尼 Sriwijaya 大学	热带农业资源

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）工作基地和海南大学环南海陆域生物多样性研究中心，以海南大学近五年引进的生态学与生物学专业青年人才为骨干，联合和引进海内外高端智力，聚焦海南省与环南海区域的生物多样性与生态资源、区域生态安全与生态系统服务功能优化与提升、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、国家生态文明试验区（海南）、中国特色自由贸易港建设。

（一）生物多样性与生态保育

主要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、能源植物、药用植物、观赏花木等的发掘、引种与基础生物学研究。针对海南岛热带雨林、淡水湿地、珊瑚礁、红树林与城市关键海岸带等，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

针对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”关键节点等特点，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，为海南省的国家公园、国家生态文明试验区、国家重大战略服务保障区等建设保驾护航。

（三）传统生态文化与当代生态文明建设

发掘海南省及环南海区域的优秀生态文化，特别是入选国家级文化遗产与非物质文化遗产如洋浦千年古盐田晒盐技艺、山兰稻作文化以及海南特有的木棉-梯田耕作体系等，从现代科学理论与技术角度，揭示其生物学基础与生态学原理。同时，探索传统生态文化的现存价值及其在现代社会中的传承途径，积极开展自然教育与科普宣讲，提升海南地方民族及中华民族的民族自信、文化自信，实现“把论文写在海南大地上”，切实参与国家生态文明试验区（海南）建设。

三、大事记

➢ 中国科协海智计划海南（海南大学）工作基地正式挂牌

2020 年 6 月，主要依托我中心申报的中国科协海外智力为国服务行动计划（简称“海智计划”）海南（海南大学）工作基地正式获批建设。工作基地聚焦海南岛、粤港澳大湾区和环南海区域的生物多样性与生态安全等重大课题，引进海外华裔学者和外籍人士服务国家生态文明试验区（海南）、海南热带雨林国家公园以及海南自贸港建设，从粤港澳大湾区和环南海区域的科教合作与交流角度，积极践行“一带一路”倡议。

2020 年 10 月 27 日，中国科协书记处宋军书记、中国科协国际联络部刘阳部长等人一行在海南省科协有关领导的陪同下，对工作基地进行了现场调研，并举行了揭牌仪式。海南大学武耀廷书记出席了调研活动和揭牌仪式，工作基地负责人任明迅教授汇报了工作基地的建设现状与发展规划。宋军书记和武耀廷书记对工作基地汇聚海外智力、服务海南地方社会经济做出的贡献给予了高度肯定，并鼓励工作基地继续在基础较好的生态环境与生命健康领域做出更大的贡献。

➢ 新加坡科学院院士 Chou Loke Ming 院士创新团队建立

2020 年 8 月，海南大学生态与环境学院依托工作基地成功引进了新加坡科学院院士 Chou Loke Ming（邹乐明），在海南大学成立了院士创新团队。

邹乐明院士主要研究珊瑚礁生态与珊瑚虫生态毒理学研究，在海洋生态与环境保护方面有着很高的知名度。Chou Loke Ming 院士创新团队与工作基地前期引进的海南省李百炼院士工作站一起，形成了聚焦环南海区域生态环境研究的海陆联动的海智“双核”。

➢ 积极参与海南大学“一院一校”国际化办学计划

依托工作基地/研究中心的国际合作研究基础，海南大学生态与环境学院成功获批 2 项海南大学“一院一校”国际化办学计划，分别是：战略合作伙伴项目（新加坡国立大学）、高端外专引智项目（新加坡南洋理工大学）。这使得我院和生态学科成为我校唯一同时获批两项“一院一校”项目的学院和学科。

此外，工作基地/研究中心和菲律宾大学筹建的环南海陆域生物多样性研究中心也进入了学校的国际联合科研平台培养项目库，将经过 1 年的合作研究与联合培养学生，积极申报中国科协“一带一路”国际科技组织合作平台建设项目。

➢ 全程参与海南热带雨林国家公园体制机制建设巡查与调研

2020 年 7-8 月，工作基地/研究中心负责人任明迅教授、骨干成员杜彦君博士受邀参加了由世界自然保护联盟物种生存委员会执委解焱副教授、北京师范大学国家公园研究院院长张希武教授（原国家林业局野生动植物保护与自然保护区管理司司长）带队的海南热带雨林国家公园体制机制建设巡查活动，全程参与了鹦哥岭、五指山、吊罗山等地的实地调研，并与海南省林业局举行了座谈会。

➢ 海南热带雨林国家公园综合科考与迎评报告顺利完成

工作基地/研究中心骨干成员杨小波教授主持、任明迅教授等多位成员参与的海南省林业局专项《海南热带雨林国家公园综合科考（植物部分）》项目（总经费 298 万元），通过近 1 年的数据整理、野外补充调查及系统研究，于 12 月 21 日顺利通过结题。该项目对国家公园内的主要生态系统类型、珍稀保护植物、古树名木、特有植物、海南长臂猿食源植物、野生观赏植物、有害及入侵植物和农业生物多样性等重要植物类群开展了分类调查与综合研究。这项工作摸清了海南热带雨林国家公园生态系统、植被类型及各类植物资源本底，对进一步开展该热带雨林国家公园生物多样性保护与生态功能优化与提升具有积极的促进作用。

参与了海南热带雨林国家公园自然禀赋及试点成效评估的调研工作，承担了成效评估及生态系统代表性与面积适宜性子项目（HD-KYH-2020125-2）、结构完整性和功能完整性子项目（HD-KYH-2020125-8）的编写工作，在短短 1 个月的时间，收集了近 100 多篇文献、整理了大量第一手资料，撰写了近 10 万字的文字材料，保障了海南热带雨林国家公园迎评工作的顺利通过。

➢ 《国家生态文明试验区（海南）背景下热带雨林国家公园体制机制创新研究》获批立项

受中国工程科技发展战略海南研究院资助，工作基地/研究中心引进的李百炼教授和任明迅教授联合牵头申报获批了 1 项咨询研究项目：《国家生态文明试验区（海南）背景下热带雨林国家公园体制机制创新研究》。该项目资助经费 58 万元、执行期 1 年（2020-2021），将从国家公园科学研究、海南生态文化挖掘、高校及高校演习林方式参与国家公园建设等方面探索海南热带雨林国家公园的体制机制创新。

李百炼教授是工作基地引进的首席“海智专家”，是世界知名的生态学家，主要从事生态规划、人类与城市生态学等方面的研究。李百炼教授在海南省的工作将主要依靠工作基地和院士工作站，围绕海南省及环南海区域生态恢复、生态安全等方面开展深入研究。

➢ 《海南热带雨林国家公园高速公路穿越段的环境监测与生态恢复技术》获批立项

依托工作基地/研究中心建立的海南省李百炼院士工作站于 2020 年 10 月获批了海南省科技厅资助的海南省院士创新平台科研专项（YSPTZX202015）：海南热带雨林国家公园高速公路穿越段的环境监测与生态恢复技术。

该项目执行期 2020-2023 年、经费 50 万元，项目负责人是李百炼和任明迅教授，拟针对海南中线高速公路穿越国家公园的约 40km 路段开展环境监测和道路径流的收集与净化，主要采用人工湿地等技术。该研究有望保障昌化江流域生态安全，优化和提升海南热带雨林国家公园的水源涵养等生态服务功能。

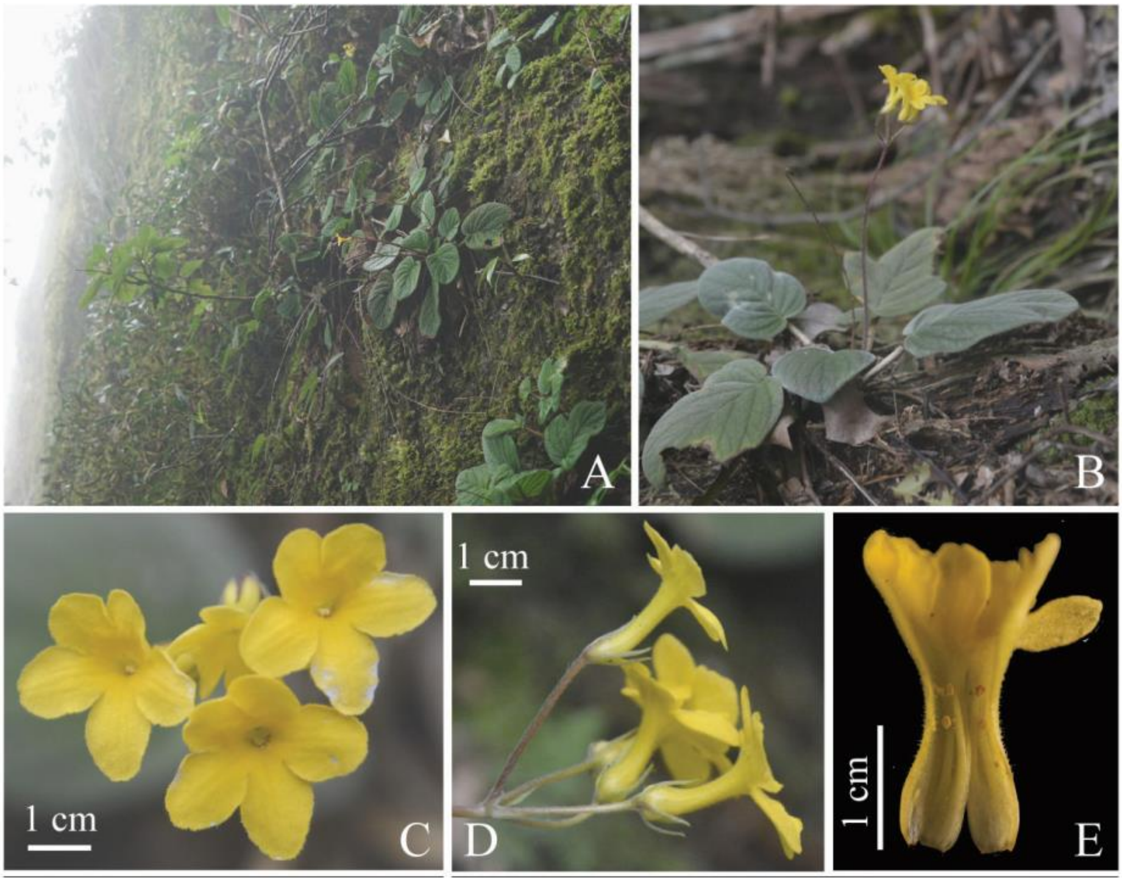
四、代表性成果

➢ 研究方向一：生物多样性与生态保育

工作基地/研究中心骨干成员杨小波教授主持、任明迅教授等多位成员参与的海南省林业局专项《海南热带雨林国家公园综合科考（植物部分）》项目（总经费 298 万元），通过近 1 年的数据整理、野外补充调查及系统研究，摸清了国家公园内的主要生态系统类型、珍稀保护植物、古树名木、特有植物、海南长臂猿食源植物、野生观赏植物、有害及入侵植物和农业生物多样性等各类植物资源本底，对进一步开展该热带雨林国家公园生物多样性保护与生态功能优化与提升具

有积极的促进作用。同时，承担了海南热带雨林国家公园自然禀赋及试点成效评估的调研工作中的成效评估及生态系统代表性与面积适宜性子项目(HD-KYH-2020125-2)、结构完整性和功能完整性子项目(HD-KYH-2020125-8)的编写工作。

先后公开发表植物新种 5 个：海南岛特有的迎春花马铃苣苔(*Oreocharis jasminina* S.J.Ling, F.Wen & M.X. Ren)、云南省特有的弯翅风筝果(*Hiptage incurvatum*)和泸水风筝果(*Hiptage lushuiensis*)、重庆特有的正宇梅花草(*Parnassia zhengyuana*)和四面山梅花草(*P. simianshanensis*)。尤其是海南岛高山云雾林中发现的新种“迎春花马铃苣苔”，具有鲜艳的黄色花瓣、辐射对称的花冠、管状的花冠筒，进化地位特殊、具有较高的园艺引种价值，是海南岛热带雨林原真性的一个生动证据(PhytoKeys, 2020, 157: 121–135; PhytoKeys, 2020, 135: 91–104)。



海南热带雨林国家公园特有的迎春花马铃苣苔(PhytoKeys 2020, 157: 121–135)

通过植物进化稳定繁殖对策和数学模型，提出了植物同株异花受精可能存在主动适应意义的新假说：自交的胚珠可能在植株水平受到选择性流产，从而降低了植物同株异花受精的代价。这一理论假说能够解释两性花植株同株异花受精现象的普遍存在，已发表在《American Journal of Botany》（2020, 107（3）: 1-4）。

在我国特有的苦苣苔科植物长冠苣苔(*Rhabdothamnopsis sinensis*)中发现了一种新型的镜像花(Flora, 2020, 272: 151694)。该植物的花冠筒底部在不同的花中发生了向左或向右的弯折，导致花柱向右或向左斜靠在花冠筒内壁；而着生于花冠上的两个可育雄蕊的花丝扭曲，偏向于花柱的另一侧，形成了互补镜像花。

迄今为止，从环南海区域采集的战略植物资源（热带作物野生近缘种、药用植物、油料植物、观赏植物、亚洲热带植被建群种等）共有秋苦苣苔科、金虎尾科、木棉科、梅花草属、海棠科、兰科、唇形科、旋花科、风毛菊属以及苔藓植物腊叶标本约近 2000 份、DNA 种质资源近 2500 份。

- **研究方向二：环南海区域生态安全**

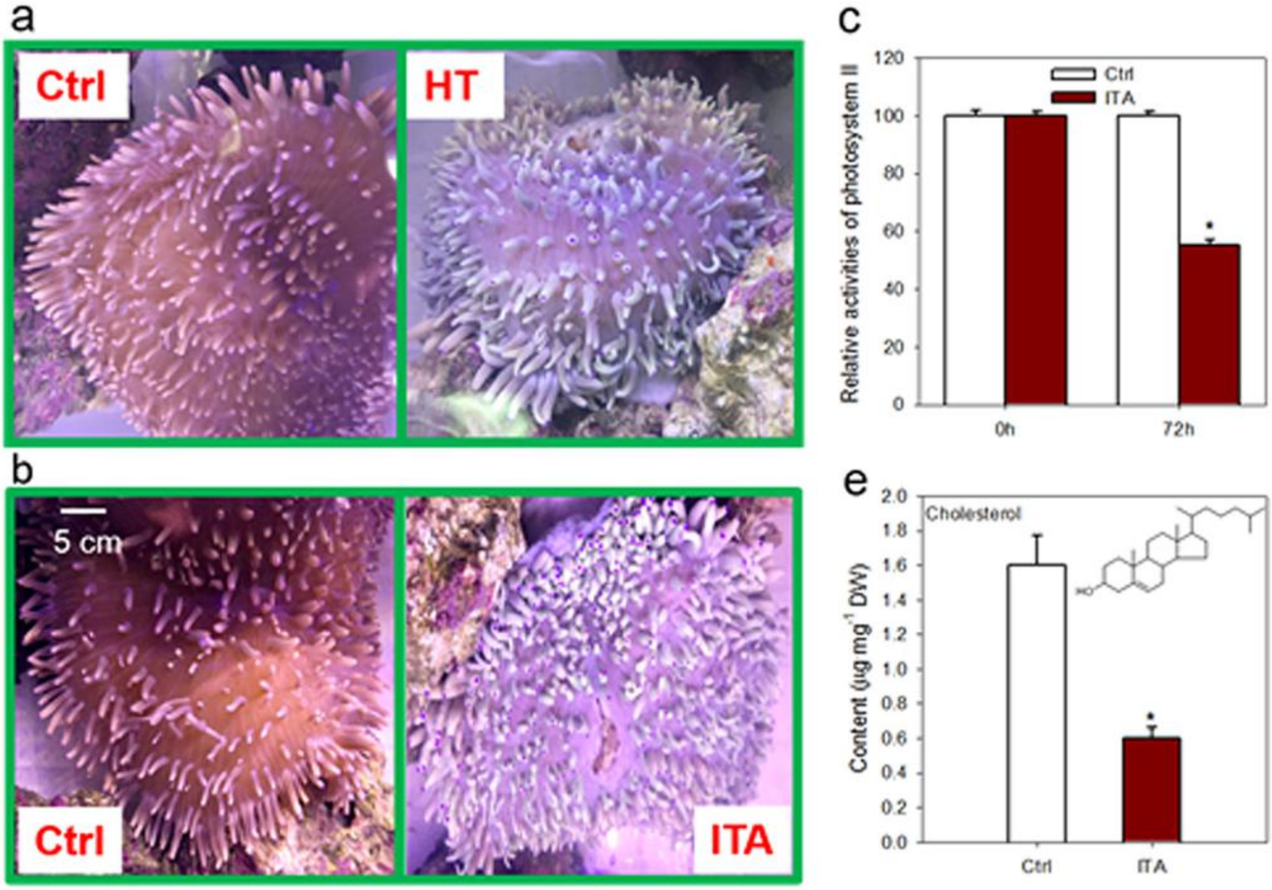
牵头组建了海南省发展和改革委员会批准的《海南省热带生态环境修复工程研究中心》，并于 2020 年 11 月举行了第一届学术委员会成立会议暨第一届学术研讨会。中国科学院水生生物研究所吴振斌研究员、中国科学院武汉植物园江明喜研究员、厦门大学李杨帆教授、东北师范大学卜兆君教授、海南省环境科学研究员杨安富高级工程师等人受邀担任学术委员会委员并出席了会议，美国加利福尼亚大学河滨分校的李百炼教授担任学术委员会主席，并在线参加了会议。

海南省热带生态环境修复工程研究中心主要依托海南大学生态与环境学院，将围绕自然生态系统保育、退化生态系统恢复、污染防控与环境修复等三大领域

开展科技研发与工程实践，服务国家生态文明试验区（海南）建设。

引进了珊瑚生态学家邹乐明院士创新团队与工作基地/研究中心骨干人员赵洪伟副教授一起开展了深入合作，从海洋生态修复方向开展珊瑚礁与海草床的修复研究。2020 年 11 月，在海南大学“一院一校”项目的支持下，邹乐明院士及其团队成员与我校刁晓平教授、李秀保教授、赵洪伟副教授等人召开了《人类活动影响下的珊瑚礁研究和管理》线上研讨会。

针对珊瑚礁“白化”现象（污染等胁迫使得珊瑚虫及共生藻类死亡，导致珊瑚礁漂白的现象），发现了海葵及其共生藻类的甲藻甾醇的生物合成途径类似于高等动物与植物、环境胁迫对甲藻甾醇生物合成的特异性干扰可损害健康珊瑚礁的共生关系(mSystems, 2020, 5: e00765-20)。



珊瑚礁白化对海葵及共生体甾醇代谢途径的影响(mSystems, 2020, 5: e00765-20)

工作基地/研究中心参与了日本东京大学牵头的日本学术振兴会资助的 C2C 项目《亚洲森林长期监测研究》，任明迅教授代表海南大学合作方做了大会报告，与马来西亚、印尼、斯里兰卡、中国台湾等地专家探讨了亚洲森林生态系统合作研究等。

2020 年 11 月，三亚中科遥感研究所与我中心签订合作研究合同，双方就海南省东寨港红树林保护区和五指山国家级自然保护区近年来的历史遥感影像数据及历史调查数据的收集、利用遥感影像进行野外调查实验等方面开展合作。

➢ 研究方向三：传统生态文化与当代生态文明建设

为提升我校在国家生态文明试验区（海南）建设中的作用，培养知悉生态文化、投身生态文明建设的人才，工作基地/研究中心牵头组织了面向儋州校区所有专业师生的《两院学坛》。该学坛每两周一次，以寓教于乐、文理兼容的方式，邀请国内外知名人士和青年才俊开展轻松活泼的交流，宣传科学哲学、自然博物学、海南本土优秀生态文化，通过提升生态学等专业本科生的专业认同感、荣誉感和使命感，提升专业水平和生态文明意识，积极投身于海南生态文明建设。

海南大学《两院学坛》系列学术沙龙

联合中国生态学会、全国大学生绿色营、海南三亚七加自然学校等，以我校生态学专业培养的青年博士为主成立了《绿色营海南小组》。邀请了国务院环保总局“环境使者”唐锡阳先生、中国生态学学会理事兼科普工作委员会常务副主任唐建军教授、中国生态学学会常务理事/全国大学生绿色营理事长李振基教授等人现场指导，提升我校在国家生态文明试验区（海南）建设中的显示度。

目前，工作基地/研究中心聚焦洋浦千年古盐田、昌江木棉-稻田共生系统，开展微生物宏基因组学、特异微生物类群及生态过程、田间生物多样性维持、作物可持续高产等方面的研究。有关研究将有助于解析洋浦盐田晒盐技艺历经千年不衰的生态学基础，对打造国家生态文明试验区“海南样板”具有积极意义。

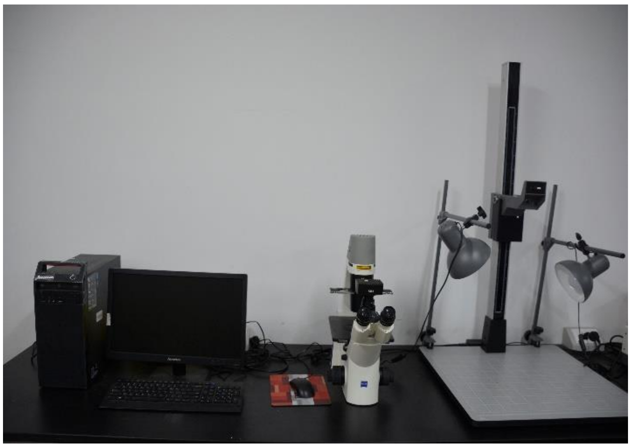
初步研究了海南岛特有的木棉-稻田共生系统的生物学基础与生态学原理，首次指出：海南传统耕作方式在稻田间保留和栽种大量木棉，可能利用了木棉春季开花吸引鸟和天敌昆虫，降低了春季插秧期的田间害虫；木棉根系还可能调节田间土壤微生物等有利于水稻丰产等。这些研究结果可为后续建议海南省昌江县木棉-稻田耕作文化系统申报中国农业文化遗产奠定基础。

海南岛悠久的木棉文化和特有的木棉-稻田共生系统

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. 资源收集与保存

➢ 植物昆虫标本库

➢ 真菌标本库

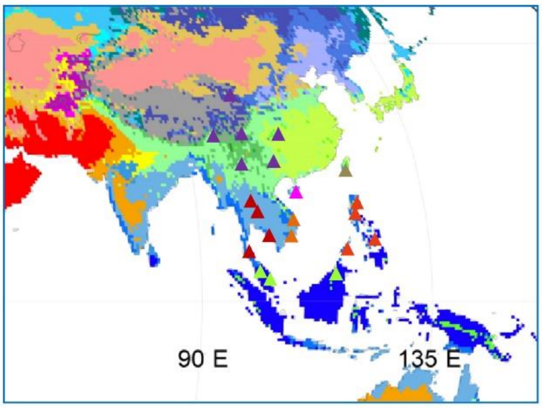
➢ 引种资源圃

➢ 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）

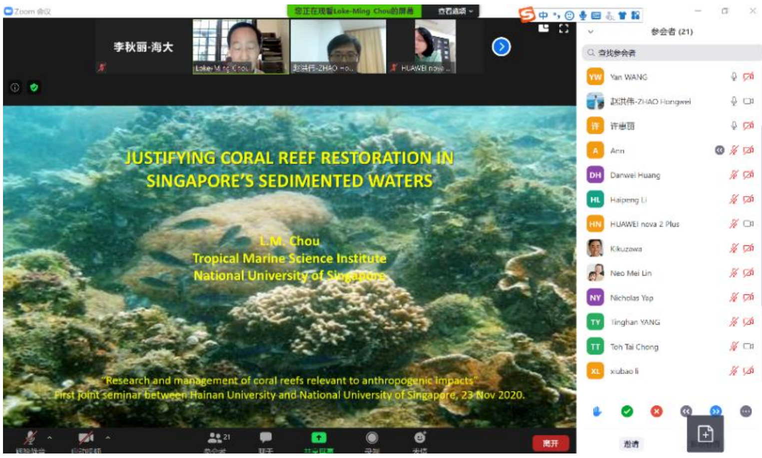
菲律宾（Arayat）

六、合作与交流

- 2020 年 7-8 月，工作基地/研究中心受邀参加了由世界自然保护联盟物种生存委员会执委解焱、北京师范大学国家公园研究院副院长张希武带队的海南热带雨林国家公园建设巡查活动，并与海南省林业局举行了座谈。

- 2020 年 4 月，参加了由海南省环境科学研究院组织的西沙群岛生态环境与植被考察活动。双方还讨论了初步的项目合作方案与人才培养计划。

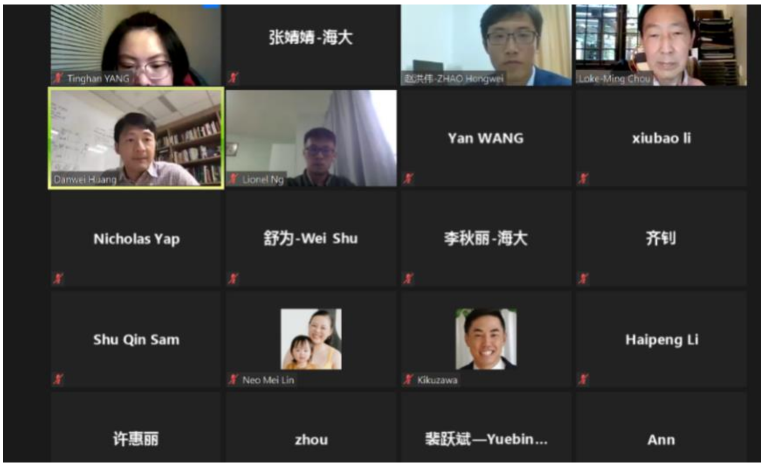
- 2020 年 11 月，参与邀请和组织中国林科院刘世荣研究员、厦门大学王文卿教授、浙江大学唐建军教授等人对我校生态文明学科群“十四五”重大科学问题和工程技术难题选题进行了审议。



JUSTIFYING CORAL REEF RESTORATION IN SINGAPORE'S SEDIMENTED WATERS

L.M. Chou
Tropical Marine Science Institute
National University of Singapore

Research and management of coral reefs relevant to anthropogenic impacts
First joint seminar between Hainan University and National University of Singapore, 23 Nov 2020.



➢ 2020 年 11 月，在海南大学“一院一校”项目的支持下，与新加坡国立大学联合召开了“人类活动影响下的珊瑚礁研究和管理”线上研讨会。来自新加坡国立大学的邹乐明教授、Huang Danwei 教授、Lionel Ng Soon Chin 博士和海南大学刁晓平教授、赵洪伟副教授等以及 30 多位研究生参加研讨会。

➢ 2019 年 11 月，美国加州大学河滨分校李百炼院士、中国台湾民享生态调查公司谢宗宇副总经理等人来访，并与海南省科协研讨了国家公园体制创新咨询。

➢ 2020 年 10 月，张莉娜副教授带队参加了中国野生植物保护协会苔藓植物专业委员会成立大会暨首届学术讨论会，研讨了我国苔藓植物资源保护与研究等。

- ➢ 2020 年 8 月，参加了海南国家公园研究院主办的海南长臂猿保护国际研讨会，参与学习了骆清铭校长的讲话，并同与会专家一起研讨了海南长臂猿保护的社区机制及生态廊道建设建议。

- ➢ 2020 年 10 月 25 日，举办了海南省农林环境过程与生态调控重点实验室学术委员会会议、海南大学生态环境高端论坛。东北农业大学张颖教授、福建农林大学周顺桂教授、浙江大学程磊教授、四川大学刘敏教授等应邀做了精彩报告。骆清铭校长、邹勇华处长以及我院领导参会。

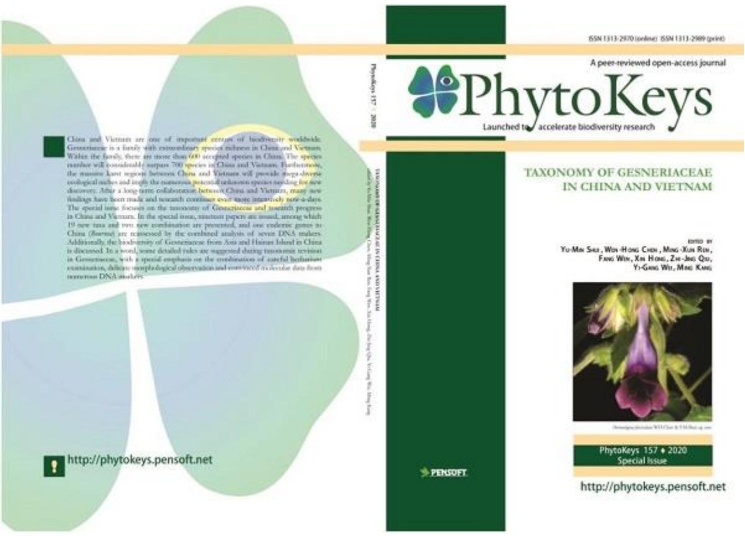
- ➢ 2020 年 12 月，任明迅教授应邀参加了贵州省铜仁市印江县的十四五发展规划座谈会，对当地生态文明建设、生态旅游规划等提供了政策咨询意见。

- 2020 年 9 月 9 日，由海南大学林学院、生态与环境学院共建的热带雨林国家公园研究院（兴隆分院）举行了挂牌仪式。科技处邹勇华处长带队出席了仪式，任明迅教授主持了挂牌仪式。

- 2020 年 11 月，参加了联合国开发计划署和全球环境基金资助的海南农业生物多样性参与式原生境保护和可持续利用项目启动会。

- 2020 年 6 月，为落实琼中县与海南大学签署的战略合作框架协议，琼中县生态环境局向前局长一行 11 人来访，双方开展了调研交流与合作洽谈。

- 2020 年 5 月，组织了我校生态与环境学院和中国热带农业科学院环境与植物保护研究所的学术交流会，讨论了长期环境监测的合作研究与人才联合培养等。



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TAXONOMY OF GESNERIACEAE
IN CHINA AND VIETNAM

EDITED BY
Yu-Min Shui, Wen-Hong Chen, Ming-Xun Ren,
Fang Wen, Xin Hong, Zhi-Jing Qiu,
Yi-Gang Wei, Ming Kang

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- 2020 年 8 月，任明迅教授受邀参与组织了 SCI 期刊 PhytoKeys 专辑正式出版。任明迅教授团队在该专辑发表 1 篇综述、2 篇实验研究论文。

- 2020 年 6 月-7 月，在中国科协海智计划服务科技经济发展助力活动号召下，举办了“传统生态文化助力当代科技进步”活动，邀请了菲律宾大学 Malabrigo 副教授、中国台湾谢宗宇总经理在线交流。

- 2020 年 7 月，参加了海南省环境科学研究院组织的西沙群岛生态环境与植被生态学调研，对西沙群岛主要岛礁的植物多样性、植被现状进行了深入调查和分析。与海南省环科院有关人员讨论了生态修复方面的项目合作意向。

➢ 2020 年 11 月 8 日，海南省热带生态环境修复工程研究中心学术委员会成立暨第一届学术交流会举行。任明迅教授汇报了工程中心的概况，与会专家讨论了研究重点方向的设置。

李百炼院士和东北师范大学卜兆君教授在线参加了会议，并和 3 位现场专家分别做了精彩的学术报告。

➢ 2020 年 9 月 25 日至 26 日，工作基地/研究中心参加了海南省生态环境厅、海南省塑料行业协会主办的第一届海南禁塑论坛召开。骨干成员黄青教授作了《塑料在热带水土环境中的迁移转化行为》报告。

➢ 2020 年 5 月，组织了中国青少年生态环境教育示范课进校园活动（海南站）活动，与国家生态环境部宣传教育中心李原原主任、海南省生态环境厅宣教中心陈强林主任等人进行了深入讨论。

- ➢2020 年 5 月 26 日，应海南三友海洋科技有限公司邀请，工作基地/研究中心访问了三友海洋公司及其生产基地，考察了三友海洋的人工鱼礁生产基地和红树种苗培育基地。

- ➢ 2020 年 10 月 30 日，中国科学院空天信息创新研究院数字地球重点实验室副主任张丽研究员一行来访，双方围绕海南岛生态承载力及生态安全等讨论了合作意愿。

- ➢ 2020 年 11 月 26 日，参加了“第三届中国生态文明大讲坛三亚分论坛”，交流了海南的传统生态文化与当代生态文明建设方式和途径。

- ➢ 2020 年 11 月，开展了与海南三亚七加自然教育学校（生态营地）的合作，依托该营地设立了海南大学生态科普基地，并指导了绿色营海南小组的成立。

- 2020 年 12 月 22 日-23 日，邀请了北京师范大学张全国教授来访，参与了《分子与进化生态学》授课，交流了开展合作研究和研究生联合培养等事宜。

- 2020 年 12 月 7 日-8 日，邀请了东北师范大学卜兆君教授（教育部自然保护与环境生态类教指委委员）来访，参与了 6 学时的《分子与进化生态学》课程授课。

- 2020 年 1 月 3 日-4 日，邀请了北京师范大学张大勇教授来访，为儋州校区生态学本科生和研究生做了为期两天的《进化生态学》的学术报告，并与中国热带农业科学院和海南大学专家座谈。

- 2020 年 1 月，邀请了中国科学院昆明植物研究所星耀武研究员来访，做了《生物地理学研究》的学术报告，并考察了中心实验室和标本库。

➢ 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
环南海区域生物多样性与生态文化	国际会议 （线上）	2020 年 6 月	60
人类活动影响下的珊瑚礁研究和管理	国际会议 （线上）	2020 年 11 月	50
海南自贸区（港）背景下热带雨林保护与国家公园建设国际交流会	国际会议 （海口）	2019 年 12 月	60
第三届中国生态文明大讲坛	全国会议 （海口主会场）	2020 年 11 月	300

➢ 学术报告情况

报告名称	报告人	会议名称	地点	时间
Chiral enantiomers of the plant growth regulator paclobutrazol selectively affect community structure and diversity of soil microorganisms	赵洪伟	美国化学学会 2020 秋季年会网上虚拟会议	线上	2020.08
海南岛森林生态系统与南海生态安全	谭正洪	国际生态岛科学研讨会	上海	2020.07
海南的传统生态文化与当代生态文明建设	任明迅	第三届中国生态文明大讲坛三亚分论坛	三亚	2020.11
南海岛礁生态辐射和能量的平衡	谭正洪	第二届海上新丝路生命生态科学大会	海口	2020.12
亚洲热带植物扩散的“一带一路”	任明迅	第二届海上新丝路生命生态科学大会	海口	2020.12
海南微塑料的环境行为与生态毒理效应	黄青	第二届海上新丝路生命生态科学大会	海口	2020.12
塑料在热带水土环境中的迁移转化行为	黄青	第一届海南禁塑论坛	海口	2020.09

海南省热带生态环境修复工程研究中心概况及发展规划	任明迅	海南省热带生态环境修复工程研究中心学术委员会成立仪式暨第一次学术会议	海口	2020.11
珊瑚-虫黄藻共生体响应扑草净胁迫的分子机制	赵洪伟	海南省热带生态环境修复工程研究中心学术委员会成立仪式暨第一次学术会议	海口	2020.11
海南霸王岭云雾林树附生苔藓植物研究	徐雪艳	首届中国野生植物保护协会苔藓植物专业委员会成立大暨第一届学术讨论会	遵义	2020.10

- 参加学术会议情况

会议名称	会议类别	会议时间	参会人员
全国系统与进化植物学研讨会暨第十四届青年学术研讨会	全国会议（北京）	2020.11	凌少军、向文倩
全国海洋生态环境保护与监测技术研讨会	全国会议（深圳）	2020.12	赵洪伟
中国科协 2020 年海智计划工作会	全国会议（成都）	2020.11	向文倩、任明迅
中国野生植物保护协会苔藓植物专业委员会成立大会暨第一届学术讨论会	全国会议（遵义）	2020.10	张莉娜、徐雪艳、杜梦雪、毕胜、邓袓

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-
	《热带生物学报》	编委	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	副主任	2019-
	海南省热带生态环境修复工程研究中心	主任	2019-
	海南省李百炼院士工作站	负责人	2018-
	海南省林学会	副秘书长	2018-
	海南省植物学会	理事	2016-
谭正洪	《热带生物学报》	执行主编	2020-
	中国林学会国家公园分会	副理事长	2019-
	海南省生态学会	理事	2018-
	云南省生态学学会	理事	2014-
	中国科学院青年创新促进会	会员	2013-

张莉娜	中国植物学会苔藓专业委员会	委员	2010-
	中国野生植物保护协会苔藓植物专业委员会	委员	2020-2025
赵洪伟	中国太平洋学会珊瑚礁分会	会员	2018-
	海南省蓝丝带海洋环境保护协会	共同发起人	2018-
	中国未来海洋联盟	成员	2014-
	美国化学学会	会员	2012-
	海南省邹乐明院士创新团队	平台负责人	2020-
	海南省热带生态环境修复工程研究中心	副主任	2019-
黄青	《亚热带植物科学》	编委	2020-
	海南省贺泓院士工作站	负责人	2020-

八、在研项目

国家自然科学基金：面上项目

- ■ 环南海区域线柱苣苔属物种分化历史与长距离扩散格局(负责人：任明迅，执行期：2019.01－2022.12，总经费：60 万)
- ■ 我国龙脑香树木叶片物候与碳收支的季节关联(负责人：谭正洪，执行期：2018.01－2021.12，总经费：69 万)
- ■ 金虎尾科“花保守性”在亚洲的适应转变与进化后果——以风筝果属的镜像花为例(负责人：任明迅，执行期：2017.01－2020.12，总经费：62 万)

国家自然科学基金：地区科学基金

- ■ 龙脑香科青梅属不同果实类型传播与适应的生态遗传学研究(负责人：唐亮，执行期：2021.1－2024.12，35 万)。
- ■ 尖峰岭热带山地雨林叶内生与附生真菌-细菌的多层互作网络及其驱动因子研究(负责人：丁琼，执行期：2020.01－2023.12，40 万)
- ■ 造礁珊瑚-虫黄藻共生体响应扑草净胁迫的分子机制(负责人：赵洪伟，执行期：2019.01－2022.12，40 万)
- ■ 军委科技委国防科技创新特区项目保密项目(珊瑚相关研究)(负责人：赵洪伟，执行期：2018.11-2021.03，125 万)
- ■ 强季节性干旱区热带森林碳素分配的优先序(负责人：谭正洪，执行期：2019.01－2022.12，37 万)
- ■ 海南东岸热带滨海森林群落植物多样性恢复与维持对台风的响应(负责人：杨小波，执行期：2018.01－2021.12，总经费：35 万)
- ■ 海南热带山地云雾林苔藓植物多样性与谱系结构(负责人：张莉娜，执行期：2018.01－2021.12，总经费：38 万)
- ■ 热带森林自养呼吸时空异质性及其形成机理：以橡胶林为例(负责人：谭正洪，执行期：2017.01－2020.12，总经费：39 万)
- ■ 海南热带山地雨林林窗对土壤呼吸的影响研究(负责人：刘文杰，执行期：2017.01－2020.12，总经费：40 万)
- ■ 海南热带雨林群落优势种 BVOCs 释放及其对氮沉降的响应(负责人：何禾，执行期：2017.01－2020.12，总经费：35 万)

- 海南省松涛水库消落区植被恢复适宜物种的筛选及耐水淹机制研究(负责人：杨帆，执行期：2017.01－2020.12，总经费：39 万)
- 鸟巢蕨巢基结构发育及其高位土的形成机制研究(负责人：徐诗涛，执行期：2017.01－2020.12，总经费：39 万)
- 昌化江河谷对海南岛两种特有植物种群分布与基因流的隔离作用(负责人：唐亮，执行期：2017.01－2020.12，总经费：38 万)

省部级项目

- 海南省林业局专项：海南热带雨林国家公园综合科考(植物部分) (负责人：杨小波，执行期：2020-2021，经费：298 万)
- 海南省林业局专项：海南热带雨林国家公园自然禀赋及试点成效评估相关报告(结构完整性、功能完整性)(负责人：任明迅，执行期 2020-2021，经费：5 万元)
- 海南省林业局专项：海南热带雨林国家公园自然禀赋及试点成效评估相关报告(生态系统代表性、面积适宜性)(负责人：谭正洪，执行期 2020-2021，经费：5 万元)
- 中国工程科技发展战略海南研究院 2020 年咨询研究项目：国家生态文明试验区(海南)背景下热带雨林国家公园体制机制创新研究(负责人：李百炼、任明迅，执行期：2020-2021，经费：58 万)
- 海南省院士创新平台 2020 年科研专项项目：海南热带雨林国家公园告诉公路穿越段的环境监测与生态恢复技术(负责人：李百炼、任明迅，执行期：2020-2023，经费：50 万)
- 海南省自然科学基金创新团队项目：环南海区域植物长距离扩散与演化动态研究(负责人：任明迅，执行期：2018-2020，经费：30 万)。
- 海南省重大科技专项：海南农业面源污染减排技术研究与示范(课题：畜禽粪便无害化利用与种养结合生态循环模式研究与示范)(子课题负责人：赵洪伟，执行期：2017.01-2020.06，821 万(海大到账财政经费 144 万))
- 德国教研部(BMBF)中德合作项目(01DO17018)：Tracking environmental change Issues of China's coastal Aquatic Systems: Networking, capacity building and knowledge exchange (主要参与：赵洪伟，执行期：2017-2020，直接经费 20 万欧元)
- 海南省院士工作站(外籍)专项：(负责人：赵洪伟，执行期：2020.1-2023.12，100 万 (海南省科技厅 50 万、海南大学 50 万)
- 海南省贺泓院士工作站专项：(负责人：黄青，执行期：2020.1-2023.12，60 万 (海南省科技厅 30 万、海南大学 30 万)
- 东南大学生物电子学国家重点实验室开放基金：造礁珊瑚共生体适应高温胁迫的生理与分

子响应机制(负责人：赵洪伟，执行期：2019.01-2020.12，6 万)

- 清华大学环境模拟与污染控制国家重点联合实验室开放基金：(负责人：赵洪伟，执行期：2020.06-2022.06，8 万)
- 海南省重大科技计划项目(zdkj201815)：热带花卉(三角梅、文心兰)优质高效生产技术研究与示范(课题 1)(负责人：丁琼，执行期：2018-2020，直接经费：20 万)
- 海南省“海智计划”海南大学工作站建设与运行专项经费(负责人：任明迅，执行期：2017-2020，经费：13 万)
- 海南省高等学校科学研究重点项目：海南热带山顶矮林苔藓植物多样性随环境及空间尺度变化的研究(负责人：张莉娜，执行期 2017-2020, 经费 5 万)
- 琼中县第二次古树名木资源普查(负责人：唐亮，执行期 2018-2020, 经费 27 万)
- 海南省自然科学基金项目：基于养分回收的种苗基质开发(负责人：黄青，执行期 2019.03-2021.12，经费 10 万)

九、主要论著目录

➢ 论文

1. Spatial and seasonal variations of chloramphenicol resistance genes and their co-occurring analysis with bacteria in a typical mangrove area of Hainan island, China. **Estuarine, Coastal and Shelf Science**, 2020, 233: 106541. (责任作者: 赵洪伟)
2. Clade-specific sterol metabolites in dinoflagellate endosymbionts are associated with coral bleaching in response to environmental cues. **mSystems**, 2020, 5:e00765-20. (责任作者: 赵洪伟)
3. Plasticity in selective embryo abortion may limit the mating costs of geitonogamy in self-compatible plants: a hypothesis. **American Journal of Botany**, 2020, 107(3): 390–393. (责任作者：任明迅等)
4. Isolation and characterization of twelve polymorphic microsatellite markers in the endangered *Hopea hainanensis* (Dipterocarpaceae). **Ecology and Evolution**, 2020, DOI: 10.1002/ece3.7077. (责任作者: 唐亮)
5. Genome-wide codon usage pattern analysis reveals the correlation between codon usage bias and gene expression in *Cuscuta australis*. **Genomics**, 2020, 112: 2695–2702. (责任作者: 谢尚潜)
6. Phytomelatonin: An overview of the importance and mediating functions of melatonin against environmental stresses. **Physiologia Plantarum**, 2020, 1–27. (责任作者：任明迅)
7. Exogenous melatonin enhances salt stress tolerance in tomato seedlings. **Biologia Plantarum**, 2020, 604–615. (责任作者：任明迅)
8. Genetic diversity and population structure in the endangered tree *Hopea hainanensis* (Dipterocarpaceae) on Hainan Island, China. **PLoS ONE**, 2020, 15(11): e0241452. (责任作者: 唐亮、任明迅)
9. Biogeography and evolution of Asian Gesneriaceae based on updated taxonomy. **PhytoKeys**, 2020, 157: 7–26. (责任作者：任明迅)
10. Genetic delimitation of *Oreocharis* species from Hainan Island. **PhytoKeys**, 2020, 157: 59–81. (责任作者：任明迅)

11. *Oreocharis jasminina* (Gesneriaceae), a new species from mountain tops of Hainan Island, South China. **PhytoKeys**, 2020, 157: 121–135. (责任作者：任明迅)
12. Reducing bioavailability of heavy metals in contaminated soil and uptake by maize using organic-inorganic mixed fertilizer. **Chemosphere**, 2020, 261: 128122. (责任作者: 黄青)
13. Effects of plastic mulch film residues on soil-microbe-plant systems under different soil pH conditions **Chemosphere**, 2020, 128901. (责任作者: 黄青)
14. A new species of *Hiptage* (Malpighiaceae) from Nujiang Gorge, southwest China. **Nordic Journal of Botany**, 2020, 38(3). (责任作者：任明迅)
15. A novel type of mirror-image flowers caused by lateral bending of the floral tube in a bumblebee-pollinated plant. **Flora**, 2020, 272: 151694. (责任作者：任明迅)
16. High haplotype diversity with fine-scale structure in a recently established population of an endangered orchid. **Plant Species Biology**, 2020, 35(3):1–9. (责任作者：任明迅)
17. Morphological and physiological responses of *Dalbergia odorifera* T. Chen seedlings to different culture substances. **PLoS ONE**, 2020, 15(5): e0232051. (责任作者：杨帆)
18. Distribution Patterns of DNA N6-Methyladenosine Modification in Non-coding RNA Genes. **Frontiers in Genetics**, 2020, 11: 1–8. (责任作者: 谢尚潜)
19. Evaluating Structural Variation Detection Tools for Long-Read Sequencing Datasets in Saccharomyces cerevisiae. **Frontiers in Genetics**, 2020, 11: 159. (责任作者: 谢尚潜)
20. Palladium-Catalyzed Divergent Imidoylative Cyclization of Multi-Functionalized Isocyanides: Tunable Access to Oxazol-5(4H)-ones and Cyclic Ketoimines. **The Journal of Organic Chemistry**, 2020, 85: 7297-730. (责任作者: 王健等)
21. Development of Rapid Curing SiO_2 Aerogel Composite-Based Quasi-Solid-State Dye-Sensitized Solar Cells through Screen-Printing Technology. **ACS Applied Materials & Interfaces**, 2020. (责任作者: 周扬等)
22. The genome evolution and domestication of tropical fruit mango. **Genome Biology**, 2020, 21(1): 1–17. (责任作者: 王鹏)
23. Comparative study of polycyclic aromatic hydrocarbons (PAHs) and heavy metals (HMs) in corals, sediments and seawater from coral reefs of Hainan, China. **Environmental Pollution**, 2020, 264,114719. (责任作者: 赵洪伟)
24. Occurrence and origin of triazine herbicides in a tropical coastal area in China: A potential

ecosystem threat. **Estuarine, Coastal and Shelf Science**, 2020, 235, 106612. (责任作者: 赵洪伟)

25. Reef benthic composition and coral communities at the Wuzhizhou Island in the South China Sea: the impacts from Anthropogenic disturbance. **Estuarine, Coastal and Shelf Science**, 2020, 243, 106863. (责任作者: 赵洪伟)
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十、代表性论著首页

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RESEARCH ARTICLE
Host-Microbe Biology

Clade-Specific Sterol Metabolites in Dinoflagellate Endosymbionts Are Associated with Coral Bleaching in Response to Environmental Cues

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ABSTRACT Cnidarians cannot synthesize sterols (which play essential roles in growth and development) *de novo* but often use sterols acquired from endosymbiotic dinoflagellates. While sterol availability can impact the mutualistic interaction between coral host and algal symbiont, the biosynthetic pathways (in the dinoflagellate endosymbionts) and functional roles of sterols in these symbioses are poorly understood. In this study, we found that itraconazole, which perturbs sterol metabolism by inhibiting the sterol 14-demethylase CYP51 in dinoflagellates, induces bleaching of the anemone *Heteractis crispa* and that bleaching perturbs sterol metabolism of the dinoflagellate. While Symbiodiniaceae have clade-specific sterol metabolites, they share features of the common sterol biosynthetic pathway but with distinct architecture and substrate specificity features of participating enzymes. Tracking sterol profiles and transcripts of enzymes involved in sterol biosynthesis across time in response to different environmental cues revealed similarities and idiosyncratic features of sterol synthesis in the endosymbiont *Breviolum minutum*. Exposure of algal cultures to high levels of light, heat, and acidification led to alterations in sterol synthesis, including blocks through downregulation of squalene synthase transcript levels accompanied by marked growth reductions.

IMPORTANCE These results indicate that sterol metabolites in Symbiodiniaceae are clade specific, that their biosynthetic pathways share architectural and substrate specificity features with those of animals and plants, and that environmental stress-specific perturbation of sterol biosynthesis in dinoflagellates can impair a key mutualistic partnership for healthy reefs.

KEYWORDS coral bleaching, symbiosis, sterols, *Heteractis crispa*, Symbiodiniaceae

Corals and sea anemones are marine invertebrates of the phylum Cnidaria. Many are symbiotic species that engage as hosts in mutualistic partnerships (symbioses) with photosynthetic, algal endosymbionts (1). The major symbiotic algae associated with cnidarians are members of the dinoflagellate family Symbiodiniaceae, which has high phylogenetic diversity (2). Annotated genomes are available for several taxa of the family, including *Symbiodinium microadriaticum* (clade A) (3), *Breviolum minutum* (clade B, formerly *S. minutum*) (4), *Cladocopium goreaui* (clade C, formerly *S. goreaui*) (5), and *Fugacium kawagutii* (clade F, formerly *S. kawagutii*) (6). The dinoflagellate endosymbionts supply their cnidarian hosts with photosynthetic products (7) while benefiting from using CO_2 and nutrients in the host's waste products and their stable position in the water column with exposure to light (1). As the reefs provide numerous socioeconomic and ecological benefits in addition to high biodiversity (*inter alia*, tourist and recreational attractions, shoreline protection, and fisheries), there are urgent needs for

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NEWS & VIEWS

ON THE NATURE OF THINGS: ESSAYS

New Ideas and Directions in Botany

Plasticity in selective embryo abortion may limit the mating costs of geitonogamy in self-compatible plants: a hypothesis

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KEY WORDS geitonogamy; plant mating; pollen limitation; reproductive assurance; seed and pollen discounting; selective embryo abortion; self-fertilization.

Geitonogamy involves pollination of flowers by pollen from other flowers on the same plant. In hermaphroditic plants with multiple flowers in anthesis at the same time, this mode of pollination is likely to be near ubiquitous (de Jong et al., 1993; Harder and Barrett, 1995; Vaughton and Ramsey, 2010). In self-compatible species, geitonogamy may incur fitness costs because of inbreeding depression (i.e., the reduction in fitness of selfed seeds relative to outcrossed seeds), seed discounting (i.e., a reduction in the production of outcrossed seeds because seeds are selfed), and pollen discounting (i.e., a decrease in outcross siring success because self-pollen deposition reduces opportunities for cross pollination) (Lloyd, 1992; Busch and Delph, 2012). Because of these mating costs, geitonogamy is commonly recognized as a pervasive and non-adaptive by-product of floral display size leading to the evolution of diverse floral strategies that function to limit geitonogamy (Lloyd, 1992; de Jong et al., 1993; Barrett, 2003). However, if geitonogamy is both ubiquitous and unavoidable, it is worth considering how self-compatible plants cope with geitonogamy after ovules are selfed, but this has not been explored in the literature on plant reproductive ecology.

In this essay, we propose a novel hypothesis for how self-compatible plants may take advantage of the benefits of reproductive assurance through geitonogamy while avoiding the seed discounting cost after geitonogamous selfing has occurred. We propose that after ovules are selfed through geitonogamy, they can mature into seeds, providing reproductive assurance if cross-fertilized ovules are limiting, but that selfed ovules will be preferentially aborted if cross-fertilized ovules are abundant. Such post-fertilization mating flexibility in stochastic pollination and fertilization environments may allow geitonogamy to provide reproductive assurance with limited seed discounting costs. It is important to emphasize that according to the hypothesis we propose here geitonogamous seed discounting can be reduced but not pollen discounting, which may still be significant (Harder and Barrett, 1995).

Our hypothesis depends on the key assumption that maternal parents can selectively abort ovules fertilized by low-quality pollen (self-pollen or pollen of close relatives) when resources are limiting but not when resources are abundant; i.e., there is plasticity in selective embryo abortion. For example, in several studies fruit or ovule abortion was lower and progeny vigor higher in intact flowers or inflorescences than in those receiving hand-thinning treatment, indicating that otherwise viable embryos were aborted when resources were limiting (Stephenson and Winsor, 1986; Casper, 1988; Rocha and Stephenson, 1991; Melser and Klinkhamer, 2001). However, there is also evidence indicating that selective embryo abortion caused

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NATURE NOTES

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Isolation and characterization of twelve polymorphic microsatellite markers in the endangered *Hopea hainanensis* (Dipterocarpaceae)

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Abstract

Microsatellite markers were isolated and characterized for *Hopea hainanensis* Merrill & Chun, an endangered tree species with scattered distribution in Hainan Island and northern Vietnam. Twenty-six microsatellite markers were developed based on next-generation sequencing data and were genotyped by capillary electrophoresis on an ABI 3730xl DNA Analyzer. Twelve markers were found to be polymorphic in *H. hainanensis*. GENODIVE analyses indicated that the number of alleles ranged from 2 to 6 per locus, and the observed and expected heterozygosity varied from 0 to 0.755 and from 0.259 to 0.779, respectively. Primer transferability was tested with *Hopea chinensis* Hand.-Mazz. and *Hopea reticulata* Tardieu, in which 3 and 7 microsatellite markers were found to be polymorphic, separately. The results showed that *H. reticulata* and *H. hainanensis* had similar levels of genetic diversity. A neighbor joining dendrogram clustered all individuals into two major groups, one of which was exclusively constituted by *H. hainanensis*, while the other consisted of two subgroups, corresponding to *H. reticulata* and *H. chinensis*, respectively. The 12 polymorphic microsatellite markers could be applied to study genetic diversity, population differentiation, mating system, and fine-scale spatial genetic structures of *H. hainanensis* as well as its close relatives, facilitating the conservation and restoration of these endangered but valuable *Hopea* species.

KEYWORDS

Dipterocarpaceae, endangered species, *H. hainanensis*, microsatellite markers, next-generation sequencing

1 | INTRODUCTION

Hopea hainanensis Merrill & Chun is a large evergreen tree that can grow up to 20 m. It is found in tropical lowland forest of Hainan Island and northern Vietnam (Li et al., 2007). *Hopea hainanensis* is known for its highly valued timber which is extremely durable and suitable for making boats and building bridges and houses (Li et al., 2007). As a result, adult trees of this species had been overly logged, leading to a reduction of 50%–70% population in the last three hundred years (Ly et al., 2018). The remaining population of *H. hainanensis* is severely fragmented and isolated in a few reserves in Hainan Island. This species is scarce in its natural habitat and is assessed as

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Genome-wide codon usage pattern analysis reveals the correlation between codon usage bias and gene expression in *Cuscuta australis*

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ABSTRACT

The protein-coding genes and pseudogenes of *Cuscuta australis* had the diverse contribution to the formation and evolution of parasitism. The codon usage pattern analysis of these two type genes could be used to understand the gene transcription and translation. In this study, we systematically analyzed the codon usage patterns of protein-coding sequences and pseudogenes sequences in *C. australis*. The results showed that the high frequency codons of protein coding sequences and pseudogenes had the same A/U bias in the third position. However, these two sequences had converse bias at the third base in optimal codons: the protein coding sequences preferred G/C-ending codons while pseudogene sequences preferred A/U-ending codons. Neutrality plot and effective number of codons plot revealed that natural selection played a more important role than mutation pressure in two sequences codon usage bias. Furthermore, the gene expression level had a significant positive correlation with codon usage bias in *C. australis*. Highly-expressed protein coding genes exhibited a higher codon bias than lowly-expressed genes. Meanwhile, the high-expression genes tended to use G/C-ending synonymous codons. This result further verified the optimal codons usage bias and its correlation with the gene expression in *C. australis*.

1. Introduction

The central principle is one of the core principles of biology, and the triple codon is the most important part of biological activity when the genetic information is transmitted from mRNA to protein. Each codon corresponds to one amino acid, and each amino acid refers to up to six codons or at least one codon [1]. The multiple codons encode the same amino acid are the synonymous codons with each other [2], but the frequencies of synonymous codons usage are not equal during protein synthesis [3]. The usage of codon in different genes or species has a preference for some certain codons [4]. The codon preference of synonymous codon usage, known as codon usage bias (CUB), is widespread in the genomes and reflects non-uniform use of codon for gene encoding and plays a role in the gene regulation [5–8].

Selection-mutation-drift, included natural selection, mutation pressure and gene drift, was the representative theory to explain codon usage bias [9–12]. The assessment of the factors for CUB included the relative synonymous codon usage (RSCU), neutrality plot, effective number of codons (ENC), parity rule 2 bias analysis and frequency of optimal codons (FOP) and so on. And the different selection of above indictors was used to measure the CUB among different species or conditions [13–16]. Besides, the GC component of genes was an important feature to assess the CUB, and GC content in the third position of a codon (GC3) is considered to be the direct reflection for codon usage pattern [17]. In general, the G/C-terminated codons are more frequently used in monocotyledonous plants, and A/T-terminated codons are more common in dicotyledonous plants [18–20]. Moreover, gene expression levels and gene length were associated with the formation of CUB [8], and the codon usage pattern of higher expression genes was biased [21]. In addition, the relationship between codon preference and gene expression was also reported in *Trypanosoma brucei* [22], *Escherichia coli* [23] and *Drosophila* [24].

Cuscuta australis, a root and leafless parasitic model plant, uses a specialized haustorial organ to extract water and nutrients through vascular connections with the hosts [25–27]. Although the extract of *C. australis* is an important medicinal component for the treatment of sores, measles and liver diseases [28], the mainly investigate of *C. australis* still focused on the evaluation of parasitism [27] and the functional effects of bidirectional movement between host and parasite [26]. Recently, a high-quality reference genome of *C. australis* was assembled and released in Dodder Genome Database (DGD, http://groups.english.kib.cas.cn/epb/dgd/) [27], which provided a genome-wide insight for the annotated protein-coding sequences and pseudogenes sequences of *C. australis*. The codon usage bias can be used as an

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Physiologia Plantarum

SPECIAL ISSUE ARTICLE

Phytomelatonin: An overview of the importance and mediating functions of melatonin against environmental stresses

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Abstract

Recently, melatonin has gained significant importance in plant research. The presence of melatonin in the plant kingdom has been known since 1995. It is a molecule that is conserved in a wide array of evolutionary distant organisms. Its functions and characteristics have been found to be similar in both plants and animals. The review focuses on the role of melatonin pertaining to physiological functions in higher plants. Melatonin regulates physiological functions regarding auxin activity, root, shoot, and explant growth, activates germination of seeds, promotes rhizogenesis (growth of adventitious and lateral roots), and holds up impelled leaf senescence. Melatonin is a natural bio-stimulant that creates resistance in field crops against various abiotic stress, including heat, chemical pollutants, cold, drought, salinity, and harmful ultra-

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Abbreviations: ABA, abscisic acid; SA, salicylic acid; PAO, pheophorbide an oxygenase; ROS, reactive oxygen species; APX, ascorbate peroxidase; POX, peroxidase; CAT, catalase; ET, ethylene; IAA, indole-3-acetic acid; PSII, photosystem II; JA, jasmonic acid; RNS, reactive nitrogen species; SDG, secoisolariciresinol DiGlucoside; SOD, superoxide dismutase.

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Exogenous melatonin enhances salt stress tolerance in tomato seedlings

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Abstract

Melatonin (N-acetyl-5-methoxytryptamine) is an essential molecule which regulates plant growth and development and alleviates the damaging effects of abiotic stresses. To evaluate the important functions of melatonin in response to salinity stress, the effects of exogenous melatonin on the antioxidant system and growth of tomato (*Solanum lycopersicum* L.) under 150 mM NaCl stress were investigated. The application of 100 µM melatonin compensated the growth inhibition caused by salt-stress. Melatonin treated seedlings had an increased fresh and dry masses of shoots and roots. The application of 1 - 200 µM melatonin notably enhanced the relative chlorophyll content (SPAD index), root characteristics, and gas exchange in tomato seedlings subjected to salt stress compared to seedlings treated with salt stress alone. Moreover, melatonin pretreatment minimized accumulation of reactive oxygen species and improved activities of antioxidative enzymes including catalase, superoxide dismutase, glutathione reductase, and ascorbate peroxidase.

Additional key words: abiotic stresses, antioxidative enzymes, chlorophyll, NaCl, oxidative damage, photosynthesis.

Introduction

Environmental stress, such as salinity, directly impacts plants growth and development through osmotic and particular ion effects, and by leading to oxidative stress due to enhanced reactive oxygen species (ROS) production (Hasanuzzaman *et al*. 2013, Jiang *et al.* 2017). According to Ahuja (2010) and Zhang *et al.* (2011), many environmental stresses as drought, salinity, extreme temperatures are devastating for crops causing yield loses. Kaya *et al.* (2013) and Peng *et al.* (2017) declared soil salinity as a global problem. As described by Khan and Hemalatha (2016) and Liu *et al.* (2018) photosystems get impaired, production of reactive oxygen species is accelerated, and growth is reduced due to excessive NaCl concentration. Firstly, cellular organelles are damaged due to high concentrations of Na^+, thus causing changes in of enzymatic activities, protein synthesis, respiration, and photosynthesis. Secondly, an imbalance in nutrients is resulted due to salinity, as it causes a decline in uptake and transport nutrients towards the shoot. Further, plants face a physiological drought condition as salinity hurdles root water uptake due to decreased osmotic potential of soil (Ruiz-Lozano *et al.* 2012).

Melatonin (N-acetyl-5-methoxytryptamine) is an organic compound with low molecular mass and exerting various biological activities; it represents a ubiquitous molecule in all living organisms from bacteria to mammals (Hardeland *et al.* 2011, Reiter *et al.* 2014, Nawaz *et al.* 2016). The first discovery of melatonin in higher plants was reported by Dubbels *et al.* (1995) and Hattori *et al.* (1995). Later on, clear occurrence of melatonin in all organs of

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Abbreviations: APX - ascorbate peroxidase; CAT - catalase; c_i - intercellular CO_2 concentration; E - transpiration rate; EL - electrolyte leakage; GR - glutathione reductase; g_s - stomatal conductance; MDA - malondialdehyde; PDM - plant dry mass; PFM - plant fresh mass; P_N - net photosynthetic rate; RDM - root dry mass; RFM - root fresh mass; ROS - reactive oxygen species; SOD - superoxide dismutase.

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PLOS ONE

RESEARCH ARTICLE

Genetic diversity and population structure in the endangered tree *Hopea hainanensis* (Dipterocarpaceae) on Hainan Island, China

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Abstract

Hopea hainanensis Merrill & Chun (Dipterocarpaceae) is an endangered tree species restricted to Hainan Island, China and a small part of Northern Vietnam. On Hainan Island, it is an important indicator species for tropical forests. However, because of its highly valued timber, *H. hainanensis* has suffered from overexploitation, leading to a sharp population decline. To facilitate the conservation of this species, genetic diversity and population structure were assessed using 12 SSR markers for 10 populations sampled across Hainan Island. Compared to non-threatened *Hopea* species, *H. hainanensis* exhibited reduced overall genetic diversity and increased population differentiation (AMOVA: $F_{ST} = 0.23$). Bayesian model-based clustering and principal coordinate analysis consistently assigned *H. hainanensis* individuals into three genetic groups, which were found to be widespread and overlapping geographically. A Mantel test found no correlation between genetic and geographical distances ($r = 0.040$, $p = 0.418$). The observed genetic structure suggests that long-distance gene flow occurred among *H. hainanensis* populations prior to habitat fragmentation. A recent population bottleneck was revealed, which may cause rapid loss of genetic diversity and increased differentiation across populations. Based on these findings, appropriate strategies for the long-term conservation of the endangered species *H. hainanensis* are proposed.

Introduction

Earth's biodiversity is rapidly declining as a consequence of agricultural expansion, overexploitation, deforestation, pollution and climate change [1–3]. Approximately 40% of plant species are threatened with extinction [4]. Conservation genetics, a new discipline that applies the concepts and tools of population genetics to biological conservation, is aimed at preserving endangered species from extinction [1]. Endangered species are commonly characterized by small, fragmented populations and restricted gene flow among populations [3]. In small, isolated populations, mating occurs more frequently among relatives, and a shift to selfing may be observed in hermaphroditic plants. Inbreeding leads to homozygosity in detrimental

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RESEARCH ARTICLE

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Biogeography and evolution of Asian Gesneriaceae based on updated taxonomy

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Abstract

Based on an updated taxonomy of Gesneriaceae, the biogeography and evolution of the Asian Gesneriaceae are outlined and discussed. Most of the Asian Gesneriaceae belongs to Didymocarpoideae, except *Titanotrichum* was recently moved into Gesnerioideae. Most basal taxa of the Asian Gesneriaceae are found in the Indian subcontinent and Indo-China Peninsula, suggesting Didymocarpoideae might originate in these regions. Four species diversification centers were recognized, i.e. Sino-Vietnam regions, Malay Peninsula, North Borneo and Northwest Yunnan (Hengduan Mountains). The first three regions are dominated by limestone landscapes, while the Northwest Yunnan is well-known for its numerous deep gorges and high mountains. The places with at least 25% species are neoendemics (newly evolved and narrowly endemic) which were determined as evolutionary hotspots, including Hengduan Mountains, boundary areas of Yunnan-Guizhou-Guangxi in Southwest China, North Borneo, Pahang and Terengganu in Malay Peninsula, and mountainous areas in North Thailand, North Sulawesi Island. Finally, the underlying mechanisms for biogeographical patterns and species diversification of the Asian Gesneriaceae are discussed.

Keywords

Didymocarpoideae, endemic, species diversification, limestone landscape, monsoon, long-distance dispersal

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Genetic delimitation of *Oreocharis* species from Hainan Island

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Abstract

Hainan Island harbours an extraordinary diversity of Gesneriaceae with 14 genera and 23 species, amongst which two species and one variety are recognised in the genus *Oreocharis*. These three *Oreocharis* taxa are all Hainan-endemics and show a complex geographical distribution pattern with considerable morphological intermixtures. In this study, we combined DNA (nuclear ITS sequences and cpDNA *trn*L-*trn*F and *ycf1b*) to evaluate genetic delimitation for 12 *Oreocharis* populations from the island, together with morphological similarity analysis using 16 morphological traits. The results showed Hainan *Oreocharis* taxa were monophyletic with relative low genetic diversity within populations, highly significant genetic differentiation amongst populations and a significant phylogeographical structure. The 12 populations formed three genetically distinct groups, roughly correspondent to the currently recognised two species and one unknown lineage. The PCA analyses of morphological traits indicate three distinctive groups, differing mainly in petal colour and corolla shapes. The roles of river and mountain isolations in the origin and distribution of these three lineages are discussed.

Keywords

genetic differentiation, genetic diversity, morphological similarity, *Oreocharis*

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Oreocharis jasminina (Gesneriaceae), a new species from mountain tops of Hainan Island, South China

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Abstract

A new species of Gesneriaceae, *Oreocharis jasminina* S.J.Ling, F.Wen & M.X. Ren from Hainan Island, south China, is highlighted and described. The new species is distinguished by its actinomorphic corolla, narrow floral tube and ovate anthers hidden in the floral tube. The new species also showed clear geographic and altitudinal isolation from the three currently-recognised *Oreocharis* species on the Island. Molecular phylogenetic analysis, based on nuclear ITS1/2 and plastid *trn*L-*trn*F sequences, supported the delimitation of the new species, which forms a single lineage with all the other *Oreocharis* species from Hainan Island. The roles of geographic and floral isolation in the evolution of the new species and its affinities are discussed.

Keywords

Hainan Island, new taxon, *Oreocharis*

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Reducing bioavailability of heavy metals in contaminated soil and uptake by maize using organic-inorganic mixed fertilizer

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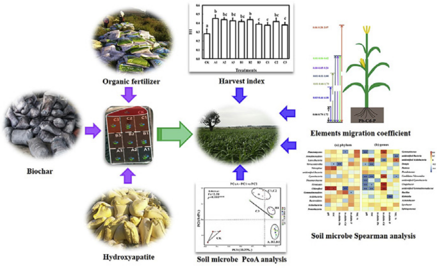
HIGHLIGHTS

- Soil pH and crop yield were significantly improved in the A1 treatment.
- The bioavailability of Cd was remarkably decreased with the application of A1 amendment.
- The microbial community was shaped by additions with increases in groups likely to immobilize Cd.

GRAPHICAL ABSTRACT



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ABSTRACT

Heavy metals in soil are harmful to human health via the food chain, but little is known about the mechanism of reducing bioavailability of Cd or Pb to maize (*Zea mays* L.) by applying complex amendments to soil. A field experiment was conducted at a tropical site in Hainan Province, China, that had been subjected to soil pollution by Cd and Pb from past mining activities. There were ten treatment groups comprising a mixture of biochar, hydroxyapatite (HAP), manure, and plant ash in varying proportions and at three different rates. Compared with untreated soil, all treatments increased pH by 2–3 units in bulk soil or 1–2 units in rhizosphere soil. For all amendments, the concentration of Cd in all parts of maize plants was decreased compared with unamended soil, but this effect was much smaller for Pb. The greatest effect was found with a mixture containing the ratio of HAP:manure:biochar:plant ash as 6:4:2:1 when applied at 20.1 t ha^{-1}. The dominant microbial group in contaminated soil was Proteobacteria. There is evidence that this group can immobilize Cd by mechanisms that include biosorption and bioprecipitation. It was concluded that the mixed amendments containing biochar, HAP, manure, and plant ash can be useful in decreasing Cd uptake by maize. The amendment in this study likely

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Effects of plastic mulch film residues on soil-microbe-plant systems under different soil pH conditions

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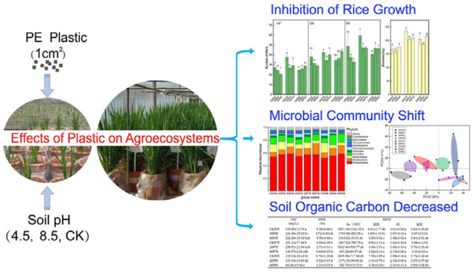
HIGHLIGHTS

- Plastic mulch film residues (PMFR) affect the rhizophere bacterial communities.
- Microbe significant correlations with SOM and SOC when response to PMFR.
- Negative effects of PMFR on rice growth were stronger under acidic conditions.
- SOC declined significantly more in alkaline soils with PMFR concentrations.

GRAPHICAL ABSTRACT



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ABSTRACT

Plastic mulch film residues (PMFR) accumulated throughout mulching years can result in serious environmental problems, especially in hotter areas with frequent farming (e.g. the tropics). The effects of long-term mulching on the soil-microbe-plant system, however, are largely unknown. As mulching years is positively correlated with PMFR concentrations, we used a controlled pot experiment to investigate the effects of mulching years (20a: The concentration of PMFR is about 2 g kg^{-1}, 60a: About 6 g kg^{-1}) on rice growth, rhizosphere bacterial communities, and soil organic carbon (SOC) under different soil pH conditions. Mulching years reduced rice growth; 20a showed more negative effects than 60a on rice tillers number and biomass. PMFR changed the composition, diversity, and metabolic function of the rhizosphere bacterial communities. The content of SOC decreased as mulching residues increased; total organic carbon (TOC), soil organic matter (SOM), Fn (355), and humification index (HIX) declined by 30.24%, 55.97%, 59.74%, and 70.24%, respectively. Furthermore, significant correlations between bacterial communities and SOC were observed in the soil-microbe-plant system. PMFR showed stronger negative effects on rice growth in acidic soil (pH 4.5); however, in basic soil (pH 8.5), there were stronger

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NORDIC JOURNAL OF
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Research

A new species of *Hiptage* (Malpighiaceae) from Nujiang Gorge, southwest China

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Hiptage lushuiensis, a new species from the Hengduan Mountains, northwestern Yunnan Province, China, is described and illustrated here. This species was found growing at the margin of an open forest in the Nujiang Gorge of Lushui City. *Hiptage lushuiensis* is distinctive for its pink petals, 2 or more calyx glands, and large and pink samara with white hairs. This species is isolated in the deep gorge (25°51′N, 98°51′E, altitude 917 m), at the northern edge distribution range of the genus. These distinctive morphological differences and the geographic isolation suggest a history of long-distance dispersal and allopatric speciation. *Hiptage lushuiensis* has a shorter filament but larger herkogamy than related species, suggesting that *H. lushuiensis* may have adapted to other pollinators with short but fat body such as *Amegilla* or *Bombus* spp.

Keywords: Asian flora, Malpighiales, taxonomy, tetrapteroid clade

Introduction

Hiptage Gaertn. (1971, p. 22) is a genus of woody lianas in the Malpighiaceae growing mainly at forest edges, riversides or on limestone hills in tropical and subtropical Asia (Chen and Funston 2008, Ren 2015). The genus comprises ca 30 species (Anderson et al. 2006, Chen and Funston 2008, Ren et al. 2013, Ren 2015), of which seven are endemic to China (Chen and Funston 2008). Due to the dominating summer monsoons in Asia (Ren 2015, Jiang et al. 2017), *Hiptage* reach to more than 25° northern latitude in Yunnan, Guangxi, southeast Tibet and South Guizhou in southwestern China, and some narrowly-endemic *Hiptage* species are found here (Chen and Funston 2008, Ren 2015, Yang et al. 2018, Tan et al. 2019).

Hiptage is distinctive by its diagnostic three-winged samara and mirror-image flowers with heteranthery (Ren et al. 2013, Yang et al. 2018). Mirror-image flowers are a sexual polymorphism in which the style is deflected either to the left (left-styled flower) or the right (right-styled flower) (Barrett et al. 2000, Jesson and Barrett 2002), and it is recognized as a specialized insect-pollination mechanism (Jesson and Barrett 2002, Ren et al. 2013). The three-winged samara makes the fruit flying in a helicopter-like mode, an adaptation facilitating long-distance dispersal (Davis et al. 2002, Ren 2015, Qian and Ren 2016, Tan et al. 2018).

NORDIC SOCIETY OIKOS

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A novel type of mirror-image flowers caused by lateral bending of the floral tube in a bumblebee-pollinated plant

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ABSTRACT

We studied a previously unreported form of mirror-image flowers in *Rhabdothamnopsis sinensis* (Gesneriaceae) endemic to China. The style in *R. sinensis* remains straight throughout the blooming period, while the basal part of the floral tube bends either to the left or right side, causing the style to lean towards the right or left side of the floral tube. *R. sinensis* has two epipetalous fertile stamens with twisted filaments, moving the fused anthers located at the opposite side of the style. This floral syndrome results in reciprocal mirror-image flowers in a relative simpler way as compared to typical types of mirror-image flowers. Pollinator observations revealed that the bending of the floral tube and twisted filament block the entrance to the floral tube, rendering long-tongued bumblebees as pollinators by transferring pollen with the side of the thorax. *R. sinensis* is self-compatible and the pollen-ovule ratio is strikingly low (37.41 ± 11.90). Thorax pollination probably is the main reason for such low pollen wastage because the thorax suffers less grooming than the abdomen, which is the main pollen-carrying part in other typical mirror-image flowers. The unusual type of mirror-image flowers described here suggests a specialized pollination adaptation with limited but high-fidelity pollinators.

1. Introduction

Mirror-image flowers are a highly-specialized sexual polymorphism in which the style deflects either to the left or right side of a flower in the same species (Todd, 1882; Barrett et al., 2000; Jesson and Barrett, 2002). Depending on whether or not there are fertile stamen(s) deflecting to the opposite side of the style, mirror-image flowers can be classified as reciprocal or nonreciprocal mirror-image flowers (Jesson and Barrett, 2002). Mirror-image flowers can be expressed at two fundamentally different patterns of organization, i.e. the left- and right-styled flowers can be produced either on the same individual (monomorphic enantiostyly) or on different individuals (dimorphic enantiostyly) (Jesson and Barrett, 2002, 2003).

Typical mirror-image flowers have no obvious floral tube and sexual organs are presented to pollinators for buzz-pollination (pollinators vibrate poricidal anthers to release pollen) (Todd, 1882; Jesson and Barrett 2002, 2005). Normally, mirror-image flowers are pollinated by large-bodied insects such as bumblebees or carpenter bees (Müller, 1883; Jesson and Barrett, 2002, 2003). These insects can touch the deflected style and stamen(s) respectively with their left or right side and consequently facilitate pollen transfer between left- and right-styled flowers (Fenster, 1995; Jesson and Barrett, 2002, 2005; Lin and Tan, 2007). Therefore, mirror-image flowers can increase the precision of cross-pollen transfer (Jesson and Barrett, 2002) and the spatial separation of the deflected style and stamen (herkogamy) is crucial for touching the left or right side of the pollinator's body, and is the key trait for successful pollen pickup and deposition (Ren et al., 2013).

As a medium-size pantropical family, Gesneriaceae is well known for the high occurrence and diversity of mirror-image flowers (Harrison et al., 1999; Lu et al., 2019). Mirror-image flowers in Gesneriaceae are restricted to the Old World subfamily Didymocarpoideae, and are known from about 80 species from seven genera (Lu et al., 2019). In contrast to most angiosperms, mirror-image flowers in Didymocarpoideae are mainly nonreciprocal, with several distinct floral traits such as united anthers and an obvious floral tube (Harrison et al., 1999; Lu et al., 2019), suggesting a specialized pollination mechanism and distinct evolutionary histories of mirror-image flowers in this subfamily.

Here, we report a previously undescribed type of mirror-image

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ORIGINAL ARTICLE

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High haplotype diversity with fine-scale structure in a recently established population of an endangered orchid

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Abstract

New populations of endangered plants may establish outside of protected areas if a suitable habitat becomes available. However, it is unclear whether such populations are genetically uniform, as a result of a founder effect, or whether they contain genetic variation resulting from continuous gene flow from source populations, and subsequent recruitment after establishment. We addressed this by examining haplotype variation in the endangered orchid, *Anacamptis robusta*, which has formed a new population outside of its protected area within the past 20 years. To assess population growth, the number of *A. robusta* flowering plants were counted every year for 22 years in both the new population and populations within the reserve. Haplotype diversity and fine-scale structure were examined with spatial autocorrelation analysis, both in the new population and representative populations from the protected area. The number of flowering individuals in the new population increased from 9 to 2,277 between 2003 and 2012, whereas within the reserve flowering population sizes varied between years. Seventeen of 23 haplotypes detected for *A. robusta* were detected in the new population, with seven of these occurring more frequently in the new population than reserve populations. In the new population, there was strong fine-scale spatial structure of haplotypes, similar to patterns found in large populations from the protected area, suggesting multiple colonization events and subsequent local recruitment. This highlights that ongoing demographic and genetic monitoring of plant populations is vital to improve our understanding of population colonization and the conservation of narrow endemics.

KEYWORDS

Anacamptis, colonization, distance matrix regression, plastid minisatellite, population expansion

1 | INTRODUCTION

Populations of endangered plants can colonize new habitats that may not necessarily occur within protected areas (Järvinen, 1982; Thomas, 1994). Indeed, human-mediated habitat disturbance or changing ecological conditions may open suitable habitats that were previously unavailable (Bazzaz, 1991). The ability of endangered plants to colonize such new habitats is crucial for their long-term persistence (Ackerman, 1998; Honnay & Jacquemyn, 2007). However, endangered species tend to have specialized ecological requirements in order to complete their life cycles (Swarts & Dixon, 2009; Tsuji & Kato, 2010), which may reduce their ability to colonize

PLOS ONE

RESEARCH ARTICLE

Morphological and physiological responses of *Dalbergia odorifera* T. Chen seedlings to different culture substances

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Abstract

Dalbergia odorifera T. Chen seedlings do not grow well in the typical red soils of tropical regions. Eighteen culture substances filled with different substrate combinations and proportions of red soil, coconut coir powder, deciduous leaf powder, and sand were used as to determine their effects on the growth, root system development, dry matter accumulation and allocation, leaf relative electrolyte leakage, chlorophyll content, root superoxide dismutase activity, root malondialdehyde content, and total soluble sugar content of *D. odorifera*. Results demonstrated that different substrate combinations and proportions had different effects on the performance of *D. odorifera*. All mixed substrates were better than any single substrate. The suitable substrate combinations and proportions of sand, coconut coir powder, and deciduous leaf powder mixed with red soil improved the growth, root architecture, and physiological characteristics of *D. odorifera* seedling. For example, groups $C1_{-2}$ (coconut coir/red soil = 2/2, v/v, the same below) and $C3_{-2}$ (red soil/sand = 2/2) exerted the best effects on plant growth and biomass accumulation. Groups $C1_{-2}$, $C2_{-2}$ (deciduous leaf powder/red soil = 2/2), and $C3_{-2}$ remarkably enhanced root system development. Group C6 (coconut coir/red soil/sand = 1/1/1) substantially promoted root nodule development. Group $C3_{-1}$ (red soil/sand = 3/1) exhibited the best effects on physiological characteristics. On the basis of the comprehensive evaluation of Euclid's multidimensional space mathematical model, we found that the suitable substrate combinations followed the order of $C1_{-2} > C3_{-1} > C2_{-2}$. This research provides scientific guidance for the proper seedling culture of *D. odorifera* and the rational utilization of solid wastes such as coconut coir and deciduous leaves of *Ficus elastica*.

Introduction

Dalbergia odorifera T. Chen, also named yellow flower pear, is a species that belongs to Family Leguminosae. This tree can reach 10–15 m in plant height [1]. *D. odorifera* is a fragrant

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ORIGINAL RESEARCH
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Distribution Patterns of DNA N6-Methyladenosine Modification in Non-coding RNA Genes

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N6-methyladenosine (6mA) DNA modification played an important role in epigenetic regulation of gene expression. And the aberrational expression of non-coding genes, as important regular elements of gene expression, was related to many diseases. However, the distribution and potential functions of 6mA modification in non-coding RNA (ncRNA) genes are still unknown. In this study, we analyzed the 6mA distribution of ncRNA genes and compared them with protein-coding genes in four species (*Arabidopsis thaliana*, *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Homo sapiens*) using single-molecule real-time (SMRT) sequencing data. The results indicated that the consensus motifs of short nucleotides at 6mA location were highly conserved in four species, and the non-coding gene was less likely to be methylated compared with protein-coding gene. Especially, the 6mA-methylated lncRNA genes were expressed significant lower than these genes without methylation in *A. thaliana* (p = 3.295e-4), *D. melanogaster* (p = 3.439e-11), and *H. sapiens* (p = 9.087e-3) all four species. The detection and distribution profiling of 6mA modification in ncRNA regions from four species reveal that 6mA modifications may have effects on their expression level.

Keywords: non-coding RNAs, model species, DNA methylation, gene expression, 6mA modification

INTRODUCTION

DNA methylation, refers to the addition of a methyl group (CH3) to the DNA molecule, plays a critical role in epigenetic regulation of genes expression. Previous studies have paid more attention to 5-methylcytosine (5mC) in eukaryotes genomic DNA (gDNA) due to its abundance and significance (Zhang et al., 2006; Zilberman et al., 2007; Law and Jacobsen, 2010; Jones, 2012). In contrast, N6-methyladenosine (6mA) has been found at a significant level and commonly characterized in prokaryotes. Particularly, 6mA modifications in bacteria are involved in diverse biological processes such as DNA replication, DNA mismatch repair, host–pathogen interaction, and gene expression (Ratel et al., 2006; Wion and Casadesus, 2006). Recently, 6mA has been identified as a novel epigenetic mark in eukaryotes (Sun et al., 2015). And owing to the developed high-through sequencing technologies, 6mA modifications have been detected in diverse eukaryotes such as *Chlamydomonas* (Fu et al., 2015), *Arabidopsis thaliana* (Liang et al., 2018), *Caenorhabditis elegans* (Greer et al., 2015), *Drosophila melanogaster* (Zhang et al., 2015), *Mus*

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ORIGINAL RESEARCH
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Evaluating Structural Variation Detection Tools for Long-Read Sequencing Datasets in *Saccharomyces cerevisiae*

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Structural variation (SV) represents a major form of genetic variations that contribute to polymorphic variations, human diseases, and phenotypes in many organisms. Long-read sequencing has been successfully used to identify novel and complex SVs. However, comparison of SV detection tools for long-read sequencing datasets has not been reported. Therefore, we developed an analysis workflow that combined two alignment tools (NGMLR and minimap2) and five callers (Sniffles, Picky, smartie-sv, PBHoney, and NanoSV) to evaluate the SV detection in six datasets of *Saccharomyces cerevisiae*. The accuracy of SV regions was validated by re-aligning raw reads in diverse alignment tools, SV callers, experimental conditions, and sequencing platforms. The results showed that SV detection between NGMLR and minimap2 was not significant when using the same caller. The PBHoney was with the highest average accuracy (89.04%) and Picky has the lowest average accuracy (35.85%). The accuracy of NanoSV, Sniffles, and smartie-sv was 68.67%, 60.47%, and 57.67%, respectively. In addition, smartie-sv and NanoSV detected the most and least number of SVs, and SV detection from the PacBio sequencing platform was significantly more than that from ONT ($p = 0.000173$).

Keywords: structural variation, long-read sequencing, PacBio and ONT, SV caller, Saccharomyces cerevisiae

INTRODUCTION

Structural variation (SV) is generally defined as a large-scale structural difference region of genomics DNA that are inherited and polymorphic in species (Mills et al., 2011). It accounts for the greatest number of divergent base pairs, including insertion (INS), deletion (DEL), inversion (INV), duplication (DUP), and translocation (TRA)/breakend (BND) (Weischenfeldt et al., 2013). SV represents a major form of genetic variations and contributes to polymorphic variations and phenotypes in organisms. Somatic SVs revealed that the deletion and rearrangement of chromosomal structure result in gene suppression and phenotypic transform, such as cancers (Stankiewicz and Lupski, 2010; Patel et al., 2014) and neurological disorders (Weischenfeldt et al., 2013; Brand et al., 2014). The genomic deletion of *D.*

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Palladium-Catalyzed Divergent Imidoylative Cyclization of Multifunctionalized Isocyanides: Tunable Access to Oxazol-5(4*H*)-ones and Cyclic Ketoimines

Jian Wang,* Ling Zhong, Shi Tang, Yuan Liu, Shumin Ding, Lianjie Li, Haixia Zhao, Chen Chen, and Yongjia Shang*

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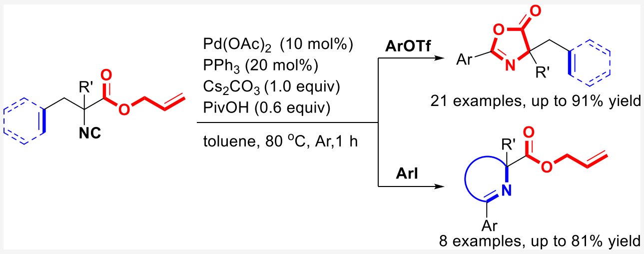
ABSTRACT: A palladium-catalyzed tunable imidoylative cyclization of multifunctionalized isocyanides to construct diverse imine-containing heterocycles has been developed. Oxazol-5(4*H*)-one derivatives were obtained exclusively when allyl-2-benzyl(or allyl)-2-isocyanoacetates were used in the reaction with aryl triflates as electrophiles, whereas cyclic ketoimines were generated in the presence of aryl iodides with the allyl ester group remaining unreacted. The reactions proceeded smoothly under mild conditions with a wide functional group tolerance.



■ INTRODUCTION

Selective catalytic transformation of organic molecules is one of the most challenging tasks in modern synthetic chemistry.[1] The construction and modification of nitrogen-containing heterocycles are of vital importance, which are ubiquitous in natural products, pharmaceutical chemistry, and material sciences. In this regard, divergent heterocycles could be accessed by conditions-controlled selective reactions from the same molecules, which could facilitate the assembly of complex compounds.[2] For example, a solvent-controlled site-selective (2/3 position) alkenylation reaction of indoles was developed by the Gaunt group in 2005.[3] Tunable cyclization of 2-aryl cyclic 1,3-dicarbonyl compounds with alkynes and alkenes leading to fused or spiro N-heterocycles was reported by the Lam group using palladium or ruthenium catalysis,, respectively.[4] Very recently, Fan and co-workers reported an elegant annulation reaction of 2-arylindazoles with maleimides for the divergent synthesis of indazo-lo[2,3-*a*]pyrrolo[3,4-*c*]quinolinones or spiroindolo[1,2-*b*]indazole-11,3′-pyrrolidinones, which could be simply switched by resorting to different additives.[5a−d]

In the past decades, isocyanide was widely investigated in transition-metal-catalyzed insertion reactions,[6] multicomponent reactions,[7] cycloaddition reactions,[8] and even biorthogonal reactions[9] because of its diverse reactivities. As an equivalent of carbon monoxide (CO), C1 insertion reactions of isocyanide under palladium catalysis have been applied in the construction of numerous N-containing compounds.[10] Because of the adjustable R group of isocyanides, an efficient access to N-heterocycles by the strategy of functionalized isocyanide was successfully developed, in which multiple atoms (including both nitrogen and carbon atoms of isocyanide) were introduced to the formed cycle, demonstrating the advantage over carbon monoxide-participated carbonylation reactions. For instance, camptothecins,[11] indoles,[12] oxazoles,[13] phenanthridines,[14] β-carbolines,[15] tetrasubstituted imidazolones,[16] and cyclic imines[17] were successfully prepared by applying this approach. In 2017, the Zhu group developed the first enantioselective palladium-catalyzed C−H bond imidoylation reaction *via* a desymmetrization strategy (Scheme 1a).[18a] Later on, a site-selective imidoylative cyclization was reported by the same group (Scheme 1b).[19] The selectivity of the formation of six- or five-membered ketoimines was tuned by using bulky Ad_2PnBu or bidentate DPPB as the ligands. However, to the best of our knowledge, selective and tunable cyclization of isocyanides bearing different functional groups, which could offer divergent access to different types of heterocycles, remains unprecedented. Herein, we developed the first palladium-catalyzed imidoylative cyclization of multifunctionalized isocyanides, affording diverse imine-containing heterocycles. Oxazol-5(4*H*)-one derivatives were obtained exclusively when allyl-2-benzyl(allyl)-2-isocyanoacetates were conducted in the reaction with aryl triflates as electrophiles. When aryl iodides were used as the coupling partner, cyclic ketoimines were generated selectively with the allyl ester group remaining unreacted. A wide range of functional groups were

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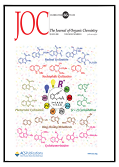

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Research Article

Development of Rapid Curing SiO_2 Aerogel Composite-Based Quasi-Solid-State Dye-Sensitized Solar Cells through Screen-Printing Technology

Shouzheng Jiao, Zhicheng Sun,* Jinyue Wen, Yuanyuan Liu, Furong Li, Qingqing Miao,* Weixia Wu, Luhai Li, and Yang Zhou*

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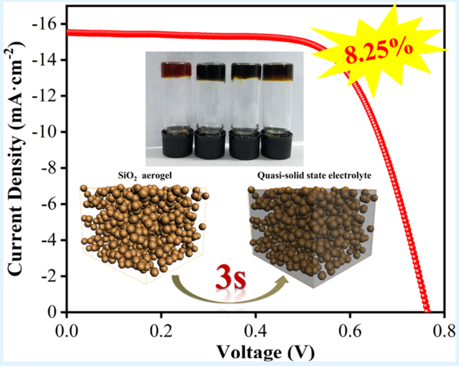

ABSTRACT: Grätzel's dye-sensitized solar cells (DSSCs) can readily convert sunlight into electricity, attracting considerable attention of global scientists. The fabrication efficiency of DSSCs was greatly limited by the slow fabrication (~3.5−24 h) of quasi-solid (QS) electrolytes to date. In this study, novel composites of SiO_2 aerogel with graphene (GR), multi-walled carbon nanotubes, or polyaniline were proposed in the fabrication of QS-state electrolytes. The morphology of these composites was characterized. The gels with SiO_2 aerogels as QS electrolytes of DSSCs can be rapidly cured in ~3 s. Using the screen-printing technology, these QS electrolytes can be readily utilized to construct the QS-DSSC to provide high efficiency and great stability. The photovoltaic parameters and interfacial charge-transfer resistances of the QS-DSSC incorporated with our synthetic composites were investigated in detail. Specifically, the SiO_2 aerogel composed of GR (SiO_2@GR) as a gel can greatly improve the performance of QS-DSSCs up to 8.25%. It is likely that these SiO_2 aerogel composite electrolytes could provide a rapid curing process in the preparation of QS-state DSSCs, which might be useful to promote the development of DSSCs for future industrialization.

KEYWORDS: *dye-sensitized solar cells, SiO_2 aerogel, quasi-solid-state electrolyte, rapid curing, screen printing*

INTRODUCTION

Grätzel's dye-sensitized solar cells (DSSCs) have attracted worldwide attention in the renewable energy field due to their ease of manufacturing, low cost, and environmental friendliness.[1] The photovoltaic performance and the long-term stability of DSSCs are highly dependent on the properties of electrolytes.[2] Specifically, the electrolyte serves as an electron donor, which can effectively reduce the oxidized dye. In addition, it plays a crucial role as an electron acceptor on the counter electrode, which is readily reduced by the electrons from external circuit, thereby completing the internal circulation of solar cells.[2−9] The traditional liquid electrolyte is composed of an iodide/triiodide (I^-/I_3^-) redox couple and additives in volatile organic solvents (such as acetonitrile[6,10] or ethylene carbonate[11,12]). Using this I^-/I_3^- and the cobalt liquid electrolyte, the power conversion efficiency (PCE) can reach up to 12.4 and 14%, respectively.[6,13] However, the organic solvents are greatly volatile and can easily leak out due to their evaporation. Therefore, a tight sealing technology is necessarily required during the fabrication of DSSCs. Furthermore, the corrosive I_3^- ion generated in the electrolyte can partially absorb visible light,[14−16] limiting the long-term stability and the PCE of DSSCs.

To solve these current problems of electrolytes, many efforts have been made on the development of nonvolatile liquid electrolytes (such as ionic liquids)[17−20] and the modification of liquid electrolytes incorporating gelling agents (such as polymers,[21−23] inorganic nanoparticles,[24,25] and supramolecular or low molecular mass organogelators[26−28]). In the gelling solidification approach, a quasi-solid (QS) sol−gel electrolyte in three-dimensional (3D) network structures can be generated through physical or chemical cross-linking to inhibit the leakage of the electrolyte and to improve the long-term stability of DSSCs.[29−32] As compared to the polymers as gelling agents, specifically, inorganic materials with abundant pores and large surface areas can bring about effectively interfacial interactions with liquid electrolytes to greatly improve the conductivity. More importantly, the presence of inorganic particles can significantly increase the viscosity of electrolytes without affecting the PCE.[33−36] To date, SiO_2,

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Genome Biology

RESEARCH Open Access

The genome evolution and domestication of tropical fruit mango

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Abstract

Background: Mango is one of the world's most important tropical fruits. It belongs to the family Anacardiaceae, which includes several other economically important species, notably cashew, sumac and pistachio from other genera. Many species in this family produce family-specific urushiols and related phenols, which can induce contact dermatitis.

Results: We generate a chromosome-scale genome assembly of mango, providing a reference genome for the Anacardiaceae family. Our results indicate the occurrence of a recent whole-genome duplication (WGD) event in mango. Duplicated genes preferentially retained include photosynthetic, photorespiration, and lipid metabolic genes that may have provided adaptive advantages to sharp historical decreases in atmospheric carbon dioxide and global temperatures. A notable example of an extended gene family is the chalcone synthase (CHS) family of genes, and particular genes in this family show universally higher expression in peels than in flesh, likely for the biosynthesis of urushiols and related phenols. Genome resequencing reveals two distinct groups of mango varieties, with commercial varieties clustered with India germplasms and demonstrating allelic admixture, and indigenous varieties from Southeast Asia in the second group. Landraces indigenous in China formed distinct clades, and some showed admixture in genomes.

Conclusions: Analysis of chromosome-scale mango genome sequences reveals photosynthesis and lipid metabolism are preferentially retained after a recent WGD event, and expansion of CHS genes is likely associated with urushiol biosynthesis in mango. Genome resequencing clarifies two groups of mango varieties, discovers allelic admixture in commercial varieties, and shows distinct genetic background of landraces.

Keywords: Mango genome, Whole-genome duplication, Photosynthesis, Urushiol, Germplasm

Background

Mango, commonly known as the "king of fruits," is one of the most popular fruits in the world [1]. Mango is widely cultivated in tropical and warmer subtropical areas in the world. India, China, and Thailand are the top three producers. In 2016, the global production of mango was 46.5 million tons, which ranks as the fifth most produced fruit crop worldwide (http://www.fao.org/faostat/). Mango fruits are mainly consumed fresh, while some are processed into products like nectar, juice, jam, and powder [1]. The fruits demonstrate attractive visual appearance and offer a favorable sensory experience to consumers, making them growingly popular among world consumers. Nevertheless, like many other Anacardiaceae plants such as poison ivy, sumac, and cashew, mango produces phenolic compounds (e.g., urushiols) that can induce contact dermatitis, an undesired quality for fresh mango consumption [2]. The biosynthetic pathways for these compounds

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东南亚生物多样性热点地区的形成与演化

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摘要:东南亚地处热带,生物多样性极为丰富,可分为 4 个热点地区:印度-缅甸区的中南半岛、巽他区(含马来半岛、婆罗洲、苏门答腊岛)、菲律宾区(菲律宾群岛)、华莱士区(苏拉威西岛、爪哇岛、马鲁古群岛、小巽他群岛等)。中南半岛在泥盆纪便已是欧亚大陆的一部分,在印度板块撞击欧亚大陆之后受挤压而出;巽他区来自于冈瓦纳古陆和澳洲古陆;菲律宾群岛部分来自于劳亚古陆的碎片向南漂移,部分来自于太平洋西南岛弧的向北迁移;华莱士区则是劳亚古陆碎片、太平洋西南岛弧以及澳洲古陆北侧碎片的组合。巽他区地处赤道,常年温湿;菲律宾区、华莱士区、中南半岛则都受到不同程度的季风气候决定的干湿季变动。地质历史和季风气候影响程度的不同,奠定了东南亚 4 个生物多样性热点地区的雏形。华莱士区保存有大量的早期被子植物原始类群如睡莲目(Nymphaeales)和木兰藤目(Austrobaileyales),是现代被子植物起源地和冰期避难所之一。巽他区(婆罗洲)和中南半岛是亚洲热带植物的现代分布中心和“进化前沿”,是整个东南亚地区重要的种源;而华莱士区的爪哇岛和小巽他群岛主要是物种迁入和中转的种库。这样的物种形成历史与迁移格局,塑造了东南亚 4 个生物多样性热点地区物种多样性水平与地理范围的基本格局。巽他区和印度-缅甸区曾在冰期通过陆桥相连,使得东南亚成为周边植物扩散交汇的一个“十字路口”。但是,人们对东南亚生物多样性热点地区的物种长距离扩散规律及植物地理学分区仍存在分歧;东南亚与邻近生物多样性热点地区如新几内亚岛、西高止山脉-斯里兰卡、中国横断山区的历史联系,还尚待深入解析。利用现代分子生物学技术,覆盖整个东南亚地区进行全域取样开展代表性类群的物种迁移与生物地理学研究,有望进一步揭示东南亚生物多样性热点地区的形成过程与演化趋势。

关键词:马来群岛;生物地理学;生物多样性热点地区;长距离扩散;物种形成

Origin and evolution of biodiversity hotspots in Southeast Asia

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Abstract: Southeast Asia has the largest archipelagos and probably has the most complex geological history in the world. The overwhelming monsoon climate further promotes the extremely rich biodiversityin Southwest Asia. A large number of primitive taxa of angiosperms including Austrobaileyales and Nymphaeales were found in this region. Several tropical groups such as *Cyrtandra*, *Aeschynanthus*, and *Begonia*are distributed in Southeast Asia, especially in Borneo Island and Indo-China Peninsula. Thus, Southeast Asia is not only a ‘museum’ of early angiosperms, but also acts as an ‘evolutionary front’ for some tropical taxa. Based on the plant distribution pattern, climate, and geographic history, the whole of Southeast Asia can be divided into four phytogeographic regions, i.e., Indo-China Peninsula (a part of Indo-Burma

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WU LX，YANG XB，LI DH，et al. Population structure and dynamics of *Schefflera octophylla* in Tongguling，Hainan Province [J]. Guihaia，2020，40(8) : 1101-1110.

海南铜鼓岭鸭脚木种群动态特征研究

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摘　要: **鸭脚木(** *Schefflera octophylla*) **是海南文昌铜鼓岭国家级自然保护区内滨海森林的优势种，也是海南其他地区热带森林常见伴生种。为深入了解该区滨海森林内鸭脚木种群的生存现状、更新机制以及未来发展的动态变化特点，该研究通过对海南热带滨海森林** 2.56 hm^2 **样地中鸭脚木种群的调查，以径级结构代替龄级结构，编制鸭脚木种群静态生命表，并结合种群动态量化指数、生存函数、时间序列预测模型等方法定量分析鸭脚木种群结构和数量动态变化。结果表明:** (1) **研究区域内共记录鸭脚木数量**2 814**株，按照径级大小共划分为** 12 **个龄级，龄级结构呈倒** J **字型，属于趋向稳定型种群。**(2) **该区鸭脚木的存活曲线趋于** Deevey-Ⅱ **型，种群各径级的死亡率相接近。**(3) **鸭脚木种群的量化指数显示，**$V_{pi}=30.685>0$，$V_{pi}'=0.236>0$，**说明该种群现处增长阶段并且相对稳定。**(4) **据时间序列模型预测鸭脚木种群在未来的** 3、6、9 a **内各龄级的种群个体数量整体呈现增加的趋势。综上分析认为，该区生境有利于鸭脚木种群的生长且该种群形成了良好的生存策略，其幼龄个体较多且后备资源丰富，能较好地补充各龄级个体自然死亡造成的损失，对森林的天然更新起到一定促进作用。**

关键词: 种群结构，静态生命表，生存分析，时间序列预测

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Population structure and dynamics of *Schefflera octophylla* in Tongguling，Hainan Province

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Abstract: *Schefflera octophylla* is the dominant species of coastal forest in Tongguling National Nature Reserve in Wenchang，Hainan，and is also a common associated species of tropical forests in other areas of Hainan. Based on the field investigation of sample plot (2.56 hm^2)，the dynamic characteristic changes of *S. octophylla* population were

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海南三亚滨海雨林、半落叶季雨林到落叶季雨林的植物群落多样性及种间联结研究

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摘要 为了探索三亚沿海地区（自东向西）从滨海雨林过渡到半落叶季雨林、落叶季雨林的物种多样性及种间关系的变化趋势，采用了植物群落学调查方法对三种植被类型进行群落调查，进一步使用物种丰富度指数（d_{GL}）、Shannon-wiener 指数（H）、Simpson 指数（P）和 Pielou 均匀度指数（E）来表征各植被类型的物种多样性水平，并使用联结系数 AC、共同出现百分率 PC 及 Spearman 秩相关系数检验三种方法来表征各植被类型的种间关系。结果表明：（1）从滨海雨林过渡到半落叶季雨林再到落叶季雨林的生态序列变化过程中，森林优势物种组成逐渐由喜湿树种过渡为耐旱性较强的树种；（2）生物多样性的变化与降雨量呈正相关，均呈现自东向西逐渐递减；（3）三种植被类型共有物种的种间关系分析反映出，三种植被类型种间关系松散，种间联结强度滨海雨林相对较高，半落叶季雨林与落叶季雨林相似；进一步表明从滨海雨林到落叶季雨林物种间的协同共存关系在减弱，排斥竞争关系在增强。无论是物种组成、物种多样性水平还是种间关系，半落叶季雨林与落叶季雨林更相似。

关键词 三亚滨海丘陵，物种多样性，联结系数，相关系数，年降水量
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Study on plant community diversity and inter-specific relationship of coastal rain forest，semi-deciduous monsoon forest to deciduous monsoon forest in coastal hills of Sanya City, Hainan Province

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Abstract To explore the changing trend of species diversity and interspecific relationship of the forests in Sanya coastal hills (from east to west) from coastal rain forest to semi-deciduous monsoon forest and deciduous monsoon forest, the phytocoenological investigation methods were used to investigate those three types of vegetation communities in our field works. The species diversity in different types of vegetation were analyzed by the species richness index (d_{GL}), Shannon-wiener index (H), Simpson Index (P) and Pielou evenness index (E). The interspecific relationships in different types of vegetation were analyzed by association coefficient (AC), co-occurrence percentage (PC) and Spearman's rank correlation coefficient test. The results showed that: (1) dominant species gradually changed from hygrophilous species to drought-tolerant species during the process of ecological sequence change from coastal rain forest to semi-deciduous forest and then to deciduous forest; (2) the change trend of species diversity was positively related to the annual precipitation, which decreased gradually from east to west; (3) interspecific relationship of the three vegetation types was relatively loose; while the intensity of interspecific association in coastal rain forest was relatively high, and shows likeness between the semi-deciduous monsoon forest and deciduous monsoon forest. Those indicated that the co-existence of species was weakened from coastal rain forest to deciduous monsoon forest while the repelling competition was strengthened. In conclusion, the species composition,

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淹水和盐胁迫对降香黄檀植株生理生态特性的影响

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摘　要: 为了研究降香黄檀(*Dalbergiaodorifera* T. Chen)对水淹、盐、水淹-盐组合胁迫耐受程度以及生理生态响应,设计了4个实验:对照(CKM)、水淹(水淹高度5 cm; WM)、盐处理(200 mM NaCl; SM)和水淹-盐组合(100 mM NaCl; SWM). 结果显示:经过6 d处理,3种胁迫处理均降低了叶片气孔导度g_s、净光合速率Pn、水势Ψ_l和相对含水量;在植株叶片激素水平上,生长素在WM中呈下调、在SM中呈上调状态,脱落酸在3个处理组均上调,玉米素核苷在SM和SWM中呈下调状态,赤霉素在WM中上调. 除此之外,叶片激素水平的胁迫响应具有处理差异性. 经过30 d处理,SM和SWM处理条件下的降香黄檀幼苗存活率分别为83.33%和66.67%. 此外,幼苗能经历130 d的水淹完全存活.

关键词: 叶片水势; ABA; 气孔导度; 净光合速率; 根系导水率

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降香黄檀(*Dalbergiaodorifera* T. Chen)是海南特有半落叶乔木,在广西、广东及福建等地亦有引种[1],是我国重要的红木树种. 其材质坚硬、纹理清晰、色泽美丽且气味芳香,具有很高的实用和艺术价值,广泛用于高档家具、艺术品及乐器制造[2]. 此外,其心材亦是中国传统中药材,称之"降香",有活血化瘀、理气止痛之功效[3],药用价值较高. 降香提取成分富含黄酮类、醌类、香精油以及酚类等活性物质[4-5],有抗氧化、抗炎、抗肿瘤等生物活性[6-7],是现代药理学研究的领域之一.

降香黄檀是慢生树种,在自然生长条件下心材形成较慢. 一棵20年树龄的此树,茎粗大约17~20 cm,其心材约2~5 cm[5]. 由于人类活动以及对其经济和药用价值的过渡开发,此树种已被我国列入重点保护野生植物[2]. 此外,降香黄檀能形成根瘤,在生物固氮和土壤改良上亦发挥着重要的生态作用[8-9]. 因此,扩大其种植范围,是平衡利用与保护,充分发挥其综合效益的可行之举. 在海南有很多滩涂、河流库塘等淡水湿地资源;在一些海岸区域也分布着由于海水漫灌导致的高盐土地,当这些高盐土地遭遇强降水等事件时亦会形成短时间渍水现象,使生长于此地的植物面临盐-水复合胁迫,但此时的盐浓度较降水之前因雨水稀释而降低. 针对降香黄檀的研究主要集中在活性成分的鉴定及药理学研究,非生物胁迫相关研究较少. 目前有学者在温度[10]等方面对降香黄檀展开研究,而针对水淹、盐,特别是两者复合胁迫的研究尚未见报道,关于降香黄檀如何响应水淹、盐,水淹-盐复合胁迫尚不清楚,需要开展此方面研究.

植物的固着性决定了其在生活史期间面临各种各样的环境干扰时,不能采取及时有效的空间逃避策略. 为了经受住短期或者长期干扰,植物采取了从胁迫信号感知与转导、基因选择性表达、蛋白质合成与修饰、代谢状态调整直到表型改变等一系列的应对策略. 这些应对策略因植物种类和耐受性差异而不同,大致涉及胁迫规避、短时间内代谢调整来忍受胁迫,或者通过生理、表型、结构等一系列变化长期适应胁迫等类型. 在水淹条件下,陆生植物可以通过糖酵解加速、酶促或非酶促抗氧化物质积累等代谢状态的调整短时间应对水淹导致的根部氧气匮乏以及由此带来的部分根系功能障碍,有些植物还能通过形成不定

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LI Youjia, YANG Fan, LÜ Baoqian, et al. Analysis of haplotype diversity of an invasive leaf-eating pest *Opisina arenosella*[J]. Journal of South China Agricultural University, 2020, 41(4): 76-81.

入侵性食叶害虫椰子织蛾的单倍型多样性分析

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摘要:【目的】分析危害棕榈科 Palmae 植物的一种重要入侵食叶害虫椰子织蛾 *Opisina arenosella* 单倍型在原产地和入侵地的分布特点，揭示椰子织蛾入侵我国的虫源信息。【方法】利用线粒体 *COI* 基因分析 16 个地理种群共计 172 个样本，比较椰子织蛾印度种群和入侵地 (中国、马来西亚和泰国) 种群的遗传关系。【结果】片段长度为 625 bp 的 172 条序列共鉴定出 12 个单倍型，包含 15 个变异位点，构成 2 个明显的单倍型分支，其中一个分支由 11 个单倍型 (IN1~IN11) 组成，均来自印度种群，单倍型 IN1 是 6 个印度种群的共享单倍型，IN2~IN11 为独享单倍型；另一个分支为单倍型 HAP，由来自中国、马来西亚和泰国的种群共享；HAP 与 11 个来自印度的单倍型 IN1~IN11 均存在 4 个变异位点。【结论】入侵地区的椰子织蛾种群来自同一基因型或者具有相同的入侵源；椰子织蛾种群入侵后受环境选择压力，在新栖息地产生新的突变或杂交。

关键词: 椰子织蛾; 线粒体 DNA; 单倍型; 地理种群; 入侵
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Analysis of haplotype diversity of an invasive leaf-eating pest *Opisina arenosella*

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Abstract: 【Objective】*Opisina arenosella* is an important invasive leaf-eating pest that attack Palmae plants. The goal was to analyze the distribution characteristics of haplotypes of *O. arenosella* in native and invaded zones, and reveal the insect source information of *O. arenosella* invading China.【Method】A total of 172 samples from 16 geographical populations were analyzed by mitochondrial *COI* gene, and the genetic relationship of *O. arenosella* from India and invading areas (China, Malaysia and Thailand) was compared.【Result】Twelve haplotypes were identified in 172 sequences with fragment length of 625 bp. Fifteen variation sites were detected in the haplotype alignment. Two obvious haplotype branches were formed, one of which was composed of 11 haplotypes IN1-IN11 and they were all from Indian populations. Haplotype IN1 was shared by

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大羽藓形态学性状及挥发性成分的 GC-MS 分析

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摘　要: 为探究传统中药大羽藓的形态学特征及挥发性化学成分，以海南黎母山的大羽藓 (*Thuidium cymbifolium* (Dozy et Molk.) Dozy et Molk.) 为研究材料，对其形态性状进行了描述，比较了该种与 4 个近缘种或变种的形态差异，并采用石油醚快速溶剂萃取技术结合 GC-MS 法对其挥发性物质进行萃取和化学成分分析。共鉴定出 31 种挥发性成分，占总组分的 91.1%，主要成分类型包括酯类 (25.48%)，萜类 (22.64%)，酮类 (20.64%) 及甾醇类 (10.61%); 主要成分为丁酸丁酯 (18.96%)、4−庚酮 (10.90%)、角鲨烯 (10.75%) 和 3−甲基−4−庚酮 (9.74%)。

关键词: 大羽藓; 形态学性状; 挥发性成分; 气相色谱−质谱

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苔藓植物是介于藻类和维管植物之间的高等植物类群，被划分为苔类植物门 (Marchantiophyta)、藓类植物门 (Bryophyta) 和角苔门 (Anthocerotophyta)3 大门类，全世界约有 21 000 种[1－2]。苔藓植物在数量上仅次于被子植物，但具有个体微小、结构简单、种间常混杂生长、形态上不易区分等特点，物种鉴定较困难，而且难以做到大量采集，因而该类群化学成分的研究及应用受到极大制约。目前，全世界仅对不足其物种总量 10% 的苔藓植物 (以苔类为主) 开展了化学成分的研究，分离和发现了大量为该类群所特有的结构新颖的次生代谢产物，表现出多样而显著的生物活性[3－5]。苔藓植物次生代谢产物中含有丰富的萜类、联苄、双联苄、黄酮类及脂肪酸衍生物等，被认为是苔藓植物具有抗细菌、抗真菌和抗病毒等活性的物质基础[6－8]，多种化合物还表现出抗肿瘤、抗氧化、昆虫拒食、调节植物生长以及预防有害生物体等生物学功能[7－10]。苔藓植物被誉为生物活性天然产物的宝库，然而对这一类群的研究和应用还十分匮乏，具有非常大的开发潜能。大羽藓 (*Thuidium cymbifolium* (Dozy et Molk.) Dozy et Molk.) 隶属于藓类植物门羽藓科 (Thuidiaceae) 羽藓属 (*Thuidium*)，多生于海拔 400～1 400 m 的热带和亚热带山地森林，分布于我国中部、东部及西南部[11]。该种为我国传统药用植物资源，可全草入药[12－13]。大羽藓不仅植株矮小，而且在形态上与同属的种类十分接近不易区分，尤其是与大羽藓分布区一致或分布区相重叠的一些种，如灰羽藓 (*T. pristocalyx* (Müll.Hal.) A.Jaeger)、绿羽藓 (*T. assimile* (Mitt.) A.Jaeger) 及短肋羽藓 (*T. kanedae* Sakurai) 等，在野外采集时仅凭借肉眼无法将它们准确鉴别，在室内通过显微镜观察标本进行鉴定也具有一定难度，而分类上的困难严重阻碍了人们对该物种在化学成分和药用方面的进一步了解及应用。因此，笔者对大羽藓的形态学性状进行了描述，阐明该种及其近缘种的形态差异，同时采用 GC-MS 法对其

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海南海口温泉真菌、细菌多样性及其环境影响因素分析

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摘要：【目的】海南海口含有丰富的温泉资源，对温泉微生物多样性进行研究，有助于进一步开发和利用海南温泉微生物资源。【方法】本文采用Illumina HiSeq高通量测序技术对海口3个温泉[海甸岛荣域温泉(S1)、火山口开心农场温泉(S2)和西海岸海长流温泉(S3)]水样中微生物ITS序列和16S rRNA基因V3−V4区进行测序及生物信息学分析，探究海口市3个不同区域的温泉真菌多样性与细菌多样性。【结果】(1) α多样性分析表明，真菌群落中，S3>S1>S2，而在细菌群落中，S2>S1>S3。β多样性分析表明，3个温泉真菌群落和细菌群落组成差异皆显著。(2) 分类分析表明，温泉真菌群落优势菌门为子囊菌门(*Ascomycota*)和担子菌门(*Basidiomycota*)，细菌群落优势菌门为变形菌门(*Proteobacteria*)、拟杆菌门(*Bacteroidetes*)、*Thermi*、硝化螺旋菌门(*Nitrospirae*)、绿菌门(*Chlorobi*)、厚壁菌门(*Firmicutes*)、绿弯菌门(*Chloroflexi*)、放线菌门(*Actinobacteria*)。(3) CCA (Canonical correspondence analysis)分析表明，3个温泉的真菌群落主要影响因子是温度，细菌群落主要影响因子是总磷。【结论】海南省海口市温泉中含有丰富的微生物资源，其微生物群落组成受多种环境因子影响，且影响真菌和细菌的主要环境因子不同。

关键词：海口，温泉，高通量测序，微生物多样性

温泉是一种地下自然涌出的泉水，水温较高于周围地区的气温，具有丰富的微生物资源[1]。泉环境与地球早期环境比较接近，独特理化特征促进了特殊微生物群体的形成，嗜热等适合极端环境条件生存的微生物聚集于温泉环境，形成了微生物多样性[2]。对温泉的微生物进行研究有助于认识生命的起源和进化，同时温泉中的微生物具有耐热的生理特性，使其成为各种高温酶的潜在来源而具有较高的应用价值[3–4]。

温泉一直是国内外研究的热点之一。目前国

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李歌, 凌少军, 陈伟芳, 等. 昌化江河谷隔离对海南岛特有植物盾叶苣苔遗传多样性的影响 [J]. 广西植物, 2020, 40(10): 1505-1513.

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昌化江河谷隔离对海南岛特有植物盾叶苣苔遗传多样性的影响

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摘 要: 为评估盾叶苣苔的遗传多样性与遗传分化格局,探索影响盾叶苣苔遗传变异地理分布的因素,该研究采集盾叶苣苔(*Metapetrocosmea peltata*)11 个种群 172 份材料,通过 PCR 扩增和测序分析核糖体转录间隔区(ITS)序列的变异式样。结果表明:(1)盾叶苣苔物种水平的遗传多样性很高($H_T = 0.998$, $\pi = 0.0235$),种群间基因流很弱($N_m = 0.04$)且存在强烈的遗传分化($G_{ST} = 0.375$)。(2)单倍型分析显示,盾叶苣苔的单倍型大多是种群特异的,仅白马岭与南茂岭种群有共享单倍型。(3)Mantel test 表明,遗传距离和地理距离存在一定相关性(相关系数 $r = 0.322, P = 0.010$)。(4)Structure 聚类分析将盾叶苣苔划分为 6 种遗传成分,其地理分布与昌化江河谷导致的隔离样式基本一致,基于 Nei 遗传距离的种群聚类分析支持这一结果,显示盾叶苣苔遗传多样性的分布受到昌化江河谷的隔离作用。(5)AMOVA 分析确定 67%的变异来自地区间,表明地理隔离是盾叶苣苔种群分化的重要因素。这表明昌化江及其支流所引起的海南岛山地内部隔离是盾叶苣苔种群发生强烈遗传分化的重要原因,从而导致盾叶苣苔在物种水平具有较高的遗传多样性。上述研究结果为海南特有苦苣苔资源盾叶苣苔的保护和可持续利用提供了理论指导,将有助于理解海南岛特有植物和其他海岛植物遗传变异的地理分布及其影响因素。

关键词: 盾叶苣苔, 遗传多样性, 遗传结构, 地理隔离, 岛屿特有种

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Effects of geographic isolation caused by Changhua River on genetic diversity of Hainan-endemic *Metapetrocosmea peltata* (Gesneriaceae)

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海南岛 1988—2018 年畜禽粪尿氮磷负荷量及环境效应

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摘要：【目的】揭示海南畜禽养殖业发展过程中粪尿氮磷养分流动情况及其对环境的影响，为区域农业发展规划和畜禽养殖结构调整提供参考。【方法】基于统计资料和文献数据，定量估算 1988—2018 年海南岛畜禽粪尿养分产生量、单位耕地面积养分承载量，并利用畜禽粪尿耕地负荷预警值和环境风险指数深入分析其对环境的影响，当畜禽粪尿耕地负荷预警值＜0.4 时，可认为对环境无威胁，而当环境风险指数在 1.00 以下时，对环境的风险可忽略，在安全数值以上即会对环境产生不同程度的影响。【结果】1988—2018 年间，海南岛畜禽粪尿产生量变化经历了 3 个阶段，1988—2005 年整体上升，2006—2008 年下降较多，此后缓慢发展并趋于稳定，到 2018 年畜禽粪尿产生量为 10.50×10^6 t，就养分产生量来看，粪尿氮磷年际间变化趋势相似，2005 年产生量最多，2006 年出现较大幅度下降，到 2018 年粪尿氮产生量为 7.41×10^4 t，粪尿磷产生量为 1.01×10^4 t。单位耕地面积氮磷负荷量也经历了先增加后稳定的过程，到 2018 年耕地氮负荷 168.80 kg·hm^{-2}，耕地磷负荷为 23.05 kg·hm^{-2}。2018 年区域间差异较大，东部和北部地区单位耕地面积氮磷负荷量较高，西部和中部地区偏低，其中氮和磷负荷最高的是定安（分别为 288.50 和 40.35 kg·hm^{-2}），最低的是东方（分别为 61.66 和 8.83 kg·hm^{-2}）。就环境效应来看，1988—2018 年海南岛畜禽粪尿耕地负荷预警值始终处于较高水平，大多数年份在 1.0—1.5，分级标准中达到Ⅳ级，对环境有较严重的威胁。2018 年，定安和澄迈等地预警值分别为 2.66 和 4.59，预警分级达Ⅵ级，对环境有很严重的威胁，仅东方处于安全水平，数值为 0.36，为Ⅰ级。就环境风险评价结果来看，海南岛耕地上畜禽粪污环境风险较高，近年随着养殖总量的控制有所降低，2018 年环境风险指数下降到 1.99（以氮计）和 1.32（以磷计）。在区域水平上，就氮素的环境污染风险，2018 年定安环境风险指数最高，为 3.39，东方最低，为 0.73；对于磷素的环境污染风险，东方环境风险指数最低，为 0.50，可认为磷素对环境潜在威胁较低，对环境有严重影响的是定安，风险值高达 2.31。总的来说，畜禽粪尿耕地负荷预警值和环境风险指数均表明海南岛畜禽粪污潜在环境风险大，从空间分布看，定安、万宁等东部市（县）环境风险要高于临高、东方等西部地区，并且大多数市（县）对环境均有较高程度的威胁。【结论】受养殖规模和耕地面积影响，海南岛单位耕地面积氮负荷较高，区域潜在环境风险不容忽视。因此，未来海南岛畜禽养殖发展规划更应着眼于污染物的控制以及区域优化布局和管理上，并通过减少畜禽粪尿环境排放和循环利用模式以实现海南岛畜禽粪污的资源化利用和绿色发展。

关键词：海南岛；畜禽粪尿；氮磷负荷量；环境效应

Nitrogen and Phosphorus Loads and Their Environmental Effects of Animal Manure in Hainan Island from 1988 to 2018

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海南岛农业绿色发展指标时空变化特征*

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摘　要: 海南自建省以来农业生产规模、结构及生产方式均发生了很大改变, 影响了其农业绿色发展程度。本文借助中国农业绿色发展指标体系, 利用 NUFER 模型(NUtrient flows in Food chains, Environment and Resources use), 选取并定量计算 1988—2017 年海南岛 20 项农业绿色发展指标, 研究其时空变化特征, 探究制约海南岛农业绿色发展的影响因素。研究表明: 30 年间海南省农业绿色发展水平总体呈下降趋势, 较低级别(Ⅲ、Ⅳ级)指标数量由 12 个增加至 15 个, 较高级别(Ⅰ、Ⅱ级)指标数量由 8 个减少至 5 个。随着蔬菜、水果等经济作物种植比例增加, 畜禽养殖规模扩大与集约化程度提高, 海南农业产值与社会发展水平不断升高, 农业产值和农业机械化投入分别从 0.62×10^4 ¥$\cdot$hm^{-2} 和 3 kW$\cdot$hm^{-2} 增加至 16.1×10^4 ¥$\cdot$hm^{-2} 和 13 kW$\cdot$hm^{-2}。30 年来农业资源(氮素、磷素、农药和农膜)过量投入, 其中农药和农膜的使用强度增幅最大, 分别从 8.0 kg$\cdot$hm^{-2} 和 0 kg$\cdot$hm^{-2} 增加至 41.9 kg$\cdot$hm^{-2} 和 34.7 kg$\cdot$hm^{-2}; 由于生产力水平较低, 导致养分(农田氮素盈余量、农田氮素径流量、农业源氨挥发等)环境排放量大幅增加, 农业源氨挥发和单位播种面积农田氮素盈余增幅最大, 分别从 61.0 kg$\cdot$hm^{-2} 和 152.1 kg$\cdot$hm^{-2} 增加至 131.4 kg$\cdot$hm^{-2} 和 297.9 kg$\cdot$hm^{-2}。农业资源投入过量、农牧分离导致的环境污染是制约海南岛农业绿色发展的主要原因。在空间上, 由于中部为山地林区, 是国家重点生态功能保护区, 开发力度较小, 因此沿海平原的资源投入增长更快、养分环境损失量更多, 经济增长、社会发展和农业生产 3 类指标提升更为迅速。今后海南岛应合理优化沿海地区种植结构, 提高生产管理水平, 加强农牧结合减少资源损失, 实现海南岛农业绿色发展。

关键词: 农业绿色发展; NUFER 模型; 种植业结构变化; 农牧系统; 热带农业

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Spatial and temporal characteristics of agricultural green development indicators in Hainan Island*

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