实验室代码：2009DP173234

2017 年度报告

实验室名称：中国科学院植物种质创新与特色农业重点实验室

归口领域：生命科学

依托单位：中国科学院武汉植物园

实验室主任：韩月彭

联系人：周玲

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填报时间：2018 年 3 月

目　录

第一部分 实验室基本情况

实验室中文名称	中国科学院植物种质创新与特色农业重点实验室		
实验室英文名称	Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, Chinese Academy of Sciences		
实验室代码	2009DP173234		
实验室类型	中科院重点实验室		
依托单位	中国科学院武汉植物园		
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学术委员会主任	朱玉贤		
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实验室网址	http://pg.wbgcas.cn/		
研究性质	应用基础研究		
归口领域	生命科学		
	学科 1	学科 2	学科 3
硕士点	植物学	园林植物与观赏园艺	
博士点	植物学		
博士后流动站	生物学		

定位			
面向国家特色农业植物资源收集保护与可持续利用需求，立足于园林园艺经济植物、能源植物、药用植物、水生经济植物等特色农业资源种质创新与开发利用，系统研究植物濒危机制与保育原理、关键类群的系统发育重建、谱系地理与分子进化，致力于植物资源评价与功能基因发掘、种质创新与新品种培育、功能化合物开发与产业化研究及技术创新，为我国特色农业的快速可持续发展提供理论与技术支撑。			
序号	研究方向	研究内容	对应研究所一三五
1	特色农业资源植物保育原理	特色农业植物资源遗传评价、核心种质和相应指纹图谱的建立、种质资源迁地保育原理；重要特色农业经济植物的系统发育与保育基因组学；重要农业植物资源遗传多样性分布格局、基因流动态和适应性进化。围绕资源保育与开发利用的共性机理，为特色农业资源植物可持续利用提供理论基础和关键技术支撑。	植物资源引种驯化与综合保育

2	特色农业资源植物优质和抗性性状的生物学基础	特色农业资源植物优良品质和特异抗性/耐性的生理生化基础；特种资源植物次生代谢的分子机制；优良品质、特异抗性/耐性相关的重要基因的克隆和生物学功能；重要功能基因的分子标签或紧密连锁分子标记的开发。针对特有的优良品质和抗性/耐性深入开展应用基础研究，阐明其分子和生理生化机制，并为这些优良性状向大田作物的转移提供基因和分子标记资源。	特色农业植物重要经济性状分子调控和新品种创制
3	特色农业资源植物的种质创新和可持续利用	研究特色资源植物的育种、繁殖、栽培和综合开发利用的技术体系，为特种资源植物的可持续利用提供优良种苗和相应的技术保障。重点培育适应性强并具有自主知识产权的特色资源作物新品种；特色资源植物的高效繁殖和转基因技术；研发特种资源植物的优质高产和绿色生态栽培技术体系。	县域特色生态农业模式研发与示范
参与四类机构情况			
1	参与中国科学院种子创新研究院华中分部		
2			

第二部分 年度总结

一、研究水平与贡献

1. 承担任务

本年度在研科研课题共 119 项，合同总经费 15943 万元，当年实到经费 2187 万元，其中 2017 年新增课题 30 项，新增科研合同经费 1794 万元。2017 年度获国家自然科学基金资助项目（2018 年开始执行）10 项，其中面上项目 7 项，青年科学基金项目 3 项，资助经费总额 495 万元。

主持完成的“特色猕猴桃新品种选育及产业化应用”获神农中华农业科技一等奖；以第二单位参加的“葡萄种质创新与新品种选育推广团队”获中国科学院科技促进发展奖；发表 SCI 论文 67 篇，其中本学科领域 1 区论文 46 篇，占 SCI 论文总数的 2/3 以上；国家授权发明专利 11 项；参与选育的桃新品种‘徽黄 2 号’和‘徽黄 4 号’均通过安徽省园艺学会园艺作物品种认定委员会认定。

列举不超过 5 项当年新增的重要科研任务。

序号	课题名称	课题编号	负责人及单位	起止时间	总经费（万元）	本年度实到经费（万元）	经费来源	类别	类型	研究方向
1	国家现代农业产业技术体系岗位科学家	CARS-30-1-02	韩月彭，中科院武汉植物园	2017.1-2020.12	280	70	其他	省部委	主要负责	2
2	滨海盐碱地植物资料利用与经饲草产业化开发	Y729451X03	陈良，中科院武汉植物园	2017.1-2018.12	150	60	中科院	中科院项目	主要负责	3
3	软枣猕猴桃生产示范及品系优化筛选	Y749361A01	王彦昌，中科院武汉植物园	2017.7-2023.6	150	25	其他	横向项目	主要负责	3
4	华中-本土植物清查与保护	KFJ-3W-No1-131	梁琼，中科院武汉植物园	2016.6-2019.5	120	0	中科院	中科院项目	主要负责	1
5	油桐副产品高值化加工利用关键技术研究	2017YFD0600703-5	吕世友，中科院武汉植物园	2017.7-2020.12	60	22.4	科技部	国家重点研发计划	参与	3

2. 代表性研究工作进展

	名称	本实验室固定人员参加名单	所属研究方向
代表性工作 1	东亚温带植物区系为主的特征成分系统发育和生物地理研究	王恒昌、李新伟、闫娟、孟爱平、孙延霞	1
简要介绍	植物之间的系统亲缘、地理分布格局的研究是生物学的基础，可为物种保育、保护区分区划界以及农业种质资源利用提供理论指导。对东亚温带区系的若干被子植物重要类群开展了分类、系统演化和生物地理学研究，发表论文 14 篇，主要进展如下： （1）在系统与进化研究方面，阐述物种在大的地理尺度和小的适应性进化模式中的演化机制。以蔷薇科委陵菜族为研究对象，该族包含超过 1000 个种，广泛分布于北温带，以高山草本类群为主，在青藏高原和欧洲地中海地区分别形成多样性中心。委陵菜族植物种类多、形态变异丰富，其中委陵菜属和羽衣草属发生过快速辐射分化、草莓属中存在大量杂交物种形成事件，给该族的分类学研究带来了很大困难，导致其属下种间分类一直比较混乱，族下属间分类系统也存在很大争议。中国西南横断山-青藏高原是全球生物多样性热点地区之一，也是委陵菜族的分化中心之一，孕育着委陵菜族大部分属和约一半的物种。在广泛的野外调查和标本馆查阅的基础上，基于核基因和叶绿体基因标记构建了委陵菜族的分子系统进化树，并探讨了：1）委陵菜族的系统进化历史；2）关键形态性状的进化及其分类学价值；3）委陵菜族的生物地理学；4）蕨麻属的分类修订及新种描述。通过祖先状态重建对委陵菜族三个关键的形态性状（雄蕊数目、花药结构和花柱类型）进行分析，明确了花药结构和花柱类型在委陵菜族族下属间水平上具有一定的系统学价值，适合作为族下系统的分类指标。提出了新的委陵菜族的分类系统，包含即草莓亚族、委陵菜属和蕨麻属三大分支，此分类系统既考虑了传统分类，避免了过多的分类学名称变更，又符合系统发育的理论框架，反映出了委陵菜族的进化历史。此外，发现委陵菜属始于新世中期起源于亚洲西南地区，随后向欧洲及北美地区迁移扩散，并在当地发生区系特有性辐射分化，并伴随着欧亚-北美洲际间的多次双向的迁移扩散，分别在青藏高原地区和地中海地区发生辐射分化，形成两大多样性中心。委陵菜属和蕨麻属在青藏高原地区具有很高的特有性，同时它们的起源及多样化在时间上与青藏高原的隆升过程相吻合，因此推测它们可能受到高原隆升的影响，物种形成速率加快，发生辐射分化。 （2）在族下属间研究的基础上，进一步深入到种水平上，探讨山莓草符合群的物种界限及其环北极间断分布模式的形成机制。综合形态、地理和分子的多种证据，发现在青藏高原地区存在山莓草的隐性种，不同隐种之间可能由于横断山的地理阻隔而发生生殖隔离进而分化成种。基于叶绿体基因标记的谱系地理学分析表明，山莓草起源于横断山地区，分别向东西两个方向通过白泠路桥和北大西洋路桥传播到北美，形成环北极间断分布的模式。 （3）委陵菜族是高山脆弱生态系统的重要组成部分，通过类似研究，可以确定物种的分布中心和分化中心，进一步对植物区系划分提出理论依据，并提出优先保护策略。也可以发现新的隐形种类以及适应性较强类群，为潜在的生态恢复提供种质资源。总之，系统与进化研究不仅可以认知植物之间的亲缘，而且也为生物多样性保护和某些资源植物的收集和利用提供指导。		

代表性工作 2	名称	本实验室固定人员参加名单	所属研究方向
	特色果树重要性状的遗传机理与新品种创制	韩月彭、钟彩虹、王彦昌、姚小洪、周晖、王鲁、张琼、李大卫、李黎、黄文俊、廖燎	2,3

简要介绍

在果树果实品质、抗性等重要性状的遗传机理及新材料创制等方面取得了一些创新性研究进展，正式发表 SCI 论文 15 篇，授权国家发明专利 8 项，申请国家专利 16 项；申报 2 个特色品种的专利权保护，完成 3 个专利品种的现场考察；2017 年猕猴桃新品种示范推广种植新增 28 万余亩，年均增加社会经济效益 38 亿余元。“特色猕猴桃新品种选育及产业化应用”获神农中华农业科技奖（科研类成果一等奖）。具体如下：

（1）揭示了猕猴桃网状进化与杂交物种形成机制：对猕猴桃属 25 个种 40 基因型进行了重测序，发现该属存在广泛的网状杂交基因流并形成了 11 个骨干类群，这些骨干类群促进了网状基因流的发生并形成更多类群，这是猕猴桃属物种表型和遗传多样性丰富的原因。研究结果发表于 *New Phytologis*t 杂志；同时参与了国际猕猴桃基因组联盟共同完成猕猴桃基因组重新组装，将之前红阳猕猴桃基因组中未组装的 164 Mb scaffold 锚定到染色体，并对错误注释进行了校正；发现了全基因组范围内复制现象，明确了染色体间的共线性。

（2）阐明了特色果树一些重要性状的遗传基础与规律：1）在果实品质方面，明确了栽培苹果和野生种连锁不平衡（LD）衰减均非常快，且栽培种与野生种连锁不平衡区域（LD block）在染色体上的分布明显不同，其中栽培苹果多数 LD block 位于果实品质性状 QTL 区间内，这表明了果实品质性状在苹果驯化过程中受到了选择；同时发现野生苹果抗坏血酸（Vc）含量显著高于栽培种，苹果 Vc 含量与果实酸度存在显著正相关，而与果实大小和甜度呈显著负相关，苹果幼果期 Vc 含量极高为成熟果实的 8-13 倍，暗示大果、低酸、甜度的选择会伴随着 Vc 含量下降的搭车效应。此外，完成了猕猴桃 29 份野生资源和 45 份栽培种成熟果实糖酸组分与含量的测定，发现栽培种的糖、酸各组分含量均高于野生种，但糖酸比非常接近，杂交后代果实糖酸组分与含量呈现偏父遗传；构建了基于 RAD 技术的猕猴桃高密度遗传图谱，利用山梨猕猴桃和中华猕猴桃种间杂交群体进行果实品质性状基因定位研究，获得了果实大小及糖酸含量 QTLs 及其分子标记。2）在性别遗传方面，在猕猴桃基因组重组抑制区检查的基础上，发现 25 号染色体上一个遗传多样性极低区段，在此区段发现了 4 个与性别共分离位点，并结合转录组研究获得了 1 个控制性别的候选基因。3）在抗性方面，与新西兰 Paul Raniey 院士合作完成了来自全球的 80 株猕猴桃细菌性溃疡病（Psa）菌株的基因组测序与分析，揭示了 Psa 起源于日本和韩国，然后从野生软枣猕猴桃迁移至栽培中华猕猴桃并全球传播的过程，研究结果发表在 *Genome Biology and Evolution* 上。完成了我国猕猴桃主产区真菌性软腐病、黑斑病及炭疽病的病原菌调查，确定拟茎点霉菌是我国猕猴桃果实软腐病的主要病原菌，葡萄座腔菌、盘多毛孢菌、链格孢菌属次要病原菌，且不同地区的主要致病菌种类存在明显差异；确定 *Nigrospora oryzae* 及 *Colletotrichum gloeosporioides* 分别是黑斑病及炭疽病的主要致病菌。这些结果抗性机理研究、抗病品种选育及防治等工作奠定了基础。

（3）资源收集与创新：收集了我国东北及山东软枣资源 30 余份以及中华、中越、黄毛、毛花等野生资源 20 余份，充实了国家资源圃；获得了 3000 余株杂交后代雌株，并完成了其开花和果实性状的系统评价；建立一套用于猕猴桃重要物种和品种鉴定的分子标记。

<table>
<tr><td rowspan="2">代表性工作 3</td><td>名称</td><td>本实验室固定人员参加名单</td><td>所属研究方向</td></tr>
<tr><td>药用植物活性成分发掘及其生物合成机理研究</td><td>章焰生、郭明全、陈方方、王欣、李长福、张春云</td><td>2</td></tr>
<tr><td>简要介绍</td><td colspan="3">以药用植物为研究材料，开展了具重要药用价值的新型化合物的创新发掘或已知化合物新功能的发现、重要活性成分分析的新技术与新方法的建立、重要药用代谢物的生物合成与调控及转运的分子机理解析等研究，主要进展如下：
（1）针对挥发性药用成分，建立了一套溶剂辅助固相基质饱和的顶空分析技术。该技术通过向固体粉末样品表面添加少量高沸点有机溶剂，使得固体表面形成饱和的单层溶剂膜，从而增大挥发物由内向外的传至动力，可有效提高固体基质中挥发物的顶空提取效率，该技术原理如下：当固体表面溶剂量较少未达到饱和时，溶剂润湿部分固体表面，增强萃取动力；当固体表面溶剂量较多达到过饱和时，提取的挥发物会溶解到溶剂相中，降低顶部空间的浓度和顶空分析灵敏度；当溶剂量刚好使得固相表面饱和时，可达到最大提取效率。该技术可用于提高药用植物中挥发物顶空分析灵敏度，目前该技术已在国际著名杂志 *Journal of Chromatography A* 期刊公开发表。
（2）利用 HPLC-UV/ESI-MS/MS 方法，比较分析了分别源自中国与非洲国家的三种花椒品种生物碱合成特征，评价了中非两地花椒生物碱对 4 种肿瘤细胞的抑制活性。明确了中非两地花椒生物碱无论是其分子结构还是含量特征均存在明显差异；在抗肿瘤活性方面，除了 *Z. ailanthoides* 花椒生物碱对 Hep G2 细胞的增殖抑制活性较弱，源自其它花椒品种的生物碱对 4 种肿瘤细胞的增殖均呈现出了较强的抑制活性，其抑制率为 60%-93%，花椒生物碱对 HT-29 肿瘤细胞增殖抑制活性最强，而季铵碱则是花椒中最具潜力的抗肿瘤细胞增殖活性生物碱类型。以上研究成果已在 *BMC Complementary and Alternative Medicine* 期刊上发表。
（3）在重要药用代谢物生物合成机制解析方面，以湖北恩施地区特色药用植物旋覆花为研究材料，成功解析了抗癌活性分子 C12,8 型倍半萜内酯的形成机理。通过植物特定细胞分离与代谢组学表征分析技术，明确了大根香叶烯 A 酸（Germacrene A acid）是 C12,8 型倍半萜内酯化合物的母体结构；结合植物分子生物学以及生物化学技术，分离了控制该类化合物内酯环形成的关键 P450 氧化酶基因(该基因被命名为 *CYP71BL6*)，揭示了该类化合物 C12,8 内酯环形成机理如下：即大根香叶烯 A 酸在特种 P450 氧化酶 CYP71BL6 作用下，在其 C8 位置生成羟基，该羟基由于位邻效应随即攻击 C12 位的羧基，经植物细胞酸性环境下自由脱水从而形成该类化合物的活性基团 C12,8 内酯环。相关成果已在植物学国际权威期刊 *Plant Journal* 上发表。
（4）在重要药用代谢物生物合成调控方面，基于转录组文库筛选，发现了液泡分选蛋白 DID2 控制了萜类药物的生物合成。过量表达 *DID2* 基因显著提升了萜类药物的合成滴度，进一步研究表明 DID2 是通过与萜类代谢物生物合成途径某些关键酶形成蛋白复合体，增强了这些关键酶的蛋白稳定性，从而提升了萜类药物的合成通量。相关成果已在国际 SCI 杂志 *Frontiers in Microbiology* 期刊上发表。</td></tr>
</table>

<table>
<tr><td rowspan="2">代表性工作 4</td><td>名称</td><td>本实验室固定人员参加名单</td><td>所属研究方向</td></tr>
<tr><td>莲基因组学与遗传育种</td><td>杨平仿、宋世勇、石涛、杨美、邓显豹、杨东</td><td>2</td></tr>
<tr><td>简要介绍</td><td colspan="3">莲是真双子叶基部类群，也是我国重要的水生经济植物，具有重要的研究与利用价值。在已完成中国古代莲全基因组测序和注释的基础上，进一步开展了莲功能基因组学研究，并在 miRNA 表观遗传及生物碱活性物质合成调控方面取得了进展，具体如下：
（1）莲 miRNA 的相关研究：在全基因组范围对温带莲与热带莲 miRNA 序列差异进行分析，发现 miRNA 序列分化加速温带型和热带型莲发育过程中靶基因表达模式的分化，对地下茎分化具有重要推进作用。
（2）莲资源的遗传结构特征：基于莲的种质资源丰富的遗传多样性，在全基因组范围内解析了莲的遗传结构和功能基因进化，研究结果为莲的核心资源的保育及分子育种提供了技术支撑；同时还以温带莲（花莲、藕莲、子莲、野生莲）、热带莲（泰国莲）和美洲黄莲为研究材料，结合基因组重测序和群体变异位点分析，揭示了莲各类种质资源的遗传结构和进化关系；发现了促进温带莲与热带莲特异性状遗传及表型分化相关的关键候选基因。
（3）活性物质生物碱合成与调控：生物碱是荷叶中的主要活性成分，具有降脂降压的功效，但目前荷叶碱的生物合成与调控机制尚不清楚。选用荷叶碱含量存在显著差异的两个莲品种为研究材料，开展了荷叶碱的比较转录组学研究，获得了荷叶碱代谢的差异基因，包括生物碱合成途径中已知基因 NCS、6OMT、CNMT、NMCH、4'OMT 和 CTS；在此基础上进一步构建了荷叶碱的 WGCNA 共表达网络图，鉴定了荷叶碱生物合成途径下游路径的候选基因，研究结果不仅有助于深入解析莲生物碱代谢调控的分子机制，而且为高生物碱品种选育提供了分子工具。</td></tr>
</table>

代表性工作 5	名称	本实验室固定人员参加名单	所属研究方向
	特色经济植物抗逆分子机制及推广应用	陈良、辛海平、李惠英、胡涛、谢燕	2,3
简要介绍	开展了特色经济作物响应非生物胁迫的应答机理研究，在植物耐寒、抗盐机制方面取得了进展，主要成果如下: （1）阐明棘孢曲霉真菌在狗牙根耐盐方面的应用潜力：狗牙根具有生长快，适应能力强等特点，广泛用作饲草和草坪草，但缺乏高耐盐碱品种，限制了狗牙根在我国盐碱地区的广泛应用。近年来，利用微生物改善植物的耐盐性受到很多学者的关注。棘孢曲霉是我们前期从狗牙根根际土壤中分离筛选出的一株耐镉真菌，为了明确棘孢曲霉对狗牙根耐盐能力的影响，我们对棘孢曲霉的耐盐及促生特性进行评价，并通过外源添加试验，研究了棘孢曲霉对狗牙根生长、光合及离子平衡的影响。结果显示，棘孢曲霉真菌具有很好的耐盐能力及促生特性，依据前人对菌类耐盐性的分类标准，可被划分为“轻度嗜盐耐盐菌”。此外，棘孢曲霉可减轻狗牙根盐害，具体表现为促进根系生长，提高抗氧化能力及光合作用能力，提高离子平衡能力。相关研究成果已在*Molecular Plant-Microbe Interactions*国际期刊上发表。 （2）发掘鉴定了参与狗牙根应答低温、高盐以及盐寒（高盐+低温）双重胁迫的miRNA及其靶基因：低温、盐，尤其盐寒双重胁迫是限制狗牙根生长发育及推广应用的主要因素，为了揭示狗牙根miRNA及其靶基因调节的逆境胁迫应答，我们以狗牙根耐寒种质为实验材料，利用高通量测序结合转录组数据，构建了4个（对照、低温、高盐、低温高盐双重胁迫）小RNA文库，获得了449个成熟的miRNA，挖掘出203个新的miRNA，其中包括102个差异表达的miRNA。差异表达miRNA的2200个靶基因也被预测，其中涉及多个与胁迫相关的转录因子。相关研究成果已在*Environmental and Experimental Botany*国际期刊上发表。 （3）建立了山葡萄愈伤转化体系，为研究其抗寒旱机理提供了重要平台：我国酿酒葡萄主栽区冬季低温干旱，目前所种植的欧亚种葡萄需要埋土防寒，导致种植成本居高不下，是制约我国葡萄和葡萄酒产业发展的主要因素之一。山葡萄是葡萄属属种最抗寒旱的种质，对其抗性机理的挖掘将会为培育适合我国气候条件的酿酒葡萄新品种提供理论依据。课题组在2017年开展了包括*WRKY14*，*MYB-like*等胁迫相关基因的功能验证。同时，利用山葡萄组培苗叶柄，建立了愈伤转化系统，为进一步研究抗性相关基因的在胁迫过程中的调控机理提供了平台。相关研究工作于2017年获得中国科学院科技促进发展奖（武汉植物园为第二单位） （4）耐盐草坪草示范推广成效显著：在中科院STS项目“滨海盐碱地植物资源利用与经饲草产业化开发”支持下，目前已在山东东营建立了耐盐草坪草规模化繁育基地，显著提升了当地的生态和社会效益。		

3. 合作研究的组织情况与实施效果

聚焦重点突破方向，积极响应国家“走出去”战略，不断推进国际化进程。根据重点实验室国际合作中长期发展规划，2017 年继续稳步推进国际交流与合作工作，科研合作国际化水平和国际科技影响力有力进一步提升。

目前，实验室已与美国康奈尔大学、美国伊利诺伊大学、美国肯塔基大学、美国克莱姆森大学、法国波尔多大学、新西兰植物和食品研究所、澳大利亚昆士兰大学、日本名古屋大学和筑波大学等国外高校或科研院所建立了长期合作关系。本年度共有科研人员 20 人次赴国外参加国际会议或开展合作交流；13 人次在国际学术会议上作报告；邀请国（境）内外专家来室讲学 24 人次，其中来自国（境）外单位的专家 9 人次。

在国际合作重点突破方向上，推进“中-非联合研究中心”建设，服务“一带一路”倡议，不断推进国际化进程，科研合作水平显著提升，国际影响力不断加强。目前在研院国际合作局海外科教基地项目 5 项，合同总经费 1270 万元，年度到账经费 207 万元。本年度共 8 人次赴肯尼亚执行项目并开展合作交流。

本年度与国（境）外单位合作发表SCI论文9篇，其中1区论文4篇，闫娟副研究员与奥地利维也纳大学和瑞士伯尔尼大学合作论文“Population transcriptomic characterization of the genetic and expression variation of a candidate progenitor of *Miscanthus* energy crops”在权威期刊*Molecular Ecology*上发表，该刊物影响因子6.086，JCR分区TOP 5.88%。

加强与地方的科技合作，签订北京市门头沟区软枣猕猴桃（奇异莓）工作站合作协议（北京清水云峰果业有限公司）、浙江省江山市猕猴桃产业发展合作协议（江山市林业局/市政府）、湖北省兴山县白及产业发展科技合作协议（宜昌神草生态科技有限公司）。

本年度共邀请了24位国内外专家到重点实验室开展学术交流，具体情况如下：

序号	时间	报告人	报告人单位	报告题目
1	5 月 24 日	周功克	中科院青岛生物能源与过程研究所	植物生态修复及资源化利用
2	5 月 24 日	李强	加拿大科学院和 University of Saskatchewan	Dynamic Lipid Metabolism in Plants
3	6 月 5 日	刘继红	华中农业大学	植物多胺合成转录调控网络解析：以柑橘 ADC 基因为例
4	6 月 5 日	徐强	华中农业大学	柑橘基因组及无融合生殖基因的克隆
5	6 月 6 日	邹吉涛	加拿大国家研究院植物生物技术研究所	植物甘油脂代谢研究及生物技术应用
6	6 月 8 日	张蕾	Elsevier（励德爱思唯尔科技）出版社	Understanding and Benefiting from the Publishing Process

7	6 月 16 日	郭振飞	南京农业大学	狗牙根抗逆基因功能研究
8	6 月 22 日	张献龙	华中农业大学	棉花纤维发育及基因组驯化生物学
9	6 月 22 日	郭文武	华中农业大学	分子辅助柑橘细胞工程与种质创新
10	6 月 29 日	郝玉金	山东农业大学	光温和糖信号调控苹果果实品质的调控网络
11	7 月 25 日	梅洁	华中农业大学	鱼类性别异形和性别决定的遗传基础及其在育种中的应用
12	7 月 25 日	殷平	华中农业大学	Pentatricopeptide Repeat Proteins: Coding for base; Decoding for us
13	8 月 31 日	宋士勇	新加坡国立大学	OsFTIP1 Regulation of Florigen Transport in Rice
14	10 月 26 日	杨继良	华智水稻生物技术有限公司分子育种中心	SNP 技术使植物分子育种乘高铁快速奔驰
15	10 月 27 日	吴俊	南京农业大学	梨基因组和分子遗传育种
16	11 月 4 日	肖建波	澳门大学	天然多酚的稳定性
17	11 月 9 日	Jia-Long Yao	新西兰植物与食品研究所	The ABC model of apple fruit development
18	11 月 9 日	徐娟	华中农业大学	果实品质相关转录因子的筛选及验证
19	11 月 16 日	徐明良	中国农业大学	ZmAuxRP1, encoding an auxin-regulated protein, coordinates the balance between growth and defense in maize
20	12 月 2 日	刘爱忠	中国科学院昆明植物研究所	蓖麻种子油脂累积与基因印迹研究
21	12 月 4 日	伍建林	澳门科技大学	基于衍生化的 Carboxylomics 分析方法及应用
22	12 月 4 日	李娜	澳门科技大学	基于 LC-MS 研究药物活性代谢产物的肝毒性
23	12 月 6 日	范恩国	中国医学科学院	桶状蛋白与新型抗生素开发
24	12 月 12 日	陈国防	美国圣约翰大学	Pristine metal nanostructures: green synthesis and applications

二、队伍建设和人才培养

1. 队伍结构与团队建设

重点实验室现有固定人员 72 名，包括正高级职称人员 14 人；副高级职称人员 37 人，其中 40 岁以下青年人员 23 人（截止 2017 年 12 月 31 日），占副高级人员总数的 62%；中级职称人员 19 名。实验室技术及管理人员 9 名。

本年度引进“中国科学院百人计划”1 名，青年博士 2 名，晋升副研究员 4 名。拥有 2 个硕士点，1 个博士点和 1 个博士后流动站。现有研究生导师 32 名，其中博士生导师 10 名，硕士生导师 22 名；在读研究生 79 名，其中博士生 35 名（含留学生 5 名），硕士生 44 名（含留学生 5 名）。本年度毕业研究生 20 名，其中博士生 7 名，硕士生 13 名（含留学生 2 名）。在站博士后 1 名，本年度出站博士后 1 名。

本年度钟彩虹研究员获“中国科学院特聘研究员骨干人才”称号；韩月彭研究员入选“农业部现代农业产业技术体系岗位科学家”；陈良和杨美副研究员入选“中国科学院青年创新促进会”。

实验室现有“中国科学院百人计划”入选者 8 名，国务院政府特殊津贴获得者 1 名，湖北省政府专项津贴获得者 1 名，湖北省突出贡献中青年专家 3 名，中国科学院特聘研究员（骨干人才）3 名，中国科学院青年创新促进会会员 3 名，农业部现代农业产业技术体系岗位科学家 1 名。实验室基本形成了一支以高水平学术带头人为核心、中青年科学家为中坚力量、结构合理的科研队伍。

2. 实验室主任和学术带头人简介

姓名	韩月彭	身份类型	实验室主任
性别	男	年龄	49 岁
最后学位	博士	获得最后学位所在院校	扬州大学
任职时间	2017 年	依托单位职务	研究员
学习及工作经历	2008/11-至今　中国科学院武汉植物园，研究员，从事果树遗传与改良研究 2016/10-2016/12　新西兰植物食品研究院合作研究，新西兰Li Lairong 奖学金资助 2004/08-2008/10　美国伊利诺伊大学厄巴纳－香槟分校，博士后，从事苹果基因组学研究 1998/09-2004/06　扬州大学，硕士、博士研究生，作物学专业		
研究方向	果树果实品质性状遗传与改良		
代表性工作	主要从事果树遗传与改良研究，在果实色泽与风味遗传研究方面形成特色并取得了开创性成果，实现了我国首例基于图位克隆法分离果树功能基因，致力于果实品质分子辅助选择育种；以通讯和第一作者发表 SCI 论文 50 余篇，获国家授权专利 3 项。		
个人荣誉	中科院“百人计划”和“特聘研究员”；湖北省有突出贡献的中青年专家和湖北省科协“科技创新源泉工程”创新创业人才；新西兰 Li Lairong 奖学金；2017 年被聘为农业部现代农业产业技术体系岗位科学家。		
学术兼职	2009 年至今担任湖北省遗传学会理事；2017 年至今中国园艺分子育种学会理事。		
学术期刊兼职	国际期刊 Plant Molecular Biology Reporter、Canadian Journal of Plant Science、Horticulture Research 副主编，PLoS One 编委，国内期刊《植物科学学报》副主编。		

姓名	章焰生	身份类型	实验室副主任
性别	男	年龄	45 岁
最后学位	博士	获得最后学位所在院校	中国科学院植物研究所
任职时间	2017 年	依托单位职务	研究员
学习及工作经历	2010/04-至今　中国科学院武汉植物园，研究员 2008/04-2010/03　加拿大国家植物生物技术研究所，助理研究员 2006/04-2008/03　加拿大国家植物生物技术研究所，博士后 2005/04-2006/03　美国丹佛斯植物科学中心，博士后 2001/09-2005/03　中国科学院植物研究所，获博士学位		
研究方向	天然产物生物合成		
代表性工作	在天然药用物质代谢机制及其生物合成方面取得了很好的研究进展，相关成果已在 *Journal of the American Chemical Society*、*Plant Biotechnology Journal* 、*Plant Journal* 以及 *Journal of Biological Chemistry* 等知名杂志上发表 SCI 研究论文 40 余篇，代表性学术成果如下： 1）在药用植物药用品质形成机制解析方面，成功分离了著名抗疟药青蒿素合成路径关键还原酶基因，引领了国内外青蒿素合成生物学研究热潮，相关成果发表于国际著名生物化学杂志 *Journal of Biological Chemistry*，已被他引 SCI200 余次；成功分离了中国传统中药葛根素合成路径中的关键糖基转移酶基因，解析了该糖碳苷形成机制，相关成果发表于国际著名植物学杂志 *Plant Journal*。 2）在重要药用成分生物合成体系建立方面，基于抗癌物质白黎芦醇代谢路径上下游关键酶催化特征，构建了高效地催化了白黎芦醇的生物合成非天然酶分子，实现了白黎芦醇在酵母细胞中的高效合成，相关成果发表于世界顶级化学杂志 *Journal of the American Society Chemistry*；同时实现了抗癌原料药白桦脂酸的在酵母系统生物合成，为白桦脂酸产业化提供了技术支撑。		
个人荣誉	2010 年入选中国科学院“百人计划”		
学术兼职	2012 年至今担任中国国家自然科学基金委植物学学科基金项目评审人； 2012 年至今担任中国科学院大学药学专业硕士培养教指委员会委员； 2014 年至今担任能源林产业技术创新战略联盟理事； 2014 年至今担任天津市药用植物细胞规模培养企业重点实验室学术委员会委员； 2015 年至今分别担任中国中药产业技术创新战略联盟常务理事、湖北省黄姜产业技术创新战略联盟理事。		
学术期刊兼职	2010 年至今担任《植物科学学报》编委、2017 年至今担任国际 SCI 杂志 *Frontiers in Plant Science* 审稿编委		

姓名	杨平仿	身份类型	副主任
性别	男	年龄	43 岁
最后学位	博士	获得最后学位所在院校	中国科学院植物研究所
任职时间	2017 年	依托单位职务	研究员
学习及工作经历	2009/12-至今　中国科学院武汉植物园 研究员 2007/03-2009/12 美国密西根州立大学 博士后 2005/11-2006/11 香港科技大学 访问学者 2002/09-2005/07 中国科学院植物研究所 博士 1999/09-2002/07 华中农业大学 硕士 1993/09-1997/07 西北农林科技大学 学士		
研究方向	水生植物莲的基因组学及遗传育种		
代表性工作	利用莲基因组测序数据构建了莲基因组信息数据库，开展了莲花色、莲子、莲藕发育与产量等性状的遗传机制研究工作。对莲 miRNA 开展相关研究，初步探索了 miRNA 目标基因的进化规律，并对对热带连及温带莲的进化规律进行了研究。相关研究结果已经在 *Plant Journal*、*Journal of Integrative Plant Biology*、*Plant & Cell Physiology*、*Database* 等期刊上发表。		
个人荣誉	2011 年入选中国科学院“百人计划”		
学术兼职	Asia Oceania Agricultural Proteomics Organization （委员），中国生物化学与分子生物学会蛋白质组学专业委员会（委员），中国植物学会种子科学与技术专业委员会（委员），中国园艺学会水生蔬菜专业委员会（理事），湖北省遗传学会（理事）		
学术期刊兼职	Scientific Reports 和 Plos One 编委		

姓名	钟彩虹	身份类型	学术带头人
性别	女	年龄	49 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	猕猴桃专类园（国家猕猴桃种质资源圃主圃）主任
学习及工作经历	2015.9-至今，中国科学院武汉植物园，猕猴桃种质资源与育种中心，研究员 2013.1-2015.8，中国科学院武汉植物园，猕猴桃种质资源与育种中心，国家猕猴桃种质资源圃主圃主任，一级副研究员。 2008.9-2012.6，中国科学院大学，植物学博士 2008.05-2012.12 中国科学院武汉植物园，猕猴桃专类园（国家猕猴桃种质资源圃主圃）主任，一级副研究员 2006.10-2008.04 中国科学院武汉植物园，猕猴桃专类园，二级副研究员。 2005.01-2006.09 湖南省农业科学院园艺研究所，果树基地部，部门负责人，副研究员 1998.01-2004.12 湖南省农业科学院园艺研究所，果树基地部，部门负责人，助理研究员 1992.8-1997.12 湖南省农业科学院园艺研究所，落叶果树室，实习研究员 1988.9-1992.6 湖南农业大学，园艺学院果树专业，农学学士		
研究方向	果树种质资源收集、保护和开发利用；猕猴桃遗传育种；猕猴桃栽培生理；猕猴桃产业推广		
代表性工作	国际国内知名的猕猴桃育种、栽培专家，26 年来致力于猕猴桃种质鉴定和创新、新品种培育及栽培研究，先后主持或参加各类科研开发项目 50 余项，带领团队取得了系列创新性成果，为主培育优异新品种 17 个，获得授权国家发明专利 12 项，累计发表论文 84 篇，其中 SCI 论文 24 篇，先后出版中英文专著 10 部，累计推广‘东红’、‘金艳’等优良品种 32 万余亩，研发的新技术应用 100 余万亩。2017 年育种成果获得农业部神农中华农业科技奖（科研类）一等奖（第二完成人）、2016 年主持的种质创新科研团队获得中国科学院科技促进发展奖，2015 年育种成果获得湖北省技术发明奖一等奖（第二完成人），为提高我国猕猴桃领域育种、栽培技术水平，促进猕猴桃产业发展做出了积极的贡献。		
个人荣誉	多次获得中科院“优秀共产党员”、湖北省直机关“优秀共产党员”、湖北省“女职工建功立业标兵”等各级荣誉称号。		
学术兼职	中国园艺学会猕猴桃分会理事长、中国园艺学会理事、中科院奇异莓专家工作站首席科学家		
学术期刊兼职			

姓名	李夜光	身份类型	学术带头人
性别	男	年龄	55 岁
最后学位	硕士	获得最后学位所在院校	中国科学院武汉植物研究所
任职时间		依托单位职务	研究员
学习及工作经历	1987 年至今，在中国科学院武汉植物园工作；1995-1996 年，在澳大利亚 Murdoch 大学微藻生物技术研究室访问学者。		
研究方向	微藻生物技术		
代表性工作	在国内率先完成规模培养红球藻生产虾青素中试，与云南绿 A 公司合作，实现红球藻产业化；筛选出适合规模培养的产油微藻优良藻种油球藻 *Graesiella* sp.WBG-1，建立了开放池规模培养产油微藻的全套技术工艺，1000m^2 开放池培养油球藻 *Graesiella* sp.WBG-1，总脂含量超过 30%。		
个人荣誉	国家政府特殊津贴获得者；湖北省有突出贡献的中青年专家；武汉市第二届优秀科技青年创业奖；第五届湖北省青年科技奖；云南省省院省校合作先进个人。		
学术兼职	中国海洋湖泊学会理事；中国藻类学会常务理事		
学术期刊兼职			

姓名	王恒昌	身份类型	学术带头人
性别	男	年龄	50 岁
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	研究员
学习及工作经历	2012 年-至今，中国科学院武汉植物园研究员 2006 年 1 月-2007 年 1 月，美国佛罗里达大学访问学者； 2016 年 12 月-2017 年 3 月，美国东卡罗莱纳大学访问学者 2009 年，中国科学院武汉植物园研究员 2006 年，中国科学院武汉植物园副研究员 2002 年-2005 年，中国科学院武汉植物园，博士 1997 年-2000 年，中国科学院昆明植物研究所，硕士		
研究方向	植物分类、系统发育与生物地理学		
代表性工作	2009 年以第一作者在 *PNAS* 发表了在美国访问学者期间的工作，对被子植物最大的分支蔷薇类的系统发育和演化开展了分子生物学研究；目前主要结合形态、生态和分子生物学手段开展被子植物若干关键类群的生物多样性和进化研究。其中，对蔷薇科委陵菜族的分类和系统发育及生物地理开展了研究；对真双子叶植物基部类群的系统学关系进行了梳理；对真菊类基部类群的安息香科的系统发育开展了研究。以上工作取得了较好研究成果，以通讯作者在国际著名期刊 *Journal of Biogeography*、*Molecular Phylogeny and Evolution*、BMC Genomics 等发表论文。目前主要开展东亚植物区系的生物地理学工作。		
个人荣誉			
学术兼职			
学术期刊兼职	Plant Diversity 编委		

姓名	郭明全	身份类型	学术带头人
性别	男	年龄	43 岁
最后学位	博士	获得最后学位所在院校	中国科学院长春应用化学研究所
任职时间		依托单位职务	研究员
学习及工作经历	2012/08－至今 中国科学院武汉植物园，研究员 2007/10－2012/07 美国南加州大学，研究助理 2006/03－2007/09 美国加州大学劳伦斯伯克利国家实验室，博士后 2004/07－2006/02 美国国家卫生研究院，博士后 1998/09－2004/03 中国科学院长春应用化学研究所，硕博连读、博士研究生		
研究方向	药用植物化学生物学		
代表性工作	主要开展了富含生物碱成分的非洲特色药用植物石蒜、石松和花椒中生物碱类成分的结构、活性及其作用机理的研究，共分析鉴定出 150 余个具有生物活性的生物碱类成分。在生物活性的研究中，发现这些生物碱类成分对人肝癌、肠癌和胃癌细胞均具有显著的抗肿瘤细胞增殖活性。同时，发展了基于药物分子靶标（如 DNA 拓扑异构酶等）的亲和超滤筛选方法，成功筛选到具有很强抗肿瘤细胞增殖活性的化合物，并对部分化合物进行了分子模拟对接分析和细胞药理学的验证。这些成果累计在相关领域发表 TOP 30%以上的 SCI 论文 20 余篇。		
个人荣誉	无		
学术兼职	2016-2018 年先后 3 次担任欧洲和亚洲植物化学会举办的国际会议学术委员会成员，分会主持。		
学术期刊兼职	Current Analytical Chemistry 客座编辑 Phytochemical Analysis 编委与客座编辑		

姓名	吕世友	身份类型	学术带头人
性别	男	年龄	43 岁
最后学位	博士	获得最后学位所在院校	解放军军需大学
任职时间		依托单位职务	研究员
学习及工作经历	2013/02-今中国科学院武汉植物园，资源植物研究中心，研究员 2010/10-2013/01，沙特阿拉伯国王科技大学，博士后 2007/01-2010/09，美国普渡大学，园艺系，博士后 2004/09-2006/12，清华大学，生物科学与技术系，博士后 2004/07-2006/10，吉林大学，农学部，讲师		
研究方向	能源植物油桐高油脂新种质创新；油桐高油脂合成及调控关键基因鉴定；植物蜡合成及调控机制探讨及作为新能源材料的开发利用；植物蜡响应逆境胁迫机理探讨；		
代表性工作	以油脂类植物（油桐、山桐子）为研究对象，主要从事种质资源的收集、评价及重要性状的遗传基础研究，首次揭示了油桐及山桐子种子或果肉油脂富集的分子机制。近 5 年主持国家级课题 3 项，以第一和通讯作者在国际著名期刊上发表论文 20 余篇，其中 5 篇 IF〉6。授权国家发明专利 1 项，培养研究生 7 名，其中一名获得中国科学院院长优秀奖。		
个人荣誉	2012 年底入选中国科学院引进海外杰出人才“百人计划”		
学术兼职			
学术期刊兼职			

姓名	张秀军	身份类型	学术带头人
性别	男	年龄	38 岁
最后学位	博士	获得最后学位所在院校	上海大学
任职时间		依托单位职务	副研究员
学习及工作经历	2016/08 至今，中国科学院武汉植物园，百人计划 C 类，课题负责人 2014/04-2016/08 新加坡南洋理工大学/新加坡基因组研究所，博士后 2013/09-2014/03 美国加州大学洛杉矶分校，博士后 2011/05-2013/05 法国昂热大学，联合培养博士 2009/09-2013/07 上海大学，生物信息学与系统生物学，博士		
研究方向	生物信息学与植物基因组学		
代表性工作	主要开展了生物信息学方向的研究，在基因调控网络构建、RNA 编辑位点识别、选择性剪切突变等方面进行了一系列的研究工作。主要代表性工作包括提出了基于条件互信息和路径匹配算法的基因调控网络构建方法 PCA-CMI，提出了基于降噪去冗余技术的基因调控网络预测高性能算法 NARROMI，提出了一种准确定量调控关系和强度的基因调控网络构建方法 CMI2NI。目前已在 *Nucleic Acids Research*、*Bioinformatics*、*PNAS*、*Nature Chemical Biology* 等国内外重要期刊发表论文 15 篇。		
个人荣誉	2016 年中科院“百人计划”C 类		
学术兼职			
学术期刊兼职			

姓名	宋士勇	身份类型	学术带头人
性别	男	年龄	32 岁
最后学位	博士	获得最后学位所在院校	中科院植物研究所
任职时间		依托单位职务	副研究员
学习及工作经历	2017.10- 至今 中科院武汉植物园，中科院百人计划 C 类，课题组长 2013.06–2017.09 Research Fellow，National University of Singapore 2012.05–2013.06 Research Assistant，National University of Singapore 2008.09–2013.06 博士，中科院植物研究所 2003.09–2007.06 学士，合肥工业大学		
研究方向	莲等水生植物花色和花器官的分子遗传育种		
代表性工作	主要以拟南芥、水稻和苜蓿等为研究对象，利用基因编辑和分子蛋白相关技术，阐明了一批与产量、穗型、抗逆和花期等重要农艺性状的基因的分子作用机制，在国际上首次阐释了水稻成花素的转运途径，对农作物的开花调控有重要的指导意义。研究成果先后发表在 *Plant Cell*、*Developmental Cell* 和 *JXB* 等国际主流杂志上，被引用近三百余次。		
个人荣誉	无		
学术兼职	无		
学术期刊兼职			

姓名	梁琼	身份类型	学术带头人
性别	女	年龄	42 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	园纪委书记
学习及工作经历	2017.1-今　中科院武汉植物园纪委书记，副研究员 2015.5 -2016.12　中科院武汉植物园主任助理，园艺中心主任，副研究员 2005.2-2015.4　中科院武汉植物园科研处员工，副处长，处长 2008.9-2012.7　中国科学院大学，获博士研究生学位 2003.9-2005.1　中科院武汉植物园园艺中心，员工 2000.9-2003.7　华中农业大学，获硕士学位 1994.9-1998.7　华中农业大学，获学士学位		
研究方向	药用植物资源筛选评价；新种质创制；特色经济植物保育与开发利用		
代表性工作	发表各类学术论文 10 余篇，申请发明专利 8 项，获湖北省科技进步一等奖 1 项（主要参加），主持《白及规范化栽培》湖北省地方标准。		
个人荣誉			
学术兼职	中国野生植物保护协会迁地保护委员会副主任；中国中药产业技术创新战略联盟常务理事		
学术期刊兼职			

姓名	陈良	身份类型	学术带头人
性别	男	年龄	36 岁
最后学位	博士	获得最后学位所在院校	华中师范大学
任职时间		依托单位职务	青年研究员
学习及工作经历	2016.01-至今，　中国科学院武汉植物园，青年研究员 2016.11-2017.11　美国康奈尔大学，访问学者 2014.09- 2015.12　中国科学院武汉植物园，副研究员 2011.07- 2014.08　中国科学院武汉植物园，助理研究员 2010.10　美国丹佛斯植物科学中心，访问交流 2005.09-2011.06　华中师范大学生命科学学院，博士		
研究方向	草坪草与牧草逆境胁迫应答、抗逆新种质创制与示范		
代表性工作	以草坪草与牧草为研究对象，主要从事种质资源的收集、评价及重要性状（抗逆及品质性状）的分子遗传机理研究，为培育抗逆草坪草及优异品质性状牧草奠定了坚实的科学依据，相关研究成果以第一和通讯作者在国际主流期刊上发表论文 20 余篇，已被国际期刊引用 500 余次；选育出了一批抗逆能力强（耐盐、耐寒、耐荫、耐高温等）的草坪草新种质，并进行了示范推广。		
个人荣誉	2016 年 中科院武汉植物园“卓越青年人才计划”（青年研究员） 2016 年 入选中国科学院青年创新促进会会员 2016 年 中科院植物园 2016 年学术论坛三等奖 2013 年 中科院植物种质创新与特色农业重点实验室优秀青年人才计划		
学术兼职			
学术期刊兼职	Frontiers in Plant Sciences 期刊 Review Editor		

姓名	杨美	身份类型	学术带头人
性别	女	年龄	36 岁
最后学位	博士	获得最后学位所在院校	华中农业大学
任职时间		依托单位职务	副研究员
学习及工作经历	2016/3-2017/3 University of Illinois at Urbana-Champaign，Plant biology department，国家公派访问学者 2010/7-至今 中国科学院武汉植物园，水生植物基因组学与遗传育种学科组，副研究员 2006/9–2010/6 华中农业大学， 植物营养遗传学,博士 2003/9–2006/6 华中农业大学， 植物营养学， 硕士 1999/9–2003/6 河南农业大学， 植物营养学， 学士		
研究方向	莲重要性状解析与遗传改良		
代表性工作	参与莲首张基因组图谱绘制，首次构建了莲遗传连锁图谱。在莲花色、花期、莲子和地下茎发育遗传机制研究方面取得了重要成果，致力于特色优质花莲、子莲的遗传改良和分子育种。目前在国内外刊物上发表论文 25 篇，其中以第一作者和通讯作者发表 SCI 研究论文 15 篇，获得国家发明专利授权 2 项。		
个人荣誉	2011 年 湖北省优秀博士学位论文; 2015 年 中国科学院植物园 2015 年学术论坛三等奖; 2016 年 入选中国科学院青年创新促进会会员; 2016 年 入选中国科学院武汉植物园科研骨干人才计划.		
学术兼职	中国园艺学会水生花卉分会 常务理事		
学术期刊兼职	无		

姓名	王彦昌	身份类型	优秀青年骨干
性别	男	年龄	45 岁
最后学位	博士	获得最后学位所在院校	沈阳农业大学
任职时间		依托单位职务	研究员
学习及工作经历	2005.9-至今　中国科学院武汉植物园 2012.1-2012.12　University of Waikato科学与工程学院，教育部公派访问学者 2003.9-2005.9 武汉大学生命科学学院，博士后； 1999.9-2003.7 沈阳农业大学园艺学院，博士； 1999.7-2000.9 新疆石河子农学院，讲师； 1996.9-1999.7 新疆石河子农学院蔬菜学专业，硕士； 1992.9-1996.7 新疆石河子大学农学院园艺专业，本科；		
研究方向	猕猴桃分子生理学		
代表性工作	武汉植物园研究员，博士生导师，主要从事猕猴桃分子遗传学、果实品质代谢生理及调控技术研究、红肉猕猴桃、软枣猕猴桃遗传育种等。 主持农业部农业公益性行业科研专项子课题、国家自然科学基金面上项目、中国科学院知识创新工程重要方向性项目、武汉市青年科技晨光计划项目及四川省地方合作项目等 18 项，在国内外园艺专业刊物及重要专业会议上发表论文 30 多篇。研究基地及产业服务范围涉及四川、重庆、湖北、陕西、浙江、江苏、辽宁等猕猴桃主产区。保存杂交群体、野生资源及中间育种材料 3 万余份，主持选育出一批红肉猕猴桃新品系，申请保护了多个猕猴桃红肉新品系，其中‘红昇’已经开始在四川、重庆、湖北等红肉猕猴桃主产区大面积发展。选育出软枣猕猴桃新品系‘小紫晶’、‘甜猕 A8’及‘紫猕 A12’等，已有 4 个申请农业部植物新品种保护。指导建设了多个产区大规模商业果园规划建设与果园管理技术实施。指导培训猕猴桃技术管理人员超过 2000 人次，技术指导惠及猕猴桃果园生产面积规模 15 万亩。		
个人荣誉			
学术兼职	中国园艺学会会员，中国园艺学会小浆果分会理事，猕猴桃分会常务理事，湖北遗传学会会员		
学术期刊兼职			

姓名	姚小洪	身份类型	优秀青年骨干
性别	男	年龄	42 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	研究员
学习及工作经历	2016.09- 中国科学院武汉植物园猕猴桃种质资源与育种学科组 研究员 博士生导师 2010.11-2011.11 美国密西根大学生态与进化系 访问学者 2009.09-2016.08 中国科学院武汉植物园猕猴桃种质资源与育种学科组 副研究员 硕士生导师 2006.07-2009.08 中国科学院武汉植物园植物保育遗传学学科组 助理研究员 2003.09-2006.06 中科院武汉植物研究所攻读植物学博士学位 2000.09-2003.07 江西农业大学园艺系攻读果树学硕士学位 1996.09-2000.07 江西农业大学园艺系攻读园艺学学士学位		
研究方向	猕猴桃种质资源		
代表性工作	从事植物群体遗传学以及猕猴桃遗传育种工作。在国际上，首次报道了猕猴桃科的叶绿体基因组，构建了猕猴桃种内杂交群体高密度遗传图谱，揭示了猕猴桃属植物的杂交物种形成模式以及基因流动态，为猕猴桃属植物的进化以及重要农艺性状 QTL 定位研究奠定了坚实基础。首次用实例报道了植物园迁地保护可能存在的遗传学风险，揭示了生境片断化的遗传学效应，探讨了物种分布范围限制的进化机制，揭示了川东鄂西植物多样性维持的机制。研究紧扣国际前沿，在 *New Phytologist* 和 *Annals of Botany* 等国际知名期刊上发表论文 20 余篇，被引用 500 多次。		
个人荣誉			
学术兼职	中国园艺学会猕猴桃分会理事		
学术期刊兼职			

姓名	辛海平	身份类型	优秀青年骨干
性别	男	年龄	38 岁
最后学位	博士	获得最后学位所在院校	武汉大学
任职时间	-	依托单位职务	无
学习及工作经历	2016.12-至今　武汉植物园，副研究员二级 2013.11-2016.11　武汉植物园，副研究员二级 2011.1-2013.10　武汉植物园，副研究员一级 2011.2-2011.8　美国伊利诺伊大学，访问学者 2008.11-2011.1　武汉植物园，助理研究员 2003.9-2008.8　武汉大学，发育生物学专业，博士		
研究方向	葡萄抗逆分子机理		
代表性工作	主要葡萄低温和干旱适应性机制研究，利用葡萄抗性资源-山葡萄开站了一系列工作，挖掘了数个参与葡萄低温和干旱应答的基因，并对其调控机理进行了深入研究，目前在在 *Plant journal*、*Journal of experimental Botnay*、*BMC Plant Biology* 等期刊上发表论文 20 余篇		
个人荣誉	2015 年入选中国科学院青年创新促进会		
学术兼职	无		
学术期刊兼职	无		

姓名	张燕君	身份类型	412822198009210108
性别	女	年龄	38
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	副研究员
学习及工作经历	2014,9-2015,1 公安部物证鉴定中心，访问学者 2011,9-至今 中国科学院武汉植物园，副研究员 2009,2-2011,8 中国科学院武汉植物园，助理研究员 2004,9-2009,1 中国科学院武汉植物园，硕博连读获博士学位		
研究方向	药用植物学		
代表性工作	对我国药用植物淫羊藿资源进行了系统的评价，作为主要科研骨干，培育了 3 个国家级新品种，成功开展了淫羊藿产业化种植。		
个人荣誉			
学术兼职	中国民族医药学会药用资源分会常务理事		
学术期刊兼职			

姓名	邓显豹	身份类型	优秀青年骨干
性别	男	年龄	42 岁
最后学位	博士	获得最后学位所在院校	赫尔辛基大学
任职时间		依托单位职务	副研究员
学习及工作经历	2014.08－ 至今　中国科学院武汉植物园，副研究员 2014.02－2014.04 纽约州立大学布法罗分校（美国），访问博士后 2013.11－2014.07 赫尔辛基大学(芬兰)，博士后 2008.01－2013.11 赫尔辛基大学(芬兰)，植物育种，博士研究生 2004.09－2007.12 赫尔辛基大学(芬兰)，园艺学，硕士研究生 2003.01－2004.05 北京合纵力源农业高科技有限公司，副总经理 1999.07－2002.12 北京青龙湖农业高科技有限公司，历任技术员、生产部经理、总经理助理、常务副总经理 1995.09－1999.07 中国农业大学，园艺学，本科		
研究方向	莲生物碱合成调控		
代表性工作	莲富含具有极高药用价值的苄基异喹啉生物碱类。以中国科学院武汉植物园保育的 600 余份莲种质资源为基础，主要开展以下工作： 1）建立莲不同品种、不同器官生物碱组分及含量数据库； 2）解析莲生物碱的合成途径，对重要的合成酶基因进行克隆及功能鉴定； 3）解析莲生物碱合成的调控机理，利用群体重测序、转录组、代谢组等手段，筛选重要的转录调控因子，并做功能鉴定； 4）选育高生物碱含量的莲品种，并进行开发推广。 已在 *New Phytoloigst, Plant Biotechnology Journal, Molecular Plant and Microbe Interactions* 等期刊发表文章 10 余篇。		
个人荣誉	2013 年国家优秀自费留学生奖学金		
学术兼职	无		
学术期刊兼职	无		

姓名	周晖	身份类型	优秀青年骨干
性别	男	年龄	30 岁
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	副研究员
学习及工作经历	2016/03-至今　中国科学院武汉植物园 果树分子育种组 副研究员 2009/09-2016/01 中国科学院武汉植物园 植物学 硕博连读 2005/09-2009/07 上海交通大学 植物科学系 本科		
研究方向	果实色泽及发育调控机理		
代表性工作	血桃性状的分子遗传机理解析：利用图位克隆结合比较转录组学的方法筛选出控制血桃性状的 NAC 转录因子 **BL**，并解析了 NAC 转录因子复合体调控果实着色的分子机理。这是在植物中第一次对 NAC 转录因子调控花青苷合成的分子机理进行系统地报道，为桃果肉着色性状的遗传育种提供了理论指导和分子工具。		
个人荣誉	2015 年获中国科学院院长优秀奖 第十六届湖北省自然科学优秀学术论文 2016 三等奖		
学术兼职	无		
学术期刊兼职	无		

姓名	闫娟	身份类型	优秀青年骨干
性别	女	年龄	36 岁
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	副研究员
学习及工作经历	2012.09 - 至今　中科院武汉植物园　副研究员　植物学 2015.04 - 2016.04　奥地利维也纳大学　院公派“青年访问学者” 2010.07-2012.08　中科院武汉植物园　助理研究员　植物学 2005.09-2010.06　中科院武汉植物园　植物学　博士 2001.09-2005.06　河南师范大学　生物技术　学士		
研究方向	种群遗传学和进化生态学		
代表性工作	主要以苜蓿属 (*Medicago*) 和芒属 (*Miscanthus*) 重要资源植物为研究对象，从事种群遗传学和进化生态学相关研究。发现生活史、繁育系统和种子分布方式塑造了花苜蓿和天蓝苜蓿的种群结构和地理分布格局，这些生物学特征在植物适应性进化过程中发挥重要作用（Yan *et al*., 2009）；基于不同生态环境的南荻形态、生理及分子变异研究，揭示南荻在不同环境梯度下均表现出生态适应性强，与其水分利用效率高及相关基因在压力环境下表达显著上调相一致（Yan *et al*., 2012；2015；Fan *et al*., 2015; Xing *et al*., 2016）。对南荻全分布区野生种群进行种群遗传分析，发现南荻遗传多样性高，种群间分化低，其基因流格局受地形和人为因素的双重影响（Yan *et al*., 2016）。进一步对其进行种群转录组分析，阐明基因表达变异是种群维持稳定的重要因素之一；基因表达和遗传变异间存在补偿效应，这种效应是植物适应环境的重要模式，在适应性进化研究中有重要意义（Yan *et al*., 2017）。 目前，以第一及共同通讯发表 SCI 论文 11 篇（Top 10% 8 篇），其中 Yan *et al*. (2012，GCBB)被该杂志以“Miscanthus adapts”专题报道，引起广泛关注; Yan *et al*. (2016，GCBB)以封面文章发表；Yan *et al*. (2017, *Molecular Ecology*)被 reviewers 评议为“开创了种群遗传研究的新思路，为适应性进化过程的研究提供了新视角”。		
个人荣誉	2009 年 中国科学院朱李月华优秀博士生奖 2018 年 中国科学院青年促进会第 8 批会员		
学术兼职	无		
学术期刊兼职	GCBB 审稿人		

姓名	张琼	身份类型	优秀青年骨干
性别	女	年龄	37 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	副研究员
学习及工作经历	2016 年 2 月-2017 年 2 月　新西兰皇家植物与食品研究院 访问交流 2015 年 9 月-至今　中国科学院武汉植物园 副研究员 2012 年 9 月-2015 年 8 月　中国科学院武汉植物园 助理研究员 2011 年 8 月-2012 年 8 月　美国伊利诺伊大学香槟分校 访问交流 2009 年 6 月-2012 年 6 月　中国科学院武汉植物园 理学博士 2006 年 7 月-2009 年 8 月　中国科学院武汉植物园 科研管理		
研究方向	猕猴桃果实品质及性别调控		
代表性工作	收集猕猴桃种质资源，进行遗传多样性分析，建立重要物种和品种的分子指纹图谱，为猕猴桃种质资源及品种鉴定提供分子依据。构建猕猴桃种间高密度遗传图谱，提升基因组组装效果；定位性别区间，开发猕猴桃早期性别鉴定标记；探讨猕猴桃物种的杂交起源。对猕猴桃物种及品种进行糖酸组分及香气成分分析，探究其遗传规律；结合遗传连锁图谱数据，定位糖酸 QTL 位点，开发分子元件，辅助猕猴桃分子育种。 近年来，在 *Genome Biology*、*New Phytologist*、*DNA Research*、*BMC Genomics* 等杂志发表 SCI 论文 15 篇；参与编著猕猴桃中英文专著 4 本。获国家发明专利授权 5 项。获国家自然科学基金青年项目和面上项目资助各 1 项。		
个人荣誉	2016 年中科院促进发展团体一等奖 2016-2017 年度神农中华农业科技奖一等奖		
学术兼职	中国园艺学会猕猴桃分会 秘书长		
学术期刊兼职			

姓名	李大卫	身份类型	优秀青年骨干
性别	男	年龄	35 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	副研究员
学习及工作经历	2016-2017　新西兰植物与食品研究所，访问学者 2011-至今　中国科学院武汉植物园，工作 2006-2010 年 中国科学院武汉植物园，硕博连读 2001-2005 年 武汉大学生物技术专业		
研究方向	猕猴桃优异野生资源收集及驯化；猕猴桃多倍体研究及育种		
代表性工作	主要从事猕猴桃的资源收集和评估、多倍体育种、功能基因发掘及应用研究。近年来，在 *NEW PHYTOL*、*FRONT PLANT SCI*、*TGG*、*MGG* 等杂志发表与猕猴桃相关 SCI 论文 14 篇；参与编著猕猴桃中英文专著 4 本，撰写英文章节 1 节；参与选育猕猴桃品种 9 个；获得湖北省技术发明一等奖、中科院促进发展一等奖和农业部中华农业科技一等奖各 1 项。		
个人荣誉	中国科学院青促会会员		
学术兼职	中国园艺学会猕猴桃分会 理事		
学术期刊兼职			

姓名	王鲁	身份类型	优秀青年骨干
性别	男	年龄	42 岁
最后学位	博士	获得最后学位所在院校	武汉大学
任职时间		依托单位职务	副研究员
学习及工作经历	2011 年 10 月-至今　中国科学院武汉植物园 果树分子育种课题组 助理研究员（2016 年晋升为副研究员） 2008 年 7 月-2011 年 7 月 中国农业科学院烟草研究所 生物技术学科组 助理研究员 2001 年 9 月-2008 年 1 月　就读于武汉大学 生命科学学院植物发育生物学专业，获理学博士 1998 年 9 月-2001 年 7 月　就读于武汉大学 生命科学学院生物化学与分子生物学专业，获理学硕士 1994 年 9 月-1998 年 7 月　就读于武汉大学 生命科学学院生物化学与分子生物学专业，获理学学士		
研究方向	果树分子育种、桃果实风味品质基因的发掘及其应用		
代表性工作	在我园工作以来，根据学科组方向，从事果树功能基因学的研究，引进了高通量测序分析技术，从桃花果叶等多个组织的转录组中挖掘丰富的新基因和非编码 RNA，并调查了可变剪切、功能性 SNP、优势表达基因和特征性转录因子等，发表第一作者文章于 SCI 期刊 *Plant Molecular Biology*（2013 年，国内果树功能基因组学较早的报道文献，被引用记录 36 次，领域内引用率较高的文献之一）。为定位克隆果树品质相关的重要基因，借助作图群体和种质资源进行桃果实酸度性状基因定位，发展与酸度连锁的 CAPS 和 dCAPS 标记，成功锁定关键的候选基因，并将进行相关功能验证。同时为研究果树基因组遗传变异的分子基础，及转座子在基因组范围内跳跃造成的 DNA 片段插入或缺失变异的遗传特征，在桃基因组中发现了一类新的 hAT MITE 型转座子，命名为 MoShan 转座子，并对该家族进行系统的筛选和分析，提出该类转座子起源和进化的假说，发表第一作者文章于 *Plant Molecular Biology* 期刊（2016 年）。		
个人荣誉	无		
学术兼职	无		
学术期刊兼职	曾为 Plant Molecular Biology、PLoS ONE、Tree Genome and Genetics 等植物科学、园艺科学或果树学 SCI 期刊审稿		

姓名	王中杰	身份类型	优秀青年骨干
性别	男	年龄	34 岁
最后学位	博士	获得最后学位所在院校	中国科学院水生生物研究所
任职时间		依托单位职务	副研究员
学习及工作经历	2015 年 9 月-至今　　中国科学院武汉植物园，副研究员 2012 年 9 月-2015 年 8 月 中国科学院武汉植物园, 助理研究员 2007 年 9 月-2012 年 7 月 中国科学院水生生物研究所，硕博连读，水生生物学 2003 年 9 月-2007 年 7 月 郑州大学生命科学学院，生物技术，本科		
研究方向	微藻生物技术		
代表性工作	1. 首次建立了完善的微藻固碳潜力评价方法,为微藻在二氧化碳减排领域的应用提供了方法基础。 2. 在中试规模上系统评价了微藻固碳效率及附加产物产率。 3. 以 *Graesiella* sp. WBG-1 为材料,首次实现了油脂产率与固碳效率同步最大化,为微藻固碳与产油的结合提供了新的技术途径。 4. 首次解析了 C4 途径在 *Graesiella* sp. WBG-1 固碳中的作用,发现了微藻全基因组加倍现象。		
个人荣誉	无		
学术兼职	无		
学术期刊兼职	无		

姓名	孙延霞	身份类型	优秀青年骨干
性别	女	年龄	34 岁
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	副研究员
学习及工作经历	2016.09 - 至今 中国科学院武汉植物园 副研究员三级 2015.09 - 2016.08 中国科学院武汉植物园 助理研究员一级 2014.08 - 2015.08 中国科学院武汉植物园 助理研究员二级 2013.08 -2014.08 North Carolina State University, USA (国家公派博士联合培养) 2011.09 - 2014.06 中国科学院武汉植物园-植物学 （获理学博士学位） 2008.09 - 2011.06 中国科学院新疆生态与地理研究所-植物学（获理学硕士学位） 2003.09 - 2007.07 山东师范大学-生命科学学院（获理学学士学位）		
研究方向	植物系统发育、谱系地理与基因组进化		
代表性工作	近年来，一直从事真双子叶植物基部类群的研究工作，包括高级分类单元（科）的系统基因组学研究，相关研究结果被 APG 分类系统采用；包括第三纪孑遗植物水青树的谱系地理学研究，通过分子证据和化石考证资料对水青树的进化历程进行了探讨；包括叶绿体基因组结构进化研究，推测了真双子叶植物基部类群祖先的叶绿体基因组结构，并先后报道了两项真双子植物基部类群特有的叶绿体基因组结构；也致力于真双子叶植物基部类群中特殊物种的适应性进化方面的研究，目前正在开展濒危珍稀高山植物独叶草适应性进化的分子机制研究。		
个人荣誉	1. 2014 年度中国科学院朱李月华优秀博士生奖学金 2. 2013 年国家留学基金委资助出国留学资格 3. 2013 年博士研究生国家奖学金 4. 2013 年重点实验室首场学术交流会优秀报告奖		
学术兼职	无		
学术期刊兼职	无		

姓名	张玲玲	身份类型	优秀青年骨干
性别	女	年龄	33
最后学位	博士	获得最后学位所在院校	中国科学院武汉植物园
任职时间		依托单位职务	副研究员
学习及工作经历	2015/9－至今　中科院武汉植物园，能源植物生物学学科组，副研 2013/8－2015/8 中科院武汉植物园，能源植物生物学学学科组，助研 2008/8 - 2013/6 中科院武汉植物园，植物学，博士 2004/9 - 2008/6 贵州大学，生态学，学士		
研究方向	木本油料植物种子脂肪酸合成代谢		
代表性工作	科研工作主要涉及种子脂肪酸合成代谢，可细分成两方面内容： 1） 桐油中高桐酸含量分子机制：完成了油桐树全基因组的测序工作等，基于酵母，发现桐酸的β 氧化可能是油桐种子高桐酸含量的分子机制之一。 2）油桐种子高低含油率的分子机制：基于转录组分析，发现 WRL1 等多个基因的差异表达是单株间含油率差异的分子机制之一。		
个人荣誉	无		
学术兼职	无		
学术期刊兼职	无		

姓名	王欣	身份类型	优秀青年骨干
性别	男	年龄	36 岁
最后学位	博士	获得最后学位所在院校	中国科学院水生生物研究所
任职时间		依托单位职务	副研究员
学习及工作经历	2017.10 -至今　美国北德克萨斯大学生物学系，访问学者 2015.9-至今　中国科学院武汉植物园，副研究员 2013.8-2015.8　中国科学科院武汉植物园，助理研究员 2010.10-2013.7　武汉大学生命科学学院，博士后 2006.9-2010.7　中国科学院水生生物研究所，攻读遗传学专业博士学位 2004.9-006.7　武汉大学，攻读遗传学专业硕士学位 2000.9-2004.7　华中师范大学，攻读生物科学专业学士学位		
研究方向	植物次生代谢产物生物合成途径及调控机理		
代表性工作	以野葛为研究材料，通过比较转录组学对野葛不同组织的差异表达谱分析，成功地对参与异黄酮合成途径中关键酶基因进行了功能预测分析，为进一步深入研究其黄酮类化合物生物合成途径及其调控机理打下了基础。相关结果以第一作者发表于《*Plant Cell Reports*》。 从前期已建立的野葛转录组库中，成功克隆了 2 个具有重要功能的糖基转移酶基因，并通过一系列的体内与体外的方法对它们的功能进行了分析。首次解析野葛中特有活性化合物葛根素的生物合成路径，为将来在微生物（酵母）或其他植物中异源合成异黄酮化合物提供有用的基因资源。相关结果以第一作者分别发表于国际主流 SCI 期刊《*The Plant Journal*》与《*Frontiers in Plant Science*》。		
个人荣誉	无		
学术兼职	无		
学术期刊兼职	无		

姓名	胡涛	身份类型	优秀青年骨干
性别	男	年龄	37 岁
最后学位	博士	获得最后学位所在院校	中国科学院大学
任职时间		依托单位职务	副研究员
学习及工作经历	2016/03-2017/03 普渡大学，朱健康老师实验室，访问学者 2012/09-至今 中国科学院武汉植物园，草业资源与分子育种学学科组，副研究员/助理研究员 2009/09-2012/06 中国科学院武汉植物园，博士 2006/09-2009/06 福建农林大学，园艺学院，硕士 2002/09-2006/06 武汉纺织大学，环境工程学院，学士		
研究方向	草业种质资源创新与抗性分子机理		
代表性工作	鉴定到抗 1.2%含盐量多年生黑麦草种质 8 份，耐高温高羊茅种质 5 份，SSR 关联位点 116 个，构建了相关杂交群体 6 个；利用 RNA-Seq，GC-MS，iTRAQ 多组学联合分析，鉴定到的抗逆候选基因 600 余个。目前，正以鉴定的抗逆候选基因和遗传群体，利用 CRISPR/Cas9 基因编辑技术和分子标记辅助育种手段进行种质创新。		
个人荣誉	中国科学院优秀毕业生 2017 年中国科学院武汉植物园园学术年会报告三等奖		
学术兼职			
学术期刊兼职			

3. 国际学术机构和国际学术期刊任职情况

序号	姓名	学术组织/期刊名称	职务	任职时间
1	陈　良	Frontiers in plant sciences	Review editor	2017-
2	付金民	Ecotoxicology	编委	2010-
3	郭明全	Current Analytical Chemistry	客座编辑	2012-
		Phytochemical Analysis	编委	2017-
		Phytochemical Analysis	客座编辑	
4	韩月彭	Plant Molecular Biology Reporter	副主编	2008-
		Canadian Journal of Plant Science	副主编	2010-
		Horticulture Research	副主编	2017-
		PLoS ONE	编委	2013-
5	杨平仿	Asia Oceania Agricultural Proteomics Organization (AOAPO)	Council Member	2011-
		Scientific Reports	编委	2016-
		PLoS ONE	编委	2014-
6	章焰生	Frontiers in plant sciences	Reviewing editor	2017-

三、开放交流与运行管理

1. 对外开放

1）参照国家留学基金管理委员会的要求和《中国科学院公派出国留学研修管理办法》，积极组织优秀骨干人才申报国家公派留学项目和院公派留学项目，鼓励优秀中青年骨干赴国外先进科研机构（大学）进行访学，了解世界科技前沿，提升其把握学科发展方向和主持科研项目的能力。受国家留学基金管理委员会（CSC）的资助，2017 年共派出 3 人，其中：

陈良副研究员于 2016 年 11 月-2017 年 11 月在美国康奈尔大学（Cornell University）整合植物科学学院（School ofIntegrative Plant Science）开展访学研究，指导老师为康奈尔大学终身教授 Susheng Gan（甘苏生）教授。访学期间，陈良主要在甘教授的指导下进行衰老关键调控基因 AtNAP 参与应答非生物胁迫的机制研究，研究发现敲除 AtNAP 基因的突变体植株呈现出更强的耐受非生物胁迫（盐、干旱、高温、紫外线等）能力，目前这部分的研究内容已整理成文，同时陈良还与甘苏生教授就国内开展的科研工作进行了深入交流，并就双方长期科研合作达成了初步意向。访学期间陈良还积极参加校内外的各种学术活动，积极参加多个 Seminar 和 Workshop，与多位著名专家学者进行了广泛深入的学术交流。

王恒昌研究员于 2016 年 12 月-2017 年 3 月在美国 East Carolina 大学开展访学研究，与东卡大学生物系生物信息学与进化生物学专家黄锦林教授开展合作研究。在访学期间，主要就整个真核生物领域，从大尺度了解物种的水平基因转移现象和机理，从更深和广的层次学习和讨论了物种进化的复杂过程。澄清了以前在进化生物学中的模糊概念和理解上的局限。

具体对基金项目的实验数据进行了讨论并于 2018 年整理发表。黄锦林教授现在为中国科学院昆明植物研究所客座研究员，通过此次访问，为以后双方在植物分子进化领域特别是生物信息学领域的沟通和合作建立了较好的意向。

王欣副研究员于 2017 年 10 月赴美国北德州大学开展为期 1 年的访学研究，目前该项目正在执行中。

2）受中国科技部“亚非杰出青年科学家来华工作计划”资助，埃及农业部沙漠研究所 Mohamed Hamdy Amar 副教授来到重点实验室，开展了桃基因组学合作研究，完成了野生桃光核桃（*Amygdalus mira*）和两个栽培桃叶绿体基因组测序与组装，光核桃和栽培桃叶绿体基因组大小分别为 85,610、85,924 bp，都包含 133 个基因和 128 个基因间隔区间，平均 GC 含量为 36.8%。发现了 600 个叶绿体 SSR 多态性位点，其中 6bp 重复 SSR 位点频率最高，且多数 SSR 位点在光核桃和栽培桃之间存在多态性。同时发现了 331 个单碱基变异位点和 51 个 Indels，明确了桃叶绿体基因组存在 45 个高变异区域，这些高变异区域是导致光核桃和栽培桃叶绿体基因组变异的主要原因。此外，叶绿体序列进化树分析表明，栽培桃与山桃血缘关系比光核桃近。上述研究为李属果树分子标记开发、物种分子指纹开发以及种间近缘关系鉴定提供了资源与分子工具。

3）开放课题：根据“开放、流动、联合、竞争”的运行要求，重点实验室紧密围绕三个研究方向设置开放课题。 目前在研开放课题 4 项，其中 2017 年新增 2 项，与华中农业大学、中国农业科学院深圳农业基因组研究所、湖北省农业科学院果树茶叶研究所和中国科学院植物研究所分别就莲、药用植物、果树等方面的研究开展深入合作。

2. 科学传播

重点实验室以植物科研为选题，利用大众喜闻乐见的表现形式制作科普产品，大力普及传播了前沿科技知识，创新了科学传播的方式，也取得了非常好的传播效果。

1）借助大型科普活动开展科学传播

2017 年湖北省科技活动周于 5 月 19 日在中科院武汉植物园正式启动。在开幕式现场，重点实验室展出各种药用植物，并请科研人员介绍其植物性能、营养和药理等，同时还介绍日常生活中常见的外观相似但功效却不相同的植物，使公众深入了解传统医药养生保健知识，并将其运用到生活中，贴近民生的科普活动吸引了大批社会公众的观看与参与。

7 月 13 日，2017 年青少年高校科学营植物科学专题营在中国科学院武汉植物园启动，专题营吸引了来自重庆、安徽、广西、河南、湖南、福建、四川、湖北的百名优秀高中生和 10 名带队老师的参与。本届植物科学专题营以“探秘植物专类园”为主题，依托武汉植物园丰富的植物专类园资源，精心设计了“濒危植物及其濒危机制探究”、“莲与睡莲的区别”、“花的形态多样性及虫媒花与昆虫的协同进化”、“多肉植物干旱适应性研究”和“植物香气成分的探究”等 10 个科学探究课题。各个课题强调理论、实践与探究的结合，兼具科学性、趣味性、可操作性，既传播了相关领域的科学知识，也让营员化身小植物学家直接开展科学探究。 在植物香气成分探究小组，科研人员带领学员实地考察药园，认识有天然香气

的植物，引导营员提出问题并设计实验，利用科学实验进行论证。植物香气成分探究小组和珍稀濒危植物探究小组带领营员参观公共实验平台，讲述部分大型仪器的基本原理及运用，并让营员亲自操作。在药用植物课题小组，设计“制作彩色糯米饭”和“棉织物扎染”环节，采摘、研磨、熬制、上色，使营员们了解药用植物染料，以及几种常见黄色系药用植物染料的染色分析与应用。

2）借助武汉植物园主题花展、科普课堂等开展科普教育

重点实验室收集保存观赏型、实用型、和观赏食用兼备型的桃百余个品种，主要集中在桃花园、野果园区域，向大众展示了桃不同树型、枝型、叶型、叶色等各种类型。桃花品种丰富，花瓣似菊花的“菊花桃”，一树开红白两种花色的“红白花桃”，小枝拱形下垂，树冠犹如伞盖的“垂枝条”，花大且花朵密集，花开如满天红霞的“满天红”，观赏食用并举的“迎春”，可食用的“金花露”、“晚蟠桃”等品种。

10 月 28 日，第二届中科院武汉植物园金玉猕猴桃品鉴节在武汉植物举行。由重点实验室选育的“CUSTMO 金玉”猕猴桃，个头小、口感香甜，皮也能吃，受到市民和游客的喜爱。 在品鉴现场，80 名市民代表分别品尝了“CUSTMO 金玉”成熟的果肉。

10 月 15 日和 29 日，武汉植物园自然学校在猕猴桃园开展了两次以“猕猴桃的那些事”为主题的课程，为孩子们打开了猕猴桃的私密生活。介绍了猕猴桃的成长过程、形态差异及果实由涩到甜的原因，带领小朋友积极调动自身的触觉、嗅觉、视觉、听觉、味觉。引导孩子们触摸猕猴桃果皮，辨别粗糙与光滑，感受猕猴桃的果香，观察猕猴桃果肉颜色的不同，探寻猕猴桃果实落地后昆虫啃食的声音，品鉴猕猴桃的“甜、酸、辣”味。通过孩子们的感官来探究猕猴桃的小秘密。

3）应用新媒体取得新成效

3 月初，由武汉植物园制作的科普微视频《小猕猴桃大学问》荣获中国科学院十大优秀科普微视频奖项”。武汉植物园依托世界上遗传资源覆盖最广的猕猴桃种质资源圃，采用二维动画的技术手段，制作了《小猕猴桃大学问》的科普微视频，该视频从猕猴桃的历史出发，介绍了猕猴桃的起源及丰富的品种资源，展示了我园关于猕猴桃种质资源选育的科研成果、同时介绍了猕猴桃的营养价值、猕猴桃膨大剂等有关社会热点。视频通过科学、生动的展示手段，将科学家的科研成果向公众推广，把深奥的科学知识变得生动有趣，让公众感受到科学就在身边。

重点实验室工程师张鹏在中国科学院网络科普联盟“科学启明星”计划中，荣获“2017 年科普启明星（个人）”的称号。张鹏撰写的《猕猴桃家族的颜值担当—中国原产的红心猕猴桃》一文，语言生动有趣、知识丰富翔实，被各大门户网站转载，广泛传播，入选科学大院“2017 年度十佳科普文章”。

《植物寻香记》科普微视频以实拍和三维动画的方式展示了人类对植物香气成分的探究，

内容兼科学性与趣味性为一体。视频以常见的芳香植物为切入点，引出香气成分如何获得的问题。随后，科研人员以柚子皮为实验原材料开展科学实验，介绍了蒸馏法提取植物香气成分的操作和原理。最后，视频进行升华，介绍了植物香气成分在多个领域的广泛应用，传达了科技让生活更美好的理念。

四、依托单位的支持

1. 依托单位在人、财、物条件方面的保障和支持

类别	上一年度	本年度	增长数	增长比率
专职管理人员（个）	1	1	0	0
专职技术人员（个）	6	6	0	0
硕士研究生招生（个）	17	16	-1	-5.9%
博士研究生招生（个）	13	10	-3	-30%
单位配套运行费（万元）	60	155	95	158.3%
单位配套设备费（万元）	440	218	-222	-50.5%
实验室总面积（平米）	3149	5876	2727	86.6%
实验室总资产（万元）	5242	5647	405	7.7%

2. 依托单位给予的其他支持

1）人才支持

在人员配备和聘用方面，依托单位根据科技创新发展规划，制定了相应的高级人才引进管理办法。2017 年，武汉植物园为实验室引进新加坡国立大学宋士勇博士作为中国科学院率先行动“百人计划”青年俊才（C 类），他的加盟将促进重点实验室在水生植物分子育种方面的研究。武汉植物园引进青年博士 2 名，推荐 2 人入选青促会，4 人入选武汉植物园青年骨干人才计划，不断充实和加强实验室的研究团队。同时，支持实验室聘请国内外知名学者来室开展多形式的合作研究工作，另外还根据申请，派遣实验室中青年研究骨干到境外著名实验室进行访问、进修、合作研究和参加国际学术会议。

2）资源支持

依据依托单位的整体部署，重点实验室于2017年10月整体搬迁至武汉植物园光谷园区，实验室科研，办公条件得到极大改善，而且依托单位为实验室提供了集中的实验空间，使其具有相对的独立性和联合的开放性。

2017 年，依托单位在武汉市新洲区选取地块 1000 亩，作为实验室特色经济作物种质创新与应用示范综合基地。

第三部分 人员情况

1. 固定人员名单

序号	姓名	性别	出生年月	职称等级	实验室职务	所学专业	工作性质	最后学位	学位取得时间	授予单位	进入实验室时间	离开实验室时间	职称名称	研究方向	国别	国籍
1	程中平	男	1963-9	正高级		植物学	研究	博士	2007-6-30	中国科学院大学	2009-12-30	至今	研究员	1	国内	中国
2	付金民	男	1961-12	正高级		园艺学	研究	博士	2003-5-1	肯萨斯州大学	2009-12-30	2017-10	研究员	3	国内	中国
3	郭明全	男	1975-10	正高级		化学	研究	博士	2004-3-27	中国科学院长春应用化学研究所	2012-8-1	至今	研究员	2	国内	中国
4	韩月彭	男	1968-11	正高级	实验室主任	作物遗传育种	研究	博士	2004-6-30	扬州大学	2009-12-30	至今	研究员	2	国内	中国
5	李夜光	男	1962-5	正高级		植物学	研究	硕士	1987-9-1	中国科学院大学	2009-12-30	至今	研究员	3	国内	中国
6	吕世友	男	1974-10	正高级		植物分子生物学	研究	博士	2004-6-30	解放军农牧大学	2013-5-1	至今	研究员	2	国内	中国
7	王恒昌	男	1967-3	正高级		植物学	研究	博士	2006-3-1	中国科学院武汉植	2009-12-30	至今	研究员	1	国内	中国

										物园						
8	王彦昌	男	1973-9	正高级		农学	研究	博士	2003-6-30	沈阳农业大学	2009-12-30	至今	研究员	3	国内	中国
9	杨平仿	男	1975-7	正高级	实验室副主任	植物蛋白质组学	研究	博士	2006-3-1	中国科学院植物研究所	2009-12-30	至今	研究员	2	国内	中国
10	姚小洪	男	1975-11	正高级		植物学	研究	博士	2006-7-30	中国科学院大学	2009-12-30	至今	研究员	3	国内	中国
11	章焰生	男	1972-12	正高级	实验室副主任	植物学	研究	博士	2005-3-31	中国科学院植物研究所	2010-4-8	至今	研究员	2	国内	中国
12	钟彩虹	女	1968-2	正高级		植物学	研究	博士	2013-1-6	中国科学院武汉植物园	2009-12-30	至今	研究员	3	国内	中国
13	陈良	男	1981-2	副高级	实验室秘书	植物分子遗传学	研究	博士	2011-6-19	华中师范大学	2011-7-1	至今	副研究员	3	国内	中国
14	邓显豹	男	1975-8	副高级		园艺	研究	博士	2013-12-10	赫尔辛基大学	2014-8-8	至今	副研究员	2	国内	中国
15	高磊	男	1981-5	副高级		植物学	研究	博士	2010-4-1	中国科学院武汉植物园	2009-12-30	至今	副研究员	1	国内	中国
16	何冬丽	女	1977-11	副高级		藻类遗传与生物技术	研究	博士	2010-7-10	中国科学院水生生物研究所	2010-4-1	至今	副研究员	2	国内	中国

17	胡涛	男	1981-10	副高级		植物学	研究	博士	2012-7-1	中国科学院武汉植物园	2012-7-1	至今	副研究员	3	国内	中国
18	黄文俊	男	1981-5	副高级		植物学	研究	博士	2012-1-7	中国科学院武汉植物园	2012-6-1	至今	副研究员	3	国内	中国
19	黎佳	女	1982-2	副高级		微生物学	研究	博士	2010-7-15	中国科学院武汉病毒研究所	2010-6-21	至今	副研究员	2	国内	中国
20	李大卫	男	1983-5	副高级		植物学	研究	博士	2010-12-31	中国科学院武汉植物园	2010-10-1	至今	副研究员	3	国内	中国
21	李惠英	女	1977-3	副高级		植物学	研究	博士	2009-4-1	中国科学院水生生物研究所	2009-12-30	至今	副研究员	3	国内	中国
22	李黎	女	1985-12	副高级		微生物学	研究	博士	2011-6-19	华中农业大学	2012-2-1	至今	副研究员	3	国内	中国
23	李明	男	1982-10	副高级		植物学	研究	博士	2014-7-6	中国科学院武汉植物园	2014-7-1	至今	副研究员	2	国内	中国
24	李荣俊	男	1979-4	副高级		发育生物学	研究	博士	2006-6-10	武汉大学	2014-1-1	至今	副研究员	2	国内	中国
25	李晓东	男	1966-11	副高级		植物学	研究	博士	2007-3-1	中国科学院武汉植物园	2009-12-30	至今	副研究员	1	国内	中国

26	李新伟	男	1974-10	副高级		植物学	研究	博士	2007-6-30	中国科学院武汉植物园	2009-12-30	至今	副研究员	1	国内	中国
27	李作洲	男	1967-5	副高级		植物学	研究	博士	2006-7-30	中国科学院武汉植物园	2009-12-30	至今	副研究员	3	国内	中国
28	梁琼	女	1975-5	副高级		植物学	研究	博士	2013-7-7	中国科学院大学	2009-12-30	至今	副研究员	3	国内	中国
29	刘艳玲	女	1976-12	副高级		园林植物与观赏园艺	研究	博士	2013-6-20	华中农业大学	2009-12-30	至今	副研究员	2	国内	中国
30	宋士勇	男	1986-5	副高级		细胞生物学	研究	博士	2013-7-7	中国科学院大学	2017-10-12	至今	副研究员	2	国内	中国
31	孙延霞	女	1984-2	副高级		植物学	研究	博士	2014-7-6	中国科学院大学	2014-8-1	至今	副研究员	1	国内	中国
32	王鲁	男	1976-12	副高级		发育生物学	研究	博士	2008-6-30	武汉大学	2011-11-1	至今	副研究员	2	国内	中国
33	王欣	男	1982-3	副高级		遗传学	研究	博士	2012-7-8	中国科学院水生生物研究所	2014-1-1	至今	副研究员	2	国内	中国
34	王中杰	男	1984-8	副高级		水生生物学	研究	博士	2012-7-8	中国科学院水生生物研究所	2012-9-1	至今	副研究员	3	国内	中国
35	辛海平	男	1980-2	副高级		发育生物学	研究	博士	2010-12-30	武汉大学	2009-12-30	至今	副研究员	2	国内	中国

36	闫娟	女	1982-10	副高级		植物学	研究	博士	2010-7-1	中国科学院武汉植物园	2010-7-1	至今	副研究员	1	国内	中国
37	杨美	女	1981-8	副高级		植物遗传学	研究	博士	2010-6-18	华中农业大学	2010-10-1	至今	副研究员	2	国内	中国
38	张玲玲	女	1985-3	副高级		植物学	研究	博士	2013-7-7	中国科学院武汉植物园	2012-7-1	至今	副研究员	2	国内	中国
39	张琼	女	1981-1	副高级		植物学	研究	博士	2012-12-20	中国科学院武汉植物园	2009-12-30	至今	副研究员	3	国内	中国
40	张秀军	男	1979-3	副高级		生物信息学	研究	博士	2013-7-3	上海大学	2016-8-15	至今	副研究员	2	国内	中国
41	张燕君	女	1980-9	副高级		植物学	研究	博士	2009-4-1	中国科学院武汉植物园	2009-12-30	至今	副研究员	3	国内	中国
42	周晖	男	1987-1	副高级		植物学	研究	博士	2016-1-10	中国科学院大学	2016-2-24	至今	副研究员	2	国内	中国
43	陈方方	女	1982-2	中级		作物生物技术	研究	博士	2011-12-22	华中农业大学	2011-11-1	至今	助理研究员	2	国内	中国
44	陈桂林	男	1984-8	中级		植物学	研究	博士	2017-6-30	中国科学院大学	2017-7-26	至今	助理研究员	2	国内	中国
45	陈丽	女	1982-10	中级		植物学	研究	博士	2010-7-1	中国科学院武汉植物园	2010-7-1	2017-8	助理研究员	1	国内	中国

46	丁奕	女	1986-10	中级		水生生物学	研究	博士	2013-7-7	中国科学院水生生物研究所	2014-1-1	至今	助理研究员	3	国内	中国
47	廖燎	男	1984-7	中级		园林植物与观赏园艺	研究	博士	2013-6-20	华中农业大学	2011-6-1	至今	助理研究员	2	国内	中国
48	潘程	男	1983-3	中级		植物遗传学	研究	博士	2012-12-30	武汉大学	2014-4-1	至今	助理研究员	2	国内	中国
49	石涛	男	1985-3	中级		植物学	研究	博士	2012-7-1	中国科学院大学	2015-11-17	至今	助理研究员	2	国内	中国
50	温小斌	男	1984-7	中级		植物学	研究	博士	2014-7-6	中国科学院大学	2016-8-15	至今	助理研究员	3	国内	中国
51	谢燕	女	1987-8	中级		植物学	研究	博士	2015-7-1	中国科学院大学	2015-9-1	至今	助理研究员	3	国内	中国
52	张爱娣	女	1984-11	中级		遗传学	研究	博士	2014-7-1	中国科学院大学	2017-7-18	至今	助理研究员	2	国内	中国
53	张春云	男	1988-2	中级		植物学	研究	博士	2015-6-30	华南理工大学	2015-8-1	至今	助理研究员	2	国内	中国
54	吴金清	男	1963-6	正高级		植物学	研究	硕士	1989-7-1	中国科学院大学	2009-12-30	至今	正高级工程师	1	国内	中国
55	姜正旺	男	1965-5	副高级		果树学	研究	学士	1985-7-1	华中农学院	2009-12-30	至今	高级工程师	3	国内	中国
56	李长福	女	1971-12	副高级		昆虫学	研究	硕士	2003-7-1	安徽农业大学	2010-6-1	至今	高级工程师	2	国内	中国
57	刘松柏	男	1970-4	副高级		植物学	技术	硕士	2003-7-1	中国科学院武汉植	2009-12-30	至今	高级工程师	1	国内	中国

										物园						
58	孟爱平	女	1968-7	副高级		植物学	研究	硕士	2004-8-28	中国科学院武汉植物园	2009-12-30	至今	高级工程师	1	国内	中国
59	杨东	男	1981-7	副高级		生态学	研究	博士	2013-7-7	中国科学院大学	2012-7-1	至今	高级工程师	2	国内	中国
60	张莉俊	女	1982-11	副高级		园林植物与观赏园艺	技术	博士	2008-6-30	北京林业大学	2009-12-30	至今	高级工程师	1	国内	中国
61	耿亚洪	女	1962-6	副高级		经济管理学	研究	学士		湖北省委党校	2009-12-30	至今	高级实验师	3	国内	中国
62	刘贵华	男	1968-7	正高级		植物学	管理	博士	2005-7-30	中国科学院武汉植物园	2009-12-30	至今	处长		国内	中国
63	陈美艳	女	1980-9	中级		生药学	技术	硕士	2006-7-11	中国协和医科大学	2014-3-3	至今	工程师	3	国内	中国
64	韩飞	男	1986-9	中级		园艺	技术	学士	2009-6-30	孝感学院	2009-7-1	至今	工程师	3	国内	中国
65	何艳	女	1987-12	中级		药用植物	研究	硕士	2015-6-19	华中农业大学	2015-8-1	至今	工程师	3	国内	中国
66	吕海燕	女	1983-12	中级		园林植物与观赏园艺	研究	硕士	2009-6-20	华中农业大学	2009-7-1	至今	工程师	3	国内	中国
67	满玉萍	女	1985-11	中级		生物化学与分子生物学	研究	硕士	2012-6-25	中南民族大学	2013-6-1	至今	工程师	3	国内	中国

68	田华	女	1985-2	中级		植物学	研究	硕士	2009-7-4	中国科学院武汉植物园	2009-9-1	至今	工程师	3	国内	中国
69	张鹏	男	1986-10	中级		园林	技术	学士	2007-6-25	华中农业大学	2014-6-1	至今	工程师	3	国内	中国
70	周玲	女	1984-9	中级		植物营养学	管理	硕士	2010-6-30	西北农林科技大学	2010-12-1	至今	工程师		国内	中国
71	潘慧	女	1984-11	初级		植物学	技术	硕士	2010-6-18	华中农业大学	2015-10-8	至今	助理工程师	3	国内	中国
72	靳莲新	女	1980-7	初级		行政管理	管理	学士	2003-7-1	西南政法大学	2012-6-1	至今	助理工程师	2	国内	中国

2. 流动人员名单

序号	姓名	性别	出生日期	职称等级	所学专业	最后学位	学位取得时间	授予单位	进入实验室时间	离开实验室时间	工作单位	职称名称	国别	国籍	是否为本实验室博士后
1	Mohamed Hamdy Amar	男	1970-7-12	副高级	遗传学	博士	2008-05-22	埃及艾因夏姆斯大学	2017-1-14	2018-1-14	埃及农业部沙漠研究所	副教授	国外	埃及	否，执行科技部“亚非杰出青年科学家来华工作计划”
2	杨贤鹏	男	1989-11-20	其他	植物学	博士	2017-6-30	中国科学院武汉植物园	2017-7-3			其他	国内	中国	是
3	汪巍	男	1982-6-3	其他	植物学	博士	2014-1-10	复旦大学	2013-11-14	2017-7-3		其他	国内	中国	是
4	刘霞	女	1993-3-9		植物学	学士	2017-6-30	湖北民族学院	2017-9-1		西藏大学		国内	中国	否，为联培生
5	罗舒予	女	1992-7-25		植物学	学士	2016-6-30	山西农业大学	2017-9-1		西藏大学		国内	中国	否，为联培生
6	乔匿骏	女	1994-9-11		遗传学	学士	2016-6-30	湖南农业大学	2017-12-5		湖南农业大学		国内	中国	否，为联培生
7	赵力	男	1991-3-13		作物遗传育种	学士	2015-6-30	西北民族大学	2017-3-1		福建农林大学		国内	中国	否，为联培生
8	王彩红	女	1993-4-16		园林	学士	2015-6-30	河南农业大学	2016-7-10		云南农业大学		国内	中国	否，为联培生

3. 实验室研究单元

研究单元	研究方向	学术带头人	其他固定人员名单
1	特色农业资源植物保育原理	王恒昌	程中平、吴金清、闫娟、张莉俊、李新伟、孙延霞、孟爱平、刘松柏、李晓东、陈丽、高磊
2	特色农业资源植物优质和抗性性状的生物学基础	韩月彭	章焰生、杨平仿、郭明全、吕世友、张秀军、宋士勇、张春云、陈桂林、王鲁、周晖、廖燎、靳莲新、张玲玲、李荣俊、潘程、杨美、邓显豹、杨东、李明、何冬丽、石涛、张爱娣、王欣、黎佳、李长福、陈方方、刘艳玲、辛海平
3	特色农业资源植物的种质创新和可持续利用	钟彩虹	付金民、李夜光、梁琼、陈良、王彦昌、姚小洪、姜正旺、李作洲、李大卫、张琼、黄文俊、李黎、张燕君、田华、陈美艳、韩飞、张鹏、潘慧、何艳、吕海燕、满玉萍、李惠英、胡涛、谢燕、耿亚洪、王中杰、丁奕、温小斌

4. 重要人才情况

	中国科学院院士	中国工程院院士	杰青	优青	千人计划			长江学者	百人计划	万人计划		
					长期（A类）	短期（B类）	青年千人			杰出人才	领军人才	青年拔尖人才
姓名									韩月彭			
									付金民			
									杨平仿			
									章焰生			
									郭明全			
									吕世友			
									张秀军			
									宋士勇			
数量	0	0	0	0	0	0	0	0	8	0	0	0

5. 基金委创新研究群体

序号	研究方向	学术带头人	参加人员	获批年份

6. 研究生培养情况

在读硕士一览表

序号	姓名	出生年月	导师姓名	生源校	入学时间	专业	获奖
1	Wamaua Albert Owiti	19880606	韩月彭	肯尼亚肯雅塔大学	20140901	植物学	
2	包维红	19900216	李新伟	华中农业大学	20150901	植物学	
3	梁沁	19910104	章焰生	广西师范大学	20150901	植物学	
4	林楠	19931019	王恒昌	西北大学	20150901	植物学	
5	刘梦迪	19930715	章焰生	西北农林科技大学	20150901	植物学	
6	陆建军	19910617	吕世友	海南大学	20150901	植物学	中科院大学“三好学生”
7	程程	19930929	辛海平	华中农业大学	20150901	园林植物与观赏园艺	
8	高营营	19930508	辛海平	山东农业大学	20150901	园林植物与观赏园艺	
9	镇巧玲	19911122	韩月彭	湖北工程学院	20150901	园林植物与观赏园艺	
10	李会	19900624	杨平仿	河南师范大学	20150901	生物工程	
11	汪志	19920819	李作洲	安徽师范大学	20150901	生物工程	中科院大学“三好学生”
12	胡裕凤	19940810	杨　美	华中农业大学	20160901	植物学	
13	卢雯莹	19940628	吕世友	福建农林大学	20160901	植物学	
14	周子琳	19951013	章焰生	海南大学	20160901	植物学	
15	蒋小涵	19940308	张秀军	华中农业大学	20160901	植物学	
16	刘美慧	19921003	杨平仿	西北农林科技大学	20160901	植物学	
17	张奥棋	19920606	李夜光	鲁东大学	20160901	植物学	
18	张富萍	19931107	张秀军	华中农业大学	20160901	植物学	
19	胡莲莲	19940306	吕世友	华中农业大学	20160901	园林植物与观赏园艺	

20	黄雪冰	19920413	陈　良	广西师范大学	20160901	园林植物与观赏园艺	
21	徐胜利	19910613	韩月彭	九江学院	20160901	园林植物与观赏园艺	
22	杨秋瑞	19930427	韩月彭	沈阳农业大学	20160901	园林植物与观赏园艺	
23	李璐璐	19930606	钟彩虹	山西师范大学	20160901	生物工程	
24	鲁雪梅	19950122	王彦昌	安徽师范大学	20160901	生物工程	
25	朱振飞	19920925	辛海平	河南科技大学	20160901	生物工程	
26	Isidore Moraa Mosongo	19920402	章焰生	肯尼亚乔莫•肯雅塔农业与科技大学	20160901	植物学	
27	Tonny Maraga Nyonga	19900710	杨平仿	肯尼亚乔莫•肯雅塔农业与科技大学	20160901	植物学	
28	Duncan Kiragu Gichuki	19910930	辛海平	肯尼亚乔莫•肯雅塔农业与科技大学	20160901	植物学	
29	方静	19950420	章焰生	海南大学	20170901	植物学	
30	侯小玉	19940510	李夜光	内蒙古农业大学	20170901	植物学	
31	张旭	19950701	王恒昌	河南农业大学	20170901	植物学	
32	甄兆孟	19951110	郭明全	海南大学	20170901	植物学	
33	李师鹏	19950501	吕世友	西北农林科技大学	20170901	植物学	
34	宋贺云	19940815	杨美	河南师范大学	20170901	植物学	
35	徐勇兵	19940323	郭明全	南昌大学	20170901	植物学	
36	赖恩惠	19941201	韩月彭	安徽农业大学	20170901	园林植物与观赏园艺	
37	刘晓莹	19930914	李大卫	广西师范大学	20170901	园林植物与观赏园艺	
38	申瑞楠	19950529	姚小洪	河南科技大学	20170901	园林植物与观赏园艺	
39	纪康	19950118	陈良	河南师范大学	20170901	生物工程	

40	刘芳兵	19931212	宋士勇	华东师范大学	20170901	生物工程	
41	申俊	19941006	宋士勇	河南农业大学	20170901	生物工程	
42	王腾飞	19950416	张秀军	河南科技大学	20170901	生物工程	
43	赵苗苗	19940403	张秀军	滨州学院	20170901	生物工程	
44	Sylvia Cherono	19931102	韩月彭	肯尼亚乔莫•肯雅塔农业与科技大学	20170901	植物学	

在读博士一览表

序号	姓　名	出生日期	导师姓名	专业	生源校	入学时间	获奖
1	冯涛	19860817	王恒昌	植物学	河南科技大学	20130901	研究生国家奖学金
2	李缘君	19890720	章焰生	植物学	湖北师范学院	20130901	
3	黄龙雨	19880817	杨平仿	植物学	河北农业大学	20140901	中国科学院大学“三好学生”
4	张郎郎	19880927	李绍华	植物学	浙江大学	20140901	中国科学院大学“三好学生”
5	柴风梅	19900206	李绍华	植物学	河南科技大学	20150301	
6	方庭	19901006	韩月彭	植物学	西北农林科技大学	20150901	中国科学院大学“三好学生”
7	郭瑞	19881201	王恒昌	植物学	浙江大学	20150901	
8	户正荣	19901001	付金民	植物学	山东农业大学	20150901	
9	李娟娟	19890928	杨平仿	植物学	西南大学	20150901	中国科学院大学“三好学生”
10	李勋	19841013	郭明全	植物学	江汉大学	20150901	
11	乔玮博	19881217	章焰生	植物学	沈阳农业大学	20150901	
12	吴攀	19910118	吕世友	植物学	武汉大学	20150901	
13	Kole Fredrick Adelalu	19830824	王恒昌	植物学	Obafemi Awolowo University, Ile-Ife, Osun state Nigeria	20150901	
14	蔡亚明	19940916	韩月彭	植物学	河南农业大学	20160901	

15	张亮	19920401	宋士勇	植物学	西北农林科技大学	20160901	
16	张越	19940405	杨平仿	植物学	华中农业大学	20160901	
17	赵磊	19920511	韩月彭	植物学	西北农林科技大学	20160901	
18	林钟员	19880125	杨平仿	植物学	南京农业大学	20160901	
19	刘彩霞	19891214	李夜光	植物学	中国科学院海洋研究所	20160901	
20	张华杰	19900516	王恒昌	植物学	中国科学院西双版纳热带植物园	20160901	
21	周晨	19900910	章焰生	植物学	中国科学院武汉植物园	20160901	
22	Rebecca Njeri Damaris	19870217	杨平仿	植物学	中国科学院武汉植物园	20160901	
23	Erick Amombo	19900127	付金民	植物学	中国科学院武汉植物园	20160901	
24	Flora Didii Saleri	19890308	郭明全	植物学	中国科学院武汉植物园	20160901	
25	Collins Otieno Ogutu	19840806	韩月彭	植物学	中国科学院武汉植物园	20160901	
26	彭倩	19911210	韩月彭	植物学	中国科学院武汉植物园	20170301	中国科学院大学2017年度博士研究生国际合作培养计划综合项目
27	曹仃仃	19910626	杨平仿	植物学	中国科学院武汉植物园	20170901	
28	范民霞	19890510	郭明全	植物学	中国科学院西北高原生物研究所	20170901	
29	李东海	19880825	吕世友	植物学	浙江理工大学	20170901	

30	李梦辉	19900610	郭明全	植物学	海南大学	20170901	
31	李晓宁	19900425	付金民	植物学	中国科学院武汉植物园	20170901	中国科学院大学“三好学生”
32	刘秀林	19910302	吕世友	植物学	中国科学院武汉植物园	20170901	
33	王广阳	19930906	付金民	植物学	中国科学院武汉植物园	20170901	
34	余敏	19890228	王彦昌	植物学	华中农业大学	20170901	
35	朱亚如	19900920	章焰生	植物学	武汉大学	20170901	

当年毕业研究生一览表

序号	姓名	性别	攻读学位	专业	指导教师	论文题目	毕业去向	获奖
1	杨路路	女	博士	植物学	王　瑛	我国三种药用甘草遗传多样性和居群遗传结构评价及核心种质的构建	中国科学院武汉植物园	
2	刘翠霞	女	博士	植物学	李绍华	葡萄果实单萜化合物含量的 QTL 定位及其合成调控的候选基因筛选	商洛学院	
3	闫明慧	女	博士	植物学	王恒昌	安息香科的叶绿体系统发育基因组学研究	信阳师范学院	
4	李林懋	女	博士	植物学	吕世友	拟南芥表皮蜡质生物合成调控的分子机制解析	武汉大学	武汉教育基“优秀毕业生”
5	杨贤鹏	男	博士	植物学	吕世友	拟南芥表皮蜡质合成相关基因 CER17 的功能解析	中国科学院武汉植物园	中国科学院“院长优秀奖”；中国科学院大学“三好学生标兵”

6	陈桂林	男	博士	植物学	郭明全	基于拓扑异构酶 I 的超滤质谱法快速筛选天然活性成分的研究	中国科学院武汉植物园	中国科学院大学“三好学生”
7	苟君波	男	博士	植物学	章焰生	倍半萜内酯合成关键酶基因挖掘与功能分析	中国农业科学院深圳基因组研究所	中国科学院大学“三好学生”
8	王宙雅	女	硕士	植物学	吕世友	古代莲超长链脂肪酸延伸相关基因 NnCER26 的克隆及功能分析	中国科学院遗传与发育生物学研究所	
9	刘奥	男	硕士	植物学	付金民	狗牙根低温高盐胁迫耐性 miRNA 挖掘及生理应答机制研究	美国达特茅斯学院	中国科学院大学“优秀毕业生”
10	许岩	男	硕士	植物学	李夜光	微藻高效固碳并联产高附加值产物的初步研究	焦作市国土资源局不动产登记中心	中国科学院大学“三好学生”
11	李玲	女	硕士	植物学	杨平仿	莲高密度遗传连锁图谱的构建及花期 QTL 定位	武汉市武昌区绿化队	
12	李晓华	女	硕士	植物学	章焰生	薯蓣皂素合成基因富集、挖掘及其功能分析系统建立	武汉启瑞药业有限公司	武汉教育基地“优秀毕业生”
13	邱子栋	男	硕士	植物学	郭明全	南方山荷叶化学成分的研究	中国药科大学	
14	郑斌	男	硕士	植物学	闫　娟	龙胆属头花组和多枝组的分类学研究	武汉谷语自然文化发展有限公司	
15	唐萍	女	硕士	植物学	姚小洪	猕猴桃属叶绿体基因组进化及其系统发育关系重建	美因健康科技（北京）有限公司	
16	GITAU MARGARET MUKAMI	女	硕士	植物学	付金民	狗牙根遗传多样性与饲用性状的关联分析		

17	SOSPETER KARANJA KARUNGO	男	硕士	植物学	李绍华	VaWRKY55 在山葡萄低温和干旱胁迫响应中的功能研究		
18	赵亭亭	女	硕士	园林植物与观赏园艺	辛海平	高效、快速山葡萄遗传转化体系的建立		
19	毕傲月	女	硕士	生物工程	付金民	高羊茅耐高温生理分析及 HSP17.8 和 HSP17.9 分子克隆	中国科学院遗传与发育生物学研究所	武汉教育基地“优秀毕业生”
20	刘秀林	男	硕士	生物工程	吕世友	高浓度 CO_2 调控表皮蜡质合成的研究	中国科学院武汉植物园	

第四部分 承担任务及经费

1. 承担任务一览表

序号	项目名称	项目来源	项目类别	开始时间	结束时间	总经费（万元）	实到经费（万元）	负责人	参与类型
1	毒品原植物快速鉴定及替代资源研发	科技部	国家重点研发计划	2016.7	2019.6	100	28	梁琼	参与
2	水稻蛋白磷酸化平台构建及应用	科技部	国家重点研发计划	2016.7	2020.12	65.3	12.7	杨平仿	参与
3	油桐副产品高值化加工利用关键技术研究	科技部	国家重点研发计划	2017.7	2020.12	60	22.4	吕世友	参与
4	苹果果实糖酸性状的全基因组关联分析及其遗传调控网络研究	基金委	基金重点	2015.1	2019.12	278	0	韩月彭	主要负责
5	安息香科的系统发育基因学和花形态发生研究	基金委	其他基金项目	2014.1	2017.12	80	0	王恒昌	主要负责
6	东亚特有植物水青树的谱系地理学研究	基金委	其他基金项目	2014.1	2017.12	80	0	李建强	主要负责
7	中华猕猴桃复合体及其近缘种的分子谱系地理学研究	基金委	其他基金项目	2014.1	2017.12	80	0	李作洲	主要负责
8	拟南芥 ABA 受体相互作用蛋白的鉴定和功能解析	基金委	其他基金项目	2014.1	2017.12	80	0	产祝龙	主要负责
9	拟南芥蜡质合成 CER16 的功能解析	基金委	其他基金项目	2014.1	2017.12	80	0	吕世友	主要负责
10	倍半萜药用化合物苍耳素生物合成关键 P450 基因的分离与功能分析	基金委	其他基金项目	2014.1	2017.12	80	0	章焰生	主要负责

11	解析蕨类植物叶绿体基因组高变区的进化式样、过程和机制	基金委	其他基金项目	2014.1	2017.12	80	0	王艇	主要负责
12	葡萄高密度遗传图谱构建及果实糖酸含量 QTL 定位	基金委	其他基金项目	2014.1	2017.12	85	0	李绍华	主要负责
13	苹果果实酸度 QTLs 区域液泡膜 H+-ATPase 及相关调节基因的关联分析和功能研究	基金委	其他基金项目	2014.1	2017.12	80	0	韩月彭	主要负责
14	蕨类植物叶绿体 RNA 编辑及其适应性进化研究	基金委	其他基金项目	2015.1	2017.12	26	0	高磊,	主要负责
15	拟南芥 CER9 基因参与调节种子油脂合成的机理研究	基金委	其他基金项目	2015.1	2017.12	24	0	李荣俊	主要负责
16	鬼伞属真菌中抗肿瘤 guanacastane 类二萜及其作用机制研究	基金委	其他基金项目	2015.1	2017.12	25	0	刘源振	主要负责
17	基于谱系地理学的濒危植物银鹊树的保护生物学研究	基金委	其他基金项目	2015.1	2017.12	24	0	田华	主要负责
18	低温响应转录因子 CdCAMTA1 在野生狗牙根抗寒中的功能及其抗寒分子机理研究	基金委	其他基金项目	2015.1	2017.12	25	0	陈良	主要负责
19	高羊茅耐热相关 miRNA 及靶基因的发倔与功能解析	基金委	其他基金项目	2015.1	2018.12	85	21.3	付金民	主要负责
20	萝卜细胞质雄性不育育性恢复新机制的分子解析	基金委	其他基金项目	2015.1	2018.12	85	21.3	汪志伟	主要负责
21	桃三个 MADS-box 基因调控果实发育其分子机理的研究	基金委	其他基金项目	2015.1	2018.12	86	0	韩月彭	主要负责

22	WRKY28 和 WRKY43 调控葡萄耐寒的分子机理研究	基金委	其他基金项目	2015.1	2018.12	85	21.3	辛海平	主要负责
23	结合连锁分析和关联分析定位莲花期和地下茎 QTL 及候选基因鉴定	基金委	其他基金项目	2015.1	2018.12	85	21.3	杨美	主要负责
24	水稻 OsSRO1c 基因在干旱胁迫诱导的叶片衰老中的功能研究	基金委	其他基金项目	2016.1	2018.12	24	1.3	游均	主要负责
25	油桐经济性状关联分析	基金委	其他基金项目	2016.1	2018.12	24	1.3	张玲玲	主要负责
26	苹果 MdLAR1 和 MdNR2 基因等位变异的发掘及其果实原花青素含量的关联分析	基金委	其他基金项目	2016.1	2018.12	26.4	10.3	廖燎	主要负责
27	红肉猕猴桃 AcMYB1 功能鉴定及其调控机制研究	基金委	其他基金项目	2016.1	2018.12	23.8	1.3	满玉萍	主要负责
28	基于 SSR 关联分析发掘中国狗牙根耐镉基因位点	基金委	其他基金项目	2016.1	2018.12	22.8	1.3	付金民	主要负责
29	基于转录分析的小球藻同步生长与产油的分子基础	基金委	其他基金项目	2016.1	2018.12	23.9	1.3	王中杰	主要负责
30	拟南芥 miR156 调节表皮蜡质合成的功能及机理解析	基金委	其他基金项目	2016.1	2019.12	75.6	22.1	吕世友	主要负责
31	中华猕猴桃复合体跨倍性杂交子代倍性分离及果实性状遗传规律研究	基金委	其他基金项目	2016.1	2019.12	75.5	22.0	钟彩虹	主要负责
32	生态及遗传因子对枸杞叶品质的影响研究	基金委	其他基金项目	2016.1	2019.12	80.4	23.5	梁琼	主要负责
33	猕猴桃细菌性溃疡	基金委	其他基	2016.1	2019.12	78.0	22.7	李大卫	主要

	病抗性遗传规律研究及抗病基因发掘		金项目						负责
34	小檗科系统基因组学及叶绿体基因进化研究	基金委	其他基金项目	2017.1	2019.12	18	12.0	孙延霞	主要负责
35	猕猴桃中糖苷键合态 C6 醇/醛类香气物质的气调游离化机制研究	基金委	其他基金项目	2017.1	2019.12	21	13.9	张春云	主要负责
36	两个串联 NAC 基因控制果实成熟期的分子机理研究	基金委	其他基金项目	2017.1	2019.12	20	13.3	周晖	主要负责
37	灵芝三萜酸下游合成路径关键CY450s基因挖掘与功能分析	基金委	其他基金项目	2017.1	2019.12	20	13.3	陈方方	主要负责
38	VaNAC26 通过茉莉酸信号通路调控山葡萄耐寒性的机理研究	基金委	其他基金项目	2017.1	2020.12	65	35.6	辛海平	主要负责
39	茉莉酸信号组分 CdMY2 及其调节的 CdWRKY26 基因在野生狗牙根抗寒中的功能及抗寒分子机理	基金委	其他基金项目	2017.1	2020.12	65	35.8	陈良	主要负责
40	基于功能蛋白组学和超滤质谱技术研究石蒜抗癌的作用机制与化学物质基础	基金委	其他基金项目	2017.1	2020.12	57	31.4	郭明全	主要负责
41	淫羊藿高密度遗传图谱构建及类黄酮含量 QTL 定位	基金委	其他基金项目	2017.1	2020.12	61	33.4	张燕君	主要负责
42	桃 PpOA3 基因参与果实酸度调控的功能及机理解析	基金委	其他基金项目	2017.1	2020.12	65	35.8	韩月彭	主要负责
43	薯皂素合成下游路径关键P450酶基因的分离与功能分析	基金委	其他基金项目	2017.1	2020.12	62	34.0	章焰生	主要负责

44	水稻种子萌发过程中赤霉素信号传递所介导的蛋白质磷酸化级联反应及其功能分析	基金委	其他基金项目	2017.1	2020.12	64	35.2	杨平仿	主要负责
45	中国产油微藻调查	科技部	省部委	2012.5	2018.12	105	0	李夜光	参与
46	猕猴桃种质资源收集、编目、更新与利用	其他（农业部）	省部委	2012.1	2022.12	300	30	钟彩虹	主要负责
47	主要果树新品种选育	科技部	省部委	2013.1	2018.12	1087	0	李绍华	主要负责
48	泛喜马拉雅地区植物综合考察与植物志编研	科技部	省部委	2013.6	2018.12	20	0	李建强	参与
49	南水北调（中线）水源地生物群落环境调查	科技部	省部委	2015.5	2019.5	1089	0	胡涛	参与
50	黄河中上游半干旱-半漠境区盐碱地植物种质资源调查及数据库构建	科技部	省部委	2015.1	2018.12	70	31.4	付金民	参与
51	湖北秦岭冷杉专项调查	其他	省部委	2015.12	2019.12	65.9	5.8	李晓东	主要负责
52	植物园迁地栽培植物志	科技部	省部委	2015.1	2018.12	10	45	吴金清	参与
53	三峡库区水生高等植物多样性调查及图鉴制作	科技部	省部委	2014.5	2018.4	70	33.5	吴金清	参与
54	猕猴桃香气成分原位全组分检测机理研究	其他	省部委	2016.1	2018.12	3	0	张春云	主要负责
55	油桐种子桐酸合成通路相关基因等位变异与功能标记开发	其他	省部委	2016.1	2018.12	5	0	张玲玲	主要负责
56	优质多抗猕猴桃新品种选育和种质资源创新利用	其他	省部委	2016.5	2019.5	100	0	钟彩虹	主要负责
57	新型因果逻辑模型及基于因果关系的预测研究	其他	省部委	2017.1	2018.12	30	25	张秀军	参与

58	国家现代农业产业技术体系岗位科学家	其他	省部委	2017.1	2020.12	280	70	韩月彭	主要负责
59	非洲特有药用植物开发利用合作研究	其他	省部委	2017.1	2019.12	20	20	郭明全	主要负责
60	猕猴桃果实采后应答软腐病菌发生的关键抗性基因筛选和功能解析	其他	省部委	2017.1	2018.12	3	4	李黎	主要负责
61	非洲和亚洲地区水稻生物和非生物胁迫抗性基因资源的转录组学和蛋白质组学比较研究	中科院	中科院项目	2013.1	2020.12	220	30	杨平仿	主要负责
62	咖啡野生种质资源的收集与保育	中科院	中科院项目	2013.1	2020.12	100	32	韩月彭	主要负责
63	药用植物化学生物学	中科院	中科院项目	2013.12	2020.12	260	40	郭明全	主要负责
64	葡萄抗逆分子机理	中科院	中科院项目	201.1	2020.12	40	20	辛海平	主要负责
65	丹江口库区高效生态农业示范	中科院	中科院项目	2015.7	2020.12	540	0	钟彩虹	主要负责
66	莲基因组进化和驯化机制的研究	中科院	中科院项目	2016.8	2020.12	250	60	杨美	主要负责
67	非洲天然产物开发利用	中科院	中科院项目	2016.1	2020.12	700	125	郭明全	主要负责
68	葡萄科适应性进化	中科院	中科院项目	2016.1	2020.12	100	20	辛海平	主要负责
69	植物抗逆分子机制	中科院	中科院项目	2016.1	2020.12	150	0	产祝龙	主要负责
70	红球藻技术研发与示范	中科院	中科院项目	2016.1	2018.12	60	18	李夜光	主要负责
71	特色经济作物示范种植	中科院	中科院项目	2016.5	2018.12	360	180	钟彩虹	主要负责
72	基于大数据处理的生物信息学平台开发	中科院	中科院项目	2016.9	2019.8	80	40	张秀军	主要负责
73	珍稀濒危药用植物白及优异种质创制与规模化栽培技术研发	中科院	中科院项目	2016.1	2018.12	66	30	梁琼	主要负责

74	新兴工业原料植物山桐子新种质创制	中科院	中科院项目	2016.1	2018.12	50	25	吕世友	主要负责
75	新型特色水果三叶木通的重要农艺性状遗传机理及新种质创制研究	中科院	中科院项目	2016.1	2018.12	50	25	姚小洪	主要负责
76	华中-湖北本土植物清查与保护	中科院	中科院项目	2016.6	2019.5	120	0	梁琼	主要负责
77	莲花期和地下茎发育的遗传机制研究	中科院	中科院项目	2017.1	2020.12	80	20	杨美	主要负责
78	草坪草逆境生理与分子遗传机理解析	中科院	中科院项目	2017.1	2020.12	80	20	陈良	主要负责
79	滨海盐碱地植物资源利用与经饲草产业化开发	中科院	中科院项目	2017.1	2020.12	150	60	陈良	主要负责
80	植物分子遗传改良	中科院	中科院项目	2017.10	2020.10	80	0	宋士勇	主要负责
81	油桐种质资源创新	中科院	中科院项目	2014.1	2017.12	260	50	吕世友	主要负责
82	特种功能蔬菜推广种植	其他	横向项目	2010.10	2018.12	35	0	张燕君	主要负责
83	红肉猕猴桃新品种东红	其他	横向项目	2012.2	2032.4	950	60	钟彩虹	主要负责
84	功能蔬菜和神农金菊的种植	其他	横向项目	2012.4	2018.12	50	4.2	王庆	主要负责
85	黄肉新品种金圆的开发技术研究	其他	横向项目	2013.2	2033.2	830	0	钟彩虹	主要负责
86	天然药用植物系列复合天然功能保健品研发	其他	横向项目	2013.5	2018.12	50	0	郭明全	主要负责
87	神农架猕猴桃种质技术服务	其他	横向项目	2014.6	2019.12	100	0	王彦昌	主要负责
88	都江堰市国际猕猴桃博览馆布展项目	其他	横向项目	2014.6	2018.12	20	0	李大卫	主要负责
89	红昇猕猴桃品种示范技术服务	其他	横向项目	2014.8	2019.12	550	0	王彦昌	主要负责
90	产油微藻病虫害控制	其他	横向项目	2015.1	2018.12	160	0	李夜光	主要负责
91	猕猴桃新品种、新技术	其他	横向	2015.2	2020.1	1037	202.2	钟彩虹	主要

	的国内产业化开发		项目						负责
92	白桦脂酸双功能菌构建	其他	横向项目	2015.12	2020.12	100	0	章焰生	主要负责
93	软枣猕猴桃引种与示范	其他	横向项目	2016.1	2018.12	30	17.8	王彦昌	主要负责
94	有机猕猴桃生产关键技术研究集成与示范	其他	横向项目	2016.6	2018.6	42	0	钟彩虹	主要负责
95	软枣猕猴桃种质鉴定和新品种选育	其他	横向项目	2016.12	2022.11	90	0	王彦昌	主要负责
96	孝义市矿山生态修复及湿地景观建设	其他	横向项目	2017.6	2018.12	28	18.7	闫娟	主要负责
97	软枣猕猴桃生产示范及品系优化筛选	其他	横向项目	2017.7	2023.6	150	25	王彦昌	主要负责
98	淫羊藿优良品种选育与示范栽培	其他	横向项目	2017.8	2020.8	15	10	张燕君	主要负责
99	彩叶苗木新品种快繁	其他	横向项目	2016.1	2017.12	40	12	梁琼	主要负责
100	湖北后河种子植物调查和名录编研	其他	横向项目	2017.6	2018.6	9.5	9.5	王恒昌	主要负责
101	东湖植物资源调查与利用	其他	其他	2008.1	2023.12	32	0	程中平	主要负责
102	武汉长山口垃圾生态修复	其他	其他	2010.12	2026.12	60	0	程中平	主要负责
103	猕猴桃种质资源圃成果推广	其他	其他	2012.5	2022.12	50	0	龚俊杰	主要负责
104	香榧指纹图谱构建	其他	其他	2015.3	2019.3	40	0	姚小洪	主要负责
105	泰顺县猕猴桃科技服务	其他	其他	2016.5	2021.5	200	40	姚小洪	主要负责
106	莲推广与产业化	其他	其他	2016.1	2020.12	100	14.0	杨平仿	主要负责
107	高产优质子莲品种的保育、创制与产业化	其他	其他	2016.1	2018.12	30	0	杨美	主要负责
108	基于高密遗传图谱的猕猴桃糖酸含量的 QTL 定位	其他	其他	2016.1	2018.12	30	0	姚小洪	主要负责
109	基于新一代测序数	其他	其他	2016.9	2019.8	50	0	张秀军	主要

	据的植物功能基因组学分析研究								负责
110	枸杞育种、反季节栽培	其他	其他	2016.1	2018.12	20	0	杨天顺	主要负责
111	水稻 OsSAP8 基因调控赤霉素合成和种子萌发的分子机理研究	其他	其他	2017.7	2019.7	10	10	李明	主要负责
112	芒属植物的系统进化学研究	其他	其他	2017.1	2019.12	30	15	闫娟	主要负责
113	山葡萄抗寒旱分子机理	其他	其他	2017.1	2019.12	30	15	辛海平	主要负责
114	水生植物分子育种	其他	其他	2017.10	2020.10	50	50	宋士勇	主要负责
115	毒品原植物快速鉴定及替代资源研发匹配	其他	其他	2016.7	2019.6	45	0	梁琼	主要负责
116	通山富水湖国家湿地公园生物多样性调查	其他	其他	2017.7	2018.12	15	10	李新伟	主要负责
117	国际猕猴桃研讨会	其他	其他	2017.1	2017.12	45	40.2	钟彩虹	主要负责
合计	/	/	/	/	/	14928	2162.4	/	/

2. 国际合作项目一览表

序号	项目名称	合作国别	合作单位	开始时间	结束时间	总经费(万元)	本年实到经费（万元）	负责人
1	新品种授权商业开发	意大利	Consorzio Kiwigold	2005.8	2028.12	1000	9.9	钟彩虹
2	亚非国家杰出青年科学家来华工作计划	埃及	埃及农业部沙漠研究所	2017.1	2017.12	15	15	韩月彭
合计	/	/	/	/	/	1015	24.9	/

第五部分 研究成果

1. 获奖情况

序号	成果名称	级别	类别	等级	完成人	排名
1	特色猕猴桃新品种选育及产业化应用	省部级	神农中华农业科技奖	科研类成果一等奖	黄宏文、钟彩虹、刘义飞、姜正旺、李大卫、张忠慧、龚俊杰、姚小洪、韩飞、张琼、刘小莉、李黎、陈美艳、张鹏	1
2	葡萄种质创新与新品种选育推广团队	省部级	中国科学院科技促进发展奖		辛海平（排名第六）	2（第二完成单位）

2. 发表论文一览表

序号	论文名称	期刊名称	卷、期、页	影响因子	收录类型	是否为1区论文	作者	通迅作者(固定人员)	通迅作者(非固定人员)	完成情况
1	The acyl Desaturase CER17 is Involved in Producing Wax Unsaturated Primary Alcohols and Cutin Monomers	Plant Physiology	2017: 173:1109 -1124	6.456	SCI	是	Yang XP, Zhao HY, Kosma DK, Tomasi P, Dyer JM, Li RJ, Liu XL, Wang ZY, Parsons EP, Jenks MA, Lv SY	Lv SY		第一完成人（非独立完成）

2	Population transcriptomic characterization of the genetic and expression variation of a candidate progenitor of *Miscanthus* energy crops	Molecular Ecology	2017,26: 5911－5922	6.086	SCI	是	Yan J, Song ZH, Xu Q, Kang LF, Zhu CY, Xing SL, Liu W, Greimler J, Züst T, Li JQ, Sang T	Li JQ	Sang T	第一完成人（非独立完成）
3	The evolution of plant microRNAs: insights from a basal eudicot sacred lotus	Plant Journal	2017,89: 442-457	5.901	SCI	是	Shi T, Wang K, Yang PF	Yang PF		独立完成
4	Molecular characterization of the C-glucosylation for puerarin biosynthesis in *Pueraria lobata*	Plant Journal	2017,90: 535-546	5.901	SCI	是	Wang X, Li CF, Zhou C, Li J, Zhang YS	Zhang YS		独立完成
5	Variation of ascorbic acid concentration in fruits of cultivated and wild apples	Food Chemistry	2017,225 : 132-137	4.529	SCI	是	Fang T, Zhen QL, Liao L, Owiti A, Zhao L, Korban SS, Han YP	Han YP		第一完成人（非独立完成）
6	Rapid Screening for α-Glucosidase Inhibitors from *Gymnema sylvestre* by Affinity Ultrafiltration-HPLC-MS	Frontiers in Pharmacology	2017,8:228	4.40	SCI	是	Chen GL, Guo MQ	Guo MQ		独立完成
7	Identification of differentially expressed proteins in bermudagrass response to cold stress in the presence of ethylene	Environmental and Experimental Botany	2017, 139: 67-78	4.369	SCI	是	Hu ZR, Liu A, Bi AY, Amombo E, Gitau MM, Huang XB, Chen L, Fu JM	Chen L, Fu JM		独立完成
8	Amelioration of Salt Stress on Bermudagrass by the Fungus *Aspergillus aculeatus*	Molecular Plant-Microbe Interactions	2017,30(3):245-254	4.332	SCI	是	Xie Y, Han SJ, Li XN, Amombo E, Fu JM	Fu JM		独立完成

9	Exogenous Calcium Enhances the Photosystem II Photochemistry Response in Salt Stressed Tall Fescue	Frontiers in Plant Science	2017.8, 2032	4.291	SCI	是	Wang GY,Bi AY, Amombo E, Li HY, Zhang L, Cheng C, Hu T, Fu JM	Hu T, Fu JM		第一完成人（非独立完成）
10	ABA Is Involved in Regulation of Cold Stress Response in Bermudagrass	Frontiers in Plant Science	2017,8, 1613	4.291	SCI	是	Huang XB, Shi HY, Hu ZR, Liu A, Amombo E, Chen L, Fu JM	Chen L, Fu JM		第一完成人（非独立完成）
11	Melatonin is Involved in Regulation of Bermudagrass Growth and Development and Response to Low K^+ Stress	Frontiers in Plant Science	2017,8,2038	4.291	SCI	是	Chen L, Fan JB, Hu ZR, Huang XB, Amombo E, Liu A, Bi AY, Chen K, Xie Y, Fu JM	Chen L		第一完成人（非独立完成）
12	Functional Characterization of a Novel R2R3-MYB Transcription Factor Modulating the Flavonoid Biosynthetic Pathway from *Epimedium sagittatum*	Frontiers in Plant Science	2017,8:1274	4.291	SCI	是	Huang WJ, Lv HY, Wang Y		Wang Y	第一完成人（非独立完成）
13	Development and Application of Transcriptome-Derived Microsatellites in *Actinidia eriantha* (Actinidiaceae)	Frontiers in Plant Science	2017,8:1383	4.291	SCI	是	Guo R, Landis JB, Moore MJ, Meng AP, Jian SG, Yao XH, Wang HC	Yao XH, Wang HC		第一完成人（非独立完成）
14	The Alleviation of Heat Damage to Photosystem II and Enzymatic Antioxidants by Exogenous Spermidine in Tall Fescue	Frontiers in Plant Science	2017,8,1747	4.291	SCI	是	Zhang L, Hu T, Amombo E, Wang GY, Xie Y, Fu JM	Xie Y, Fu JM		独立完成
15	Screening for Natural Inhibitors of Topoisomerases I from *Rhamnus davurica* by Affinity Ultrafiltration and High-Performance Liquid	Frontiers in Plant Science	2017,8:1521	4.291	SCI	是	Chen GL, Guo MQ	Guo MQ		独立完成

	Chromatography-Mass Spectrometry									
16	Involvement of Ubiquitin-Conjugating Enzyme (E2 Gene Family) in Ripening Process and Response to Cold and Heat Stress of *Vitis vinifera*	Scientific Reports	2017,(7): 13290	4.259	SCI	是	Gao YY, Wang Y, Xin HP, Li SH, Liang ZC		Liang ZC	第一完成人（非独立完成）
17	The Fungus *Aspergillus* aculeatus Enhances Salt-Stress Tolerance, Metabolite Accumulation, and Improves Forage Quality in Perennial Ryegrass	Frontiers in Microbiology	2017, 8:1664	4.076	SCI	是	Li XN, Han SJ, Wang GY, Liu XY, Amombo E, Xie Y, Fu JM	Xie Y, Fu JM		独立完成
18	Discovery of Several Novel Targets that Enhance β-Carotene Production in *Saccharomyces cerevisiae*	Frontiers in Microbiology	2017,8:1 116	4.076	SCI	是	Li J, Shen J, Sun ZQ, Li J, Li CF, Li XH, Zhang YS	Zhang YS		独立完成
19	Isolation and characterization of an endoparasite from the culture of oleaginous microalga *Graesiella* sp. WBG-1	Algal Research	2017,26: 371-379	3.994	SCI	是	Ding Y, Peng XA, Wang ZJ, Wen XB, Geng YH, Li YG	Li YG		独立完成
20	Investigation of changes in endocannabinoids and N-acylethanolamides in biofluids, and their correlations with female infertility	Journal of Chromatography A	2017,150 9:16-25	3.981	SCI	是	Ding J, Luo XT, Yao YR, Xiao HM, Guo MQ	Guo MQ		第一完成人（非独立完成）
21	Solvent-saturated solid matrix technique for increasing the efficiency of headspace extraction of volatiles	Journal of Chromatography A	2017,151 1:9-14	3.981	SCI	是	Zhang CY, Guo MQ	Guo MQ		独立完成

22	Reduced representation genome sequencing reveals patterns of genetic diversity and selection in apple	Journal of Integrative Plant Biology	2017,59 (3): 190-204	3.962	SCI	是	Ma BQ, Liao L, Peng Q, Fang T, Zhou H, Korban SS, Han YP	Han YP		第一完成人（非独立完成）
23	Complete plastomes sequencing of both living species of Circaeasteraceae (Ranunculales) reveals unusual rearrangements and loss of the *ndh* gene family	BMC Genomics	2017,18: 592	3.729	SCI	是	Sun YX, Moore MJ,Lin N, Adelalu KF, Meng AP, Jian SG, Yang LS, Li JQ, Wang HC	Li JQ, Wang HC		第一完成人（非独立完成）
24	Transcriptome profilings of two tall fescue (*Festuca arundinacea*) cultivars in response to lead (Pb) stress	BMC Genomics	2017, 18:145	3.729	SCI	是	Li HY, Hu T, Amombo E, Fu JM	Fu JM		独立完成
25	Low genetic diversity and functional constraint of miRNA genes participating pollen–pistil interaction in rice	Plant Molecular Biology	2017,95: 89-98	3.356	SCI	是	Wang K, Wang X, Li M, Shi T, Yang PF	Shi T, Yang PF		独立完成
26	First Report of *Alternaria alternata* Causing Postharvest Rot of Kiwifruit in China	Plant Disease	2017, 101(6):1 046	3.173	SCI	是	Li L, Pan H, Liu W, Chen MY, Zhong CH	Zhong CH		第一完成人（非独立完成）
27	First Report of *Diaporthe actinidiae* Causing Stem-end Rot of Kiwifruit During Post-Harvet in China	Plant Disease	2017, 101(6):1 054	3.173	SCI	是	Li L, Pan H, Liu W, Chen MY, Zhong CH	Zhong CH		第一完成人（非独立完成）
28	First Report of Anthracnose Caused by *Colletotrichum gloeosporioides* on kiwifruit (*Actinidia chinensis*) in China	Plant Disease	2017, 101(12): 2151	3.173	SCI	是	Li L, Pan H, Chen MY, Zhang SJ, Zhong CH	Zhong CH		独立完成

29	Genome-wide identification of heat stress-responsive small RNAs in tall fescue (*Festuca arundinacea*) by high-throughput sequencing	Journal of plant physiology	2017, 213:157-165	3.121	SCI	是	Li HY, Hu T, Amombo E, Fu JM	Fu JM		独立完成
30	Proteomics analysis identified a DRT protein involved in arsenic resistance in *Populus*	Plant Cell Reports	2017,36: 1855-1869	2.869	SCI	是	Liu YL, Damaris RN, Yang PF	Yang PF		独立完成
31	Comparative Analysis of Saponins from Different Phytolaccaceae Species and Their Antiproliferative Activities	Molecules	2017,22: 1077	2.861	SCI	否	Saleri FD, Chen GL, Li X, Guo MQ	Guo MQ		独立完成
32	An efficient method for transgenic callus induction from *Vitis amurensis* petiole	PLoS ONE	2017,12 (6):e0179730	2.806	SCI	是	Zhao TT, Wang ZM, Su LY, Sun XM, Cheng J, Zhang LL, Karungo SK, Han YP, Li SH, Xin HP	Xin HP		第一完成人（非独立完成）
33	Comparative transcript profiling explores differentially expressed genes associated with sexual phenotype in kiwifruit	PLoS ONE	2017, 12(7):e0180542	2.806	SCI	是	Tang P, Zhang Q, Yao XH	Yao XH		独立完成
34	Effects of cadmium-resistant fungi *Aspergillus aculeatus* on metabolic profiles of bermudagrass [Cynodondactylon (L.)Pers.] under Cd stress	Plant Physiology and Biochemistry	2017, 114:38-50	2.724	SCI	是	Li XN, Gitau MM, Han SJ, Fu JM, Xie Y	Fu JM, Xie Y		独立完成

35	Carbonylated protein changes between active germinated embryos and quiescent embryos give insights into rice seed germination regulation	Plant Growth Regulation	2017,83: 335-350	2.646	SCI	是	Zhang H, He DL, Li M, Yang PF	Li M, Yang PF		独立完成
36	The *Arabidopsis* endoplasmic reticulum associated degradation pathways are involved in the regulation of heat stress response	Biochemical and Biophysical Research Communications	2017,487 :362-367	2.466	SCI	否	Li LM, Liu XL, Li RJ	Li RJ		独立完成
37	Construction of a SNP-based genetic linkage map for kiwifruit using next-generation restriction-site-associated DNA sequencing (RADseq)	Molecular Breeding	2017,37: 139	2.465	SCI	是	Liu CY, Li DW, Zhou JH, Zhang Q, Tian H, Yao XH	Yao XH		第一完成人（非独立完成）
38	Assessment of calcium and zinc accumulation in cultivated and wild apples	Journal of the Science of Food and Agriculture	2017,97: 4258-4263	2.463	SCI	是	Liao L, Fang T, Ma BQ, Deng XB, Zhao L, Han YP	Han YP		独立完成
39	Comparative study on alkaloids and their anti-proliferative activities from three *Zanthoxylum* species	BMC Complementary and Alternative Medicine	2017,17: 460	2.288	SCI	是	Tian YQ , Zhang CY, Guo MQ	Guo MQ		独立完成

40	Phylogenetic study of the tribe Potentilleae (Rosaceae),with further insight into the disintegration of *Sibbaldia*	Journal of Systematics and Evolution	2017,55(3):177－191	2.050	SCI	否	Feng T, Moore MJ, Yan MH, Sun YX, Zhang HJ, Meng AP, Li XD, Jian SG, Li JQ, Wang HC	Li JQ, Wang HC		第一完成人（非独立完成）
41	Analysis and Differentiation of the Volatile Compounds in Red and White Wines Using Desiccated Headspace Gas Chromatography-Mass Spectrometry Coupled with Chemometrics	Food Analytical Methods	2017,10:3531-3537	2.038	SCI	否	Zhang CY, Guo MQ	Guo MQ		独立完成
42	Flavonoids of Lotus (*Nelumbo nucifera*) Seed Embryos and Their Antioxidant Potential	Journal of Food Science	2017, 82(8):1834-1841	1.815	SCI	否	Zhu MZ, Liu T, Zhang CY, Guo MQ	Guo MQ		独立完成
43	Genetic diversity and association mapping of forage quality in diverse bermudagrass accessions	Euphytica	2017, 213(10): 234	1.626	SCI	是	Gitau MM, Fan JB, Xie Y, Fu JM	Xie Y, Fu JM		第一完成人（非独立完成）
44	Characterization and development of EST-derived SSR markers in *Sinowilsonia henryi* (Hamamelidaceae)	Applications in Plant Sciences	2017,5(11):1700080	1.492	SCI	否	Li ZZ, Tian H, Zhang JJ	Zhang JJ		第一完成人（非独立完成）
45	Ammonium bicarbonate supplementation as carbon source in alkaliphilic *Spirulina* mass culture	Aquaculture Research	2017,48:4886-4896	1.461	SCI	否	Ding Y, Li XL, Wang ZJ, Li ZK, Yin DC, Geng YH，Li YG	Li YG		独立完成
46	The first complete plastome sequence of the basal asterid family Styracaceae	Plant Systematics	2017,303 : 61-70	1.239	SCI	否	Yan MH, Moore MJ, Meng AP, Yao XH, Wang	Wang HC		第一完成人（非独立完

	(Ericales)reveals a large inversion	and Evolution					HC			成）
47	Changes of Antioxidant Defense System and Fatty Acid Composition in Bermudagrass under Chilling Stress	Journal of the American Society for Horticultural Science	2017, 142(2): 101-109	1.125	SCI	否	Hu ZR, Amombo E, Gitau MM, Bi AY, Zhu HH, Zhang L, Chen L, Fu JM	Chen L, Fu JM		第一完成人（非独立完成）
48	Research Advances on Tall Fescue Salt Tolerance: From Root Signaling to Molecular and Metabolic Adjustment	Journal of the American Society for Horticultural Science	2017, 142(5): 337-345	1.125	SCI	否	Amombo E, Li HY, Fu JM	Fu JM		独立完成
49	Isolation and identification of pathogenic fungi causing post-harvest fruit rot of kiwifruit (*Actinidia chinensis*) in China	Journal of Phytopatholog y	2017,165 :782-790	0.853	SCI	否	Li L, Pan H, Chen MY, Zhang SJ, Zhong CH	Zhong CH		独立完成
50	Quantitative Analysis and Comparison of Flavonoids in Lotus Plumules of Four Representative Lotus Cultivars	Journal of Spectroscopy	2017, Article ID 7124354	0.761	SCI	否	Liu T, Zhu MZ, Zhang CY, Guo MQ	Guo MQ		独立完成
51	iTRAQ-based Comparative Proteomic Analyses of Two Grapevine Cultivars in Response to Cold Stress	Current Proteomics	2017,14: 42-52	0.59	SCI	否	Deng J, Yin XJ, Xiang Y, Xin HP, Li SH, Yang PF	Li SH, Yang PF		第一完成人（非独立完成）
52	*Primula hubeiensis* (Primulaceae), a New Species from Central China	Novon	2017,25: 162-165	0.512	SCI	否	Li XW, Bao DC, Huang HD, Xie JF	Li XW		第一完成人（非独立完成）

53	Rapid radiations of both kiwifruit hybrid lineages and their parents shed light on a two-layer mode of species diversification	New Phytologist	2017, 215:877-890	7.330	SCI	是	Liu YF, Li DW, Zhang Q, Song C, Zhong CH, Zhang XD, Wang Y, Yao XH, Wang ZP, Zeng SH, Wang Y, Guo YT, Wang SB, Li XW, Li L, Liu CY, McCann HC, He WM, Liu Y, Chen M, Du LW, Gong JJ, Datson PM, Hilario E, Huang HW		Huang HW	非第一完成人（非独立完成）
54	Transcriptomic characterization of candidate genes responsive to salt tolerance of *Miscanthus* energy crops	Global Change Biology Bioenergy	2017,9:1222-1237	4.655	SCI	是	Song ZH, Xu Q, Lin C, Tao CC, Zhu CY, Xing SL, Fan YY, Liu W, Yan J, Li JQ, Sang T		Sang T	非第一完成人（非独立完成）
55	Solar Radiation-Associated Adaptive SNP Genetic Differentiation in Wild Emmer Wheat, *Triticum dicoccoides*	Frontiers in plant science	2017,8,258	4.291	SCI	是	Ren J, Chen L, Jin XL, Zhan MM, You FM, Wang JR, Frenkel V, Yin XG, Nevo E, Sun DF, Luo MC, Peng JH		Sun DF, Luo MC, Peng JH	非第一完成人（非独立完成）
56	Agronomic Trait Variations and Ploidy Differentiation of Kiwiberries in Northwest China: Implication for Breeding	Frontiers in Plant Science	2017,8,711	4.291	SCI	是	Zhang Y, Zhong CH, Liu YF, Zhang Q, Sun XR, Li DW	Li DW		非第一完成人（非独立完成）
57	Acid/Salt/pH Gradient Improved Resolution and Sensitivity in Proteomics Study Using 2D SCX-RP LC-MS	Journal of Proteome Research	2017,16,3470-3475	4.268	SCI	是	Zhu MZ, Li N, Wang YT, Liu N, Guo MQ, Sun BQ, Zhou H, Liu L, Wu JL		Wu JL	非第一完成人（非独立完成）

58	Whole transcriptome sequencing of *Pseudomonas syringae* pv. *actinidiae*-infected kiwifruit plants reveals species-specific interaction between long non-coding RNA and coding genes	Scientific Reports	2017,7: 4910	4.259	SCI	是	Wang ZP, Liu YF, Li L, Li DW, Zhang Q, Guo YT, Wang SB, Zhong CH, Huang HW		Liu YF,Huang HW	非第一完成人（非独立完成）
59	Origin and Evolution of the Kiwifruit Canker Pandemic	Genome Biology and Evolution	2017,9(4) : 932-944	3.979	SCI	否	McCann HC, Li L, Liu YF, Li DW, Pan H, Zhong CH, Rikkerink EHA, Templeton MD, Straub C, Colombi E, Rainey PB, Huang HW	Huang HW	McCann HC，Rainey PB	非第一完成人（非独立完成）
60	Systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change	BMC Plant Biology	2017,17: 42	3.964	SCI	是	Xu Q, Song ZH, Zhu CY, Tao CC, Kang LF, Liu W, He F, Yan J, Sang T		Sang T	非第一完成人（非独立完成）
61	iTRAQ-Based Quantitative Proteomics Analysis on Rice Anther Responding to High Temperature	International Journal of Molecular Science	2017,18: 1811	3.226	SCI	否	Mu QL, Zhang WY, Zhang YB, Yan HL, Liu K, Matsui T, Tian XH, Yang PF	Yang PF	Tian XH	非第一完成人（非独立完成）
62	Effect of flexible linker length on the activity of fusion protein 4-coumaroyl-CoA ligase::stilbene synthase	Molecular BioSystems	2017,13: 598-606	2.781	SCI	否	Guo HL, Yang YD, Xue FY, Zhang H, Huang TR, Liu WB, Liu H, Zhang FQ, Yang MF, Liu CM, Lu HS, Zhang YS, Ma LQ	Zhang YS	Ma LQ	非第一完成人（非独立完成）

63	Haplotypes phased from population transcriptomes detecting selection in the initial adaptation of Miscanthus Lutarioriparius to stressful environment	Plant Genome	2017,10（2）:1-12	2.736	SCI	是	Zhu CY, Liu W, Kang LF, Xu Q, Xing SL, Fan YY, Song ZH, Yan J, Li JQ, Sang T	Yan J	Sang T	非第一完成人（非独立完成）
64	Surface Modification of Carbon Nanotubes with an Enhanced Antifungal Activity for the Control of Plant Fungal Pathogen	Materials	2017,10:1375	2.654	SCI	否	Wang XP, Zhou ZL, Chen FF	Chen FF		非第一完成人（非独立完成）
65	Cotton *GhERF38* gene is involved in plant response to salt/drought and ABA	Ecotoxicology	2017,26:841-854	1.951	SCI	否	Ma LF, Hu LX, Fan JB, Amombo E, Khaldun ABM, Zheng Y, Chen L	Chen L		非第一完成人（非独立完成）
66	Survival, recovery and microcystin release of *Microcystis aeruginosa* in cold or dark condition	Chinese Journal of Oceanology and Limnology	2017,35(2):313-323	0.688	SCI	否	Ding Y, Gan NQ, Liu J, Zheng LL, Li L, Song LR		Li L	非第一完成人（非独立完成）
67	A New Species of *Delphinium* (Ranunculaceae) from Hubei, China	Novon	2017,25:430-432	0.512	SCI	否	Gan QL, Li XW	Li XW		非第一完成人（非独立完成）
68	猕猴桃果实采后生理研究进展	植物科学学报	2017,35（4）:622-630		其他	否	黄文俊，钟彩虹	钟彩虹		独立完成
69	两种转化因子对葫芦巴发根转化率的影响	植物科学学报	2017,35（5）:735-740		其他	否	李晓华，李长福，黎佳，刘梦迪，章焰生	章焰生		独立完成

70	珍稀植物菊科蚂蚱腿子湖北郧西分布新资料	林业世界	2017,6(4):94-97		其他	否	林楠，郑斌，包维红，徐春翼，王恒昌	王恒昌		第一完成人(非独立完成)
71	湖北龙胆和铺地龙胆的分类学处理	植物科学学报	2017,35（4）:488-493		其他	否	郑斌，闫娟*，熊兴军，李新伟，陈丽，高磊，包卫红，李建强	闫娟，李建强		第一完成人(非独立完成)
72	中华猕猴桃复合体跨倍性杂交亲和性研究	中国园艺学会2017年学术年会论文集			其他	否	钟彩虹，黄宏文，李大卫，韩飞， 张鹏 ，刘小莉	钟彩虹		独立完成
73	小水果带动大产业，猕猴桃帮助农民脱贫	科技促进发展	2017,16,6		其他	否	钟彩虹，黄宏文，李大卫，陈美艳，韩飞，张琼，李黎，张鹏	钟彩虹		独立完成

3. 其他成果一览表

序号	类别	成果名称	编号	完成人（固定人员）	完成人（非固定人员）	完成情况	授权日期	国别
1	农业新品种	桃品种徽黄 2 号	皖认果 201710	韩月彭、周晖	张金云、潘海发、苗文举、刘春燕、郭遵守、王学良、伊兴凯、高正辉、秦改花、苗兰君、盛玉、陈红莉、齐永杰	非第一完成人（非独立完成）	2018.1.3	国内
2	农业新品	桃品种徽黄 4 号	皖认果 201711	韩月彭、周晖	张金云、陈加红、钱超、	非第一完成	2018.1.3	国内

	种				齐永杰、潘海发、王学良、雷波、郭遵守、汪波涛、张传州、陈红莉、凌杰、刘春燕	人（非独立完成）		
3	发明专利	控制苹果果肉有机酸含量的苹果酸转运体基因及其应用	ZL 201510061891.6	韩月彭、马百全、王鲁、谷超		独立完成	2017-8-8	国内
4	发明专利	调控水果果肉花青苷合成的基因 PpRd 及其应用	ZL 201510062155.2	韩月彭、周晖、王鲁、谷超		独立完成	2017-9-26	国内
5	发明专利	一种猕猴桃专用丰产剂及制备方法	ZL 201510340995.0	王彦昌、满玉萍、李作洲、雷瑞、黄汉钱		独立完成	2017-2-22	国内
6	发明专利	用于猕猴桃杂交群体雌雄性别鉴定的 SSR 分子标记 A002	ZL201410524999.X	黄宏文、张琼、钟彩虹、龚俊杰、刘春燕		独立完成	2017-5-3	国内
7	发明专利	早产优质猕猴桃园建立的两段栽培法	ZL 201510341700.0	钟彩虹、余和明、黄宏文、杨虹、刘琨然、韩飞		独立完成	2017-9-26	国内
8	发明专利	一种拟茎点霉菌的快速诱导产孢方法及其应用	ZL 201510733574.4	钟彩虹、李黎、黄宏文、龚俊杰、陈美艳、潘慧		独立完成	2017-12-4	国内

9	发明专利	一种快速筛选天然产物中拓扑异构酶 I 抑制剂的方法	ZL 201610249760.5	郭明全、陈桂林、田永强、张春云		独立完成	2017-4-19	国内
10	发明专利	一种箭叶淫羊藿越冬芽快速繁殖方法	ZL 201410682416.6	王瑛、吕海燕、黄文俊		独立完成	2017-3-8	国内
11	发明专利	宁夏枸杞在华中地区的大田栽培方法	ZL 201510295111.4	王瑛、吕海燕、陈亮		独立完成	2017-5-31	国内
12	发明专利	一种与猕猴桃总糖含量性状 QTL 位点紧密连锁的分子标记及应用	ZL 201710286488.2	张琼、黄宏文、钟彩虹、刘义飞、姚小洪、刘春燕		独立完成	2017-12-12	国内
13	发明专利	一种山梨猕猴桃和中华猕猴桃种间杂交子代的分子鉴定方法	ZL 201710243107.7	张琼、黄宏文、钟彩虹、刘义飞、赵婷婷		独立完成	2017-12-7	国内

4. 出版专著一览表

序号	著作名称	类别	作者	出版单位	出版年份

第六部分 开放交流与运行管理

1. 举办的学术会议一览表

序号	会议名称	会议类型	主办/承办单位名称	会议主席	会议日期	会议地址	参加人数
1	第三届全国猕猴桃产业技术培训会	全国性	中国园艺学会猕猴桃分会、中国科学院武汉植物园、贵州省果树蔬菜工作站主办，中共大方县委、大方县人民政府、贵州省果蔬行业协会猕猴桃分会承办	钟彩虹	2017 年 8 月 13 日至 15 日	贵州省大方县	400 余人

2. 参加的学术会议一览表

序号	报告名称	报告人	会议名称	地点	时间
1	An Ultra-High Density, Sequencing-Based Genetic Map Improve the Reference Genome of Asian Lotus	杨美	第 25 届动植物基因组大会	加利福尼亚州圣地亚哥	2017 年 1 月 14 日至 18 日
2	The acyl desaturase CER17 is involved in producing cuticle wax monounsaturated primary alcohols in Arabidopsis thaliana	杨贤鹏	第十三届国际学生论坛	美国内布拉斯加州	2017 年 6 月 4 日-8 日
3	Exploring correlations between phyto-chemical components from Rhamnus davurica Pall and their biological activities using bio-affinity ultrafiltration and LC-MS	郭明全	2017 年欧洲植物化学学会青年科学家会议	法国里尔	2017 年 6 月 28 日-7 月 10 日
4	The prerequisite for natural product synthetic biology: pathway gene identification	章焰生	第四届植物代谢国际会议	中国大连	2017 年 7 月 16 至 20 日
5	水稻种子萌发过程中的蛋白质泛素化修饰及其功能	杨平仿	2017 年国际蛋白质组会议	马来西亚吉隆坡	2017 年 8 月 14 日至 18 日

6	植物表皮蜡质合成与调控的分子机理解析	吕世友	中国林学会经济林分会 2017 年学术年会	哈尔滨	2017 年 8 月 24 日至 27 日
7	新品种金圆、金梅育种进程及品质特征	钟彩虹	第九届国际猕猴桃研讨会	葡萄牙波尔图	2017 年 9 月 5 日至 14 日
8	猕猴桃多倍体进化及多倍化后分子机理	李大卫	第九届国际猕猴桃研讨会	葡萄牙波尔图	2017 年 9 月 5 日至 14 日
9	Characteristics and assessment of sugar and acid composition in kiwifruit	张琼	第九届国际猕猴桃研讨会	葡萄牙波尔图	2017 年 9 月 5 日至 14 日
10	猕猴桃溃疡病及软腐病	李黎	第九届国际猕猴桃研讨会	葡萄牙波尔图	2017 年 9 月 5 日至 14 日
11	The door is opening for commercialization of ‘Ruanzao Kiwi’ (Actinidia arguta) in China	王彦昌	第九届国际猕猴桃会议	葡萄牙波尔图	2017 年 9 月 5 日至 10 日
12	温带莲与热带莲杂交 F1 代的等位基因特异性表达研究	石涛	湖北植物生物学大会	湖北武汉	2017 年 9 月 28 日
13	水稻种子萌发过程中的蛋白质泛素化修饰及其功能	杨平仿	植物蛋白质组研究最新进展国际会议	巴基斯坦伊斯兰堡	2017 年 9 月 30 日至 10 月 5 日
14	桃色泽遗传研究进展	韩月彭	第二届中埃农业畜牧业科技大会	埃及开罗	2017 年 10 月 6 日至 11 日
15	SCREENING FOR BIOACTIVE COMPOUNDS TARGETING TOPOISOMERASE I FROM TODDALIA ASIATICA LAM	郭明全	第三届国际天然产物利用大会	保加利亚班斯科	2017 年 10 月 17 日至 22 日
16	中科院武汉植物园莲育种工作简介	杨东	第三届荷花栽培育种与国际登录学术研讨会	南京	2010 年 10 月 19 日-21 日
17	花青苷着色机制的多样性-以桃果实为例	周晖	第七届全国果树分子生物学学术研讨会	安徽合肥	2017 年 10 月 23 日至 25 日
18	高羊茅耐热分子设计育种	胡涛	2017 中国草学会年会	广东广州	2017 年 11 月 7 日
19	Phytochemical study on traditional herbal medicines	郭明全	第 12 届科技与工业化国际会议	肯尼亚内罗毕	2017 年 11 月 21 日至 26 日
20	水稻种子萌发过程中的蛋白质泛素化修饰及其功能	杨平仿	第 12 届科技与工业化国际会议	肯尼亚内罗毕	2017 年 11 月 21 日至 26 日
21	中国淫羊藿资源研究与可持续利用	张燕君	第二届中国民族医药学会药用资源分会	成都	2017 年 11 月 23 日-25 日

22	莲重要性状的分子解析与新品种选育	杨美	2017 首届全国水生植物学术研讨会	杭州	2017 年 12 月 2 日至 4 日
23	2017 中科院武汉植物园水生植物收集、保育与研究简述	杨东	2017 首届全国水生植物学术研讨会	浙江杭州	2017 年 12 月 2 日-4 日

3. 开放课题一览表

序号	课题名称	负责人	职称	工作单位	参加人员	起止时间	总经费（万元）
1	莲地下茎膨大相关基因 NnCOL5 克隆和功能验证	宋波涛	教授	华中农业大学	杨平仿、曹仃仃	2016.8.1-2018.7.31	3
2	银杏内酯下游合成路径 C1 和 C7 位置羟基化酶基因的分离和功能分析	苟君波	博士后	中国农业科学院深圳农业基因组研究所	章焰生、廖庆刚	2016.8.1-2018.7.31	3
3	软枣猕猴桃果实 C6-醛合成关键基因的克隆与表达分析	张蕾	副研究员	湖北省农业科学院果树茶叶研究所	张琼、陈庆红、钟彩虹、罗轩、高磊	2017.8.1-2019.7.31	3
4	芒属植物适应性进化	康丽芳	助理研究员	中国科学院植物研究所	林聪、赵旭红、陶程程、闫娟	2017.8.1-2019.7.31	3

4. 30 万元以上仪器设备使用情况

序号	设备类型	设备型号	设备名称	设备状况	价格（万元）	实验室研究总机时（小时）	对外服务总机时（小时）	购置时间	性能指标	用途	是否开放
1	购置	TSQ Quantum Access MAX	液相色谱质谱仪	优	151.3	2122	1280	2010 年	质量数范围: 10～3000amu。 分辨率：具有高选择性离子检测模式；扫描速度：5000 amu/s	可以在一次多残留筛查实验中定量数以百计的化合物,快速正/负离子模式转换-小于或等于 25 毫秒-适用于多残留检测	是
2	购置	X series	等离子体质谱仪、快速液相色谱仪	优	141.3	1035	512	2010 年	质量范围：2-255am；质量分辨率：在一次分析中 0.3amu-3.0amu 可调，多元素分析不同元素可以设置不同的分辨率	进行样品的定性确认、定量成分分析以及元素成分的同位素分析，与 HPLC 联用可以进行元素的化合价态、结合形态的分析和特殊要求样品的分析	是
3	购置	LI-6400 XTP	便携式光合作用仪	优	31.1	495	426	2011 年	绝对开路式非扩散红外分析器；量程范围：0~3000 μmol mol-1；波宽：10 Hz	通过红外线气体分析仪检测二氧化碳的消耗速率来测定植物光合速率	是

4	购置	7890A+5975C	气相色谱质谱联用仪	优	97.9	3090	1351	2011 年	质量数范围：1.6-1050amu，以 0.1amu 递增；分辨率：全质量范围内单位质量分辨	复杂混合物的成分分析；杂质成分的鉴定和定量分析；目标化合物残留的定量分析等	是
5	购置	Quanta250	扫描电子显微镜	优	104.4	1017	256	2011 年	放大倍数： 在 10 倍和 90 万倍能清晰看到扫描图像。30KV 分辨率	分析样品的微观结构	是
6	购置	7500 FAST	实时荧光定量 PCR 检测系统	优	39.7	626	142	2012 年	96 孔半导体控温 PCR 模块；五色滤光片分光；采用冷 CCD 摄像机成像；可实时动态检测，动态显示，可同时检测 5 种荧光染料	主要用于基因表达分析，SNP 分析，甲基化分析以及 CNVs 分析等	是
7	购置	3730	遗传分析仪	优	164.5	779	0	2012 年	48 道毛细管电泳系统；可同时进行 5 色或以上荧光实时检测；可容纳 16 块 96 孔或 384 孔样品板连续运行；全自动进样	可用于 DNA 序列测定和基因型自动分析和 SNP 分析	是
8	购置	CyFlow Cube8	多功能细胞分析系统	优	35.7	239	215	2012 年	荧光灵敏度：FITC≤100MESF，PE≤50 MESF ；检测分辨率：CV≤1％ ；颗粒检测范围：0.1～200um	倍体分析，植物基因组大小检测，单性生殖监测；真核细胞培养，原核细胞培养	是

9	购置	1260	高效液相色谱仪	优	53.3	216	0	2012 年	样品量：15 个； 样品瓶容量：6ml；温度稳定性：<± 0.15°C	植化、合成、生物及生化等领域的物质的提取及纯化	是
10	购置	LABCONCO	冷冻真空干燥仪	优	39.1	4141	0	2012 年	LCD 显示温度和真空度；LED 波形图显示真空度和冷阱温度；真空度连续可调；启动电源和自动程序可自动控制降温和抽真空	冷冻干燥蛋白或者菌种	是
11	购置	FLA9500	多功能激光成像仪	优	105.3	686	0	2012 年	检测模式：3 色荧光成像、2D-DIGE、化学发光和数字化成像；动态范围：5 个数量级；图像格式：16 位	用于生物分子成像	是
12	购置	FLA7000	磷屏成像分析系统	优	73.7	1966	0	2012 年	最大扫描范围：磷屏的扫描长宽 40 x 20 cm；可检测的放射性同位素种类：3H、14C、32P、33P、35S 等；分辨率：14C 磷屏检测，标准条件下不小于 2 线对/毫米	用于同位素标记的电泳凝胶放射性检测；用于采用同位素标记方法或地高辛、生物素等标记方法的核酸杂交与的蛋白印迹	是

13		PRTOEAN i12 IEF	蛋白质等电聚焦仪及大型垂直电泳槽		42.9	372	0	2012 年	收集样品数最多为 20 个; 白上样量为 35-60ml，收集量为 1.75-3ml	用于高通量地进行双向电泳第一向等电聚焦和第二向 SDS-PAGE 蛋白分离	
14	购置	MM-Meter	微电极系统	优	59.4	285	108	2013 年	四通道高级型主机包含 2 个皮安通道（可测 O2、H2S、H2、N2O、NO）、1 个毫伏通道、1 个温度通道	用于测量样品微米尺度上的微量 O2、Redox、H2S、H2、N2O、NO、pH 的变化，从而研究样品的微观结构和传质机理	是
15	购置	ND8000	紫外可见分光光度计	优	30.3	961	0	2013 年	220~750nm 全波长扫描，显示吸收曲线，并同时给出两个设定波长的吸收值；检测只需 1 ul 的样本	可以快速同时对 8 个核酸蛋白样品进行标准检测分析；适用于极微量样本的检测	是
16	购置	ICS 5000+	氨基酸分析仪	优	68.5	1100	359	2013 年	可测定一级和二级氨基酸，氨基糖类，含磷氨基酸，及含硫氨基酸中常见氧化产物，检测限可达 10-15～10-10 摩尔；可直接测定 pmol 级的各种糖类	可完成糖类、氨基酸、抗生素、小分子药物、核酸以及蛋白质、多肽等的分离测定	是
17	购置	EZ-2 Plus system	高通量溶剂蒸发工作站	优	32.7	688	553	2013 年	一体化；自带 10 个运行程序	解决溶剂浓缩和样品干燥的问题	是

18	购置	M200 PRO	多功能全波长酶标仪	优	32.2	1428	0	2013 年	激发滤光双光栅，发射滤光为双光栅 ；杂光率：≤1 x10-6；波长准确性：<±0.3nm（230-315nm），<±0.5nm（316-1000nm）	用于酶活检测、微量毒素与激素测定、ELISA 实验、DNA 和蛋白的定量、细胞毒性研究、双报告基因检测等	是
19	购置	ArcturusXT	激光捕捉显微分离系统	优	116.4	1139	0	2013 年	提供多种模块以供选择；有近红外激光，笔式触摸显示器和轨迹球驱动的载物台	能将红外激光捕获和紫外激光切割技术融；可实现同一样本单细胞和大块组织细胞的收集	是
20	购置	GX-274 ASPEC	多通道固相萃取系统	优	38.1	0	0	2013 年	全自动固相萃取仪，可自动完成固相萃取的全过程；可同时自动处理≥4 个样品	应用于常规实验室中，从液体样品中萃取目标物的仪器	是
21	购置	ASE 350	全自动快速溶剂萃取仪	优	37.2	48	0	2013 年	萃取方式：顺序萃取；炉体：全自动密封反应器，温度控制最高可达 200 ℃，带温度过高安全切断	适合现有气相色谱、液相色谱、色质联用等分析仪器样品预处理	是
22	购置	BD Accuri C6	流式细胞仪	优	53.2	885	827	2013 年	光源：配置 2 根独立激光器，波长为 488nm、640nm；检测灵敏度：FITC≤150MESF，PE≤100MESF	可用于分析植物细胞 DNA 含量和倍性、高速分析海水和淡水样本、分析水生微生物等	是

23	购置	TripleTOF 5600	质谱仪	优	296.4	1093	998	2013 年	质量范围：5-40KDa m/z（飞行时间）；离子源：复合离子源，可同时使用 ESI 离子源和 APCI 离子源；纳升级 Nano 离子源	用于脂类、食品等未知化合物的研究，蛋白组学研究，蛋白质结构鉴定，蛋白质翻译后修饰， 生物标记物的确认和确证	是
24	购置	FXL950	元素分析仪		42.9	599	583	2014 年	测试舱：229(W)x305(D)x114(H)mm；分析范围：标准配置 Mg 到 U 之间的 43 种元素	用于野外环境 Mg 到 U 之间的 43 种元素的便携分析	是
25	购置	MONITORING-PAM	在线超高灵敏型叶绿素荧光仪		55.7	1289	1203	2014 年	红色 LED，630 cnm，FWHM 20 nm；调制频率测量 Fo 时 5-5000 Hz 可选，打开光化光时 1-100 kHz 可选，测量荧光诱导动力学的快相时 200 kHz；20 级可调	可测光响应曲线和快速光曲线（RLC）；可在线检测植物、微藻、地衣、苔藓等的光合作用变化	是
26	购置	OPTIMA 8000DV	等离子体原子发射光谱仪		72.3	1301	659	2014 年	自动进样器及配套进样系统，分析速度约 30 个样品/小时，每个样品中包含 8 个元素；超高灵敏度进样系统	用于各类样品中主量、微量及痕量元素的定性、半定量和定量分析	是

27	购置	CLARUS 680	气相色谱仪	优	47.4	311	287	2015 年	进样口设置 2 个，加热区 5 个 柱箱操作温度范围：40℃到 450℃ 柱温箱升温速度：最高达 140℃/min	主要用在环境化学、生物化学、农药残留分析等方面	是
28	购置	Optima XE-100	超速离心机	优	42.8	677	0	2015 年	最高转速：≥100,000 rpm；转速控制精度：≤ ± 2 rpm；温度设定范围：0-40℃，1℃步进	样品分离包括蛋白质的分离纯化、脂蛋白的分离、利用氯化铯梯度作 RNA 沉淀、质粒 DNA 等密度分离等	是
29	购置	GC-20	植物生长箱	优	33.5	1247	0	2015 年	光照强度：最大 750umol/m²/s；灯的热量：由制冷系统消除掉；温度范围：0℃- 45℃	是植物栽培、苗木、烟草、动物、昆虫等研究的理想试验设备	是
30	购置	HHTNT-55E-0017	台式扫描电镜及离子溅射镀膜仪	优	45.9	67	0	2015 年	溅射电流 0-150mA；溅射时间 1-999 秒	可满足多种样品的镀膜需求，提高扫描电镜下的成像质量	是
31	购置	TSC SP8	激光共聚焦三维扫描仪	优	173.6	1469	0	2015 年	全视野扫描视野≥22mm；扫描最大分辨率：≥8192×8192；扫描变倍范围：0.75×—48×；旋转扫描：旋转角度≥200	可观察固定的细胞、组织切片，还可对活细胞的结构形态、生化成分进行实时动态地观察和检测	是

32	购置	Optima MAX-XP	超速离心机	优	32.4	13	0	2015 年	最高转速：≥150,000 rpm；最大相对离心力：≥ 1,000,000 ×g；转速控制精度：±50 rpm；最大容量：≥ 6×32.4 ml；温度设定范围： 0-40℃，温度控制精度：2℃	通过离心分离可获得亚细胞组分、病毒、蛋白质及其它生物大分子，为进一步的化学分析、生物学功能测定以及形态学上超微结构的观察提供基础	是
33	购置	QuantStudio 6 Flex	实时荧光定量 PCR 仪	优	40.2	947	0	2015 年	反应体积:384 孔模式,1-30μL；精密度：最低可分辨 1.5 倍拷贝数差异，置信度 99.7%	能够在单重反应中检测低至 1.5 倍的变化，并获得 10 个数量级的动态范围	是
34	购置	ENCL NIMBUS4 4CH 9+2	高通量液体自动操作系统		48.3	96	72	2015 年	不少于 12 个工作板位，能定位 384 孔板，可一次性完成 96 个样本的 DNA 提取、RNA 提取、PCR 纯化、PCR 体系构建	用于核酸纯化，测序前样本处理和 PCR 体系构建	是
35	购置	DXR2	激光共聚焦显微拉曼光谱仪	优	142.9	774	721	2016 年	拉曼光谱测量范围：532nm 激光激发 50cm-1-6000cm-1 拉曼位移; 785nm 激光激发: 50cm-1-3250cm-1 拉曼位移	主要应用于材料、物力、化学、生物、地质等领域的物质结构鉴定和分子相互作用分析	是
36	购置	Nicolet iS50	红外光谱仪	优	57.5	288	288	2016 年	可以测定光谱范围：8000-80cm-1；波数精度：优于 0.005cm-1；光谱分辨	主要用于复杂混合物的定性定量分析与鉴定、痕量污染物鉴定	是

									率：优于 0.1cm-1；灵敏度：优于 55000:1		
37	购置	940	离子色谱	优	87.7	742	670	2016 年	重现性：<0.1%；电子类型：微处理控制，数字输出模式	主要用于样品中常规阴离子以及碱金属、碱土金属阳离子和脂肪胺等某些有机化合物的的分析和检测	是
38	购置	7890B	气相色谱仪	优	41.8	2201	0	2016 年	最大升温速率：1800℃/min；具有柱温箱温度的自动保护功能；最多可同时安装三个独立控温的进样单元	主要用在环境化学、生物化学、农药残留分析等	是
39	购置	7890B-7000C	高分辨气质联用仪	优	109.8	1109	909	2016 年	仪器检测限指标及灵敏度：10 fg OFN 连续 8 次进样	具备精确质量高分辨和超高灵敏度，适合生物代谢物，环境污染物等有机物的定性定量分析	是
40	购置	DMi8	倒置荧光显微镜	优	69.3	新设备尚在调试中		2017 年	具备光强自动跟踪功能：低倍物镜下观察时，自动变为低照明强度；高倍物镜下观察时，自动变为高照明强度，记忆最后设定光强	可用于观察并记录植物样本活体细胞的生理状态及利用报告基因检测基因表达调控分析	是

41	购置	SMZ25	电动体视荧光显微成像系统	优	49.5	新设备尚在调试中	2017 年	分析：物镜定标、拍摄数据保存、LUT、直方图、自动测量（计数、长度、周长、面积等）、荧光强度随时间变化、光强线形分布	主要应用于植物组织器官的观察成像和特异标记荧光的分析	是
42	购置	FluorChem R	多功能成像系统	优	84.0	新设备尚在调试中	2017 年	科研级 CCD，物理像素不低于 830 万，有效分辨率不低于 3326×2504	主要应用于植物样本基因水平和蛋白水平的成像分析	是

第七部分 学委会会议情况

1. 学术委员会名单

序号	姓名	性别	出生年份	职称	学委会职务	工作单位	备注
1	傅廷栋	男	1937 年	教授	名誉主任	华中农业大学	院士
2	朱玉贤	男	1955 年	教授	主任	武汉大学	院士
3	邓秀新	男	1961 年	教授	副主任	华中农业大学	院士
4	匡汉晖	男	1967 年	教授	委员	华中农业大学	长江学者
5	戴思兰	女	1962 年	教授	委员	北京林业大学	
6	郝玉金	男	1971 年	教授	委员	山东农业大学	长江学者、泰山学者
7	陈士林	男	1961 年	研究员	委员	中国中医科学院中药研究所	长江学者创新团队负责人
8	刘吉开	男	1962 年	教授	委员	中南民族大学	
9	柯卫东	男	1963 年	研究员	委员	武汉市农业科学院蔬菜研究所	
10	丁文军	男	1967 年	教授	委员	中国科学院大学生命科学学院	
11	吴国江	男	1962 年	研究员	委员	中国科学院华南植物园	
12	陈　凡	男	1969 年	研究员	委员	中国科学院遗传与发育生物学研究所	
13	张全发	男	1965 年	研究员	委员	中国科学院武汉植物园	
14	韩月彭	男	1968 年	研究员	委员	中国科学院武汉植物园	
15	章焰生	男	1972 年	研究员	委员	中国科学院武汉植物园	
16	杨平仿	男	1975 年	研究员	委员	中国科学院武汉植物园	
17	吕世友	男	1974 年	研究员	委员	中国科学院武汉植物园	
18	陈　良	男	1981 年	副研究员	秘书	中国科学院武汉植物园	

2. 学术委员会会议

会议年度	2017 年
会议时间	2017 年 11 月 21 日 9:00--12:30
地点	中国科学院武汉植物园光谷园区行政楼 1007 会议室
学委会委员出席人员名单	傅廷栋, 朱玉贤, 匡汉晖, 戴思兰, 郝玉金, 陈士林, 刘吉开, 柯卫东, 丁文军, 吴国江, 陈凡, 张全发, 韩月彭, 章焰生, 杨平仿, 吕世友
学委会委员缺席人员名单	邓秀新, 陈良
会议纪要	一、会议公布了重点实验室第二届学术委员会的组成，并为新一届学术委员会成员颁发了聘书。 二、会议听取了重点实验室主任韩月彭研究员关于实验室 2016 年度的工作报告。报告汇报了实验室科学研究进展及研究成果、人才队伍建设与人才培养及实验室未来研究重点领域，同时，会议还听取了重点实验室闫娟副研究员、章焰生研究员和钟彩虹研究员分别作的题为“芒属植物的适应性进化研究”、“失衡的植物天然产物合成生物学研究”和“特色猕猴桃新品种选育及产业化应用”的专题学术报告。 三、会议一致认为重点实验室较上一个评估周期相比，取得了较大进步，也获得了较好的成果，实验室整体发展上升了一个新台阶。 四、学术委员会成员对实验室的发展提出了较好的建议，特别是： 1. 加强研究的系统性、完整性和持续性，进一步体现地域和专业特色，实现实验室在促进我国国民经济发展中不可替代性的地位与作用； 2. 加强重大项目的争取，提高研究的应用性，通过基础研究带动产业链的发展，为特色植物资源可持续开发利用及新兴产业的发展做出贡献； 3. 吸引博士后或青年千人的加入，加强对年轻人的培养及配套经费的支持；探讨和建立不同学科间的产业化开发和科学问题研究的合作机制，增强学科组间的整体协作及与外界的合作，培育重大科学问题攻关的研究团队； 4. 加强实验室内部的交流，年报的编写中着重体现实验室的重点工作和重大研究成果，在 2018 年上半年召开 2017 年学术委员会； 5. 结合实验室定位，进一步凝练研究方向并加强各研究方向间的衔接，制定长期发展目标和布局，与中国科学院种子创新研究院接轨，集中力量形成有重要影响力的代表性成果，为迎接下一轮重点实验室评估做准备。

第八部分 审核意见

实验室承诺所填内容属实，数据准确可靠。

实验室主任：

年　　月　　日

依托单位对实验室的年度考核意见：

依托单位负责人签字：

（单位公章）

年　　月　　日

The Acyl Desaturase CER17 Is Involved in Producing Wax Unsaturated Primary Alcohols and Cutin Monomers[1][OPEN]

Xianpeng Yang[2], Huayan Zhao[2], Dylan K. Kosma, Pernell Tomasi, John M. Dyer, Rongjun Li, Xiulin Liu, Zhouya Wang, Eugene P. Parsons, Matthew A. Jenks, and Shiyou Lü*

Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden (X.Y., R.L., X.L., Z.W., S.L.), Sino-Africa Joint Research Center (S.L.), Chinese Academy of Sciences, Wuhan 430074, China; Applied Biotechnology Center, Wuhan Institute of Bioengineering, Wuhan, 430415, China (H.Z.); University of Chinese Academy of Sciences, Beijing 100049, China (X.Y., X.L., Z.W.); Department of Biochemistry and Molecular Biology, University of Nevada, Reno, Nevada 89557 (D.K.K.); U.S. Department of Agriculture-Agricultural Research Service, U.S. Arid-Land Agricultural Research Center, Maricopa, Arizona 85138 (P.T., J.M.D.); Prairie State College, Chicago Heights, Illinois 60411 (E.P.P.); and Division of Plant and Soil Sciences, West Virginia University, Morgantown, West Virginia 26506-6108 (M.A.J.)

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We report *n*-6 monounsaturated primary alcohols ($C_{26:1}$, $C_{28:1}$, and $C_{30:1}$ homologs) in the cuticular waxes of Arabidopsis (*Arabidopsis thaliana*) inflorescence stem, a class of wax not previously reported in Arabidopsis. The Arabidopsis *cer17* mutant was completely deficient in these monounsaturated alcohols, and *CER17* was found to encode a predicted ACYL-COENZYME A DESATURASE LIKE4 (ADS4). Studies of the Arabidopsis *cer4* mutant and yeast variously expressing *CER4* (a predicted fatty acyl-CoA reductase) with *CER17/ADS4*, demonstrated *CER4*'s principal role in synthesis of these monounsaturated alcohols. Besides unsaturated alcohol deficiency, *cer17* mutants exhibited a thickened and irregular cuticle ultrastructure and increased amounts of cutin monomers. Although unsaturated alcohols were absent throughout the *cer17* stem, the mutation's effects on cutin monomers and cuticle ultrastructure were much more severe in distal than basal stems, consistent with observations that the *CER17/ADS4* transcript was much more abundant in distal than basal stems. Furthermore, distal but not basal stems of a double mutant deficient for both CER17/ADS4 and LONG-CHAIN ACYL-COA SYNTHETASE1 produced even more cutin monomers and a thicker and more disorganized cuticle ultrastructure and higher cuticle permeability than observed for wild type or either mutant parent, indicating a dramatic genetic interaction on conversion of very long chain acyl-CoA precursors. These results provide evidence that CER17/ADS4 performs *n*-6 desaturation of very long chain acyl-CoAs in both distal and basal stems and has a major function associated with governing cutin monomer amounts primarily in the distal segments of the inflorescence stem.

Plant cuticle coats most aerial surfaces of vascular plants and plays a major role in coordinating interactions between the plant and its environment (Rensing et al., 2008; Yeats and Rose, 2013). The cuticle is primarily composed of two lipid classes, the nonpolymerized (free) cuticular waxes and the cutin polyester, both of which are synthesized by epidermal cells. Common plant wax compounds are the very long chain fatty acids (VLCFAs) and their derivatives including aldehydes, primary alcohols, alkanes, secondary alcohols, ketones, and esters (Samuels et al., 2008). As much as 4.0% of total waxes on Arabidopsis (*Arabidopsis thaliana*) inflorescence stems are composed of numerous yet unidentified wax compounds (Jenks et al., 1995). Cutin consists primarily of C_{16} and C_{18} fatty acid derivatives (e.g. hydroxy fatty acids and dicarboxylic acids), which are linked by ester bonds; however, glycerol and small amounts of longer chain cutin monomers have also been reported (Pollard et al., 2008).

In the past decade, there has been significant progress toward understanding the molecular mechanisms controlling the cuticular wax biosynthetic pathway based primarily on studies of wax-deficient mutants (Bernard and Joubès, 2013; Yeats and Rose, 2013). Synthesis of wax occurs in epidermal cells and begins with C_{16} and C_{18} long-chain acyl-coenzyme A (CoA) precursors, which are synthesized by long-chain acyl-CoA

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S.L. designed the experimental plans with input from M.A.J.; X.Y., H.Z., P.T., J.M.D., D.K.K., X.L., R.L., Z.W., and E.P.P. performed the experiments; H.Z., M.A.J., and S.L. wrote the article.

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ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOGY

Population transcriptomic characterization of the genetic and expression variation of a candidate progenitor of *Miscanthus* energy crops

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Abstract

The use of transcriptome data in the study of the population genetics of a species can capture faint signals of both genetic variation and expression variation and can provide a broad picture of a species' genomic response to environmental conditions. In this study, we characterized the genetic and expression diversity of *Miscanthus lutarioriparius* by comparing more than 16,225 transcripts obtained from 78 individuals, belonging to 10 populations distributed across the species' entire geographic range. We only observed a low level of nucleotide diversity ($\pi = 0.000434$) among the transcriptome data of these populations, which is consistent with highly conserved sequences of functional elements and protein-coding genes captured with this method. Tests of population divergence using the transcriptome data were consistent with previous microsatellite data but proved to be more sensitive, particularly if gene expression variation was considered as well. For example, the analysis of expression data showed that genes involved in photosynthetic processes and responses to temperature or reactive oxygen species stimuli were significantly enriched in certain populations. This differential gene expression was primarily observed among populations and not within populations. Interestingly, nucleotide diversity was significantly negatively correlated with expression diversity within populations, while this correlation was positive among populations. This suggests that genetic and expression variation play separate roles in adaptation and population persistence. Combining analyses of genetic and gene expression variation represents a promising approach for studying the population genetics of wild species and may uncover both adaptive and nonadaptive processes.

KEYWORDS
gene expression, *Miscanthus*, nucleotide diversity, population genetics, transcriptome

*These two authors contributed equally to this work.

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The evolution of plant microRNAs: insights from a basal eudicot sacred lotus

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SUMMARY

microRNAs (miRNAs) are important noncoding small RNAs that regulate mRNAs in eukaryotes. However, under which circumstances different miRNAs/miRNA families exhibit different evolutionary trajectories in plants remains unclear. In this study, we sequenced the small RNAs and degradome from a basal eudicot, sacred lotus (*Nelumbo nucifera* or lotus), to identify miRNAs and their targets. Combining with public miRNAs, we predicted 57 pre-eudicot miRNA families from different evolutionary stages. We found that miRNA families featuring older age, higher copy and target number tend to show lower propensity for miRNA family loss (PGL) and stronger signature of purifying selection during divergence of temperate and tropical lotus. Further analyses of lotus genome revealed that there is an association between loss of miRNA families in descendent plants and in duplicated genomes. Gene dosage balance is crucial in maintaining those preferentially retained *MIRNA* duplicates by imposing stronger purifying selection. However, these factors and selection influencing miRNA family evolution are not applicable to the putative *MIRNA-likes.* Additionally, the *MIRNAs* participating in lotus pollen–pistil interaction, a conserved process in angiosperms, also have a strong signature of purifying selection. Functionally, sequence divergence in *MIRNAs* escalates expression divergence of their target genes between temperate and tropical lotus during rhizome and leaf growth. Overall, our study unravels several important factors and selection that determine the miRNA family distribution in plants and duplicated genomes, and provides evidence for functional impact of *MIRNA* sequence evolution.

Keywords: microRNA, sacred lotus (*Nelumbo nucifera*), basal eudicot, genome duplication, evolution.

INTRODUCTION

Messenger RNA levels in the eukaryotic cell are regulated by gene transcription and degradation. Other than transcription factors (TFs) which bind to the *cis*-elements of target gene to induce or repress gene transcription, microRNAs (miRNAs) constitute other types of trans-acting elements which belong to endogenous noncoding small RNAs that function in regulating gene expression (Carrington and Ambros, 2003). Plant miRNAs are generated from stem–loop regions of longer primary transcripts by a Dicer-like (DCL) enzyme and range from 20 to 24 nucleotides (nt) in length (Papp *et al.*, 2003b; Ren and Yu, 2012). Complementary base pairing to the target mRNA, the miRNA can guide the RNA-induced silencing complex to cleave target mRNA or inhibit its translation (Llave *et al.*, 2002; Carrington and Ambros, 2003; Yu and Wang, 2010). Through repression of the target genes, miRNAs were identified to play diverse roles in plants, including development, phytohormone signaling, stress response and disease resistance (Achard *et al.*, 2004; Zhang *et al.*, 2006b; Allen *et al.*, 2007; Bartel, 2007; Reyes and Chua, 2007; Chen, 2009).

The *MIRNAs* (miRNA genes) often duplicate to form multi-copy miRNA families. The *de novo* birth of a miRNA family during plant evolution may sometimes contribute to regulatory novelty. For example, *miR824*, a newly evolved miRNA family distributed in *Brassica* species with signs of balancing selection, participates in regulation of flowering time by targeting *AGAMOUS-LIKE16* (de Meaux *et al.*, 2008; Hu *et al.*, 2014). Acquisition of different miRNA families during plant evolution has been previously summarized through parsimony approach based on their

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Molecular characterization of the *C*-glucosylation for puerarin biosynthesis in *Pueraria lobata*

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SUMMARY

***C*-glycosyltransferases (CGTs) are important enzymes that are responsible for the synthesis of the *C*-glycosides of flavonoids and isoflavonoids. Flavonoid CGTs have been molecularly characterized from several plant species; however, to date, no gene encoding an isoflavonoid CGT has been reported from any plant species. A significant example of an isoflavonoid *C*-glycoside is puerarin, a compound that contributes to the major medicinal effects of *Pueraria lobata*. Little is known about the *C*-glucosylation that occurs during puerarin biosynthesis. One possible route for puerarin synthesis is via the *C*-glucosylation of daidzein. This study describes the molecular cloning and functional characterization of a novel glucosyltransferase (PlUGT43) from *P. lobata*. Biochemical analyses revealed that PlUGT43 possesses an activity for the *C*-glucosylation of daidzein to puerarin; it shows activity with the isoflavones daidzein and genistein, but displays no activity towards other potential acceptors, including flavonoids. To validate the *in vivo* function of *PlUGT43*, the *PlUGT43* gene was over-expressed in soybean hairy roots that naturally synthesize daidzein but that do not produce puerarin. The expression of *PlUGT43* led to the production of puerarin in the transgenic soybean hairy roots, confirming a role for *PlUGT43* in puerarin biosynthesis.**

Keywords: *Pueraria lobata*, transcriptome, *C*-glucosyltransferase, soybean hairy roots, isoflavone.

INTRODUCTION

Flavonoids are a class of plant secondary metabolites that generally occur as *O*- and/or *C*-glycosides. In *O*-glycosides the sugar moieties are bonded to the hydroxyl groups of aglycones, whereas *C*-glycosides have the sugar substituents directly attached to a carbon atom of aglycones. In contrast to the labile nature of the *O*-glycosidic linkages, the *C*-glycosidic bonds are remarkably stable towards glycosidase or acid-mediated hydrolysis (Yasuda *et al.*, 1995). Flavonoid-*C*-glycosides exhibit a diverse range of physiological functions, including UV protection (Markham *et al.*, 1998), defense against pathogens (McNally *et al.*, 2003a,b; El-Alfy *et al.*, 2011), inhibition of pest growth (McMullen *et al.*, 2004; Caasi-Lit *et al.*, 2007; Khan *et al.*, 2008) and the formation of plant flower pigment (Jay, 1994). They have also been shown to confer potential health benefits, such as inhibition of cancer development (Hudson *et al.*, 2000), and to have protective effects against hypotension (Prabhakar *et al.*, 1981) and obesity (Lee *et al.*, 2010).

Studies on the biogenesis of flavonoid *C*-glycosides began in the 1970s. Early tracer experiments *in vivo* showed that the *C*-glycosylation in flavone *C*-glycoside biosynthesis might occur prior to the formation of the flavone backbone (Wallace and Grisebach, 1973). This finding was later supported by the affinity of a native flavonoid *C*-glycosyltransferase of buckwheat for 2-hydroxyflavanones but not for flavanones or flavones (Kerscher and Franz, 1987, 1988). A gene encoding 2-hydroxyflavanone *C*-glucosyltransferase has been cloned from several plant species, and the role of this enzyme in the *C*-glucosylation of plant flavonoids has been confirmed by heterologous expression studies (Brazier-Hicks *et al.*, 2009; Falcone Ferreyra *et al.*, 2013; Nagatomo *et al.*, 2014; Hirade *et al.*, 2015). Most recently, a new type of CGT, phylogenetically related to the UDP-sugar-glucosyltransferases (UGTs) that transfer sugars onto the 5-hydroxyl groups of acceptors, has been identified and functionally characterized as a

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Variation of ascorbic acid concentration in fruits of cultivated and wild apples

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ABSTRACT

Ascorbic acid (AsA) content in mature fruits of 457 apple accessions were measured, and a great variation in AsA concentration was detected. Wild fruits showed significantly higher level of AsA than cultivated fruits. Fruit AsA content was positively correlated with malic acid content, but negatively correlated with fruit weight and soluble solid content. Thus, the difference in AsA content between the wild and cultivated fruits could be attributed to an indirect consequence of human selection for larger fruit size, less acidity, and increased sweetness during apple domestication. Additionally, AsA concentration was extremely high in fruit at the juvenile stage, but dramatically decreased at the expanding and mature stages. The expression levels of three genes controlling AsA accumulation, *MdGGP1*, *MdDHAR3-3*, and *MdNAT7-2*, were significantly negatively correlated with AsA contents in fruits, suggesting a feedback regulation mechanism in AsA-related gene expression. Our results could be helpful for future apple breeding.

1. Introduction

Ascorbic acid (AsA), also known as vitamin C, is an essential nutrient for human beings. AsA is associated with a number of physiological functions. For example, AsA plays a fundamental role in scavenging reactive oxygen species (ROS) due to its powerful antioxidant properties. AsA also functions as a cofactor for hydroxylases and monooxygenase enzymes that are involved in the synthesis of collagen, L-carnitine, and certain neurotransmitters (Li & Schellhorn, 2007). Collagen not only serves as a crucial component of connective tissue, but also constitutes the principal protein of many tissues such as skin, bones, cartilage, tendons, blood vessels, heart valves, cornea and eye lens, accounting for about one third of the total body protein. In addition, AsA can improve the absorption of non-heme iron present in plant-based foods (Gershoff, 1993). Thus, AsA has a broad range of health benefits, such as prevention and treatment of scurvy, wound healing, strengthening the immune system, reducing the risk of cancer, curing cataracts, and controlling the symptoms of asthma (Naidu, 2003; Schlueter & Johnston, 2011).

Although plants and most animals can synthesize AsA, humans and other primates are unable to synthesize L-ascorbic acid due to a loss-of-function mutation of the gene encoding the L-gulono-1,4-lactone oxidase, the enzyme catalyzing the last step of AsA biosynthesis (Nishikimi, Fukuyama, Minoshima, Shimizu, & Yagi, 1994). Hence, adequate intake of AsA from foods is necessary for normal physiological functioning, and fruits and vegetables are the richest natural sources of AsA in the human diet. The recommended dietary allowance (RDA) for vitamin C is approximately 75 mg per day for healthy, nonsmoking adults, but it varies between different countries (Troesch, Hoeft, McBurney, Eggersdorfer, & Weber, 2012). Since an increased intake of vitamin C is associated with a reduced risk of cancer and disease, a new RDA of up to 200 mg AsA/d was suggested by the scientific community (Carr & Frei, 1999; Frei, Birlouez-Aragon, & Lykkesfeldt, 2012).

In plants, AsA is a crucial antioxidant against various biotic and abiotic stresses (Venkatesh & Park, 2014), and participates in various biological processes, such as cell division and expansion, photosynthesis, hormone biosynthesis, and signaling (Fotopoulos, De Tullio, Barnes, & Kanellis, 2008; Kotchoni, Larrimore, Mukherjee, Kempinski, & Barth, 2009). The biosynthetic pathway of AsA in plants, termed the L-galactose pathway, was initially established by Wheeler, Jones, & Smirnoff, 1998). Later, three alternative AsA biosynthetic pathways have been identified in plants, including D-galacturonate (Agius et al., 2003), L-glucose (Wolucka & Van

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Rapid Screening for α-Glucosidase Inhibitors from *Gymnema sylvestre* by Affinity Ultrafiltration–HPLC-MS

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Gymnema sylvestre R. Br. (Asclepiadaceae) has been known to posses potential anti-diabetic activity, and the gymnemic acids were reported as the main bioactive components in this plant species. However, the specific components responsible for the hypoglycemic effect still remain unknown. In the present study, the *in vitro* study revealed that the extract of *G. sylvestre* exhibited significant inhibitory activity against α-glucosidase with IC_{50} at 68.70 ± 1.22 μg/mL compared to acarbose (positive control) at 59.03 ± 2.30 μg/mL, which further indicated the potential anti-diabetic activity. To this end, a method based on affinity ultrafiltration coupled with liquid chromatography mass spectrometry (UF-HPLC-MS) was established to rapidly screen and identify the α-glucosidase inhibitors from *G. sylvestre*. In this way, 9 compounds with higher enrichment factors (EFs) were identified according to their MS/MS spectra. Finally, the structure-activity relationships revealed that glycosylation could decrease the potential antisweet activity of sapogenins, and other components except gymnemic acids in *G. sylvestre* could also be good α-glucosidase inhibitors due to their synergistic effects. Taken together, the proposed method combing α-glucosidase and UF-HPLC-MS presents high efficiency for rapidly screening and identifying potential inhibitors of α-glucosidase from complex natural products, and could be further explored as a valuable high-throughput screening (HTS) platform in the early anti-diabetic drug discovery stage.

Keywords: ***Gymnema sylvestre*, gymnemic acid, α-glucosidase, UF-HPLC-MS, high-throughput screening**

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INTRODUCTION

Characterized by high blood glucose levels, diabetes mellitus (DM) has become one of the most serious chronic endocrine metabolic dysfunction. According to the WHO, 90% of the 382 million DM patients worldwide were type 2 diabetes mellitus (T2DM) in 2013, which still shows tendency of growing. With the increase of age, many severe long-term complications, e.g., diabetic retinopathy, kidney failure, cognitive decline, and diabetic neuropathy, will badly affect the T2DM patient's physical and mental health. Furthermore, repeated postprandial hyperglycemia may facilitate the development of the above serious adverse effects, and, in extreme cases, the risk of mortality. In clinical trials, those complications could be delayed or prevented by the intensive postprandial hyperglycemia control (Li et al., 2015; Liu et al., 2016; Zhang et al., 2016). To this end, postprandial blood glucose, especially in non-insulin-dependent T2DM patients, has attracted growing attentions as a potential therapeutic target.

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Identification of differentially expressed proteins in bermudagrass response to cold stress in the presence of ethylene

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ABSTRACT

Low temperature is considered to be a key environmental factor that limits broad application of bermudagrass (*Cynodon dactylon*). The phytohormone ethylene has been confirmed to be involved in plant response to cold stress. However, there is limited knowledge concerning the proteomic alterations of ethylene-regulated cold stress response in plant. To explore the possible molecular mechanism, a proteomic approach was performed by using iTRAQ (isobaric tags for relative and absolute quantitation) system. Bermudagrass leaves were treated with the ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC) or water (as control) at 4 °C for 24 h. Among 3990 quantified proteins, 201 differentially expressed proteins by ethylene and cold stress were identified. To better understand the possible mechanism involved in the ethylene-regulated cold response in bemudagrass, eleven groups of differentially expressed proteins were further analyzed. These proteins were mainly related to lipid stability, antioxidant enzymes and antioxidants, ribosome pathway, as well as protein synthesis and degradation. Therefore, the process of ethylene-regulated cold response maybe mainly related to lipid peroxidation, stress response and denfence and protein metabolism. Taken together, this study provides some novel insights into the molecular mechanisms of ethylene in bermudagrass responses to cold stress.

1. Introduction

Plants are frequently exposed to a plethora of stress conditions, which often lead to plant growth inhibition and limits crop productivity. Among these, low temperature is one of major serious environmental stresses (Cui et al., 2005; Shi et al., 2012). Numerous alterations, at physiological and molecular levels, occur when plants are exposed to cold stress. These include changes in membrane integrity, gene expression and metabolic homeostasis (Thomashow, 1999; Zhu et al., 2004; Knight and Knight, 2012). Exploring the mechanism regarding plants' cold response is crucial for rational breeding and transgenic strategies to enhance stress resistance in plants (Cui et al., 2005; Xiong et al., 2002).

Plants have evolved a complex and efficient mechanism, including physiological and molecular alterations, to confront cold stress. During the adaptive responses process, the vital event is perception and transduction of stress signals by signaling components, which would in turn activate multiple stress-related genes (Shinozaki and Yamaguchi-Shinozaki, 2007). The products of these genes may be involved in the generation of regulatory molecules, like the plant hormones e.g. ethylene and abscisic acid (ABA).These regulatory molecules can trigger another round of signaling, which culminate in to the final plant response to cold stress (Shinozaki and Yamaguchi-Shinozaki, 2007).

Bermudagrass (*Cynodon dactylon* (L).Pers.) that grows in warm climatic regions, is widely used in parks, lawns and sport fields, due to the superior merits of traffic tolerance and fast reproduction (Fan et al., 2015; Hu et al., 2016a,b; Shi et al., 2015). As a typical warm-season turfgrass, bermudagrass is highly sensitive to low temperature. A series of physiological and biochemical changes occur when bermudagrass is exposed to low temperature; they include enzyme-activity, cell membrane integrity as well as protein and soluble sugar content (Fan et al., 2015; Hu et al., 2016a,b; Shi et al., 2014). Moreover, small chemicals (e.g. NO, melatonin) and phytohormones (such as ABA, cytokinin, ethylene) are determined to play roles in bermudagrass response to cold stress (Hu et al., 2016a,b; Shi et al., 2014). Although

Abbreviations: iTRAQ, isobaric tags for relative and absolute quantitation; SAM, *S*-adenosyl methionine; LOX, lipoxygenases; LEA, late embryogenesis abundant; ACC, 1-aminocyclopropane-1-carboxylic acid; ROS, reactive oxygen species; POD, peroxidase; SOD, superoxide dismutase; GST, glutathione S-transferase; Hsps, heat shock proteins; LEA, late embryogenesis abundant

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e-Xtra*

Amelioration of Salt Stress on Bermudagrass by the Fungus *Aspergillus aculeatus*

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There is considerable evidence that plant abiotic-stress tolerance can be evoked by the exploitation of a globally abundant microbe. *A. aculeatus*, which was initially isolated from the rhizosphere of bermudagrass, has been shown to increase heavy metal tolerance in turfgrasses. Here, we report on the potential of *A. aculeatus* to induce tolerance to salt stress in bermudagrass. Physiological markers for salt stress, such as plant growth rate, lipid peroxidation, photosynthesis, and ionic homeostasis were assessed. Results indicated that strain *A. aculeatus* produced indole-3-acetic acid (IAA) and siderophores and exhibited a greater capacity for Na^+ absorption under salt stress. The plant inoculation by *A. aculeatus* increased plant growth and attenuated the NaCl-induced lipid peroxidation in roots and leaves of bermudagrass. The fungus significantly elevated the amount of IAA and glutathione and slightly enhanced photosynthetic efficiency of salt-treated bermudagrass. Tissues of inoculated plants had significantly increased concentrations of K^+ but lower Na^+ concentrations than those of uninoculated regimes. It appears that the role of *A. aculeatus* in alleviating bermudagrass salt stress is partly to produce IAA, to increase the activity of antioxidases, to absorb Na^+ by fungal hyphae, and to prevent the plant from ionic homeostasis disruption.

Soil salinization is a serious factor restricting the expansion of agriculture, animal husbandry, and forestry around the globe. Salinity problems are prominent in arid and semiarid regions, including fertile alluvial plains, valleys, densely populated areas, and the coastal regions (Pessarakli and Szabolcs 2011). Salinity is becoming particularly widespread in many regions. Globally, more than 20% of agricultural land and approximately 50% of irrigated land is affected by salinity, which poses a serious threat to more than 50% of all arable lands by the year 2050 (Flowers and Yeo 1995; Wang et al. 2003).

Highly saline soil from irrigation water leads to a series of morphological, physiological, biochemical, and molecular changes that adversely affect plant growth and productivity (Wang et al. 2000). Under saline conditions, plants are exposed to three types of stresses, including ion toxicity, desiccation, and disruptions in the mineral nutrition of the plant (Blumwald 2000). Excessive ions (Na^+ and Cl^-) in the rhizosphere causes injury to plant roots, followed by their gradual accumulation in the aerial parts, with heavy damage to plant metabolism, which leads to stunted growth and subsequently reduced yield (Shannon 1997). Furthermore, the excessive uptake of Na^+ and Cl^- can limit the uptake of other mineral nutrition (e.g., K^+, Ca^{2+}, Mg^{2+}), and the lack of nutritional elements causes adverse effects on ionic homeostasis, which restrains cell elongation and division, causing premature leaf aging and reducing leaf and root growth (Munns 2002; Zhu 2001). Dionisio-Sese and Tobita (2000) reported that the net photosynthetic rate declined with increasing levels of salinity stress of four rice varieties (Dionisio-Sese and Tobita 2000). This might be due to the direct effect of salt on stomatal resistance via a reduction in guard cell turgor (Maxwell and Johnson 2000). Therefore, salinity is considered as one of the most decisive environmental factors limiting plant growth and productivity.

To counter negative effects of soil salinity, selection of salt tolerant plants, desalination of soil by leaching excessive salts, and application of biological processes such as plant-microbe interactions, alone or in combination, can be employed (Bandou et al. 2006; Feng et al. 2002; Munns 2005). Among the remediation tools, the desalination of soils relies on a high chemical input, hence, it is not economically viable for sustainable agriculture and is achieved at the expense of the environment (Bandou et al. 2006; Waller et al. 2005). There is considerable evidence that abiotic-stress tolerance can be evoked in plants by the exploitation of globally abundant microbes, which live in reciprocally beneficial relationships with plants (Waller et al. 2005). For example, a fungal endophyte of tall fescue (*Epichloë coenophiala*) significantly increases plant-available water and aggregate stability of rhizosphere soil and, thereby, might raise water productivity in drought periods (Hosseini et al. 2015a and b, 2016). *Piriformospora indica*, a plant root–colonizing basidiomycete fungus, was shown to provide strong growth-promoting activity during its symbiosis with barley (Baltruschat et al. 2008; Waller et al. 2005). Previous studies have demonstrated that the *Epichloë* spp. usually infect cool-season grasses such as tall fescue, meadow fescue, and perennial ryegrass and alter soil biological and biochemical properties through the production of alkaloids, phenolic compounds, and other secondary metabolites, such as carbohydrates and proline (Hosseini et al. 2015a, 2016; Malinowski et al. 2000). Microorganisms have been reported to enhance the growth of plants by stimulating plant growth, increasing mineral nutrition, and minimizing excessive ion uptake (Na^+ and Cl^-) under salt stress (Li et al. 2012; Smith and Read 2010; Waller et al. 2005). Furthermore, mutualistic symbiosis with mycorrhizal and endophytic fungi can confer salt tolerance to plants grown in saline soils (Baltruschat et al. 2008). Arbuscular

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Exogenous Calcium Enhances the Photosystem II Photochemistry Response in Salt Stressed Tall Fescue

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Calcium enhances turfgrass response to salt stress. However, little is known about PSII photochemical changes when exogenous calcium was applied in salinity-stressed turfgrass. Here, we probe into the rearrangements of PSII electron transport and endogenous ion accumulation in tall fescue (*Festuca arundinacea* Schreber) treated with exogenous calcium under salt stress. Three-month-old seedlings of genotype "TF133" were subjected to the control (CK), salinity (S), salinity + calcium nitrate (SC), and salinity + ethylene glycol tetraacetic acid (SE). Calcium nitrate and ethylene glycol tetraacetic acid was used as exogenous calcium donor and calcium chelating agent respectively. At the end of a 5-day duration treatment, samples in SC regime had better photochemistry performance on several parameters than salinity only. Such as the Area (equal to the plastoquinone pool size), N (number of Q_A^- redox turnovers until F_m is reached), ψE_0, or δRo (Efficiencdy/probability with which a PSII trapped electron is transferred from Q_A to Q_B or PSI acceptors), ABS/RC (Absorbed photon flux per RC). All the above suggested that calcium enhanced the electron transfer of PSII (especially beyond Q_A^-) and prevented reaction centers from inactivation in salt-stressed tall fescue. Furthermore, both grass shoot and root tissues generally accumulated more C, N, Ca^{2+}, and K^+ in the SC regime than S regime. Interrelated analysis indicated that ψE_0, δRo, ABS/RC, C, and N content in shoots was highly correlated to each other and significantly positively related to Ca^{2+} and K^+ content in roots. Besides, high salt increased *ATP6E* and *CAMK2* transcription level in shoot at 1 and 5 day, respectively while exogenous calcium relieved it. In root, *CAMK2* level was reduced by Salinity at 5 day and exogenous calcium recovered it. These observations involved in electron transport capacity and ion accumulation assist in understanding better the protective role of exogenous calcium in tall fescue under salt stress.

Keywords: exogenous calcium, PSII photochemistry, carbon and nitrogen assimilation, salt stress, tall fescue

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INTRODUCTION

Salinity is a major abiotic stress factor threating plant growth and crop yield (Shabala and Cuin, 2007; Türkan and Demiral, 2009). A considerable amount of fundamental processes in plant life, for instance the photosynthesis, were vulnerable with increasing salinity (Sayed, 2003; Murata et al., 2007; Chaves et al., 2009). Moreover, photosystem II (PSII) is more sensitive than

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ABA Is Involved in Regulation of Cold Stress Response in Bermudagrass

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As a representative warm-season grass, Bermudagrass [*Cynodon dactylon* (L). *Pers*.] is widely used in turf systems. However, low temperature remarkably limits its growth and distribution. ABA is a crucial phytohormone that has been reported to regulate much important physiological and biochemical processes in plants under abiotic stress. Therefore, the objective of this study was to figure out the effects of ABA on the cold-sensitive (S) and cold-resistant (R) Bermudagrass genotypes response to cold stress. In this study, the plants were treated with 100 μM ABA solution and exposed to 4°C temperature. After 7 days of cold treatment, the electrolyte leakage (EL), malonaldehyde (MDA) and H_2O_2 content were significantly increased in both genotypes compared with control condition, and these values were higher in R genotype than those of S genotype, respectively. By contrast, exogenous ABA application decreased the electrolyte leakage (EL), MDA and H_2O_2 content in both genotypes compared with those plants without ABA treatment under cold treatment condition. In addition, exogenous ABA application increased the levels of chlorophyll *a* fluorescence transient curve for both genotypes, and it was higher in R genotype than that of S genotype. Analysis of photosynthetic fluorescence parameters revealed that ABA treatment improved the performance of photosystem II under cold condition, particularly for the R genotype. Moreover, cold stress significantly increased δ13C values for both genotypes, while it was alleviated by exogenous ABA. Additionally, exogenous ABA application altered the expression of ABA- or cold related genes, including *ABF1*, *CBF1*, and *LEA*. In summary, exogenous ABA application enhanced cold resistance of both genotypes by maintaining cell membrane stability, improving the process of photosystem II, increasing carbon isotopic fractionation under cold stress, and more prominently in R genotype compared with S genotype.

Keywords: abscisic acid, Bermudagrass, cold stress, photosystem II, δ13C

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INTRODUCTION

Bermudagrass [*Cynodondactylon* (L) *Pers*.] is widely used in golf courses, sports fields and lawns globally (Fan et al., 2014). As a representative warm-season grass, its optimal growth temperature ranges from 26°C to 35°C (Fan et al., 2014). Cold stress is considered to be a key environmental factor that limits its growth and distribution (Fan et al., 2014).

When two Bermudagrass [*Cynodon dactylon* (L.) Pers. var. *dactylon*] cultivars, Riviera (cold tolerant) and Princess-77 (cold sensitive) were exposed to cold acclimation at 8/4°C (day/night), relative EL values were remarkably increased, resulting in the damage to cell membrane

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Melatonin Is Involved in Regulation of Bermudagrass Growth and Development and Response to Low K^+ Stress

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Melatonin (*N*-acetyl-5-methoxytryptamine) plays critical roles in plant growth and development and during the response to multiple abiotic stresses. However, the roles of melatonin in plant response to K^+ deficiency remain largely unknown. In the present study, we observed that the endogenous melatonin contents in bermudagrass were remarkably increased by low K^+ (LK) treatment, suggesting that melatonin was involved in bermudagrass response to LK stress. Further phenotype analysis revealed that exogenous melatonin application conferred Bermudagrass enhanced tolerance to LK stress. Interestingly, exogenous melatonin application also promoted bermudagrass growth and development at normal condition. Furthermore, the K^+ contents measurement revealed that melatonin-treated plants accumulated more K^+ in both shoot (under both control and LK condition) and root tissues (under LK condition) compared with those of melatonin non-treated plants. Expression analysis indicated that the transcripts of K^+ transport genes were significantly induced by exogenous melatonin treatment in bermudagrass under both control and LK stress conditions, especially under a combined treatment of LK stress and melatonin, which may increase accumulation of K^+ content profoundly under LK stress and thereby contributed to the LK-tolerant phenotype. In addition, we investigated the role of melatonin in the regulation of photosystem II (PSII) activities under LK stress. The chlorophyll fluorescence transient (OJIP) curves were obviously higher in plants grown in LK with melatonin (LK+Mel) than those of plants grown in LK medium without melatonin application for 1 or 2 weeks, suggesting that melatonin plays important roles in PSII against LK stress. After a combined treatment of LK stress and melatonin, the values for performance indexes (PI_{ABS}, PI_{Total}, and PI_{CS}), flux ratios (φP_0, ΨE_0, and φE_0) and specific energy fluxes (ET_O/RC) were significantly improved compared with those of LK stress alone, suggesting that melatonin plays positive roles in protecting PSII activity under LK stress. Collectively, this study reveals an important role of melatonin in regulating bermudagrass response to LK stress.

Keywords: bermudagrass, melatonin, LK stress, K^+ content, photosystem II (PSII) activity

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Functional Characterization of a Novel R2R3-MYB Transcription Factor Modulating the Flavonoid Biosynthetic Pathway from *Epimedium sagittatum*

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Epimedium species have been widely used both as traditional Chinese medicinal plants and ornamental perennials. Both flavonols, acting as the major bioactive components (BCs) and anthocyanins, predominantly contributing to the color diversity of *Epimedium* flowers belong to different classes of flavonoids. It is well-acknowledged that flavonoid biosynthetic pathway is predominantly regulated by R2R3-MYB transcription factor (TF) as well as bHLH TF and WD40 protein at the transcriptional level. *MYB* TFs specifically regulating anthocyanin or flavonol biosynthetic pathway have been already isolated and functionally characterized from *Epimedium sagittatum*, but a *R2R3-MYB* TF involved in regulating both these two pathways has not been functionally characterized to date in *Epimedium* plants. In this study, we report the functional characterization of *EsMYB9*, a *R2R3-MYB* TF previously isolated from *E. sagittatum*. The previous study indicated that *EsMYB9* belongs to a small subfamily of *R2R3-MYB* TFs containing grape *VvMYB5a* and *VvMYB5b* TFs, which regulate flavonoid biosynthetic pathway. The present studies show that overexpression of *EsMYB9* in tobacco leads to increased transcript levels of flavonoid pathway genes and increased contents of anthocyanins and flavonols. Yeast two-hybrid assay indicates that the C-terminal region of *EsMYB9* contributes to the autoactivation activity, and *EsMYB9* interacts with *EsTT8* or *AtTT8 bHLH* regulator. Transient reporter assay shows that *EsMYB9* slightly activates the expression of *EsCHS* (chalcone synthase) promoter in transiently transformed leaves of *Nicotiana benthamiana*, but the addition of *AtTT8* or *EsTT8 bHLH* regulator strongly enhances the transcriptional activation of *EsMYB9* against five promoters of the flavonoid pathway genes except *EsFLS* (flavonol synthase). In addition, co-transformation of *EsMYB9* and *EsTT8* in transiently transfected tobacco leaves strongly induces the expressions of flavonoid biosynthetic genes. The potential role of *EsMYB9* in modulating the biosynthesis and accumulation of sucrose-induced anthocyanin and flavonol-derived

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Development and Application of Transcriptome-Derived Microsatellites in *Actinidia eriantha* (Actinidiaceae)

Rui Guo[1,2], *Jacob B. Landis*[3], *Michael J. Moore*[4], *Aiping Meng*[1], *Shuguang Jian*[5], *Xiaohong Yao*[1]* *and Hengchang Wang*[1]*

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Actinidia eriantha Benth. is a diploid perennial woody vine native to China and is recognized as a valuable species for commercial kiwifruit improvement with high levels of ascorbic acid as well as having been used in traditional Chinese medicine. Due to the lack of genomic resources for the species, microsatellite markers for population genetics studies are scarce. In this study, RNASeq was conducted on fruit tissue of *A. eriantha,* yielding 5,678,129 reads with a total output of 3.41 Gb. *De novo* assembly yielded 69,783 non-redundant unigenes (41.3 Mb), of which 21,730 were annotated using protein databases. A total of 8,658 EST-SSR loci were identified in 7,495 unigene sequences, for which primer pairs were successfully designed for 3,842 loci (44.4%). Among these, 183 primer pairs were assayed for PCR amplification, yielding 69 with detectable polymorphism in *A. eriantha*. Additionally, 61 of the 69 polymorphic loci could be successfully amplified in at least one other *Actinidia* species. Of these, 14 polymorphic loci (mean $N_A = 6.07 \pm 2.30$) were randomly selected for assessing levels of genetic diversity and population structure within *A. eriantha*. Finally, a neighbor-joining tree and Bayesian clustering analysis showed distinct clustering into two groups ($K = 2$), agreeing with the geographical distributions of these populations. Overall, our results will facilitate further studies of genetic diversity within *A. eriantha* and will aid in discriminating outlier loci involved in local adaptation.

Keywords: ***Actinidia eriantha,*** **high-throughput sequencing, transcriptome, EST-SSRs, population genetic structure**

INTRODUCTION

Actinidia eriantha Benth. (Actinidiaceae) is a functionally dioecious, perennial woody vine ($2n = 58$) with a wide distribution in south central and south east China. The roots of *A. eriantha* have been used in traditional Chinese medicine to treat gastric carcinoma, nasopharyngeal carcinoma, breast carcinoma, and hepatitis (Sun et al., 2015). Polysaccharides isolated from roots have been shown to inhibit the growth of transplantable S180 sarcoma in mice, as well as promote splenocyte proliferation and natural killer cells activity (Xu et al., 2009).

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The Alleviation of Heat Damage to Photosystem II and Enzymatic Antioxidants by Exogenous Spermidine in Tall Fescue

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Tall fescue (*Festuca arundinacea* Schreb) is a typical cool-season grass that is widely used in turf and pasture. However, high temperature as an abiotic stress seriously affects its utilization. The objective of this study was to explore the effect of spermidine (Spd) on heat stress response of tall fescue. The samples were exposed to 22°C (normal condition) or 44°C (heat stress) for 4 h. The results showed that exogenous Spd partially improved the quality of tall fescue leaves under normal temperature conditions. Nevertheless, after heat stress treatment, exogenous Spd significantly decreased the electrolyte leakage of tall fescue leaves. Spd also profoundly reduced the H_2O_2 and $O_2^{\cdot -}$ content and increased antioxidant enzymes activities. In addition, PAs can also regulate antioxidant enzymes activities including SOD, POD, and APX which could help to scavenge ROS. Moreover, application of Spd could also remarkably increase the chlorophyll content and had a positive effect on the chlorophyll α fluorescence transients under high temperature. The Spd reagent enhanced the performance of photosystem II (PSII) as observed by the JIP-test. Under heat stress, the Spd profoundly improved the partial potentials at the steps of energy bifurcations (PI_{ABS} and PI_{total}) and the quantum yields and efficiencies (φP_0, δR_0, φR_0, and γRC). Exogenous Spd could also reduce the specific energy fluxes per Q_A^- reducing PSII reaction center (RC) (TP_0/RC and ET_0/RC). Additionally, exogenous Spd improved the expression level of *psbA* and *psbB*, which encoded the proteins of PSII core reaction center complex. We infer that PAs can stabilize the structure of nucleic acids and protect RNA from the degradation of ribonuclease. In brief, our study indicates that exogenous Spd enhances the heat tolerance of tall fescue by maintaining cell membrane stability, increasing antioxidant enzymes activities, improving PSII, and relevant gene expression.

Keywords: spermidine, tall fescue, heat stress, antioxidant enzymes, photosystem II, gene expression

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INTRODUCTION

Tall fescue (*Festuca arundinacea* Schreb) is a major cool-season grass that is widely used for turf, on the sports field, and as a forage grass with an optimal growth temperature of 16–24°C (Emmons, 2007). However, it is sensitive to heat stress which affects tall fescue turf quality and utilization. When the temperature exceeds the optimal range, heat stress could lead to the photosynthesis

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Screening for Natural Inhibitors of Topoisomerases I from *Rhamnus davurica* by Affinity Ultrafiltration and High-Performance Liquid Chromatography–Mass Spectrometry

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Topoisomerase I (Topo I) catalyzes topological interconversion of duplex DNA during DNA replication and transcription, and has been deemed as important antineoplastic targets. In this study, the fraction *R.d*-60 from ethyl acetate extracts of *Rhamnus davurica* showed higher inhibitory rates against SGC-7901 and HT-29 compared with the *R.d*-30 fraction *in vitro*. However, the specific active components of *R.d*-60 fraction remain elusive. To this end, a method based on bio-affinity ultrafiltration and high performance liquid chromatography/electrospray mass spectrometry (HPLC- ESI-MS/MS) was developed to rapidly screen and identify the Topo I inhibitors in this fraction. The enrichment factors (EFs) were calculated to evaluate the binding affinities between the bioactive constituents and Topo I. As a result, eight ligands were identified and six of which with higher EFs showed more potential antitumor activity. Furthermore, antiproliferative assays *in vitro* (IC_{50} values) with two representative candidates (apigenin, quercetin) against SGC-7901, HT-29 and Hep G2 cells were conducted and further validated. Finally, the structure-activity relationships revealed that flavones contain a C2-C3 double bond of C ring exhibited higher bio-affinities to Topo I than those without it. This integrated method combining Topo I ultrafiltration with HPLC-MS/MS proved to be very efficient in rapid screening and identification of potential Topo I inhibitors from the complex extracts of medicinal plants, and could be further explored as a valuable high-throughput screening platform in the early drug discovery stage.

Keywords: topoisomerases I, *Rhamnus davurica*, ultrafiltration, high performance liquid chromatography-mass spectrometry, flavonoids

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INTRODUCTION

In the early drug discovery stage of small molecules, the binding affinity between small molecular candidate and its therapeutic biomolecule targets is considered as the primary determinant of the candidate's biological activity (Qin et al., 2015). Recently, it has been found that almost half of the small-molecule drugs in the market are enzyme inhibitors according to a survey

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Involvement of Ubiquitin-Conjugating Enzyme (E2 Gene Family) in Ripening Process and Response to Cold and Heat Stress of *Vitis vinifera*

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Yingying Gao[1,2,3], Yi Wang[2,3], Haiping Xin[1], Shaohua Li[2] & Zhenchang Liang[2,4]

Ubiquitin-conjugating (UBC) E2 enzyme plays crucial roles in plant growth and development. Limited information can describe the function of UBC enzyme E2 in grapes. A total of 43 UBC enzyme E2 genes with conserved UBC domain were identified in grapes. These genes were divided into five groups based on phylogenetic tree with tomatoes. Sequence analyses indicated that *VvUBCs* in the same group possessed similar gene structures and conserved motifs. Gene distribution in chromosomes was uneven, and gene duplication existed in 36 *VvUBCs*. Transcriptome and qRT-PCR analysis indicated that most *VvUBCs* are involved in ripening and post-harvest stage, and feature functional roles in grape organs. According to the transcriptome and qRT-PCR results, seven and six *VvUBCs* in grape responded to cold and heat stress, respectively, whereas no remarkable *VvUBCs* change was noted under salt or water-deficit stress. This study provides new insights to physiological and developmental roles of these enzymes and regulation mechanism of E2 genes in grapes.

Ubiquitination is an important type of post-translational modification of proteins among all eukaryotes. This important process regulates a wide range of biological processes[1], including intracellular translocation of proteins, chromosomal organization, DNA repair, cell cycle control, and apoptosis[2–4].

Ubiquitin covalently binds with target proteins, causing a series of enzyme catalytic effects. This process requires coordination of three types of enzymes, namely, ubiquitin-activating enzyme (E1), ubiquitin-conjugating (UBC) enzyme (E2), and ubiquitin-ligase enzyme (E3)[5]. Ubiquitin is activated in an ATP-dependent manner linked with E1; E2 accepts ubiquitin from E1, passes it to active-site cysteine, and then transfers ubiquitin to a targeted protein aided by E3[5]. Additional ubiquitin can be further ligated to initial ubiquitin molecule through sequential ubiquitination cycles, ultimately forming a poly- ubiquitin chain; finally, targeted proteins are modified[5]. Then, substrates can be degraded to generate other biological effects. E2 plays a crucial role in ubiquitination and is responsible for attachment of ubiquitin to targeted proteins[5]. E2 protein contains a conserved catalytic domain, called the UBC domain, spanning 140–200 amino acids in length. Various studies indicated that UBC domain mediates the interaction between E2 and E3[6–10]. A special interaction occurs between UBC domain in E2 and RING domain in E3[11].

E2 genes exist as a multi-gene family and are involved in many plant physiological activities. A total of 14, 50, 41, 39, and 75 E2 genes were identified in *Saccharomyces cerevisiae*[12], humans[13], *Arabidopsis*[14], rice[15], and maize[16], respectively. A number of E2 genes are involved in environmental stresses. For example, *VrUBC1* of mung bean responded to osmotic[17] stress, and E2 genes in soybean and peanut reacted to drought and salt stress in transgenic *Arabidopsis*[18–20]. Recently, researchers discovered that fruit-ripening regulator (RIN) can directly bind to the

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The Fungus *Aspergillus aculeatus* Enhances Salt-Stress Tolerance, Metabolite Accumulation, and Improves Forage Quality in Perennial Ryegrass

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Perennial ryegrass (*Lolium perenne*) is an important forage grass with high yield and superior quality in temperate regions which is widely used in parks, sport field, and other places. However, perennial ryegrass is moderately tolerant to salinity stress compared to other commercial cultivars and salt stress reduces their growth and productivity. *Aspergillus aculeatus* has been documented to participate in alleviating damage induced by salinity. Therefore, the objective of this study was to investigate the mechanisms underlying *A. aculeatus*-mediated salt tolerance, and forage quality of perennial ryegrass exposed to 0, 200, and 400 mM NaCl concentrations. Physiological markers and forage quality of perennial ryegrass to salt stress were evaluated based on the growth rate, photosynthesis, antioxidant enzymes activity, lipid peroxidation, ionic homeostasis, the nutritional value of forage, and metabolites. Plants inoculated with *A. aculeatus* exhibited higher relative growth rate (RGR), turf and forage quality under salt stress than un-inoculated plants. Moreover, in inoculated plants, the fungus remarkably improved plant photosynthetic efficiency, reduced the antioxidant enzymes activity (POD and CAT), and attenuated lipid peroxidation (decreased H_2O_2 and MDA accumulation) induced by salinity, compared to un-inoculated plants. Furthermore, the fungus also acts as an important role in maintaining the lower Na/K ratio and metabolites and lower the amino acids (Alanine, Proline, GABA, and Asparagine), and soluble sugars (Glucose and Fructose) for inoculated plants than un-inoculated ones. Our results suggest that *A. aculeatus* may be involved in modulating perennial ryegrass tolerance to salinity in various ways.

Keywords: perennial ryegrass, salt stress, *Aspergillus aculeatus*, physiological markers, forage quality, metabolites

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Abbreviations: ADF, acid detergent fiber; CAT, catalase; CF, crude fat; Chl, Chlorophyll; CP, crude protein; EL, electrolyte leakage; GABA, γ-aminobutyric acid; GC-MS, gas chromatography–mass spectrometry; HCA, hierarchical clustering analysis; H_2O_2, hydrogen peroxide; MDA, malondialdehyde; MSTFA, N-Methyl-N-(trimethylsilyl)trifluoroacetamide; NDF, neutral detergent fiber; OH^-, hydroxyl radical; OJIP curve: F_0, minimal reliable recorded fluorescence, at 20 ms with the pulse-amplitude modulation (PAM) fluorometer; F_J, fluorescence intensity at the J-step (2 ms) of OJIP; F_I, Fluorescence intensity at the I-step (30 ms) of OJIP; F_P, maximal recorded fluorescence intensity, at the peak P of OJIP; O_2^-, superoxide radical; P, phosphorus; PCA, principal component analysis; POD, peroxidase; RGR, relative growth rate; SOD, superoxide dismutase; TOC, total organic carbon.

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Discovery of Several Novel Targets that Enhance β-Carotene Production in *Saccharomyces cerevisiae*

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β-Carotene is the precursor of vitamin A, and also exhibits multiple pharmaceutical functions by itself. In comparison to chemical synthesis, the production of β-carotene in microbes by metabolic engineering strategy is relatively inexpensive. Identifying genes enhancing β-carotene production in microbes is important for engineering a strain of producing higher yields of β-carotene. Most of previous efforts in identifying the gene targets have focused on the isoprenoid pathway where the β-carotene biosynthesis belongs. However, due to the complex interactions between metabolic fluxes, seemingly irrelevant genes that are outside the isoprenoid pathway might also affect β-carotene biosynthesis. To this end, here we provided an example that several novel gene targets, which are outside the isoprenoid pathway, have improving effects on β-carotene synthesis in yeast cells, when they were over-expressed. Among these targets, the class E protein of the vacuolar protein-sorting pathway (Did2) led to the highest improvement in β-carotene yields, which was 2.1-fold to that of the corresponding control. This improvement was further explained by the observation that the overexpression of the *DID2* gene generally boosted the transcriptions of β-carotene pathway genes. The mechanism by which the other targets improve the production of β-carotene is discussed.

Keywords: β-carotene biosynthesis, Did2, colony-color screening, novel amplifying targets, *Saccharomyces cerevisiae*

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INTRODUCTION

β-Carotene is a carotenoid compound with multiple physiological and pharmaceutical functions: e.g., it functions in photosynthesis as a light-harvesting pigment in naturally carotenoid-producing organisms such as higher plants and photosynthetic microorganisms (Yamano et al., 1994), and has been applied as a natural pigmentation ingredient in food industry; moreover, for humans, β-carotene is the precursor of vitamin A and was ever proposed for cancer treatments (Giovannucci et al., 1995). Although β-carotene is now supplied mainly by chemical synthesis, there has been much interest in engineering the synthesis of this compound in microbes, such as the fungus *Neurospora crassa* (Armstrong and Hearst, 1996), the yeast *Candida utilis* (Miura et al., 1998), the yeast *Saccharomyces cerevisiae* (Yamano et al., 1994; Verwaal et al., 2007; Yan et al., 2012; Li et al., 2013; Xie et al., 2014), and *Escherichia coli* (Yoon et al., 2009; Zhao et al., 2013; Yang and Guo, 2014). Given the safety of the downstream applications and the convenience of genetic manipulations,

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Isolation and characterization of an endoparasite from the culture of oleaginous microalga *Graesiella* sp. WBG-1

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ABSTRACT

Oleaginous microalgae are an important potential feedstock for biodiesel production. However, a problem in mass cultivation of microalgae is the frequent occurrence of infection by algal parasites. In the present study, an endoparasite WZ01 was isolated from an open raceway pond of oleaginous *Graesiella* sp. WBG-1, and caused epidemics resulting in algal population collapse. According to 18S rDNA-based phylogenetic analyses, morphology, ultrastructure and life cycle, strain WZ01 was identified as a member of Aphelidea, *Amoeboaphelidium protococcarum*, although it had some minor differences from *A. protococcarum* X-5 and FD95. Examination via transmission electron microscopy demonstrated that zoospores of the parasite WZ01 were amoeboid, which can produce two types of pseudopodia (multiple filopodia and short anterior lamellipodium), but the pseudocilium was not observed. Interestingly, amoeboid zoospores contained numerous dense-body vesicles, which have not been previously described. Moreover, our results revealed the presence of a microtubule inside the penetration tube, indicating that the contents of the cyst were injected into the host not only by vacuole pressure but also by using a microtubule-mediated mechanism. In addition, of the 42 tested algal species, only cultures of coccoid green algae *Chlorococcum* sp. A213 and *Chlorococcum* sp. GP1 rapidly and intensively developed infections by parasite WZ01. This is the first report on endoparasitic infection in oleaginous coccoid green algae. Our results will enhance understanding of parasite–host relationships, which will be beneficial in developing strategies for infection control.

1. Introduction

Oleaginous microalgae are considered one of the most significant potential feedstocks for biodiesel production [1]. However, biological contamination is a major potential bottleneck that can have strong detrimental effects on production in microalgal mass cultivation [2,3]. In the context of open pond systems, microalgal growth is susceptible to biological contamination, including from zooplankton, fungi, bacteria and pathogenic viruses [4]. Although biological contamination can be better managed in closed photobioreactors, they can become prone to contamination from the water or gas supply during long periods of continuous cultivation [5]. Consequently, in either open pond systems or closed systems, it is difficult to avoid biological contamination in large scale cultivation of microalgae [4].

Microalgae are often plagued by algal parasites [6], including zoosporic fungi (Chytridomycota) and fungi-like organisms [7]. In natural ecosystems, these parasites can cause widespread microalgal death, with mortality of the host population increasing to 90% [8]. The parasite *Ectrogella perforans* has been reported to have destroyed approximately 99% of the population of the diatom *Licmophora* sp. in one season [9]. In mass algal monocultures, parasitic contamination can result in complete collapse of the algal populations and destruction of their valuable products [10,11]. For instance, the aphelid *Amoeboaphelidium occidentale* FD01 has been found to cause severe production loss of *Scenedesmus dimorphus* in commercial ponds [12,13]. Hence, more research is required on parasitic contaminations.

Aphelids are a poorly understood group of intracellular parasites of microalgae; these are currently categorized within the class Aphelidea [14]. Only four genera have been described: *Aphelidium*, *Amoeboaphelidium*, *Paraphelidium*, and *Pseudaphelidium* [15,16,17]. Aphelids share similarities with Chytridiomycetes, Cryptomycota, and Microsporidia [14]. Notably, the life cycle of aphelid shows some similarities with that of Chytridiomycetes; however, similar to nucleariids, they use phagotrophy for the uptake of nutrients, whereas most true fungi live by osmotrophy [14]. Cryptomycota is a new phylum of early-diverging fungi. They are intracellular parasites of true fungi, oomycetes and diatom algae, and have an endobiotic phagotrophic stage. The phylum is represented by multiple environmental sequences and two isolated

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Investigation of changes in endocannabinoids and N-acylethanolamides in biofluids, and their correlations with female infertility

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ABSTRACT

Female infertility is a worldwide medical problem, and the scarcity of infertility biomarkers has hindered the ability to launch preventive and therapeutic measures in a timely manner. Intriguingly, alterations in endocannabinoids (eCBs) and N-acylethanolamides (NAEs) have been observed in the biofluids of infertile females. Therefore, a hypothesis of using eCB and NAEs in biofluids as infertility biomarkers was proposed by several researchers; however, little evidence exists to verify the hypothesis. To investigate their correlations with female infertility, we developed a magnetic liquid microextraction-chemical derivatization (MLME-CD) method coupled with liquid chromatography-tandem mass spectrometry for the quantification of eCBs and NAEs in biofluids. The target compounds were first purified with magnetic toluene as sorbents, and then labeled with 4-(*N*,*N*-dimethyamino)benzoyl chloride (4-DMABC). The MLME-CD method offered several advantages, including reliable quantification results by preventing the isomerization of eCB, high throughput by requiring 20 min for sample preparation, and good sensitivity with limits of detection at 3.0-54.3 fmol. The intra-day and inter-day relative standard deviations were below 14.5%, and the recoveries were 87.4%–117.9%. Concentrations of eCBs and NAEs in the serum of 49 infertile women and 53 fertile women (controls), and in the ovarian follicular fluid of 21 infertile women and 20 controls were then quantified. Using unpaired *t* test analysis indicated significant differences in AEA and PEA in serum, and OEA in follicular fluid between infertile women and healthy controls, and the areas under the curve were in the range of 0.605-0.707.

1. Introduction

Infertility is a condition of the reproduction system that has been recognized as a public health issue worldwide by the World Health Organization [1], and affects one-sixth of the couples attempting to conceive, with more than 50% of cases due to female factors [2]. Early diagnosis of infertility, however, may provide an opportunity for timely and appropriate intervention [3–5]. Therefore, it would be of great significance to discover infertility biomarkers that could be used to diagnose reproductive defects, or that reveal any possible pathologic changes in women at an early stage.

Endocannabinoids (eCBs) constitute a group of bioactive lipid mediators released from membrane phospholipids and are produced on demand by cells [6]. The best-characterized eCBs are N-arachidonoyl ethanolamine, known as anandamide (AEA), and 2-arachidonoyl glycerol (2-AG). Their biosynthesis is catalyzed by the N-arachidonoylphosphatidyl-ethanolamine-specific phospholipase D (NAPE-PLD) and diacylglycerol lipase [7,8], and terminated by hydrolysis with the serine hydrolases fatty acid amide hydrolase (FAAH) and monoacylglycerol lipase [9,10]. As neurotransmitters, the eCBs occur in an exquisitely regulated balance between synthesis and metabolism, and bind to type-1 and type-2 cannabinoid receptors (CB1 and CB2) and GPR55 (a recently discovered putative "CB3") to perform a series of physiologic functions [11,12],

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Solvent-saturated solid matrix technique for increasing the efficiency of headspace extraction of volatiles

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ABSTRACT

Due to the slow mass transfer rate of substance in solid media, very limited amount of volatiles can be released from the solid matrix to the headspace in the static headspace analysis. Thus, low sensitivity is often the main problem of static headspace analysis of the volatiles contained in a solid sample. Here, we reported on a solvent-saturated solid matrix (SSSM) technique which successfully enhanced the headspace extraction efficiency, and improved the sensitivity of the headspace analysis of the volatiles in solid sample. By adding a small amount of high-boiling-point solvent (e.g. glycerin) onto the solid sample to form a surface-covered solvent layer, the headspace extraction efficiency can be significantly increased by up to 2.5 times higher than that of the conventional one. Based on the experimental investigation of the performance of different amounts of solvent used for the headspace extraction of volatiles in air-dried lotus flower samples, the possible mechanism for the SSSM assisted headspace extraction has been proposed and validated, which showed that a saturation point of solvent existed for a given amount of solid sample, and the maximum extraction efficiency could be obtained at this saturation point. Moreover, positive results were also achieved when applying this new technique in the headspace extraction of the volatiles to the other two solid samples, which means this newly developed technique may open up a new avenue, and also serve as a general strategy for improving the sensitivity of headspace analysis of the volatiles entrapped in solid matrices.

1. Introduction

Headspace analysis, including mainly static headspace, dynamic headspace and headspace solid phase micro-extraction (SPME), is now playing an important role in the quantification of volatile analytes in samples with complicated matrices [1–3]. Because the headspace-based analysis can effectively prevent the non-volatile species contained in samples from entering the subsequent detection system, e.g., gas chromatography (GC) or gas chromatography-mass spectrometry (GC–MS), which may avoid some of the problems associated with instrument contamination, thereby reduce sample preparation procedures, e.g., filtration, solvent extraction and column separation [4].

Among the headspace techniques, static headspace, based on in-situ evaporation and sampling [5], has shown great advantages in the analytical reproducibility and calibration over other techniques in which intermediate trap phases were involved [6,7]. In the past decades, several techniques in static headspace have been developed, which made it a powerful tool being widely used in many applications, e.g., the phase equilibrium headspace technique (the conventional one) for phase equilibrium analysis and studies [8,9], the full evaporation (FE) headspace technique for matrix-independent analysis [10,11], the phase reaction conversion (PRC) headspace technique for non-volatile species analysis [12–14], and the multiple headspace extraction (MHE) technique for process studies [15,16]. Although these techniques have expanded the application of static headspace in many areas, the low sensitivity in static headspace analysis becomes a bottle-neck problem, due to the very few amount of the analyte partitioned to the headspace and sampled to the detection system. Recent years, Hu and Chai developed a water removal by hydrate formation (WRHF) technique based on FE headspace, in which a large sample volume can be fully evaporated and sampled to GC and thereby increase the

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Reduced representation genome sequencing reveals patterns of genetic diversity and selection in apple

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Research Article

Abstract Identifying DNA sequence variations is a fundamental step towards deciphering the genetic basis of traits of interest. Here, a total of 20 cultivated and 10 wild apples were genotyped using specific-locus amplified fragment sequencing, and 39,635 single nucleotide polymorphisms with no missing genotypes and evenly distributed along the genome were selected to investigate patterns of genome-wide genetic variations between cultivated and wild apples. Overall, wild apples displayed higher levels of genetic diversity than cultivated apples. Linkage disequilibrium (LD) decays were observed quite rapidly in cultivated and wild apples, with an r^2-value below 0.2 at 440 and 280 bp, respectively. Moreover, bidirectional gene flow and different distribution patterns of LD blocks were detected between domesticated and wild apples. Most LD blocks unique to cultivated apples were located within QTL regions controlling fruit quality, thus suggesting that fruit quality had probably undergone selection during apple domestication. The genome of the earliest cultivated apple in China, Nai, was highly similar to that of *Malus sieversii*, and contained a small portion of genetic material from other wild apple species. This suggested that introgression could have been an important driving force during initial domestication of apple. These findings will facilitate future breeding and genetic dissection of complex traits in apple.

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INTRODUCTION

The domesticated apple, *Malus* × *domestica* Borkh., is an economically important fruit crop in temperate regions of the world, and over 80.8 million tons of apple fruits are produced annually worldwide (http://faostat.fao.org/). Apple belongs to the genus *Malus* in the family Rosaceae, which includes many other economically important fruit crops such as pear, peach, plum, apricot, almond, cherry, loquat, strawberry, raspberry and quince. The genus *Malus* consists of about 25 to 33 species. The edible apple is known to have originated from the wild species *M. sieversii* which is native to the Tian Shan region in central Asia, and is likely to have undergone domestication during its spread along the Silk Road between Asia and Europe (Luby et al. 2001; Harris et al. 2002; Yan et al. 2008; Richards et al. 2009). During the process of domestication, multiple *Malus* species have contributed to the genetic makeup of the domesticated apple, with the wild European crabapple *M. sylvestris* serving as a major second contributor (Velasco et al. 2010; Cornille et al. 2012).

Apple has an autopolyploidy origin, but its genome has become diploidized, with a basic chromosome number of x = 17 (Velasco et al. 2010; Han et al. 2011). The domesticated apple has a relatively small genome, with an approximately 750 Mb per haploid, and its draft genome sequence has been released (Velasco et al. 2010).

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RESEARCH ARTICLE Open Access

Complete plastome sequencing of both living species of Circaeasteraceae (Ranunculales) reveals unusual rearrangements and the loss of the *ndh* gene family

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Abstract

Background: Among the 13 families of early-diverging eudicots, only Circaeasteraceae (Ranunculales), which consists of the two monotypic genera *Circaeaster* and *Kingdonia,* lacks a published complete plastome sequence. In addition, the phylogenetic position of Circaeasteraceae as sister to Lardizabalaceae has only been weakly or moderately supported in previous studies using smaller data sets. Moreover, previous plastome studies have documented a number of novel structural rearrangements among early-divergent eudicots. Hence it is important to sequence plastomes from Circaeasteraceae to better understand plastome evolution in early-diverging eudicots and to further investigate the phylogenetic position of Circaeasteraceae.

Results: Using an Illumina HiSeq 2000, complete plastomes were sequenced from both living members of Circaeasteraceae: *Circaeaster agrestis* and *Kingdonia uniflora*. Plastome structure and gene content were compared between these two plastomes, and with those of other early-diverging eudicot plastomes. Phylogenetic analysis of a 79-gene, 99-taxon data set including exemplars of all families of early-diverging eudicots was conducted to resolve the phylogenetic position of Circaeasteraceae.

Both plastomes possess the typical quadripartite structure of land plant plastomes. However, a large ~49 kb inversion and a small ~3.5 kb inversion were found in the large single-copy regions of both plastomes, while *Circaeaster* possesses a number of other rearrangements, particularly in the Inverted Repeat. In addition, *infA* was found to be a pseudogene and *accD* was found to be absent within *Circaeaster*, whereas all *ndh* genes, except for *ndhE* and *ndhJ*, were found to be either pseudogenized (*ΨndhA*, *ΨndhB*, *ΨndhD*, *ΨndhH* and *ΨndhK*) or absent (*ndhC*, *ndhF*, *ndhI* and *ndhG*) in *Kingdonia*. Circaeasteraceae was strongly supported as sister to Lardizabalaceae in phylogenetic analyses.

Conclusion: The first plastome sequencing of Circaeasteraceae resulted in the discovery of several unusual rearrangements and the loss of *ndh* genes, and confirms the sister relationship between Circaeasteraceae and Lardizabalaceae. This research provides new insight to characterize plastome structural evolution in early-diverging eudicots and to better understand relationships within Ranunculales.

Keywords: Early-diverging eudicots, Circaeasteraceae, Plastome, Rearrangements, Gene loss, Phylogenetic analyses

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RESEARCH ARTICLE Open Access

Transcriptome profilings of two tall fescue (*Festuca arundinacea*) cultivars in response to lead (Pb) stress

Huiying Li, Tao Hu, Erick Amombo and Jinmin Fu*

Abstract

Background: Lead (Pb) is one of the most toxic heavy metal environmental pollutants. Tall fescue is an important cold season turf grass which can tolerate and accumulate substantial amount of Pb. To estimate genes related to Pb response and the molecular mechanism associated with Pb tolerance and accumulation, we analyzed the transcriptome of tall fescue in response to Pb treatment.

Results: RNA-sequencing was performed in two tall fescue cultivars, Pb tolerant Silverado and Pb sensitive AST7001. A total of 810,146 assembled unique transcripts representing 25,415 unigenes were obtained from the tall fescue leaves. Among the panel, 3,696 differentially expressed genes (DEGs) were detected between the Pb treated (1000 mg/L) and untreated samples. Gene ontology (GO) and pathway enrichment analysis demonstrated that the DEGs were mainly implicated in energy metabolism, metabolism of terpenoids and polyketides, and carbohydrate metabolism related pathways. The expression patterns of 16 randomly selected genes were in consistent with that from the Solexa analysis using quantitative reverse-transcription PCR. In addition, compared to the common transcriptional response to Pb stress in both cultivars, the regulation of numerous genes including those involved in zeatin biosynthesis, limonene and pinene degradation, phagosome was exclusive to one cultivar.

Conclusions: The tall fescue assembled transcriptome provided substantial molecular resources for further genomics analysis of turfgrass in response to heavy metal stress. The significant expression difference of specific unigenes may account for Pb tolerance or accumulation in two different tall fescue cultivars. This study provided new insights for the investigation of the molecular basis of Pb tolerance and accumulation in tall fescue as well as other related turf grass species.

Keywords: Tall fescue, Pb stress, RNA sequencing, Terpenoid and polyketide metabolism, Transport and catabolism

Background

Lead (Pb) pollution is a severe global challenge due to it harmful effects on the environment, plant, and even human beings. The Pb pollution sources can be derived from various anthropogenic activities, such as mining and smelting activities, exhaust fumes of automobiles, industrial emissions, and applications of Pb-containing chemical materials including paints, gasoline, explosives, agrochemical and fertilizers [1]. As one of the most toxic non-essential elements, Pb is readily absorbed by plant roots, then eventually transferred and accumulated in different tissues. Excess Pb in plants often results in unprecedented adverse effects, including seed germination inhibition, stunted growth of seedlings, chlorosis, and a remarkable decrease in crop productivity [2]. In addition, Pb can stimulate the generation of free radicals and reactive oxygen species, hence leading to oxidative stress and DNA damage in plant [3].

Recently, phytoremediation has been considered to be a promising technique to clean up the heavy metals and limit their bioactivities. This would be achieved by exploiting the super capacity of specialized plants to tolerate, translocate, and eventually accumulate inordinate amount of heavy metal elements in harvestable parts [4]. Currently, more than 450 plant species have been identified as heavy metal accumulators. However, Pb

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Low genetic diversity and functional constraint of miRNA genes participating pollen–pistil interaction in rice

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Abstract

Key message **In this study, we sequenced and analyzed the expression and evolution of rice miRNA genesparticipating pollen-pistil interaction that is crucial to rice yield.**

Abstract Pollen–pistil interaction is an essential reproductive process for all flowering plants. While microRNAs (miRNAs) are important noncoding small RNAs that regulate mRNA levels in eukaryotic cells, there is little knowledge about which miRNAs involved in the early stages of pollen–pistil interaction in rice and how they evolve under this conserved process. In this study, we sequenced the small RNAs in rice from unpollinated pistil (R0), pistil from 5 min and 15 min after pollination, respectively, to identify known and novel miRNAs that are involved in this process. By comparing the corresponding mRNA-seq dataset, we identified a group of miRNAs with strong negative expression pattern with their target genes. Further investigation of all miRNA loci (*MIRNAs*) across 1083 public rice accessions revealed significantly reduced genetic diversity in *MIRNAs* with strong negative expression of their targets when comparing to those with little or no impact on targets during pollen–pistil interaction. Annotation of targets suggested that those *MIRNAs* with strong impact on targets were pronounced in cell wall related processes such as xylan metabolism. Additionally, plant conserved miRNAs, such as those with functions in gibberellic acid, auxin and nitrate signaling, were also with strong negative expression of their targets. Overall, our analyses identified key miRNAs participating pollen–pistil interaction and their evolutionary patterns in rice, which can facilitate the understanding of molecular mechanisms associated with seed setting.

Keywords MicroRNA · *Oryza sativa* · Evolution · Pistil–pollination interaction

Introduction

In plants and animals, the level of messenger RNA (mRNA) in the cell is determined by gene transcription and degradation. microRNAs (miRNAs) are a group of endogenous noncoding small RNAs that regulate mRNA levels in trans (Carrington and Ambros 2003). The 20–24 nt plant miRNAs are processed from stem-loop structures of longer primary transcripts by a Dicer-like (DCL) enzyme (Papp et al. 2003). Their major function is to guide the RNA-induced silencing complex (RISC) to induce target mRNA cleavage or translation inhibition by complementary base pairing to the target mRNA (Llave et al. 2002; Carrington and Ambros 2003). Through this gene repression, miRNAs are found to play diverse roles in plants, including development, signaling, reproduction, biotic and abiotic stress responses (Achard et al. 2004; Zhang et al. 2006; Allen et al. 2007; Bartel 2007; Reyes and Chua 2007; Chen 2009).

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First Report of Alternaria alternata Causing Postharvest Rot of Kiwifruit in China

Previous Article | Next Article
June 2017, Volume 101, Number 6
Page 1046
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DISEASE NOTES

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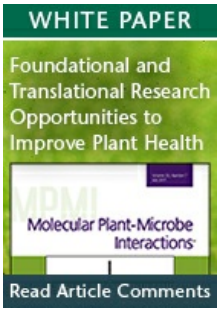

ABSTRACT

Postharvest rot diseases of kiwifruit (*Actinidia* sp.) severely damage fruits during storage, transportation, and marketing. *Botryosphaeria dothidea*, *Diaporthe ambigua*, and *D. lithocarpus* have been reported to be associated with the disease in China (†). In October to December 2015, fruits of four *Actinidia chinensis* cultivars (Jinyan, Hongyang, Jinkui, and Qinmei) were collected from nine main cultivating provinces of China (Sichuan, Shaanxi, Hubei, Fujian, Guizhou, Anhui, Hunan, Henan, and Zhejiang). During the postharvest storage period, 105 rotting kiwifruits

First Report of Diaporthe actinidiae Causing Stem-End Rot of Kiwifruit During Post-Harvest in China

Previous Article | Next Article
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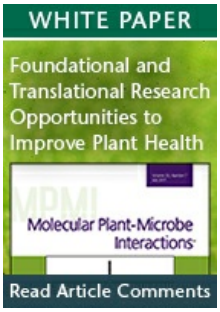

ABSTRACT

Several species of *Diaporthe* (anamorph: *Phomopsis*) have been described causing rots in kiwifruits (†; †). Between 15 and 24 October 2015, ripe kiwifruits (*n* = 70, 9% soluble solids) were collected from commercial vineyards of *Actinidia deliciosa* 'Miliang No 1' and *A. chinensis* 'Jinyan' in Chenzhou (25°32′N, Hunan Province) and Wuhan (30°32′N, Hubei Province), respectively. All fruits were stored in controlled atmosphere rooms (2% O_2, 5% CO_2) for 4 months at 1°C. After storage, fruits were incubated at 18°C for 2 weeks. By the end of the postharvest storage period, 42

First Report of Anthracnose Caused by Colletotrichum gloeosporioides on Kiwifruit (Actinidia chinensis) in China

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Previous Article | Next Article
December 2017, Volume 101, Number 12
Page 2151
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DISEASE NOTES

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- Citation

China is the leading kiwifruit producer in the world (Belrose Inc. 2016). In late September 2016, typical anthracnose symptoms were observed on young and mature leaves of kiwifruit cv. Hongyang in Taishun County, Wenzhou City, Zhejiang Province, and Liupanshui City, Guizhou Province, China. The disease symptoms began as irregularly shaped lesions, then developed into brown or black spots on infected leaves. By the later stages, the centers of the lesions had turned gray and the edges were dark brown. Twenty trees from 10 kiwifruit orchards in each city were investigated, and ~20% of trees exhibited typical anthracnose symptoms. To isolate the pathogen, 5-mm^2 pieces of symptomatic tissue of 10 infected leaves were surface-disinfected for 90 s in 1% sodium hypochlorite and then in 75% ethanol for 30 s, rinsed three times in sterile water, plated on acidified potato dextrose agar (PDA), and incubated at 25°C with a 12/12-h light/dark cycle. Three hyphal tips from the growing edge of each colony cultured for 3 days at 25°C were transferred to PDA to obtain pure cultures. After 5 days at 25°C, morphologically identical isolates were recovered on PDA. Initially, the colonies produced white mycelia, which turned gray after 5 days. The colonies produced abundant conidia that were hyaline, one celled, straight, cylindrical, and the average size of conidia was 10.45 to 15.78 × 3.56 to 5.89 μm. These morphological characteristics were generally consistent with those reported for *Colletotrichum gloeosporioides* (Cannon et al. 2012). Identification was confirmed by sequencing five typical isolates (CG 1 to 5). The internal transcribed spacer (ITS), β-tubulin (*TUB2*), and glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) gene regions of five isolates were amplified by using ITS4/ITS5, Bt2A/Bt2B, and gpd1/gpd2 primers, respectively (Damm et al. 2009; Weir et al. 2012), sequenced, and GenBank accession numbers were obtained. A BLAST search revealed that all sequences (accession nos.

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Genome-wide identification of heat stress-responsive small RNAs in tall fescue (*Festuca arundinacea*) by high-throughput sequencing

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ABSTRACT

MicroRNAs (miRNAs) play vital roles in the adaptive response of plants to various abiotic and biotic stresses. Tall fescue (*Festuca arundinacea* Schreb.) is a major cool-season forage and turf grass species which is severely influenced by heat stress. To unravel possible heat stress-responsive miRNAs, high-throughput sequencing was employed for heat-tolerant PI578718 and heat-sensitive PI234881 genotypes growing in presence and absence of heat stress (40 °C for 36 h). By searching against the miRBase database, among 1421 reference monocotyledon miRNAs, more than 850 were identified in all samples. Among these miRNAs, 1.46% and 2.29% were differentially expressed in PI234881 and PI578718 under heat stress, respectively, and most of them were down-regulated. In addition, a total of 170 novel miRNAs belonging to 145 miRNA families were identified. Furthermore, putative targets of differentially expressed miRNAs were predicted. The regulation of selected miRNAs by heat stress was revalidated through quantitative reverse transcription PCR (qRT-PCR) analysis. Most of these miRNAs shared similar expression patterns; however, some showed distinct expression patterns under heat stress, with their putative targets displaying different transcription levels. This is the first genome-wide miRNA identification in tall fescue. miRNAs specific to PI578718, or those that exhibited differential expression profiles between the two genotypes under high temperature, were probably associated with the variation in thermotolerance of tall fescue. The differentially expressed miRNAs between these two tall fescue genotypes and their putative targeted genes will provide essential information for further study on miRNAs mediating heat response and facilitate to improve turf grass breeding.

1. Introduction

MicroRNAs (miRNAs), a category of endogenous non-coding small RNAs, are vital gene regulators at post-transcriptional level which direct the cleavage of target genes or inhibit translation in organisms (Bartel, 2004). The canonical miRNAs are processed by the Dicer-like protein 1/HYPONASTIC LEAVES1 (DCL1/HYL1) complex and then transferred to the RNA-induced silencing complex (RISC) for target gene regulation, with a length of about 21 nucleotides (nt) (Kurihara et al., 2006). As a crucial component during the evolution of genetic regulation, miRNAs are highly conserved among different species (Lee et al., 2007).

It has been confirmed that plant miRNAs participate in various biological processes, such as growth, development, and signaling (Aukerman and Sakai, 2003; Chen et al., 2004; Jones-Rhoades and Bartel, 2014). In addition, recent studies have revealed that some plant miRNAs have significant regulatory effects on various stress responses (Sunkar et al., 2007; Qin et al., 2008). To date, many miRNAs have been detected and identified from diverse plants, especially in Arabidopsis (*Arabidopsis thaliana*), rice (*Oryza sativa*), and poplar (*Populus tomentosa*). For instance, the expression of miR393 is induced in Arabidopsis under cold conditions (Sunkar and Zhu, 2004). In addition, the abundance of miR393 and miR169g was increased in rice growing under drought stress (Zhao and Srivastava, 2007). Moreover, previous investigations have also elucidated that some miRNAs, including miR395, miR398, and miR399, were up-regulated in Arabidopsis exposed to differ-

Abbreviations: MiRNAs, MicroRNAs; qRT-PCR, quantitative reverse transcription PCR; DCL1/HYL1, Dicer-like protein 1/HYPONASTIC LEAVES1; RISC, RNA-induced silencing complex; nt, nucleotide; kb, kilobase; NT, normal temperature; HT, high temperature; BLAST, Basic Local Alignment Search Tool; Rfam, RNA family database; MFEI, minimal folding free energy index; DE, differentially expressed; KEGG, Kyoto encyclopedia of genes and genomes; RT, reverse transcription; sRNAs, small RNAs; snoRNAs, small nucleolar RNAs; snRNAs, small nuclear RNAs; GO, Gene ontology; ALPL, alkaline phosphatase family protein; CYP450, cytochrome P450.

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ORIGINAL ARTICLE

Proteomics analysis identified a DRT protein involved in arsenic resistance in *Populus*

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Abstract

Key message **A DRT protein was identified and proved to be involved in the poplar arsenic resistance through comparative proteomics analysis between arsenic sensitive and resistant cultivars.**

Abstract Arsenic pollution in soil has been a serious problem all over the world. It is very important to dissect plants arsenic stress-response mechanisms in phytoremediation. In this study, arsenate-tolerant *Populus deltoides* cv. 'zhonglin 2025' and arsenate-sensitive *Populus* × *euramericana cv.* 'I-45/51' were screened from 10 poplar varieties. Systematic comparisons between these two cultivars demonstrated that 'zhonglin 2025' exhibited slighter morphological and structural injury, lower ROS and MDA accumulation, and higher photosynthesis and ROS scavenging ability under arsenate stress, compared with 'I-45/51'. Through comparative proteomics analysis, we detected that most of the identified arsenate-responsive proteins were stress and defense related. Among these proteins, PdDRT102 was found to be only highly induced in 'zhonglin 2025' under arsenate stress. Heterologous overexpression of *PdDRT102* in *Arabidopsis* conferred to enhanced tolerance to arsenate and sodium chloride. *PdDRT102* localizes to the plasma membrane and the nucleus in *Arabidopsis*. Interestingly, the remarkably increased fluorescence protein signals in the nucleus were found during arsenate stress. Together, these results not only provided an overall understanding on poplar response to arsenate stress, but also revealed that DRT102 protein might involve in protecting poplar against this stress

Keywords Poplar · Proteomics · *PdDRT102* · Arsenate stress

Introduction

Heavy metal pollution (e.g., arsenic, cadmium, copper, zinc and lead) has been an increasing serious problem, which can cause not only substantial reduction in crop yield, but also permanent and irreversible health damage to human being (Ahsan et al. 2007; Garg and Singla 2011; Wang et al. 2011a, b). Arsenic, one of toxic heavy metals, is a non-essential element and group I carcinogen. Its continuous accumulation in soil and water has been occurring due to anthropogenic activities and natural processes (Panda et al. 2010; Akter et al. 2005). Arsenic-rich irrigation water further aggravated arsenic contamination in soil, and then excessive arsenic uptake by crop plants exerted adverse effects on crop productivity and food safety (Garg and Singla 2011; Akter et al. 2005; Zhao et al. 2009; Mandal and Suzuki 2002). Recently, millions of people worldwide have been at risk of arsenic poisoning,

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molecules

MDPI

Article

Comparative Analysis of Saponins from Different *Phytolaccaceae* Species and Their Antiproliferative Activities

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Abstract: The quality and the efficacy of herbal medicine are of great concern especially with the increase in their global use. Medicinal plants of different species or collected from different geographical regions have shown variations in both their contents and pharmacological activities due to the differences in the environmental conditions of the collected sites. In this study, roots of *Phytolacca acinosa* found in different provinces in south China (Sichuan and Shandong) and a species of *Phytolacca americana* were investigated. To ensure a maximum yield of the major compounds, the extraction method and conditions were optimized. The preeminent method of extraction in this analysis was determined to be the ultrasound-assisted method with specific conditions as follows: ethanol-H_2O (1:1, *v*/*v*), with a solvent: sample ratio of 1:8, and extraction was performed 3 times, each for 30 min. Under these conditions, samples from the different regions varied both in quantity and quality via the LC-MS analysis. A total of 60 triterpenoid saponins were detected within the three samples, among which 22 were identified as common in the three samples. The amounts of these common triterpenoid saponin identified varied across the samples. Moreover, the analysis led to the detection of some novel compounds that have not yet been reported in this family, while other compounds differ in their fragmentation pathways compared to previous literature. To further divulge the correlations between the bioactivities in these three samples and the quantity and quality of their bioactive components, a cytotoxic analysis was thus carried out with two cancer cell lines, and SGC-7901 and Hep G2, which evidently showed remarkable differences in their anti-proliferative activities with respect to the IC_{50} value. Samples of *P. acinosa* from Sichuan showed higher values in both cell lines (27.20 ± 1.60 and 25.59 ± 1.63 μg/mL) compared to those of Shandong and *P. americana*. For the first time, analysis and comparison of both interspecies and of different species in this family were carried out. This study will significantly contribute to the quality insurance of herbal medicine, especially in the Phytolaccaceae family.

Keywords: *Phytolacca acinosa*; *Phytolacca americana*; triterpenoid saponin; ultrasound-assisted extraction; LC-MS; antiproliferative activities

1. Introduction

Phytolaccaceae species are perennial herbs that are distributed globally with different species native to a particular place. These plant species have been used both traditionally and in modern times as herbal medicines [1]. The chemical constituents of the species in this family have shown a number of bioactive activities including antibacterial [2,3], antifungal [4–9], antimalarial [10,11], molluscicidal

PLOS ONE

RESEARCH ARTICLE

An efficient method for transgenic callus induction from *Vitis amurensis* petiole

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Competing interests: The authors have declared that no competing interests exist.

Abstract

Transformation is the main platform for genetic improvement and gene function studies in plants. However, the established somatic embryo transformation system for grapevines is time-consuming and has low efficiency, which limits its utilization in functional genomics research. *Vitis amurensis* is a wild *Vitis* species with remarkable cold tolerance. The lack of an efficient genetic transformation system for it has significantly hindered the functional identification of cold stress related genes in the species. Herein, an efficient method was established to produce transformed calli of *V. amurensis*. Segments of petioles from micro-propagated plantlets of *V. amurensis* exhibited better capacity to differentiate calli than leaf-discs and stem segments, and thus was chosen as target tissue for *Agrobacterium*-mediated transformation. Both *neomycin phosphotransferase II* (*NPTII*) and *enhanced green fluorescent protein* (*eGFP*) genes were used for simultaneous selection of transgenic calli based on kanamycin resistance and eGFP fluorescence. Several parameters affecting the transformation efficiency were optimized including the concentration of kanamycin, *Agrobacterium* stains, bacterial densities, infection treatments and co-cultivation time. The transgenic callus lines were verified by checking the integration of *NPTII* gene into calli genomes, the expression of *eGFP* gene and the fluorescence of eGFP. Up to 20% of the petiole segments produced transformed calli after 2 months of cultivation. This efficient transformation system will facilitate the functional analysis of agronomic characteristics and related genes not only in *V. amurensis* but also in other grapevine species.

Introduction

Genetic transformation systems are one of the most important platforms that are used for genetic improvement and also for functional analyses of genes in plants. As one of the most important fruit crops cultivated worldwide, the regeneration and genetic transformation of grapevines has been widely studied. Somatic embryogenesis has been reported in several *Vitis*

PLOS ONE

RESEARCH ARTICLE

Comparative transcript profiling explores differentially expressed genes associated with sexual phenotype in kiwifruit

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Competing interests: The authors have declared that no competing interests exist.

Abstract

Background

Kiwifruit is a perennial, deciduous and functionally dioecious plant. However, very little is known about the whole-genome molecular mechanisms contributing to distinct sexual phenotypes. To gain a global view of genes differentially expressed between male and female flowers, we analyzed genome-wide gene expression profiles in the flowers of male and female plants using high-throughput RNA sequencing.

Results

A total of 53.5 million reads were generated. Based on the alignments of unigenes to kiwifruit genome predicted genes, a total of 39,040 unique genes with a mean length of 970 bp were identified. There were 2,503 UniGenes differentially expressed between female and male flowers, with 1,793 up-regulated and 710 down-regulated in the female flowers. Moreover, the gene expression pattern of 17 out of 19 unigenes differentially expressed between male and female flowers revealed by RNA-Seq was confirmed by real-time quantitative PCR (qRT-PCR).

Conclusions

Here, we obtained a large number of EST sequences from female and male flowers of kiwifruit. This comparative transcriptome analysis provides an invaluable resource for gene expression, genomics, and functional genomic studies in *A. chinensis* and its related species. This study also represents a first step toward the investigation of genes involved in kiwifruit sex determination.

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Research article

Effects of cadmium-resistant fungi *Aspergillus aculeatus* on metabolic profiles of bermudagrass [*Cynodondactylon* (L.)Pers.] under Cd stress

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ABSTRACT

Plants' tolerance to heavy metal stress may be induced by the exploitation of microbes. The objectives of this study were to investigate the effect of cadmium (Cd)-resistant fungus, *Aspergillus aculeatus*, on tolerance to Cd and alteration of metabolites in bermudagrass under Cd stress, and identify the predominant metabolites associated with Cd tolerance. Two genotypes of bermudagrass with contrasting Cd tolerance (Cd-sensitive 'WB92' and Cd-tolerant 'WB242') were exposed to 0, 50, 150 and 250 mg kg^{-1} Cd for 21 days. Physiological responses of bermudagrass to Cd stress were evaluated based on the relative growth rate (RGR) and normalized relative transpiration rate (NRT). Plants inoculated with *A. aculeatus* exhibited higher RGR and NRT under Cd stress than those of non-inoculated plants, regardless of genotypes. A total of 32 Cd-responsive metabolites in leaves and 21 in roots were identified in the two genotypes, including organic acids, amino acids, sugars, and fatty acids and others. Interestingly, under Cd stress, the leaves of inoculated 'WB92' accumulated less citric acid, aspartic acid, glutamic acid, sucrose, galactose, but more sorbose and glucose, while inoculated 'WB242' leaves had less citric acid, malic acid, sucrose, sorbose, but more fructose and glucose, compared to non-inoculated plants. In 'WB92' roots, the *A. aculeatus* reduced mannose content, but increased trehalose and citric acid content, while in 'WB242', it decreased sucrose, but enhanced citric acid content, compared to Cd regime. The results of this study suggest that *A. aculeatus* may induce accumulation of different metabolites associated with Cd tolerance in bermudagrass.

1. Introduction

Heavy metals such as Cd, copper, lead and zinc enter the environment via disposal of acidified soils or urban sewage sludge, utilization of agricultural phosphate fertilizers and industrial activities, which poses considerable threat to agriculture and forestry (Barceló and Poschenrieder, 1990; Khan, 2005). Among the mentioned heavy metal pollutants, Cd, one of the most dangerous and toxic environmental pollutant, is an important abiotic stress affecting the growth of plants (Xu et al., 2012).

It has been postulated that higher plants are more sensitive to Cd stress than microorganisms. Soil Cd phytotoxicity has been associated with exposure to 1 mg kg^{-1} total Cd and higher total Cd in soils might impose phytotoxic effects on higher plants. Therefore, the presence of Cd, even at minimum quantities causes phytotoxicity to higher plants (Peterson and Alloway, 1979; Wagner, 1993; Yan et al., 2016). For microorganisms, the vast range of Cd concentration, from 20 to over 1000 mg kg^{-1}, in contaminated areas suggests a corresponding range of adaptability and sensitivity of microorganisms to Cd (Babich and Stotzky, 1977). Although Cd is a nonessential trace element in the process of plant growth; it can displace essential elements thus inhibiting plant growth (Ahsan et al., 2012). Previous research has demonstrated that Cd can restrain growth and transpiration of plants, inhibit chlorophyll synthesis and impair photosynthesis (Xie et al., 2014a, 2014b). In addition, Cd toxicity can also trigger a series of plant

Abbreviations: IAA, indole-3-acetic acid; Cd, cadmium; F, *Aspergillus aculeatus*; GC-MS, gas chromatography-mass spectrometry; GSH, glutathione; RGR, relative growth rate; ROS, reactive oxygen species; HCA, hierarchical clustering analysis; H_2O_2, hydrogen peroxide; NRT, normalized relative transpiration; OH^-, hydroxyl radical; O_{2-}, superoxide radical; PCA, principal component analysis; PGRP, plant growth-promoting rhizobacteria.

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ORIGINAL PAPER

Carbonylated protein changes between active germinated embryos and quiescent embryos give insights into rice seed germination regulation

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Abstract Rice seed germination is the determining physiological event during establishment of a new plant. Although numerous researches have focused on this complicated process, studies that disclose the carbonylated protein differences between active and quiescent rice embryos related with seed germination remain deficient. Here, protein carbonylation in rice seed embryo has been analyzed by two-dimensional electrophoresis (2-DE), anti-2,4-dinitrophenyl (DNP) immunoassay, and matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) methods. As expected, varieties of carbonylated proteins were observed to increase along with rice seed germination. Certain proteins like catalase, IAA-amino acid hydrolase, cell structural proteins, and 26S protease regulatory subunit were specifically carbonylated in 48 h embryos. We speculate that ROS directly participate in cell wall loosening, cell expansion, and radicle elongation, which are facilitated by the carbonylation damage of antioxidant enzyme catalase upon imbibition. Carbonylation degradation of IAA conjugates hydrolase and cell structural proteins were necessary for hormone regulation and materials providing in seedling establishment. We also provided evidence that Dnak-type molecular chaperone hsp70, enzymes involved in glycolysis pathway, and actins were always carbonylated in 0 and 48 h embryos. Of note, glycolytic enzymes were the most prominent carbonylated proteins. Furthermore, embryo specific cupin family proteins were intensively carbonylated in 0 h embryos thus helping in reserves mobilization to facilitate germination. These results indicate that protein carbonylation in seed embryo proteins do not occur randomly, and ROS directly or indirectly participate in rice seed dormancy breakage and seedling establishment.

Keywords 2,4-Dinitrophenylhydrazine · Embryo · Protein carbonylation · Rice · Seed germination

Abbreviations

ACN	Acetonitrile
BSA	Bovine serum albumin
DNPH	2,4-Dinitrophenylhydrazine
DTT	Dithiothreitol
IEF	Isoelectric-focusing
LC-MS/MS	Liquid chromatography tandem mass spectrometry
MALDI-TOF MS	Matrix-assisted laser desorption/ionization time of flight mass spectrometry

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The *Arabidopsis* endoplasmic reticulum associated degradation pathways are involved in the regulation of heat stress response

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ABSTRACTS

The Cytosolic Protein Response (CPR) in the cytosol and the Unfolded Protein Response (UPR) and ER-associated degradation (ERAD) in the endoplasmic reticulum are major pathways of the cellular proteostasis network. However, despite years of effort, how these protein quality control systems coordinated *in vivo* remains largely unknown, particularly in plants. In this study, the roles of two evolutionarily conserved ERAD pathways (DOA10 and HRD1) in heat stress response were investigated through reverse genetic approaches in *Arabidopsis*. Phenotypic analysis of the mutants showed that the two ERAD pathways additively play negative roles in heat tolerance, which was demonstrated by higher survival rate and lower electrolyte leakage in the loss of function mutants compared to the wild type plants. Importantly, gene expression analysis revealed that the mutant plants showed elevated transcriptional regulation of several downstream genes, including those encoding CPR and UPR marker genes, under both basal and heat stress conditions. Finally, multiple components of ERAD genes exhibited rapid response to increasing temperature. Taken together, our data not only unravels key insights into the crosstalk between different protein quality control processes, but also provides candidate genes to genetically improve plant heat tolerance in the future.

1. Introduction

Most proteins must fold into unique three-dimensional structures to perform their biological functions, yet protein folding is a fundamentally error-prone process. It was estimated that ~30% of newly synthesized proteins in mammalian cells are inappropriately folded [1,2]. The structural fragility of proteins makes cells vulnerable to damage from various environmental stressors. In organisms from bacteria to humans, exposure to heat is a particularly important form of stress. Excess heat only a few degrees above optimal physiological temperature causes misfolding and aggregation of a broad spectrum of proteins, rapidly endangering cell viability [3]. Cells have therefore evolved powerful, compartment-specific but coordinated protein quality control pathways called Heat Stress Responses (HSR) to counteract protein damage in order to maintain protein homeostasis [4]. Hence, the Unfolded Protein Response (UPR), which is induced by the accumulation of misfolded proteins in the endoplasmic reticulum (ER), recruits specific genes and pathways to regulate protein repair in that compartment, and a parallel process, the Cytosolic Protein Response (CPR), operates in the cytosol. This causes the induction of molecular chaperones that, among other effects, prevent protein aggregation and target misfolded proteins for degradation [5].

In plants, the UPR regulators show clear evolutionary conservation of the IRE1 and the ATF6 pathways [6]. *Arabidopsis* contains two functional homologs of *IRE1* (*IRE1a* and *IRE1b*). Both IRE1a and IRE1b endoribonuclease activities target *bZIP60* mRNA, a homolog of mammalian *XBP-1*. Upon heat stress, IRE1 splices bZIP60 mRNA in the cytosol, causing a frameshift leading to the synthesis of a tissue factor without a transmembrane domain, but having acquired a nuclear targeting signal. The spliced form of bZIP60 is imported into the nucleus to activate UPR target genes [7]. The mammalian *ATF6* has two homologs in *Arabidopsis*, *bZIP17* and *bZIP28*. Under heat stress conditions, both transcription factors

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Construction of a SNP-based genetic linkage map for kiwifruit using next-generation restriction-site-associated DNA sequencing (RADseq)

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Abstract Kiwifruit is a perennial horticultural crop species of the Actinidiaceae family and has high nutritional value. For a species with a long generation time, traditional breeding and genetic improvement is predicted to take more than 20 years to obtain superior cultivars. Thus, marker-assisted selection (MAS) should be used to accelerate the breeding process. Development of a genetic linkage map and molecular markers are prerequisites for MAS of crop species. Here, we report a genome-wide SNP-based genetic map of kiwifruit by analysing next-generation restriction-site-associated DNA sequencing (RADseq) reads. To construct a genetic linkage map, a 102 F1 line mapping population of *Actinidia chinensis* (2n = 58) was derived by combining parents that had contrasting phenotypic traits. The maternal map contained 4112 SNP loci and spanned a distance of 3821 cM, with an average adjacent-marker interval length of 0.929 cM. The map length of the 29 linkage groups ranged from 78.3 to 169.9 cM, with an average length of 131.8 cM. High levels of collinearity between the 29 genetic maps with the kiwifruit reference genome were found. The genetic map developed in this study can serve as an important platform to improve kiwifruit research, including anchoring unmapped scaffolds of the kiwifruit genome sequence and mapping QTLs (quantitative trait loci) that control economically important traits.

Keywords Kiwifruit · Genetic mapping · Molecular marker · RADseq

Introduction

As a successful example of plant domestication in the twentieth century, kiwifruit (*Actinidia chinensis*) is a popular horticultural crop with a delicious flavour and high nutritional value, with an annual production of 1.8 million tons (Belrose, Inc., 2015). The *Actinidia* genus is the second largest genus after *Saurauia* Willd. in the Actinidiaceae and comprises 54 species and 21 botanical varieties (Li et al. 2007). It is widely distributed in Asia, with a main centre of diversity in southwestern China. *Actinidia chinensis* possesses economic importance, as it is the species from which most commercial kiwifruit varieties (e.g. 'Hayward', 'Hort16A' and 'Jintao') have been developed (Ferguson and Huang 2007). There is increasing interest in developing new varieties with disease resistance and superior commercial traits through intraspecific or interspecific hybridization. For most fruit trees, traditional breeding is time-

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Assessment of calcium and zinc accumulation in cultivated and wild apples

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Abstract

BACKGROUND: Apple is one of the staple fruits worldwide which are a good source of mineral nutrients. However, little is known about genetic variation for mineral nutrition in apple germplasm. In this study, the calcium and zinc contents in mature fruits of 378 apple cultivars and 39 wild relatives were assessed. Mineral concentrations were quantified using flame atomic absorption spectroscopy (FAAS).

RESULTS: Both calcium and zinc accumulation showed great variation among accessions tested. Overall, wild fruits were significantly richer in zinc than cultivated fruits, while the average concentration of calcium was similar between cultivated and wild fruits. The difference in zinc concentration between wild and cultivated fruits may be an indirect result of artificial selection on fruit characteristics during apple domestication. Moreover, calcium concentration in fruit showed a decreasing trend throughout fruit development of apple, while zinc concentration in fruit displayed a complex variation pattern in the late stages of fruit development.

CONCLUSION: The finding of a wild genetic variation for fruit calcium and zinc accumulation in apple germplasm could be helpful for future research on genetic dissection and improvement of calcium and zinc accumulation in apple fruit.

Supporting information may be found in the online version of this article.

Keywords: *Malus*; mineral nutrition; fruit characteristics; FAAS

INTRODUCTION

Minerals are inorganic elements which cannot be created by living things. All minerals in the human body come directly from the diet. Based on the amount needed daily by the human body, minerals can be classified into two categories, namely macrominerals and trace minerals. Macrominerals are needed in relatively large amounts in the diet (>250 mg daily), whereas trace minerals are needed in much smaller quantities (<20 mg daily).

Minerals are believed essential for human health. For example, calcium (Ca) is the most plentiful mineral found in the human body, accounting for 1–2% of an adult human's body weight.[1] Calcium plays a critical role in maintaining structural integrity of the skeleton[2] and is also important for controlling muscle and nerve function and regulating acid/alkaline balance in the blood.[3,4] Zinc (Zn) is an essential trace mineral in human nutrition, and its importance to human health has received much more attention in recent years.[5,6] Many enzymes that are essential for metabolism use zinc as a cofactor in their catalysis. Therefore zinc is related to a variety of bodily functions, such as the immune system, wound healing, growth and development, learning and memory, and sperm production.[7,8]

Fruit is a good source of mineral nutrients. For example, most fresh fruits contain zinc, with avocado, raspberry, apricot, blackberry and pomegranate providing especially good sources of the mineral (http://www.fruitvs.com/). In addition to the nutritional value related to human health, minerals also have an effect on fruit development and quality, and calcium has received the most attention in this field. Calcium strengthens cell walls by chelating pectic substances.[9] Thus calcium accumulation can increase fruit firmness and enhance the resistance of fruit to fungal infection through maintaining or stabilizing cell wall integrity.[10] Since calcium has a low mobility in the phloem, calcium transport to fruit is exclusively via the xylem.[11,12] During the period of rapid fruit growth or low fruit transpiration, the supply of calcium to fruit is limited, which could lead to a localized calcium deficiency in the fruit.[13–15] This calcium deficiency can cause the breakdown of cell wall components and membranes, resulting in disorders such as blossom end rot in tomato and bitter pit in apple.[16,17] Therefore calcium spray treatment is a routine horticultural practice which can improve fruit cell integrity and disease resistance to prolong the storage life of horticultural products.[18,19] Moreover,

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RESEARCH ARTICLE Open Access

Comparative study on alkaloids and their anti-proliferative activities from three *Zanthoxylum* species

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Abstract

Background: Alkaloids have been considered as the most promising bioactive ingredients in plant species from the genus *Zanthoxylum*. This study reports on the compositions and contents of the *Zanthoxylum* alkaloids (ZAs) from three *Zanthoxylum* species, and their potential anti-proliferation activities.

Methods: An HPLC-UV/ESI-MS/MS method was established and employed to analyze the alkaloids in different *Zanthoxylum* extracts. The common and unique peaks and their relative contents were summarized and compared to evaluate the similarity and dissimilarity of the three *Zanthoxylum* species. Meanwhile, inhibitory activity tests to four carcinoma cell lines, i.e., stomach tumor cells (SGC-7901), cervical tumor cells (Hela), colon tumor cells (HT-29) and Hepatic tumor cells (Hep G2), were carried out in vitro to evaluate the bioactivities of the ZAs.

Results: Seventy peaks were detected in the crude total alkaloid samples, and 58 of them were identified. As a result, 13 common peaks were found in the extracts of all the three *Zanthoxylum* species, while some unique peaks were also observed in specific species, with 17 peaks in *Z. simulans*, 15 peaks in *Z. ailanthoides* and 11 peaks in *Z. chalybeum*, respectively. The comparison of the composition and relative contents indicated that alkaloids of benzophenanthridine type commonly present in all the three *Zanthoxylum* species with high relative contents among the others, which are 60.52% in *Z. ailanthoides*, 30.52% in *Z. simulans* and 13.84% in *Z. chalybeum*, respectively. In terms of activity test, Most of the crude alkaloids extracts showed remarkable inhibitory activities against various tumor cells, and the inhibitory rates ranged from 60.71 to 93. 63% at a concentration of 200 μg/mL. However, SGC-7901 cells seemed to be more sensitive to the ZAs than the other three cancer cells.

Conclusion: The alkaloid profiles detected in this work revealed significant differences in both structures and contents among *Zanthoxylum* species. The inhibitory rates for different cancer cells in this study indicated that the potential anti-cancer activity should be attributed to quaternary alkaloids in these three species, which will provide great guidance for further exploring this traditional medicinal resource as new healthcare products.

Keywords: *Zanthoxylum* alkaloids, LC-UV-ESI-MS/MS, Anti-proliferative activity, Fingerprinting analysis

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Research Article

Phylogenetic study of the tribe Potentilleae (Rosaceae), with further insight into the disintegration of *Sibbaldia*

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Abstract Potentilleae, one of 10 tribes of the Rosaceae, are mainly distributed in alpine regions of the Northern Hemisphere. The taxonomy of Potentilleae has been challenging due to extensive hybridization, polyploidization, and/or apomixis characterizing several genera of Potentilleae, such as *Alchemilla*, *Argentina*, and *Potentilla*. To help clarify relationships within Potentilleae, a phylogenetic analysis of the tribe with an emphasis on the polyphyletic genus *Sibbaldia* was carried out using nuclear ribosomal internal and external transcribed spacer regions and the plastid *trnL-F* and *trnS-G* spacer regions. In agreement with previous phylogenetic analyses, three major clades were identified in the present study: the subtribe Fragariinae, the genera *Argentina*, and *Potentilla*. The 15 species of *Sibbaldia* were recovered in five distinct clades: three in subtribe Fragariinae, one in *Argentina*, and the last in *Potentilla*. The recently established genus *Chamaecallis*, comprising a single species formerly treated in *Sibbaldia* that has intermediate floral character states with respect to Fragariinae and *Potentilla*, was recovered as sister to *Drymocallis*. Morphological character state reconstruction indicated that a reduction in the number of stamens ($\leq$10) is a derived character state that has arisen multiple times in Potentilleae. Molecular dating analyses agreed with previously published estimates and suggested that crown group Potentilleae arose in the Middle to Late Eocene, with most generic-level divergences occurring in the Oligocene and Miocene.

Key words: *Argentina*, *Chamaecallis*, character evolution, molecular dating, polyphyly, *Potentilla*, Potentilleae, *Sibbaldia*.

1 Introduction

Molecular phylogenetic studies (Potter et al., 2002, 2007; Eriksson et al., 2003) have improved our understanding of the backbone relationships of Rosaceae, which in many cases differ distinctly from traditional taxonomic groupings based on morphology (e.g., Hutchinson, 1964). Current phylogenetic-based classifications recognize 10 tribes of Rosaceae under three subfamilies (Potter et al., 2007). Potentilleae Sweet is one of the 10 tribes of Rosaceae and its taxonomy has changed dramatically with respect to the intratribal classification over its history (Table 1; also see Eriksson et al., 1998), with most changes concerning the taxonomic status of several small genera, such as *Argentina* Hill, *Comarum* L., *Dasiphora* Raf. (*Pentaphylloides* Duhamel), *Drymocallis* Fourr. ex Rydb., *Duchesnea* Smith, *Horkelia* Chamisso, *Ivesia* Torr., and *Sibbaldiopsis* Rydb.

The monophyly of Potentilleae in the modern sense was first established by Eriksson et al. (2003) using DNA sequences from nuclear internal transcribed spacer (ITS) and plastid *trnL-F* regions. The stem-based definition of Potentilleae corresponded almost exactly to the tribe Potentilleae sensu Hutchinson (1964; Table 1). More recent systematic studies using molecular data (Potter et al., 2007; Dobeš & Paule, 2010; Töpel et al., 2011) have supported the monophyly of Potentilleae as defined by Eriksson et al. (2003) and have recovered three main clades in Potentilleae, corresponding to Fragariinae Torrey & Gray, *Potentilla* L., and *Argentina*, although relationships among these three clades have been conflicting (Töpel et al., 2011; Eriksson et al., 2015; Feng et al., 2015). The four subtribes proposed by Soják (1989, 2008)—Potentillinae (*Potentilla*, *Horkelia*, *Ivesia*, *Stellariopsis* Rydb., *Tylosperma* Botsch., *Piletophyllum* (Soják) Soják), Fragariinae (*Comarum*, *Farinopsis* Chrtek & Soják, *Dasiphora*, *Drymocallis*, *Sibbaldia* L., *Sibbaldiopsis*, *Fragaria* L., *Sibbaldianthe* Juz., *Potaninia* Maxim., *Schistophyllidium* (Juz. ex Fed.) Ikonn.), Chamaerhodotinae (*Chamaerhodos* Bunge.), and Alchemillinae (*Alchemilla* L., *Aphanes* L., *Lachemilla*

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Analysis and Differentiation of the Volatile Compounds in Red and White Wines Using Desiccated Headspace Gas Chromatography-Mass Spectrometry Coupled with Chemometrics

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Abstract A well-tailored method for the fingerprinting analysis of volatile compounds in wines has been developed. Based on the complete hydrate formation between sample solvent and anhydrous salt, an in situ desiccated sampling of volatile compounds into GC-MS was achieved, which can be directly applied to the aqueous wine sample without any pretreatment. By this means, the volatile compounds in 17 wine samples have been successfully detected. To explore the common features underlying the fingerprinting differences in volatile compounds between red and white wines, PCA and PLS-DA were successively performed on 18 peaks and 10 peaks of volatile compounds in the wine samples, and good clustering was obtained for the classification of the two kinds of wines. The results showed that five characteristic components, i.e., 2-hydroxy-propanoic acid ethyl ester, butanedioic acid monomethyl ester, 4-oxo-pentanoic acid ethyl ester, 1-dodecene, and 1,2,3-trimethoxy-5-methyl-benzene, were found to be quite different in their contents between red and white wines among the other volatiles, which, to some extent, may take responsibility for the differences in their volatile aroma. This work will provide a useful tool and valuable guidance for elucidating the chemical fingerprinting differences in organoleptic quality among different wines.

Keywords Red and white wines · Volatile compounds · Desiccated headspace sampling · GC-MS · Multivariate analysis

Introduction

Wine is a complex medium composed of at least several hundred compounds from different chemical families, such as carbohydrates, alcohols, acids, phenolics, inorganic constituents, and other flavor compounds (Howard et al. 2005). Some of them originated from grape, and others are formed during wine fermentation or aging process. Among them, the volatile compounds, responsible for wine aroma, are the products of a biochemical and technological consequences that link wine quality and origin (Jiang et al. 2013). Therefore, techniques that can effectively characterize the composition of aromatic compounds in wines will be desired to ensure the organoleptic quality of wine.

Volatile compounds in wine are commonly analyzed by gas chromatography (GC) coupled with flame ionization detector (FID) or mass spectrometry (MS) (Schmidtke et al. 2013). Since MS is a universal detector and can provide data on characteristic fragment ions derived from molecular ion which are useful for the identification of molecules, it was the most widely used detection technique for the complex aroma composition in wines. However, prior to GC-MS analysis, it is mandatory to conduct a sample preparation procedure for isolating and concentrating the volatiles. Several techniques for sample preparations, e.g., distillation (Blanch et al. 1996; Bosch-Fuste et al. 2007), liquid-liquid extraction (Mamede and Pastore 2006; Mayr et al. 2014), solid phase extraction (Cabrita et al. 2007; Mateo et al. 1997), dynamic headspace extraction (Rosillo et al. 1999), and headspace solid phase micro-extraction (HS-SPME) (Antalick et al. 2010; Canuti

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Flavonoids of Lotus (*Nelumbo nucifera*) Seed Embryos and Their Antioxidant Potential

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Abstract: Flavonoids from lotus (*Nelumbo nucifera*) seed embryos were fractionated over a macroporous resin chromatography into 2 main fractions (I and II), and subsequently identified by high-performance liquid chromatography coupled with tandem mass spectrometry (HPLC-MS^2). Sixteen flavonoids were identified in lotus seed embryos, including 8 flavonoid *C*-glycosides and 8 flavonoid *O*-glycosides, in which the flavonoid *C*-glycosides were the main flavonoids. Among them, 2 flavonoid *O*-glycosides (luteolin 7-*O*-neohesperidoside and kaempferol 7-*O*-glucoside) were identified in lotus seed embryos for the 1st time. For further elucidating the effects of flavonoid *C*-glycosides to the bioactivities of lotus seed embryos, we compared the differences of the flavonoids and their antioxidant activities between leaves and seed embryos of lotus using the same methods. The results showed the antioxidant activity of flavonoids in lotus seed embryos was comparable or higher than that in lotus leaves, whereas the total flavonoid content in seed embryos was lower than lotus leaves which only contained flavonoid *O*-glycosides. The flavonoid *C*-glycosides of lotus seed embryos had higher antioxidant properties than the flavonoid *O*-glycosides presented in lotus leaves. This study suggested that the lotus seed embryos could be promising sources with antioxidant activity and used as dietary supplements for health promotion.

Keywords: flavonoid *C*-glycosides, HPLC-MS, lotus (*Nelumbo nucifera*), seed embryos

Introduction

Lotus (*Nelumbo nucifera*) is a perennial aquatic plant widely distributed throughout Asia, Australia, and North America (Kredy and others 2010). Almost all parts of lotus, including the seed embryos, have long been used as functional foods. The seed embryos have mainly been used for the treatment of nervous disorders, insomnia, and cardiovascular diseases such as hypertension and arrhythmia (National Commission of Chinese Pharmacopoeia 2010). More recently, their anti-ischemic, antioxidant, antiinflammatory, antiarrhythmic, and anti-HIV activities have been revealed (Mukherjee and others 2009). Besides being used as functional food, lotus seed embryos have also been used as Chinese traditional herbal medicines more than 2000 y in Eastern Asia (Mukherjee and others 2009). Increasing attention have been paid on analyzing bioactive components from lotus seed embryos (Zhu and others 2016).

Apart from alkaloids that have been well reported from lotus seed embryos, flavonoids have attracted enough attention due to their health benefits in treating some diseases, including neurodegenerative diseases, type II diabetes, and cardiovascular diseases (Perveen and others 2015). However, systematic studies on flavonoids composition of the lotus seed embryos are scarce, unlike for their leaves, flowers fruits, and other tissues, which have been reported to be rich in flavonoid *O*-glycosides (Chen and others 2012). Li and others (2014) 1st identified flavonoid *C*-glycosides in lotus seed embryos by high-performance liquid chromatography coupled with tandem mass spectrometry (HPLC-MS^2), and the flavonoid *C*-glycosides were also identified for the 1st time in lotus. Flavonoid *C*-glycosides received less attention as secondary plant metabolites compared with their well-understood *O*-glycosyl cousins (Courts and Williamson 2015). The *C*-glucosyl bond between the flavonoid carbon skeleton and the saccharide moiety are stable to hydrolytic effect of acidic and enzymatic treatments. This leads to big differences in the bioactivity and pharmacokinetics of these flavonoid *C*-glycosides (Courts and Williamson 2015; Xiao and others 2016). Flavonoid *C*-glycosides have multiple pharmacological benefits including antioxidant, hepatoprotective, antiviral, antiinflammatory, and anticancer activities (Courts and Williamson 2015). Further research into the flavonoid *C*-glycosides of lotus could explore more important applications in functional food industry. In addition, lotus has been widely cultivated throughout Asia and northern Australia, especially in China. It is estimated that annual harvest of dry lotus seeds in China has reached 15000 tons (Guo 2009). To explore other essential applications of lotus seed embryos in food and pharmaceutical industries, it is necessary to thoroughly investigate the constituents and activity of lotus seed embryos. Zhao and others (2014) measured the concentration of some flavonoids and alkaloids in lotus seed rhizomes from Korea, China, Vietnam, and Thailand, and evaluated the antioxidant activities of these lotus seed rhizomes. However, only 4 flavonoids in lotus seed rhizomes were measured. It is necessary to profile the flavonoids in louts seed rhizomes, especially including flavonoid *C*-glycosides.

Consequently, the total flavonoids from lotus seed embryos were fractionated by macroporous resin chromatography, and then subjected to chemical analysis with HPLC-ultraviolet detection (HPLC-UV) and HPLC-MS^2, followed by a subsequent antioxidant activity assay to explore the correlations between chemical components of lotus seed embryos and their nutritional or pharmaceutical activities.

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Genetic diversity and association mapping of forage quality in diverse bermudagrass accessions

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Abstract Bermudagrass is a warm season grass widely cultivated for turf and fodder. Nonetheless, the grass has poor forage quality because animals that consume it fail to assimilate its organic matter efficiently. Thus, identification of the marker-trait association between simple sequence repeat (SSR) markers and forage-quality-related traits in diverse bermudagrass accessions would enable efficient selection of high forage quality bermudagrass cultivars. Association mapping of 8 forage-related-quality traits with 1474 markers was conducted in 60 diverse bermudagrass accessions from five geographical regions in China. Significant variations in eight phenotypic and physiological traits were observed among the 60 accessions. A total of 1474 alleles were amplified by 104 SSR primers. The average gene diversity and polymorphic information content for the study sample were 0.2097 and 0.1748 respectively. The clustering analysis suggested that geographic origin influenced genetic distances between accessions. A total of 76 markers significantly associated with traits at $P < 0.01$; 73 with a single trait and 3 with two traits each. Nevertheless, only 41 significant marker-trait associations (MTAs) were observed after Bonferroni test was separately conducted for each trait. Forty-one microsatellites had significant associations with 8 forage-quality-related traits. These markers provide a feasible means of genetically improving forage quality in bermudagrass after further authentication.

Keywords Population structure · Kinship · Phenotypic traits · Variation · Linkage disequilibrium · Marker-trait-association

Abbreviations

ADF	Acid detergent fiber
ADL	Acid detergent lignin
AFLPs	Amplified fragment length polymorphisms
B	Biomass
CA	Crude ash
CF	Crude fat
CP	Crude protein
CTAB	Cetyl-trimethyl-ammonium-bromide
CV	Coefficient of variation
CWCs	Cell-wall-associated components

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Primer Note

Characterization and development of EST-derived SSR markers in *Sinowilsonia henryi* (Hamamelidaceae)[1]

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- *Premise of the study:* Polymorphic microsatellite markers were developed to reveal the genetic diversity of extant populations and the mating system of *Sinowilsonia henryi* (Hamamelidaceae).
- *Methods and Results:* In this study, nuclear simple sequence repeat (SSR) markers were developed using the Illumina high-throughput sequencing technique (RNA-Seq). The de novo–assembled transcriptome generated a total of 64,694 unique sequences with an average length of 601 bp. A total of 2941 microsatellite loci were detected. Of the 121 tested loci, 13 loci were polymorphic and eight were monomorphic among 72 individuals representing three natural populations of the species. The number of alleles per locus ranged from one to four, and the observed and expected heterozygosity at population level were 0.00–1.00 and 0.10–0.66, respectively.
- *Conclusions:* The developed expressed sequence tag (EST)–SSRs will be useful for studying genetic diversity of *S. henryi* as well as assessing the mating system among *Sinowilsonia* species.

Key words: Hamamelidaceae; microsatellite; RNA-Seq; *Sinowilsonia henryi*.

The tree genus *Sinowilsonia* Hemsl. is a member of the Hamamelidaceae family and comprises only one species, *S. henryi* Hemsl. This species is narrowly distributed in the mountains of central China at an elevation of 600–1400 m (Zhang et al., 2003). Currently, the natural habitats of this species are severely deteriorated and fragmented, with population sizes ranging from as few as five individuals to approximately 50 flowering plants (Zhou et al., 2014). Thus, *S. henryi* has been listed as an endangered plant species in the China Plant Red Data Book (Fu and Jin, 1992).

Knowledge of genetic diversity and genetic structure of extant populations is essential to the formulation of effective conservation and management strategies for threatened species (Frankham et al., 2002). Due to their codominance, hypervariability, and reliable scorability, microsatellite markers have been widely used in population genetic studies (Selkoe and Toonen, 2006). However, microsatellite markers for *S. henryi* are currently not available. High-throughput RNA sequencing (RNA-Seq) is one of the most useful next-generation sequencing techniques for identifying microsatellites. In the current study, we developed and characterized 21 expressed sequence tag–simple sequence repeat (EST-SSR) markers for *S. henryi* using RNA-Seq.

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METHODS AND RESULTS

Total RNAs were isolated from young leaves using a cetyltrimethylammonium bromide (CTAB) procedure (Chang et al., 1993). The poly(A)$^+$ RNA (mRNA) was purified with the RNA Clean-up Kit (Invitrogen, Carlsbad, California, USA) according to the manufacturer's instructions. The purified RNA was subsequently fragmented into small pieces (200 bp) by the fragmentation buffer. Then, the cleaved RNA fragments were used for first-strand cDNA synthesis using reverse transcriptase (Invitrogen) with random hexamer primers. Subsequently, second-strand cDNA was synthesized using RNase H and DNA polymerase I (Tiangen, Beijing, China). Illumina paired-end sequencing adapters were then ligated to the ends of the 3′-adenylated cDNA fragments. The cDNA library was sequenced by Shanghai Haiyu Biotechnology Co. Ltd. on the Illumina HiSeq 2000 instrument (Illumina, San Diego, California, USA). Before assembly, raw reads were filtered to remove those containing adapter or low-quality reads (more than 20% of nucleotides with Q-value ≤ 10) and reads containing poly N (>10% ambiguous base calls). Transcriptome assembly was performed using the Trinity package (version 2013-02-25) with the default parameters (Grabherr et al., 2011).

A total of 28.7 million 300-bp, clean, paired-end reads were obtained. All clean reads are available from the National Center for Biotechnology Information (NCBI) Short Read Archive (SRA) database (Bioproject accession no. PRJNA394173). De novo assembly of clean reads resulted in 64,694 unique sequences with an average length of 601 bp and an N50 length of 999 bp. The MIcroSAtellite identification tool (MISA; Thiel et al., 2003) was used to screen for the presence of microsatellites. The parameters used to identify microsatellites were seven repeats for di-, five for tri- and tetra-, four for penta-, and three for hexanucleotide repeats. Subsequently, SSR primers were designed with minimum GC content of 40% and an expected product size ranging from 100 to 280 bp using Primer3 (Rozen and Skaletsky, 1999).

A total of 8892 SSRs containing repeats from di- to pentanucleotides were identified from 64,694 unique sequences. Dinucleotides were the most abundant repeat type (5232), followed by trinucleotides (2198), hexanucleotides (1035), pentanucleotides (259), and tetranucleotides (168). The dinucleotide repeat $(AG/CT)_n$ (3646) was followed by $(AT/AT)_n$ (1192), $(AC/GT)_n$ (384), and $(CG/CG)_n$ (11). Among the trinucleotide repeat motifs, the most frequent SSR motif was

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Ammonium bicarbonate supplementation as carbon source in alkaliphilic *Spirulina* mass culture

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Abstract

Cyanobacterium *Spirulina (Arthrospira) platensis* is a commercial product with high content of protein and other nutritional elements, serving as a source of nutrients for food, feed and pharmaceutical industry. Generally, CO_2 gas bubbling method is a common method to supply carbon source for algae culture. However, in commercial situation where the CO_2 supply is limited, alternative bicarbonate could be utilized as a substitute carbon source in *Spirulina* cultivation. In this study, the optimum culture method of ammonium bicarbonate supplementation in open raceway pond as carbon source was firstly investigated to avoid the inhibition effect of ammonium bicarbonate. The optimal conditions estimated by experimental results for *S. platensis* cultivation were set as following: (1) the addition of ammonium bicarbonate at each time must be <2.0 mmol L^{-1}; (2) the addition rate of ammonium bicarbonate is in the range of 10–20 g m^{-2} day^{-1}. Then, *S. platensis* were cultured in eight 800 m^2 raceway ponds with fed-batch addition of ammonium bicarbonate combined with sodium bicarbonate as carbon source. The results illustrated that ammonium bicarbonate addition not only did not show any adverse impact on productivity, chlorophyll and carotenoid content of *S. platensis*, but also significantly increased the protein content of *S. platensis*. With ammonium bicarbonate supplementation as carbon source in alkaliphilic *Spirulina* mass culture, the carbon utilization efficiency was dramatically increased to approximately 70% from 38.89%, and the carbon cost was reduced by approximately 57%. Therefore, ammonium bicarbonate can be applied as supplement of carbon source for alkaliphilic *Spirulina* culture.

Keywords: ammonium bicarbonate, carbon utilization efficiency, *Spirulina platensis*, open raceway pond

Introduction

Cyanobacterium *Spirulina* (*Arthrospira*) *platensis* is a commercial product with high content of protein and other nutritional elements, serving as a source of nutrients for food, feed and pharmaceutical industry (Volkmann, Imianovsky, Oliveira & Sant'Anna 2008; Fujisawa *et al.* 2010). Moreover, the production of hydrogen and ethanol also makes this cyanobacterium a useful material for clean energy production (Amao & Nakamura 2006; Ananyev, Carrieri & Dismukes 2008). Due to its superior feature, considerable interest has been invested in mass cultivation of *S. platensis* for biomass production. Therefore, efficient methods for mass culture of *S. platensis* have become very desirable.

Carbon supply is essential for *S. platensis* cultivation, and carbon constitutes approximately 50% of

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ORIGINAL ARTICLE

The first complete plastome sequence of the basal asterid family Styracaceae (Ericales) reveals a large inversion

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Abstract Plastome sequences are rich sources of information for resolving difficult phylogenetic relationships and provide genomic data for conservation studies. Here, the complete plastome sequence of *Alniphyllum eberhardtii* Guillaumin is reported, representing the first plastome of the basal asterid family Styracaceae (Ericales). The plastome is 155,384 bp in length and contains 79 protein-coding genes, 30 tRNA genes and 4 rRNA genes, totaling 113 unique genes with 19 genes in the inverted repeat region. Unusual features of the plastome include the presence a large 20-kb inversion in the Large Single-Copy region, the pseudogenization of the *accD* gene, and the loss of the second intron from *clpP*. The 20-kb inversion includes 14 genes and has not been previously reported in other Ericales plastomes. Thirty-nine plastid simple sequence repeats (SSRs) that may provide genetic resources for the conservation of this economically import timber plant are characterized. Phylogenetic results inferred from ML and MP analyses of 66 plastid genes and 26 taxa reveal that the Styracaceae are sister to a clade including Actinidiaceae and Ericaceae and suggest that complete plastomes are likely to be very helpful in resolving the basal relationships among Ericales families, which have resisted resolution in smaller phylogenetic data sets.

Keywords *Alniphyllum eberhardtii* · Ericales · Inversion · Phylogenomics · Plastome · Styracaceae

Introduction

Plant plastomes are characterized by strong conservation of gene content and order, are easily amplified and have sequence regions that are useful at various phylogenetic levels, and have thus been broadly employed in phylogenetic studies (Gao et al. 2010; Ruhfel et al. 2014; Ruhlman and Jansen 2014). Comparison of complete plastome sequences provides the opportunity to explore sequence variation and molecular evolutionary patterns associated with gene loss, rearrangements, duplication, and transfer events (Wicke et al. 2011; Walker et al. 2014; Weng et al. 2014). Plastomes can also provide important basic genetic data for genetic engineering, DNA barcoding and phylogeography (Maliga and Svab 2011; Nock et al. 2011; Yang et al. 2013).

The Styracaceae are a small asterid family of 11 genera and about 160 species (Fritsch et al. 2001; APG 2016). Historically the Styracaceae were placed in various orders (e.g., Ebenales sensu Cronquist 1981, or part in Dilleniales sensu Thorne 2000). Molecular data have resolved the Styracaceae within Ericales (APG 1998) and have confirmed the monophyly of the family, although most of the infrafamilial relationships are unclear (Fritsch et al. 2001).

Currently the Styracaceae are one of 25 families treated within Ericales (APG 2016), but the backbone relationships among Ericales have been difficult to resolve with

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Changes of Antioxidant Defense System and Fatty Acid Composition in Bermudagrass under Chilling Stress

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Additional index words. low temperature, genotype, glutathione, gene expression, reactive oxygen species

Abstract. **Bermudagrass (*Cynodon dactylon*) is a typical and widely used warm-season turfgrass. Low temperature is one of the key environmental stress limiting its utility. However, little information is available about the differences of cold response between bermudagrass genotypes. Here, we analyzed antioxidant defense system and fatty acid composition in cold-resistant genotype WBD128 and cold-sensitive genotype WBDg17 exposed to chilling stress. Low temperature (4 °C) significantly decreased the relative water content, whereas increased the H_2O_2 and O_2^- contents, more profoundly for WBDg17. Under chilling condition, WBD128 had higher anti O_2^- activity than WBDg17. Besides, the contents of total glutathione, reduced glutathione (GSH) and its oxidized form (GSSG) were markedly increased by low temperature in both genotypes, whereas WBD128 had significantly higher values of GSH, total glutathione, and GSH/GSSG ratio than WBDg17. Moreover, chilling stress increased saturated fatty acids (SFAs) percentage (palmitic acid and stearic acid) in WBDg17. After chilling treatment, the proportion of linoleic acid decreased in both genotypes, particularly in WBDg17. As for unsaturated fatty acids (UFAs), the percentage of linolenic acid was increased in WBD128. In addition, chilling treatment decreased the values of double bond index (DBI), UFA/SFA ratio as well as degree of unsaturation in WBDg17. Finally, chilling stress altered the expression patterns of the genes, which encode one kind of late embryogenesis abundant proteins (*LEA*), superoxide dismutase (*Cu/Zn SOD*) C-repeat-binding factor/DRE-binding factor (*CBF1*), and peroxidase (*POD-2*). Collectively, our results revealed that natural variation of chilling tolerance in bermudagrass genotypes may be largely associated with the alterations of antioxidant defense system and fatty acid composition.**

Low temperature is one of the most detrimental abiotic stresses, which limits plant growth and productivity as well as distribution (Burke et al., 1976). The mechanisms of cold-induced injury are complex, and vary across different species and hardness degree (Baek and Skinner, 2003; Burke et al., 1976; Iswari and Palta, 1989). The status of the plasma membrane is crucial to cellular response when a plant is exposed to cold stress (Thomashow, 1999). Numerous mechanisms have been proposed to be involved in membrane damage under cold stress. This includes structural transitions and membrane phase transitions (Pearce and Willison, 1985), injury to membrane-bound ATPase (Iswari and Palta, 1989), and loss of bound water (Weiser, 1970).

Oxidative stress also has been suggested to be one of the causes of cold-induced damage (Halliwell and Gutteridge, 2015; McKersie and Bowley, 1997), which occurs when there are excessive free cellular radicals. Under normal condition, reactive oxygen species (ROS) are generated on a regular basis and at a low level (Arora et al., 2002). When plants are subjected to stresses, excessive ROS are produced, which can induce plant injury, including peroxidation of cell membrane components, enzymes denaturation, and DNA strands distortion (Halliwell and Gutteridge, 2015). To alleviate the detrimental effects of oxidative stress, plants have developed

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Research Advances on Tall Fescue Salt Tolerance: From Root Signaling to Molecular and Metabolic Adjustment

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Additional index words. transcriptional factors, phytohormones, endophyte, sugars, nonhormonal, endophyte, *Festuca arundinacea*

Abstract. **Soil salinity is one of the major abiotic stress factors that constrain plant growth and limit crop productivity. About a quarter of the global land area is affected by salinity; therefore, there is increased need to develop salt-tolerant crops. Tall fescue (*Festuca arundinacea*) is one of the most important cool-season turfgrasses, which has medium tolerance to salinity and has a promising potential to be used as a turfgrass under saline conditions. However, up to now, the maximum use of tall fescue under salinity stress is still limited by inadequate scientific literature. Recent studies have attempted to identify various adaptive responses to salinity stress at molecular, cellular, metabolic, and physiological levels in tall fescue. The successful integration of information concerning signal sensing, molecular tools with recent advances in -omics would certainly provide a clue for creating salt-tolerant tall fescue. Because salinity limits water availability to plants via hindering water absorption, and by inducing physiological drought, here we review and propose a probable mechanism of tall fescue response to salinity stress and to similar effects induced by drought based on published literature.**

Soil salinity is a critical environmental problem that affects about one-third of the world's irrigated agricultural land and is a major constraint on agricultural productivity (Allakhverdiev et al., 2000; Cheeseman, 1988). Despite being one of the most important cool-season turfgrasses, the use of tall fescue in tropical regions has been constrained by remarkably poor salt tolerance compared with warm-season turfgrasses (Alshammary et al., 2004; Watkins et al., 2011). Interestingly, there are remarkably great intraspecies cultivar variations in tall fescue water stress tolerance (Carrow, 1996). The decisive factor in the intraspecific variations has been attributed to differences in morphological characteristics especially the roots (Beard, 1989; Huang and Fry, 1998; Marcum et al., 1995; Youngner et al., 1981). Generally, the salt-tolerant cultivars usually develop longer and extensive roots compared with salt-sensitive cultivars (Fig. 1). Because roots play integral roles in nutrient uptake in tall fescue, any unfavorable soil conditions such as elevated salinity would adversely affect growth (Dean et al., 1996). Salinity and drought-triggered water deficit have been one of the major causes of root death of tall fescue; hence, to enhance salt adaptation, persistent tall fescue root growth is a prerequisite (Weaver and Zink, 1955). Understanding the mechanisms of tall fescue salt tolerance will uncover new information that can be incorporated into breeding programs to improve salinity tolerance.

Response of Tall Fescue Roots to Salinity

Water absorption efficiency by plant roots is a vital determinant of salinity resistance, and water absorption relies on the root size and its spatial distribution (Gupta and Huang, 2014). Recently, many studies on roots have focused on the morphological and growth characteristics, whereas extensive rooting has been positively correlated with increased resistance to water deficiency (Hays et al., 1991; Taylor, 1983). Tall fescue roots are closely associated with the surrounding soil and develop highly intricate branching that enables them to explore their environment (Bennett and Doss, 1960; Beyrouty et al., 1990; Bonos et al., 2004; Hu et al., 2015; Newman and Moser, 1988). Like other plants, the detrimental effects of salinity on tall fescue can be attributed to ion toxicity, and osmotic and nutrient imbalances (Bowman et al., 2006). The NaCl-induced toxicity, ionic imbalances, and water deficiency in plants result from the osmotic stress caused by excess Na^+ levels in the surrounding soil and a gross disruptions in the cytosolic Ca^{2+} as well as K^+ homeostasis (Apel and Hirt, 2004; Gorham et al., 1990; Hu et al., 2011; Lynch et al., 1989; Munns, 1988, 1993, 2011; Munns and Tester, 2008; Schachtman et al., 1991). Putatively, each of the limiting factors can be sensed by an elaborate system of stress sensors and then translated into a broad array of physiological and genetic changes that optimize plant performance under saline conditions. Moreover, it is highly probable that the salt-stress response pathways may function simultaneously (Bray, 1997). Thus, the prevention of salt-induced root desiccation and subsequent detriments is one of the mechanisms to ameliorate the adverse effects of salt (Fu et al., 2004).

Salt-Stress Signaling and Transcriptional Regulation

When plants are exposed to environmental stress, their signaling pathways undergo a complex and interlinked network of processes which triggers response. Plants specificity to stress

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ORIGINAL ARTICLE

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Isolation and identification of pathogenic fungi causing postharvest fruit rot of kiwifruit (*Actinidia chinensis*) in China

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Abstract

Kiwifruit is a very important commercial crop in China, which is the largest producer of the fruit in the world. The rapid expansion of areas of kiwifruit cultivation has resulted in the spread of postharvest rot diseases. To clarify the pathogens causing kiwifruit postharvest rots in China, 76 pure strains were isolated from 138 rotten fruits during the shelf-life period, with fruit collected from the 11 main regions of kiwifruit cultivation (Shaanxi, Sichuan, Henan, Guizhou, Hubei, Anhui, Jiangxi, Hunan, Fujian, Zhejiang and Jiangsu provinces) during 2014–2015. By examining the morphological and microscopic characteristics together with the results of pathogenicity testing and ITS (internal transcribed spacer) sequencing, four species were identified as the main pathogens causing kiwifruit postharvest rots in China. They were *Phomopsis* sp., *Botryosphaeria dothidea*, *Alternaria alternata* and *Pestalotiopsis microspora*, with identification rates of 52.6%, 23.7%, 13.2% and 10.5%, respectively. All isolates inoculated on wounded fruit were pathogenic but non-pathogenic when peels were unwounded except *B. dothidea*. These findings have important implications for resistance breeding and control of kiwifruit postharvest rots in China.

KEYWORDS
internal transcribed spacer identification, kiwifruit fungal postharvest rots, morphological analysis, pathogenicity tests

1 | INTRODUCTION

Kiwifruit (Chinese gooseberry, *Actinidia chinensis*) is becoming an increasingly popular fruit worldwide owing to its high vitamin C content and balanced nutritional components of minerals, dietary fibre and health-promoting metabolites (Huang, 2009). As the centre of wild kiwifruit diversity and the origin of domesticated cultivars, China has become the leading kiwifruit producer in the world, followed by Italy and New Zealand. The cultivation area reached 250,000 hectares at the end of 2015 (Belrose Inc., 2016).

The rapid expansion has resulted in the spread of various diseases including postharvest rots, which cause severe losses during storage, transportation, marketing and shelf-life period (Manning et al., 2016). Postharvest-diseased fruit with external symptoms always have internal symptoms. In addition, a large amount of fruit which appears to be healthy also turns out to be decayed after the skin of the fruit is peeled back (Koh, Hur, & Jung, 2005). Hence, postharvest losses have often been underestimated. The economic importance of the kiwifruit industry in China warrants urgent further study of postharvest rots.

Several fungi have been reported to be associated with postharvest rots of kiwifruit, including *Botryosphaeria* spp., *Phomopsis* sp., *Alternaria* spp., *Phoma* sp., *Colletotrichum* spp. (Hawthorne, Rees-George, & Samuels, 1982; Koh et al., 2005; Pennycook, 1985; Sommer & Beraha, 1975; Sommer, Fortlage, & Edwards, 1983), *Botrytis cinerea* and *Phialophora* sp. (Tonini, 2001), *Diaporthe actinidiae* (Beraha, 1970; Lee, Lee, Park, Hur, & Koh, 2001) and *Diaporthe ambigua* (Auger, Perez, & Esterio, 2016).

In China, *Botryosphaeria dothidea*, *Botryotinia fuckeliana*, *Pestalotiopsis* sp., *Fusarium proliferatum*, *Phomopsis* sp. and *Alternaria* sp. were isolated from fruit in Fengxin County of Jiangxi Province (Li et al., 2012). *Botryosphaeria dothidea*, *Lasiodiplodia theobromae and*

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Research Article

Quantitative Analysis and Comparison of Flavonoids in Lotus Plumules of Four Representative Lotus Cultivars

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The flavonoids in lotus plumules from four representative lotus cultivars have been analyzed using high-performance liquid chromatography coupled with ultraviolet detector and electrospray ionization triple quadrupole mass spectrometry. By this means, sixteen flavonoids were successfully measured and compared among four cultivars. Although similar flavonoid compositions were detected from these four cultivars, their flavonoid contents were significantly different. cv. Bailian from Guangchang was detected to have the most total flavonoid content, that is, 1595.86 mg/100 g, followed by cv. Xuanlian from Wuyi (1553.49 mg/100 g), cv. Xianglian from Xiangtan (1173.07 mg/100 g), and cv. Jianlian from Jianning (930.08 mg/100 g). However, similar percentages of flavonoid *C*-glycosides in the total flavonoids were found for four cultivars, which were 80.83% for cv. Bailian, 80.91% for cv. Xianglian, 79.25% for cv. Jianlian, and 78.53% for cv. Xuanlian. This work will be very useful for quality assurance and control for the lotus plumules from different origins in terms of qualitative and quantitative information about flavonoids. It will also be of special interest in the screening of lotus plumules with high flavonoid content, which are preferred due to their wide potential applications in food and pharmaceutical industries.

1. Introduction

Nenumbo nucifera is a valuable aquatic economic plant, and widely distributed in China [1]. It has more than 600 cultivars [2] and the four representative ones distributed in Hunan (cv. Xianglian), Jiangxi (cv. Bailian), Zhejiang (cv. Xuanlian) and Fujian (cv. Jianlian) province are the four most famous cultivars in Chinese history. All tissues of *Nenumbo nucifera* can be used as common foods or traditional medicines; so it is called the "full body of treasures" [3, 4]. Lotus plumule, also called *Lianzixin*, is the green seed embryo of the lotus seed. The mature lotus plumule has a bitter taste, and been recorded by Chinese Pharmacopoeia (2010 version) as a traditional Chinese medicine. Lotus plumule is also approved for dual purposes as a medical and edible plant by the Chinese Ministry of Health [5]. It is of important medical value, and could be used for the treatment of heart heat, high blood pressure and high fever [6]. It is also used as a healthcare food. In southern China, lotus plumules have been drunk as tea with boiling water. Xiao [7] developed a kind of health beverage made up of lotus plumules and *Chrysanthemum* in recent years. Lotus plumules, together with green tea and other materials, are also developed into tea beverage. With more and more lotus plumules derived products into the market, there is growing demand for raw materials of lotus plumules. Thus, quality assurance and control for raw materials and the derived products of lotus plumules are in great need, especially their natural phytochemicals and bioactive components, which may vary in cultivars from different districts. As it is known, the phytochemicals and bioactivities of plants are closely related to both the genetic strains and the environment factors including the insolation, temperature, precipitation, and other factors [8, 9]. For example, flavonols biosynthesis

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RESEARCH ARTICLE

iTRAQ-based Comparative Proteomic Analyses of Two Grapevine Cultivars in Response to Cold Stress

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Abstract: ***Background*:** Low temperature is a serious environmental factor that affects plant growth and cultivation. As one of the most popular fruit crop in the world, grapevine exhibited much difference in cold stress tolerance of different cultivars.

Objective: To understand the cold tolerance mechanism in grapevine and provide certain proteomics data may contribute to its breeding for enhancement of cold tolerance.

***Method*:** In this study, iTRAQ-based comparative proteomic analysis was conducted to identify cold-response proteins in two grape cultivars including a cold-resistant grape cultivar (Vitis amurensis) and a cold-sensitive grape cultivar (Vitis vinifera cv. Muscat of Hamburg).

***Results*:** Totally, 532 and 264 proteins were differentially expressed in Va and M, respectively, with 91 overlapping proteins. Compared to the control, most of these proteins exhibited down-regulated at 12 h, then up-regulated at 24 h, and decreased again at 48 h under cold treatment. Among these differentially expressed proteins, those involved in metabolic process, cellular process, single-organism process and response to stimuli were the most abundant group.

***Conclusion*:** Based on these findings, we proposed that proteins involved in photosynthesis, starch and sucrose metabolism, response to stimuli (such as glycine-rich RNA-binding protein, calmodulin, WSI18 protein etc.), signal transduction may play important roles for grape to resist cold stress. These results provide new insight to understand the cold tolerance mechanism in grapevine and may contribute to its breeding for enhancement of cold tolerance.

Keywords: Cold-response proteins, cold stress, grape, iTRAQ, proteomic.

INTRODUCTION

As one of the most vital fruit, grape and its products, such as fresh fruit, raisins, juice and wine were very popular and consumed worldwide. However, low temperature greatly limited the distribution of grapevine. Usually, the low temperature-tolerance grape varieties are used as the major resources for enhancing the chilling and freezing tolerance of grapevine by traditional breeding way. But this improvement is very limited without understanding the molecular mechanism of plant response to cold stress. Therefore, uncover the changes of physiological and biochemical process as well as signal transduction of grape during cold stress will help to apply genetic engineering to enhance its cold tolerance.

There are two kinds of low temperature, chilling (< 20 °C) and freezing (< 4 °C) [1, 2] which make plants suffer from cell damage, and extremely blocks plant growth and development, resulting in decrease product of crops [3]. During the long evolution process, many plants have acquired complex mechanism to defense cold stress. This phenomenon is termed cold acclimation. Under cold stress, plants firstly sense the severe environment, then the inner stress signal transduction system is activated leading to corresponding changes of transcriptional factors and genes. Finally, adjusted protective enzymes metabolites, such as synthesis of massive cryoprotectants adapt to cold stress [1, 3]. Some cold-response physiochemical indexes including malondialdehyde (MDA), proline, superoxide dismutase (SOD) activity, peroxidase (POD) activity, electroly leakage and so on were usually measured to reflect plant cold resistance [1, 4, 5]. It is reported that protein, proline, sugar and abscisic acid were accumulated in the leaves of four herba-

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Primula hubeiensis (Primulaceae), a New Species from Central China

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Abstract. We describe an interesting new *Primula* L. species, *P. hubeiensis* X. W. Li, which is similar to *P. filchnerae* R. Knuth, with leaves pinnately lobed and glandular hairs on the leaves and inflorescences. However, *P. hubeiensis* has more pinnae on the leaves (six to nine vs. three to four pairs) and smaller capsules (3–4 mm diam. vs. 10–16 mm diam.). The persistent calyx of *P. filchnerae* develops into the shape of a lantern when the fruits are mature, but the calyx of *P. hubeiensis* is elongated and split almost to the base during fruiting. *Primula filchnerae* has been placed in *Primula* sect. *Auganthus* (Link) Pax ex Balf. f. due to the character of its indument and deeply lobed leaves; *P. hubeiensis* might also belong in this section, but this needs further confirmation.

Key words: China, *Primula*, Primulaceae.

Primula L. is a large genus in China, with ca. 300 native species (Hu & Kelso, 1996). Hu and Kelso (1996) recognized, including three species in China with leaves pinnately compound or pinnately lobed to the midvein: *P. filchnerae* R. Knuth, *P. cicutariifolia* Pax, and *P. merrilliana* Schltr. Shao et al. (2012) showed that *P. ranunculoides* F. H. Chen is not a synonym of *P. cicutariifolia*, as treated by Hu (1990) and Hu and Kelso (1996), but rather a distinct entity distinguished from *P. cicutariifolia* and *P. merrilliana* by simple kidney-shaped outer leaves and a unique clonal reproductive ability. *Primula filchnerae* was once believed to have been extinct in the wild (Hu, 1990; Hu & Kelso, 1996); however, populations were rediscovered in west Hubei in China in 2006 (Gan & Li, 2015). Based on the ITS region of nuclear ribosomal DNA, Hao et al. (2002) proposed that *P. filchnerae* should be placed in *Primula* sect. *Auganthus* (Link) Pax ex Balf. f. and *P. cicutariifolia* and *P. merrilliana* in *Primula* sect. *Ranunculoides* C. M. Hu.

During our botanical expedition in the mountains in Tongshan County of south Hubei, China, we encountered a population of *Primula* on shady, damp rock crevices whose specimen was morphologically similar to *P. filchnerae* in having pilose, pinnately compound leaves. Yet, the specimen differed from *P. filchnerae* in obvious morphological traits, such as having more pinnae on the leaves and smaller capsules. *Primula filchnerae* was only found in Zhushan County and Zhuxi County of west Hubei (Gan & Li, 2015) and Yang County of southwest Shaanxi, China (Zhang et al., 2015), and the *Primula* population in Tongshan County is at least 500 km distant from those of *P. filchnerae*. We visited it several times and transplanted a few individuals to the Wuhan Botanical Garden, CAS, and observed them carefully. A literature survey (Hu, 1990; Hu & Kelso, 1996; Shao et al., 2012; Gan & Li, 2015) and herbarium research revealed that the species is undescribed. It is therefore described herein as new.

Primula hubeiensis X. W. Li, sp. nov. TYPE: China. Hubei: Tongshan Co., Xiapu Town, Gaoqiaotou Village, Dachengshan, on shady, damp rock crevices, 29°27′5.86″N, 114°27′37.88″E, 623 m, 16 May 2016, *D. C. Bao & H. D. Huang 1368-1* (holotype, HIB!). Figures 1, 2.

New Phytologist

Research

Rapid radiations of both kiwifruit hybrid lineages and their parents shed light on a two-layer mode of species diversification

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Key words: *Actinidia*, backbone phylogeny, hybrid speciation, phylogenomics, reticulate evolution.

Summary

- Reticulate speciation caused by interspecific hybridization is now recognized as an important mechanism in the creation of biological diversity. However, depicting the patterns of phylogenetic networks for lineages that have undergone interspecific gene flow is challenging.
- Here we sequenced 25 taxa representing natural diversity in the genus *Actinidia* with an average mapping depth of 26× on the reference genome to reconstruct their reticulate history.
- We found evidence, including significant gene tree discordance, cytonuclear conflicts, and changes in genome-wide heterozygosity across taxa, collectively supporting extensive reticulation in the genus. Furthermore, at least two separate parental species pairs were involved in the repeated origin of the hybrid lineages, in some of which a further phase of syngameon was triggered. On the basis of the elucidated hybridization relationships, we obtained a highly resolved backbone phylogeny consisting of taxa exhibiting no evidence of hybrid origin. The backbone taxa have distinct demographic histories and are the product of recent rounds of rapid radiations via sorting of ancestral variation under variable climatic and ecological conditions.
- Our results suggest a mode for consecutive plant diversification through two layers of radiations, consisting of the rapid evolution of backbone lineages and the formation of hybrid swarms derived from these lineages.

Introduction

Understanding the patterns and mechanisms underlying biological diversification remains central to answering questions about life on Earth. The classical phylogenetic foundation from which diversity grows in a bifurcating tree-like pattern has frequently been questioned, particularly in plants, where interspecific hybridization is prevalent (Rieseberg & Willis, 2007; Soltis & Soltis, 2009). Increasing evidence, from species divergence accompanied by gene flow to hybrid speciation, is driving the emergence of network models of diversification (Nakhleh, 2013), reflecting a dynamic process of organism evolution with genetic exchanges (Jónsson *et al.*, 2014; Lamichhaney *et al.*, 2015; Leducq *et al.*, 2016; Mallet *et al.*, 2016; Pease *et al.*, 2016). A growing body of genome-scale analyses further provides convincing examples showing reticulations across the 'Tree of Life', including analyses tracking clues of ancient introgression (Green *et al.*, 2010) and clarifying the evolutionary order of taxa with extensive interspecific gene flow (Heliconius Genome Consortium, 2012; Fontaine *et al.*, 2015), lending increasing support to the validity of the 'Web of Life' metaphor (Arnold, 2015). However, current data demonstrating the validity of reticulate diversification may represent just the tip of the iceberg given the potential for such diversification to be discovered in all domains of life.

Despite widespread interest in evolutionary networks, there remains little consensus among evolutionary biologists regarding the extent and pathways of gene flow occurring during speciation and diversification (Burke & Arnold, 2001; Mallet, 2007; Mavárez & Linares, 2008). In plants, allopolyploidy is a well-established speciation mode, while hybrid speciation without changes in ploidy levels (homoploid hybrid speciation) is less

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Transcriptomic characterization of candidate genes responsive to salt tolerance of *Miscanthus* energy crops

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Abstract

Given the growing need for biofuel production but the lack of suitable land for producing biomass feedstock, development of stress-tolerant energy crops will be increasingly important. We used comparative transcriptomics to reveal differential responses to long-term salt stress among five populations of *Miscanthus lutarioriparius* grown in the natural habitats and salinity experimental site. A total of 59 genes were found to be potentially responsive to the high-salinity conditions shared by the five populations, including those involved in detoxification, plant defense, photosynthesis, and signal transduction. Of these genes, about 70% were related to abiotic stress response. Among five populations, the most contrasting performance between relatively high survival rates and the relatively weak growing traits was in accordance with the down-regulation of genes involved in growth and up-regulation of genes related to plant stress tolerance in one of the populations. These results might reveal a potential tolerance-productivity trade-off, where resources were allocated from growth to stress resistance. The comparative transcriptomics of different populations among different environments will provide a basis for breeding and domestication of energy crops.

Keywords: bioenergy, energy crop domestication, long-term salt tolerance, marginal land, *Miscanthus lutarioriparius*, resource allocation

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Introduction

With the increasing demand for fuel production from renewable resources, the development of second-generation energy crops capable of growing on marginal land becomes increasingly urgent (Sang & Zhu, 2011; Allwright & Taylor, 2016). Given that salinity is a major adverse environmental factor affecting plant growth and productivity (Boyer, 1982), it is important to improve salt tolerance of energy crops. Considerable efforts have been undertaken to elucidate salt-responsive mechanisms of plants (Flowers & Yeo, 1995; Zhu, 2001; Zhang *et al*., 2004; Brinker *et al*., 2010; Cherel *et al*., 2014; Bushman *et al*., 2016). However, understanding of plant responding to long-term salt stress in the field conditions that could facilitate energy crop development remained limited.

Over the past decades, intense studies were devoted to understanding the mechanisms of plant responding to salt stress using model plants under short-term (several hours) salt stress in controlled laboratory or greenhouse conditions (Munns & Termaat, 1986; Zhu *et al*., 1998; Taji *et al*., 2004; Fujii & Zhu, 2009; Sun *et al*., 2010; Wang *et al*., 2015). Although this has been a powerful approach for revealing detailed molecular mechanisms, mechanistic study of salt tolerance of plants growing in salinity soil under long-term field conditions is needed to close the gap for the development of salt-tolerant crops (Zhu *et al*., 1998; Brosché *et al*., 2005; Vicente *et al*., 2016). In such efforts, plants grown in the field conditions do represent a valuable resource for elucidating the tolerance mechanisms (Brosché *et al*., 2005). The importance of acclimation process to long-term salt stress in the field is even more crucial for perennial grasses, as they face repeated episodes of abiotic stresses during their life cycles (Brosché *et al*., 2005; Moinuddin *et al*., 2014). Thus, a better understanding of long-term salt tolerance mechanisms under field

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Solar Radiation-Associated Adaptive SNP Genetic Differentiation in Wild Emmer Wheat, *Triticum dicoccoides*

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Whole-genome scans with large number of genetic markers provide the opportunity to investigate local adaptation in natural populations and identify candidate genes under positive selection. In the present study, adaptation genetic differentiation associated with solar radiation was investigated using 695 polymorphic SNP markers in wild emmer wheat originated in a micro-site at Yehudiyya, Israel. The test involved two solar radiation niches: (1) sun, in-between trees; and (2) shade, under tree canopy, separated apart by a distance of 2–4 m. Analysis of molecular variance showed a small (0.53%) but significant portion of overall variation between the sun and shade micro-niches, indicating a non-ignorable genetic differentiation between sun and shade habitats. Fifty SNP markers showed a medium ($0.05 \leq F_{ST} \leq 0.15$) or high genetic differentiation ($F_{ST} > 0.15$). A total of 21 outlier loci under positive selection were identified by using four different F_{ST}-outlier testing algorithms. The markers and genome locations under positive selection are consistent with the known patterns of selection. These results suggested that genetic differentiation between sun and shade habitats is substantial, radiation-associated, and therefore ecologically determined. Hence, the results of this study reflected effects of natural selection through solar radiation on EST-related SNP genetic diversity, resulting presumably in different adaptive complexes at a micro-scale divergence. The present work highlights the evolutionary theory and application significance of solar radiation-driven natural selection in wheat improvement.

Keywords: genetic differentiation, solar radiation, natural selection, SNP marker, wild emmer wheat

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INTRODUCTION

Wild emmer wheat, *Triticum dicoccoides*, the progenitor of modern tetraploid and hexaploid cultivated wheats, is distributed over the Fertile Crescent and can be found in ecologically highly diverse environments (Peng et al., 2011; Chen et al., 2013; Ren et al., 2013b; Nevo, 2014). It consists of genomes AABB, resulting most probably from spontaneous hybridization of wild

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Agronomic Trait Variations and Ploidy Differentiation of Kiwiberries in Northwest China: Implication for Breeding

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Polyploid plants often have higher biomass and superior crop qualities. Breeders therefore search for crop germplasm with higher ploidy levels; however, whether higher ploidy levels are associated with better performance remains unclear. *Actinidia arguta* and related species, whose commercialized fruit are referred to as kiwiberries, harbor a series of ploidy races in nature, offering an opportunity to determine the link between ploidy levels and agronomic traits. In the present study, we determined the ploidy levels of *A. arguta* var. *arguta*, *A. arguta* var. *giraldii,* and *A. melanandra* in 16 natural populations using flow cytometry, and examined 31 trait variations in fruits, leaves and flowers by field observations, microscopic examination and laboratory analyses. Our results showed that octaploid and decaploid *A. arguta* var. *giraldii* had larger dimension of leaves than tetraploid *A. arguta* var. *arguta* and *A. melanandra*, but their fruits were significantly smaller. In addition, *A. arguta* var. *giraldii* (8*x* and 10*x*) had higher contents of nutrients such as ascorbic acid and amino acids; however, some important agronomic traits, including the content of total sugar and total acid, were significantly lower in the octaploids and decaploids. Moreover, octaploids and decaploids did not result in greater ecological adaptability for the challenging environments and climates. In conclusion, the differentiation of ecological adaptability and traits among natural kiwiberries' cytotypes suggested that higher ploidy levels are not inevitably advantageous in plants. The findings of *A. arguta* and related taxa in geographical distribution and agronomic trait variations will facilitate their germplasm domestication.

Keywords: *Actinidia arguta*, kiwiberries, sympatric area, ploidy levels, morphological variation, fruit characters, taxonomy, breeding

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INTRODUCTION

Polyploidy, or whole genome duplication, has been an important feature of evolution and diversification in flowering plants (Otto and Whitton, 2000). Recent analysis basing on genomic data inferred all extant angiosperms have descended from polyploid species and undergone one or more chromosomal duplication events (Soltis et al., 2009). Plant polyploidization, is not the

Journal of proteome research

Technical Note

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Acid/Salt/pH Gradient Improved Resolution and Sensitivity in Proteomics Study Using 2D SCX-RP LC−MS

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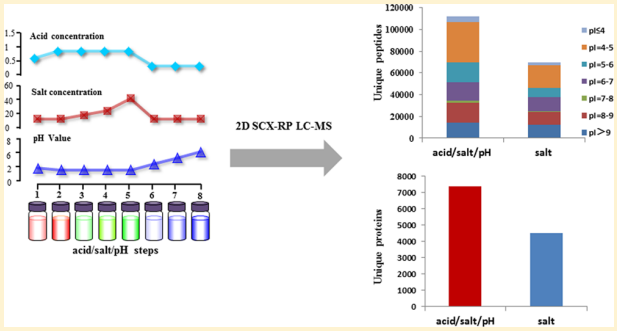
Supporting Information

ABSTRACT: The usage of strong cation exchange (SCX) chromatography in proteomics is limited by its poor resolution and nonspecific hydrophobic interactions with peptides, which lead to peptide overlap across fractions and change of peptide retention, respectively. The application of high concentration of salt (up to 1000 mM) in SCX also restricted its use in online 2D SCX-RP LC. In the present research, we first exploited the chromatographic ability of online 2D SCX-RP LC by combination of acid, salt, and pH gradient, three relatively independent modes of eluting peptides from SCX column. 50% ACN was added to elution buffer for eliminating hydrophobic interactions between SCX matrix and peptides, and the concentration of volatile salt was reduced to 50 mM. Acid/salt/pH gradient showed superior resolution and sensitivity as well as uniform distribution across fractions, consequently leading to significant improvements in peptide and protein identification. 112 191 unique peptides and 7373 proteins were identified by acid/salt/pH fractionation, while 69 870 unique peptides and 4536 proteins were identified by salt elution, that is, 62.5 and 60.6% more proteins and unique peptides, respectively, identified by the former. Fraction overlap was also significantly minimized by acid/salt/pH approach. Furthermore, acid/salt/pH elution showed more identification for acidic peptides and hydrophilic peptides.



KEYWORDS: *SCX-RP LC, acid/salt/pH gradient, resolution, sensitivity, overlap*

INTRODUCTION

In the strategy of shotgun proteomics, the efficient separation of complex protein digests is critical for the comprehensive identification of proteins.[1,2] Increasing attention has been paid to multidimensional liquid chromatography (MDLC) separation due to the high peak capacity and excellent resolving power, thereby providing an optimal delivery of peptides into the mass spectrometer.[3,4] MDLC is a popular technique that combines two or more orthogonal separation procedures in a consecutive manner. Among MDLC, 2D strong cation exchange-reversed phase liquid chromatography (2D SCX-RP LC) still represents the mainstay of bottom-up proteomics at present.[5−7] In the SCX-RP approach, the peptide mixtures are first eluted from an SCX column and then subjected to RP chromatography prior to mass spectrometry (MS) analysis. The SCX-RP system exhibits high detection sensitivity and outstanding separation performance due to the high orthogonality between SCX monolithic and RP separation materials.[8]

Salt and pH elution are two major modes for fractionating SCX-bound peptides.[5,9] Among these two modes, salt steps using nonvolatile or volatile salts are the most common mode. In this mode, salt is injected directly from the autosampler without additional pumps. The salt-step-based SCX-RP approach is thus the most simplified commercial 2D system, which is equated most widely by proteomics laboratories in the world;[5] however, even small amounts of nonvolatile salts accumulated in the ion-transfer tube also affect the ion-transfer efficiency of MS.[10] Nonvolatile salts are thus rarely used in the online SCX-RP-MS/MS platform. Compared with nonvolatile salts, volatile salts are, to some extent, tolerated in MS detection. Even so, direct contact of volatile salts with ion source of MS, especially high concentration of volatile salts, still results in source contamination of MS.[11] Furthermore, high concentration of salt easily leads to autosampler clogging and capillary blockage and causes a

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Whole transcriptome sequencing of *Pseudomonas syringae* pv. *actinidiae*-infected kiwifruit plants reveals species-specific interaction between long non-coding RNA and coding genes

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An outbreak of kiwifruit bacterial canker disease caused by *Pseudomonas syringae* pv. *actinidiae* (Psa) beginning in 2008 caused disaster to the kiwifruit industry. However the mechanisms of interaction between kiwifruit and Psa are unknown. Long noncoding RNAs (lncRNAs) are known to regulate many biological processes, but comprehensive repertoires of kiwifruit lncRNAs and their effects on the interaction between kiwifruit and Psa are unknown. Here, based on in-depth transcriptomic analysis of four kiwifruit materials at three stages of infection with Psa, we identified 14,845 transcripts from 12,280 loci as putative lncRNAs. Hierarchical clustering analysis of differentially-expressed transcripts reveals that both protein-coding and lncRNA transcripts are expressed species-specifically. Comparing differentially-expressed transcripts from different species, variations in pattern-triggered immunity (PTI) were the main causes of species-specific responses to infection by Psa. Using weighted gene co-expression network analysis, we identified species-specific expressed key lncRNAs which were closely related to plant immune response and signal transduction. Our results illustrate that different kiwifruit species employ multiple different plant immunity layers to fight against Psa infection, which causes distinct responses. We also discovered that lncRNAs might affect kiwifruit responses to Psa infection, indicating that both protein-coding regions and noncoding regions can affect kiwifruit response to Psa infection.

Kiwifruit is becoming an increasingly popular fruit worldwide owing to its high vitamin C content and balanced nutritional components of minerals, dietary fiber and health-promoting metabolites[1–3]. So far commercial kiwifruit plantings have reached more than 228,778 hectares with an annual production of 3 million tons worldwide (http://faostat.fao.org). However, since bacterial canker disease caused by a highly virulent strain of *Pseudomonas syringae* pv. *actinidiae* (Psa) was first reported in Italy in 2008, and subsequently found in other producing countries, the world kiwifruit industry has suffered a devastating blow[4]. Symptoms of this disease are characteristic dark brown spots surrounded by yellow haloes on leaves, and cankers with copious reddish exudate production on twigs and stem[4]. Psa has caused severe decline of production and death of affected kiwifruit vines even loss of entire commercial orchard[5]. Unfortunately, no effective measures has been employed to mitigate this disaster.

Psa is a hemibiotrophic pathogen of the *P. syringae* complex, which contains a large variety of plant pathogens, leading to diverse diseases of both wild and crop plants[6]. On the basis of geographic origin, physiological

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Origin and Evolution of the Kiwifruit Canker Pandemic

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Data deposition: Accession numbers (SRA and GenBank) are provided for all new sequence data analyzed in Table S1. Data for these 50 genomes will be publicly available immediately upon publication of this paper.

Abstract

Recurring epidemics of kiwifruit (*Actinidia* spp.) bleeding canker disease are caused by *Pseudomonas syringae* pv. *actinidiae* (*Psa*). In order to strengthen understanding of population structure, phylogeography, and evolutionary dynamics, we isolated *Pseudomonas* from cultivated and wild kiwifruit across six provinces in China. Based on the analysis of 80 sequenced *Psa* genomes, we show that China is the origin of the pandemic lineage but that strain diversity in China is confined to just a single clade. In contrast, Korea and Japan harbor strains from multiple clades. Distinct independent transmission events marked introduction of the pandemic lineage into New Zealand, Chile, Europe, Korea, and Japan. Despite high similarity within the core genome and minimal impact of within-clade recombination, we observed extensive variation even within the single clade from which the global pandemic arose.

Key words: pathogen evolution, genomic epidemiology, bacterial plant pathogen, plant-microbe interactions, disease emergence.

Introduction

A pandemic of kiwifruit (*Actinidia* spp.) bleeding canker disease caused by *Pseudomonas syringae* pv. *actinidiae* (*Psa*) emerged in 2008 with severe consequences for production in Europe, Asia, New Zealand, and Chile (Balestra et al. 2010; Abelleira et al. 2011; Everett et al. 2011; Vanneste et al. 2011; Koh et al. 2012; Zhao et al. 2013; Sawada et al. 2015). Earlier disease epidemics in China, South Korea, and Japan had regional impacts, however as infections were often lethal and the pathogen rapidly disseminated, *Psa* was predicted to pose a major threat to global kiwifruit production (Serizawa et al. 1989; Koh et al. 2002). Despite recognition of this threat—one subsequently realized in 2008—little was done to advance understanding of population structure, particularly across regions of eastern Asia that mark the native home of the genus *Actinidia*.

The origins of agricultural diseases and their link with plant domestication is shrouded by time. Kiwifruit (*Actinidia* spp.) is a rare exception because domestication occurred during the last century (Ferguson and Huang 2007; Ferguson 2011). Kiwifruit production and trade in plant material for commercial and breeding purposes has recently increased in Asia, Europe, New Zealand, and Chile (Shim and Ha 1999; Huang et al. 2004; Testolin and Ferguson 2009; Cruzat 2014;

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RESEARCH ARTICLE Open Access

Systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change

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Abstract

Background: Long non-coding RNA (lncRNA) is a class of non-coding RNA with important regulatory roles in biological process of organisms. The systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change are still poorly understood. Here we identified 17,610 lncRNAs and calculated their expression levels based on RNA-seq of 80 individuals of *Miscanthus lutarioriparius* from two environments, the nearly native habitats and transplanted field, respectively.

Results: LncRNAs had significantly higher expression diversity and lower expression frequency in population than protein coding mRNAs in both environments, which suggested that lncRNAs may experience more relaxed selection or divergent evolution in population compared with protein coding RNAs. In addition, the increase of expression diversity for lncRNAs was always significantly higher and the magnitude of fold change of expression in new stress environment was significantly larger than protein-coding mRNAs. These results suggested that lncRNAs may be more sensitive to environmental change than protein-coding mRNAs. Analysis of environment-robust and environment-specific lncRNA-mRNA co-expression network between two environments revealed the characterization of lncRNAs in response to environmental change. Furthermore, candidate lncRNAs contributing to water use efficiency (WUE) identified based on the WUE-lncRNA-mRNA co-expression network suggested the roles of lncRNAs in response to environmental change.

Conclusion: Our study provided a comprehensive understanding of expression characterization of lncRNAs in population for *M. lutarioriparius* under field condition, which would be useful to explore the roles of lncRNAs and could accelerate the process of adaptation in new environment for many plants.

Keywords: Population transcriptome, lncRNAs, *Miscanthus lutarioriparius*, Co-expression, Environmental response, Expression diversity

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Article

iTRAQ-Based Quantitative Proteomics Analysis on Rice Anther Responding to High Temperature

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Abstract: As one of the most important crops, rice provides the major food for more than half of the world population. However, its production is limited by many environmental factors, among which high temperature stress (HS) frequently occurs during anthesis and reduces its spikelet fertility. To explore the mechanism of HS tolerance in rice, we conducted a comparative proteomics analysis on the anthers between HS resistant and sensitive cultivars under different levels of high temperature. Under the same HS treatment, the resistant cultivar showed much higher spikelet fertility than the sensitive cultivar. Proteomic data showed that HS lead to the degradation of ribosomal proteins in the sensitive cultivar but not in the resistant one, which might result in the injury of protein biosynthetic machinery. In contrast, HS induced the increase of sHSP, β-expansins and lipid transfer proteins in the resistant cultivar, which might contribute to its ability to tolerate HS. The results provide some new insights into the mechanism of rice HS response.

Keywords: rice; high temperature; iTRAQ; proteomics; spikelet fertility

1. Introduction

With the increasing of world population, it has been a challenge to provide enough and stable food supply. Among all the crops, rice might be the most important one being the major food for more than half of the world population, especially in Asia [1]. During production, rice has to face different abiotic stresses, which negatively affect its growth and productivity. Because of their sessile characters, field grown plants have evolved diverse strategies to combat abiotic stresses depending on ecology, timing, severity and the stage of growth to improve survival [2]. With the industrialization of the world, global warming has become a threat to food production, which might lead to more than 25% decrease of the major food yield by 2050, as predicted by the International Panel on Climate Change [3]. To secure the rice supply, it is critical to develop rice cultivar with not only high yield, but also great stress tolerance.

In the last 50 years, high temperature has been one of the serious threatens for rice production. It has been reported that a 1 °C increase in temperature can lead to 7–8% of reduction in rice yield [4]. Although nearly all growth stages of the whole life cycle of rice are negatively affected by high temperature [5], anthesis is believed to be the most sensitive one [6,7]. There are over 2×10^7 ha of rice cultivation in the area along Yangtze River, which makes it one of the largest rice production areas. However, high temperature usually happens from the booting to flowering stages during rice

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Effect of flexible linker length on the activity of fusion protein 4-coumaroyl-CoA ligase::stilbene synthase†

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In order to elucidate the effect of flexible linker length on the catalytic efficiency of fusion proteins, two short flexible peptide linkers of various lengths were fused between *Arabidopsis thaliana* 4-coumaroyl-CoA ligase (4CL) and *Polygonum cuspidatum* stilbene synthase (STS) to generate fusion proteins 4CL–$(GSG)_n$–STS ($n \leq 5$) and 4CL–$(GGGGS)_n$–STS ($n \leq 4$). The fusion proteins were expressed in both *Escherichia coli* and *Saccharomyces cerevisiae*, and their bioactivities were tested *in vitro* and *in vivo* using purified proteins and engineered strains, respectively. The catalytic efficiency of the fusions decreased gradually with the increase of GSG or GGGGS repeats. In both engineered *S. cerevisiae* and *E. coli in vivo* experiments, the capacity of resveratrol production decreased gradually with increasing linker length. *In silico* analysis showed that the prediction of homology models of fusion proteins was consistent with the *in vitro* and *in vivo* results.

Introduction

Linking genes for the expression of unnatural fusion proteins is a powerful strategy for generating proteins with improved functions and bioactivities.[1–5] The linker regions between the functional domains can influence the production and properties of fusion proteins, and can be modified to improve structural folding and stability,[5–8] enhance expression,[9,10] and elevate biological activity.[11–13] The correct design of the linker peptide can be crucial for fusion protein function.[14,15] Generally, linker length, composition, hydrophobicity, sensitivity to proteases, and secondary structure are worthy of careful consideration when designing linkers,[14] wherein the flexible linker length has a direct impact on the function of the fusion protein. For constructing scFv, the short linker $(GGGGS)_1$ was demonstrated to be the best.[16] For fusing β-glucanase (Glu) and xylanase (Xyl), $(GGGGS)_2$ was the best among the tested linkers $(GGGGS)_n$ ($n \leq 3$).[8] However, only the chimera with the linker $(GGGGS)_4$ was desired when penicillin amidase and thermophilic chaperonin were fused.[6] Compared to the G5 linker, the insertion of the G8 linker greatly improved the *in vivo* function of epitope-tagged Est2p.[17] $(Gly–Ser–Gly)_n$ and $(Gly–Gly–Gly–Gly–Ser)_n$ are the most commonly used flexible linkers in the construction of fusion proteins.[8,18–20] By adjusting the copy number "*n*", the length of the linker can be optimized to achieve appropriate separation of the functional domains, or to maintain necessary inter-domain interaction.

Resveratrol is a polyphenolic compound from the stilbene family. It shows a wide range of beneficial properties such as antitumor, antithrombotic, antidiabetic, anti-inflammatory and antiaging properties.[21,22] Resveratrol is synthesized by the phenylpropanoid pathway, in which 4-coumaric acid is converted into resveratrol under the concerted activities of 4-coumaroyl-CoA ligase (4CL) and stilbene synthase (STS). After the successful elucidation of the resveratrol biosynthesis pathway, engineered microbial organisms for the production of resveratrol have been reported in many cases.[23–28] Among these efforts, the construction of unnatural fusion proteins to engineer resveratrol biosynthesis was shown to be the most powerful strategy.[18] Fusion of *Arabidopsis thaliana* 4CL and *Vitis vinifera* STS *via* a simple GSG tripeptide to give *At*4CL–GSG–*Vv*STS resulted in a 15-fold improvement in resveratrol production compared with separate expression of 4CL and STS.[18] Further crystallographic analysis of this fusion protein suggested that the improved production likely resulted from the

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ORIGINAL RESEARCH

Haplotypes Phased from Population Transcriptomes Detecting Selection in the Initial Adaptation of *Miscanthus lutarioriparius* to Stressful Environments

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Abstract

Adaptation is a characteristic that enhances the survival or reproduction of organisms; selection is the critical process leading to adaptive evolution. Therefore, detecting selection is important in studying evolutionary biology. Changes in allele frequency are fundamental to adaptive evolution. The allele frequency of entire genes at the genomic scale is more intensive and precise for analyzing selection effects, compared with simple sequence repeat and single nucleotide polymorphism (SNP) alleles from nuclear gene fragments. Here, we analyzed 29,094 SNPs derived from 80 individuals of 14 *Miscanthus lutarioriparius* L. Liou ex S.L. Chen & Renvoize populations planted near their native habitat (Jiangxia, Hubei Province, JH) and a stressful environment (Qingyang, Gansu Province, QG) to detect selection during initial adaptation. The nucleotide diversity of over 60% of genes was decreased in QG compared with JH, suggesting that most genes were undergoing selection in the stressful environment. We explored a new approach based on haplotype data inferred from RNA-seq data to analyze the change in frequency between two sites and to detect selection signals. In total, 402 and 51 genes were found to be targets of positive and negative selection, respectively. Among these candidate genes, the enrichment of abiotic stress-response genes and photosynthesis-related genes might have been responsible for establishment in the stressful environment. This is the first study assessing the change in allele frequency at the genomic level during adaptation. The method in which allele frequency detects selection during initial adaptation using population RNA-seq data would be useful for developing evolutionary biology.

Core Ideas

- A new method based on allele frequency to detect selection is proposed.
- Haplotypes were inferred from transcriptomes of 80 individuals.
- In total, 401 and 52 genes were targets of positive and negative selection respectively.
- Abiotic-related and photosynthesis-related genes were enriched in targeted genes.

ADAPTATION is a characteristic that enhances the survival or reproduction of organisms and thus evolutionary biologists always focus on studies on the critical resources of adaptation that have evolved by selection. For example, quantitative trait loci, genome scans of population diversity and divergence, and the ratio of

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Abbreviations: π, nucleotide diversity; AD, alleles with significantly decreased frequency in QG compared with those in JH; AI, alleles with significantly increased frequency in QG compared to JH; F_{ST}, index of genetic differentiation; GB, genes with both AI and AD; GD, gene with only AD; GI, genes with only AI; H_E, expected heterozygosity; JH, Jiangxia, Hubei Province; LRR, leucine-rich repeat; PPR, pentatricopeptide repeat family; QG, Qingyang, Gansu Province; SNPs, single nucleotide polymorphisms.

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Surface Modification of Carbon Nanotubes with an Enhanced Antifungal Activity for the Control of Plant Fungal Pathogen

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Abstract: The addition of surface functional groups to multi-walled carbon nanotubes (MWCNTs) expands their application in engineering, materials, and life science. In the study, we explored the antifungal activities of MWCNTs with different surface groups against an important plant pathogenic fungi *Fusarium graminearum*. All of the OH-, COOH-, and NH_2-modified MWCNTs showed enhanced inhibition in spore elongation and germination than the pristine MWCNTs. The length of spores decreased by almost a half from 54.5 μm to 28.3, 27.4, and 29.5 μm, after being treated with 500 μg· mL^{-1} MWCNTs-COOH, MWCNTs-OH, and MWCNTs-NH_2 separately. Furthermore, the spore germination was remarkably inhibited by surface-modified MWCNTs, and the germination rate was only about 18.2%, three times lower than pristine MWCNTs. The possible antifungal mechanism of MWCNTs is also discussed. Given the superior antifungal activity of surface modified MWCNTs and the fact that MWCNTs can be mass-produced with facile surface modification at low cost, it is expected that this carbon nanomaterial may find important applications in plant protection.

Keywords: MWCNTs; surface modification; antifungal activities; plant protection

1. Introduction

Carbon nanotubes (CNTs) are considered one of the most popular types of nanomaterials with unique morphologies and surface properties and have been intensively studied for various applications in bionanotechnology, including drug and gene delivery, tissue engineering, plant-technology [1,2], and other biomedical applications [3–8]. In recent years, CNTs have been found to have an active antibacterial activity and garnered a significant research interest around the use of nanotechnology-based approaches for agricultural system and plant protection [9–12]. A nanotube filter covered with a thin layer of single-walled carbon nanotubes (SWCNTs) are demonstrated to be effective in removing viral and bacterial pathogens [13–15]. Pristine SWCNTs dispersed in a biocompatible surfactant solution exhibited strong bactericidal activity against both gram-positive and gram-negative bacteria [16]. Lately, an exceptional application of CNTs in controlling plant pathogens in biological science has been described [17]. From the toxicological point of view, single-walled carbon nanotubes have higher antimicrobial properties than multi-wall carbon nanotubes (MWCNTs) [18]. At the same time, our previous studies verified that CNTs displayed superior inactivation effects on the copper-resistant plant pathogenic microorganisms *Ralstonia solanacearum*, *Fusarium graminearum*, and *F. oxysporum* [19,20]. These findings implied that CNTs may be applied to phytopathogen control in plant protection because of their superior antimicrobial activity.

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Cotton *GhERF38* gene is involved in plant response to salt/drought and ABA

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Abstract ERF (ethylene-responsive factor) transcription factors play important roles in plant stress signaling transduction pathways. However, their specific roles during diverse abiotic stresses tolerance in *Gossypium hirsutum* are largely unknown. Here, a novel ERF transcription factor, designated *GhERF38*, homologous to *AtERF38* in Arabidopsis, was isolated from cotton (*Gossypium hirsutum* L). *GhERF38* expression was up-regulated by salt, drought and ABA treatments. Subcellular localization results indicated that GhERF38 was localized in the cell nucleus. Over-expression of *GhERF38* in Arabidopsis reduced plant tolerance to salt and drought stress as indicated by a decline of seed germination, plant greenness frequency, primary roots length and the survival rate in transgenic plants compared to those of wild type plants under salt or drought treatment. Besides, stress tolerance related physiological parameters such as proline content, relative water content, soluble sugar and chlorophyll content were all significantly lower in transgenic plants than those of wild type plants under salt or drought treatment. Furthermore, over-expression of *GhERF38* in Arabidopsis resulted in ABA sensitivity in transgenic plants during both seed germination and seedling growth. Interestingly, the stomatal aperture of guard cells in the transgenic plants was larger than that in transgenic plant after ABA treatment, suggesting that *GhERF38*-over-expressing plants were insensitive to ABA in terms of stomatal closure. Furthermore, expressions of the stress-related genes were altered in the *GhERF38* transgenic plants under high salinity, drought or ABA treatment. Together, our results revealed that GhERF38 functions as a novel regulator that is involved in response to salt/drought stress and ABA signaling during plant development.

Keywords Cotton (*Gossypium hirsutum*) · *GhERF38* · Salt · Drought · ABA

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Introduction

Drought and soil salinity are the major environmental factors that influence survival, productivity and geographical distribution of agricultural crops (Shinozaki and Yamaguchi-Shinozaki 2007). Plants have evolved complex molecular, cellular, physiological and biochemical mechanisms to respond to these environmental challenges (Yamaguchi-Shinozaki and Shinozaki 2006; Shinozaki and

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Survival, recovery and microcystin release of *Microcystis aeruginosa* in cold or dark condition*

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Abstract *Microcystis* often dominates phytoplankton in eutrophic lakes and must survive a long period of cold or dark conditions. However, the survival strategies of *Microcystis* to withstand cold or dark stress are less well known. In this study, we conducted experiments on the responses of two toxic *Microcystis aeruginosa* strains (FACHB-905 and FACHB-915) and their microcystin release in conditions of low temperature (15°C or 4°C, with illumination) or darkness, and subsequent recovery in standard conditions (25°C with illumination). On exposure to 15°C, a small decrease in cell viability was observed, but the cell number increased gradually, suggesting that *M. aeruginosa* FACHB-905 and FACHB-915 cells seem in general tolerant in 15°C. Interestingly, our results show that a higher carotenoid content and microcystin release potentially enhance the fitness of surviving cells at 15°C. *M. aeruginosa* cells exposed to lower temperature light stress (4°C) did not completely lose viability and retained the ability to reinitiate growth. In darkness, the maximum quantum yield (F_v/F_m) and the maximum electron transport rate (ETR_{max}) values and cell viability of *M. aeruginosa* cells gradually decreased with time. During the recovery period, the photosynthetic efficiency of *M. aeruginosa* reverted to the normal level. Additionally, *M. aeruginosa* FACHB-905 and FACHB-915 exposed to low temperature had increased caspase-3-like activity and DNA fragmentation, which suggests the occurrence of a type of cell death in *M. aeruginosa* cells under cold stress similar to programmed cell death. Overall, our findings could confer certain advantages on the *Microcystis* for surviving cold or dark conditions encountered in the annual cycle, and help explain its repeated occurrence in water blooms in large and shallow lakes.

Keyword: *Microcystis aeruginosa*; microcystin; low temperature; darkness; Caspase-3-like activity; DNA fragmentation

1 INTRODUCTION

Microcystis is one of the most common cyanobacterial species and causes water blooms in eutrophic lakes, ponds, and reservoirs all over the world (Paerl and Otten, 2013). Some strains of *Microcystis* produce cyanobacterial hepatotoxins called microcystins, which are a threat to human and environmental health (Babica et al., 2006). *Microcystis* species are recruited from the water bottom as unicellular entities or very small colonies in early spring, grow rapidly in the water column at the end of spring, develop blooms at the water surface during the summer, sink to the bottom sediment in autumn, and overwinter in a resting state on the sediment surface (Reynolds et al., 1981). Because they are present throughout the year indicates that *Microcystis* are often exposed to fluctuating environmental conditions. For instance, *Microcystis* have been found to undergo optimal growth and photosynthesis at 25°C or above (Paerl and Huisman, 2009). However,

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A New Species of *Delphinium* (Ranunculaceae) from Hubei, China

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ABSTRACT. A new species of *Delphinium* L., *D. callichromum* Q. L. Gan & X. W. Li, from Hubei, China, is described and illustrated. It belongs to *Delphinium* sect. *Anthriscifolium* W. T. Wang, which now includes two species: *D. callichromum* and *D. anthriscifolium* Hance. Both species are similar in having pinnately divided leaves, petals broadest above the midpoint, and racemose inflorescences. *Delphinium callichromum* differs from *D. anthriscifolium* in its densely long-pilose stems, racemes with more flowers, red-brown immature anthers, oblong staminode limb with a prominent midvein, and sepals with a long claw.

Key words: China, *Delphinium*, *Delphinium* section *Anthriscifolium*, Ranunculaceae.

Delphinium L. is a large genus of the Ranunculaceae, including about 350 species in the Northern Hemisphere (Wang & Warnock, 2001). The plants are cultivated for ornament because of their beautiful flowers, and 18 species are used in Chinese traditional medicine (Wang, 1979). There are about 173 species in China, which are divided into five sections: section *Aconitoides* W. T. Wang, section *Elatopsis* Huth, section *Delphinastrum* DC., section *Oligophyllon* Dimitrova, and section *Anthriscifolium* W. T. Wang. *Delphinium* sect. *Anthriscifolium* is characterized by pinnately divided leaves, petals broadest above the midpoint, and transversely lamellate seeds (Wang & Warnock, 2001) and includes only one species, *D. anthriscifolium* Hance. In a maximum likelihood analysis of the 6-marker dataset of tribe *Delphinieae* (Wang et al., 2013), *D. anthriscifolium* was sister to all other species of genus *Delphinium* sensu Jabbour and Renner (2012).

During a botanical expedition in 2007 in Zhuxi County, western Hubei Province, China, we collected some interesting specimens of section *Anthriscifolium*. We sent the specimens to Wencai Wang (PE), who initially identified them as *D. anthriscifolium* var. *majus* Pamp. However, after a few years of observation, we noticed that the plant was quite different from *D. anthriscifolium* in that it flowers earlier (March to May vs. April to August), and its aerial part wilts much earlier (May vs. September) at similar altitudes in Zhuxi, Hubei. In 2013, some individuals from the type locality were transplanted into places where *D. anthriscifolium* occurs, and we compared their morphological characteristics. We also consulted national and local floras (Wang, 1979; Fu, 2001; Wang & Warnock, 2001) and checked specimens in herbaria. Finally we determined that our species is new to science. The new species is diagnosed by its densely long-pilose stems, many-flowered racemes, oblong staminode limb as long as or longer than the sepals with a prominent midvein, red-brown immature anthers, and sepals with a long claw.

Delphinium callichromum Q. L. Gan & X. W. Li, sp. nov. TYPE: China. Hubei: Zhuxi Co., Bingying Town, Lancaiguou Village, 32°05′05.79″N, 109°55′09.93 E″, 508 m, 22 Mar. 2015, *X. W. Li 15031* (holotype, HIB!). Figure 1.

Diagnosis. *Delphinium callichromum* Q. L. Gan & X. W. Li is similar to *D. anthriscifolium* Hance but differs from it in its densely long-pilose (vs. glabrous or retrorsely puberulent) stems; racemes with 12 to 30 (vs. 1 to 10) flowers; red-brown (vs. yellow) immature anthers; oblong (vs. dolabriform or ovate) staminode limb, as long as or longer than the sepals and with a prominent midvein; and sepals with a claw almost equaling the limb (vs. a very short or absent claw).

Plants annual. Stem 12–75 cm tall, densely long-pilose, branched. Leaf blade rhombic-ovate or deltoid-ovate, 5–15 × 8–28 cm, base broadly cuneate; leaf blade pinnately 3- to 4-lobed, primary lobes ovate-lanceolate; central lobe triangular-ovate, pinnately divided nearly to midvein, distally entire or dentate, apex acuminate; ultimate lobules narrowly ovate or obovate; proximal leaves not withered. Raceme 15–30 cm, long-pilose, 12- to 30-flowered; proximal bract leaflike; distal bracts absent. Pedicels 1.5–2 cm; bracteoles 3, borne proximally on pedicel, lanceolate-linear, 3–5 mm. Sepals bluish purple, abaxially sparsely puberulent; spur subulate, 12–20 mm, base 1.5–2.2 mm diam.; upper sepal narrowly ovate or ovate-lanceolate, 6–8 mm, constricted at middle; lateral and lower sepals with broadly ovate limb, 6–8 × 5–7 mm, and claw 5–6 mm; lower 2 sepals widely divergent. Petals 2,