四大类培养—专业型人才培养

江西农业大学农学院文件

赣农大农[2012]16号

关于印发《江西农业大学农学院本科生专业导师工作实施细则》的通知

各系、教研室、班级：

《江西农业大学农学院本科生专业导师工作实施细则》已经农学院党政联席会议通过，现予印发，请遵照执行。

江西农业大学农学院

2012年12月22日

江西农业大学农学院

本科生专业导师工作实施细则

第一章　总则

第一条　为贯彻中发[2004]16号文件精神和《国家中长期教育改革和发展规划纲要》（2010-2020），进一步加强大学生思想政治教育、创新教育和素质教育，更好地体现因材施教，促进教研育人、管理育人和服务育人，切实服务大学生成长成材，制定本实施细则。

第二条　本科生专业导师（以下简称导师）是大学生自我认知、行为养成、专业学习、科研活动、创新实践的指导者和引路人，是丰富校园文化、营造优良学风、浓厚科研氛围、促进充分就业的参与者和推动者。担任导师是高校教师的光荣任务，符合条件的教师应积极申请担任导师。

第二章　导师的配备和选聘

第三条　从2012级学生开始，学院为每位农学专业本科生配备导师，为其他专业部分本科生配备导师。

第四条　考虑相同专业背景师生比因素，每位导师指导农学专业学生人数以6—8人为宜，指导其他专业学生人数以3—5人为宜。

第五条　导师的选聘由学院统一组织，采取个人申请、组织推荐相结合的方式进行，选聘结果经公示无异议后，由学院统一颁发聘书。

第六条　在思想素质好、业务水平高、奉献精神强的本院在职和退休教师中选聘导师，基本条件如下：

（一）具有中级及以上职称或博士研究生学历，学术科研水平或实践能力强。

（二）坚持中国共产党领导，拥护党的基本路线、方针、政策，坚持社会主义办学方向，热爱和忠诚党的教育事业。

（三）师德高尚，爱岗敬业，关爱学生，作风正派，具有较好的亲和力和强烈的责任心、事业心。

（四）遵循高等教育教学规律，熟悉和遵守国家教育行政法规和学校各项规章制度。

（五）身心状况良好，有相应的精力和时间担任导师工作，能够按要求履行导师职责。

第七条　每位学生可以按顺序志愿选择导师3名，若同时选择某一位导师的学生人数超过规定上限，可以由学院按照志愿顺序进行调剂，若学生所有志愿得不到满足，则另行组织安排导师。

第八条　担任了班主任的导师不能作为本班学生的导师。导师确定后原则上不允许变更，导师不能以任何理由提出更换学生。若因特殊情况学生需要更换导师的，可以向学院提交申请，并经学院讨论后方可变更。

第九条　导师可以在相关专业在读硕士或博士研究生中自主选聘导师助理，

协助做好指导工作。原则上规定每名导师配备1名导师助理。

第三章　导师的职责和要求

第十条　导师的工作职责：

1.帮助学生了解所学专业，巩固专业思想，促进学生专业兴趣培养。

2.促进学生养成良好的学习习惯，掌握学习方法，指导学生合理安排选修课。

3.吸收学生或推荐给其他教师担任科研助理，组织学生参加校内外学术会议，指导学生参加学术、科技竞赛，促进大学生创新实践能力培养。

4.指导、推荐学生进行毕业实习，撰写毕业论文，对学生进行就业形势和择业观教育，积极为学生就业创造条件。

5.对学生进行年度考核，考核结果作为学生入团入党、素质测评、评优评先的重要依据。

6.定期或不定期组织学生召开座谈会，了解学生学习、科研情况，并协助做好学生思想引领工作。

第十一条　导师的工作要求：

（一）思想认识到位。充分认识到担任导师对青年学生成长成才产生的影响与作用，以生为本，认真履行工作职责，始终牢记责任和使命。

（二）时间精力到位。定期通过不同形式主动与学生交流沟通，认真掌握学生的基本情况与思想动态，时刻关注学生的成长变化，保持与学生、学生家长的密切联系。

（三）业务学习到位。加强学习，努力探索导师工作方式方法；积极了解和掌握大学生思想政治教育理论，主动运用新媒体，创新工作载体，不断提升导师工作能力和水平，增强工作的吸引力与感染力。

（四）工作记载到位。认真撰写导师工作日志，指导学生记载个人成长记录，协助做好学生毕业后的追踪调查工作。

第四章　导师的管理与考核

第十二条　导师工作在学院党政领导下实施，党政办、学工办是导师管理的职能部门，导师的年度考核由党政办负责，日常管理由学工办负责。

第十三条　学院高度重视导师的培训工作，积极为导师校外培训创造条件，给予经费保障。

第十四条　定期召开导师工作例会，交流情况，听取意见，对相关工作进行布置，指导和帮助导师做好工作。学院合理安排导师教学、科研工作和社会活动，保证导师有精力和时间投入工作。

第十五条　导师实行年度考核，考核结果分为优秀、称职、不称职 3 个等次，考核程序如下：

（一）每学年末，导师向学院提交学年工作总结和下学年工作计划，填写考核表。

（二）组织导师进行学年度述职，由教师代表和所指导学生对导师工作进行评议。

（三）学院设立“优秀导师”称号，“优秀导师”由学院党政联席会议根据评议结果考核导师等次确定。

（四）对“优秀导师”予以表彰，对考核等次为“不称职”的导师进行戒勉谈话。

第五章　导师的待遇和奖惩

第十六条　学院给导师按照每学年生均 5 个工作量的标准计算工作量。导师考核当年不称职的，不计算该年的工作量。

第十七条　学院对“优秀导师”按每学年 20 个工作量的标准给予物质奖励。

第十八条　导师指导学生参加学习、科技、创新创业等各类比赛获得学校和省级以上奖励或者发表高质量论文的，依据有关办法给予导师一定物质奖励。

第十九条　自主聘请导师助理的导师，导师助理有关待遇由导师协商负责。

第二十条　导师连续两年考核等次不称职的，学院予以解聘。

第六章　附则

第二十一条　本办法授权学院党政办和学工办解释。

第二十二条　本办法自 2013 年 1 月 1 日起试行。

江西农业大学农学院党政办公室　　　2012 年 12 月 22 日印发

江西农业大学农学院文件

赣农大农[2014]10号

关于激励本科生报考硕士研究生的实施意见

各系、教研室、班级：

学校已经出台《江西农业大学全日制研究生收费及奖助学金政策》，明确了录取我校研究生的国家奖助学金、江西省政府奖学金、江西省学业奖学金、“三助”岗位津贴等资助措施，特别是明确了第一志志愿或免试录取江西农业大学研究生一年级均享受5000元/年的一等奖学金，为了积极鼓励优秀本科毕业生报考研究生，经学院党政研究在学校资助政策基础上制定本实施意见。

1、研究生考试备考期间，视情况协调安排考研专用教室或者带空调的会议室供考研学生使用。

2、对于报名免试推荐研究生和全国统考研究生的，凭网银支付凭证和有效成绩给予报名费资助。

3、第一志愿或免试录取我校研究生并报到的，凭录取通知书在学校资助基础上给予500元现金奖励。

4、积极调剂录取我校研究生并报到的，凭录取通知书给予200元现金奖励。

5、班级录取（含推免）研究生比例达50%以上的，给予班主任2000元现金奖励；班级录取（含推免）研究生比例达40—50%之间的，给予班主任1500元现金奖励；班级录取（含推免）研究生比例在30—40%之间的，给予班主任1000元现金奖励。

本激励措施自2011级学生开始试行，授权学院学工办负责解释。

江西农业大学农学院
2014年9月3日

江西农业大学农学院党政办公室　　　　2014年9月4日

近年来学生在核心及以上期刊发表学术论文情况表

序号	题目	论文作者	班级
1	Crystal structure of 2-((2-(3-hydroxy-7-methylene-2,3-dihydro-7H-furo[3,2-g]chromen-2-yl)propan-2-yl)oxy)-6-(hydroxymethyl)tetrahydro-2H-pyran-3,4,5-triol – a marmesin derivative, $C_{20}H_{24}O_{10}$	李宇妍	植保 1701
2	TWO 1,2-SECO-COUMARINS FROM Clausena lansium	李宇妍等	植保 1701
3	The transcription factor AtGLK1 acts upstream of MYBL2 to genetically regulate sucrose-induced anthocyanin biosynthesis in Arabidopsis	郑雨轩	园艺 1802
4	播期对南方双季晚籼稻温光资源利用、产量及品质形成的影响	徐俊豪	种科 1801
5	褐飞虱 RNAi 显微注射试验中麻醉方法的比较	张朋稳	植保 1801
6	Genetic analysis of grain shape and weight after cutting rice husk	朱黎欣	种科 1401
7	Characterization of a Novel Weak Allele of RGA1/D1 and Its Potential Application in Rice Breeding	邱娇等	种科 1901
8	OsPLS4 Is Involved in Cuticular Wax Biosynthesis and Affects Leaf Senescence in Rice	姜志树等	种科 1601
9	精氨酸酶在植物胁迫应答中功能研究进展	刘嘉龙等	种科 1801
10	Rice husk ash addition toacid red soil improves thesoil property andcotton seedling growth	刘茜等	农学 1802
11	淹水缓解直播早籼稻苗期低温冷害的生理特性研究	刘有清	种科 1701
12	生物酶法提取铁观音茶梗中茶多酚工艺技术研究	罗兰心	茶学 1801
13	根系分泌物对紫云英油菜间作的响应	王亚君	农学 1801
14	稻米蒸煮特性 QTL 定位及与感官食味品质的相关性分析	徐伟清	农学 1402
15	QTL Mapping of Rice Cooking Characteristics and Correlation Analysis of Sensory Food Quality	徐伟清	农学 1402
16	ox-Behnken 响应面优化酶法提取宁红茶多糖工艺技术研究	罗兰心	茶学 1801
17	响应面法优化生物酶法提取滇红茶多糖工艺技术研究	汪咪娜	茶学 1801
18	Long-Term Straw Return with Reducing Chemical Fertilizers Application Improves Soil Nitrogen Mineralization in a Double Rice-CroppingSystem	陈玲等	种科 1901
19	植物铁素(Fe)营养的生理研究进展	张文静等	农学 1801
20	First report of Colletotrichum fructicola causing anthracnose on loquat in Jiangxi province, China	郭德康	植保 1701
21	稻瘟病菌中小 G 蛋白 Rho3 的假定互作蛋白 MoKin1 的功能分析	何金	植保 1702

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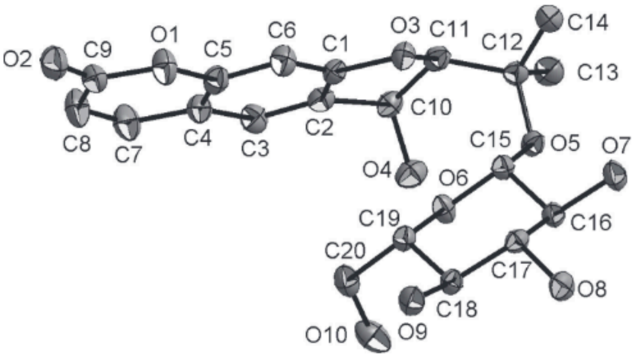
Z. Kristallogr. NCS 2020; 235(1): 171–173

Yu-Yan Li, Xu-Liang Nie, Xiao-Xiang Fu, Bao-Tong Li* and Wen-Wen Peng*

Crystal structure of 2-((2-(3-hydroxy-7-methylene-2,3-dihydro-7*H*-furo[3,2-*g*]chromen-2-yl)propan-2-yl)oxy)-6-(hydroxymethyl)tetrahydro-2*H*-pyran-3,4,5-triol – a marmesin derivative, $C_{20}H_{24}O_{10}$



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Abstract

$C_{20}H_{24}O_{10}$, orthorhombic, $P2_12_12_1$ (no. 19), $a = 6.3728(6)$ Å, $b = 14.3835(14)$ Å, $c = 20.453(2)$ Å, $V = 1874.8(3)$ Å^3, $Z = 4$, $R_{gt}(F) = 0.0272$, $wR_{ref}(F^2) = 0.0558$, $T = 296(2)$ K.

CCDC no.: 1953796

The molecular structure is shown in the figure. Table 1 contains crystallographic data and Table 2 contains the list of the atoms including atomic coordinates and displacement parameters.

Source of material

The aerial part of Clausena lansium Lour. Skeels (Rutaceae) were collected and identified by Prof. ZHANG Zhi-Yong (a botanist) of College of Agriculture, Jiangxi Agricultural University, Nanchang, China, in September, 2015. After being crushed into powder (11 kg), the plant material was extracted

Table 1: Data collection and handling.

Crystal:	Colourless block
Size:	0.20 × 0.14 × 0.12 mm
Wavelength:	Mo $K\alpha$ radiation (0.71073 Å)
μ:	0.12 mm^{-1}
Diffractometer, scan mode:	Bruker APEX-II, φ and ω
θ_{max}, completeness:	25.5°, >99%
$N(hkl)_{measured}$, $N(hkl)_{unique}$, R_{int}:	14542, 3489, 0.024
Criterion for I_{obs}, $N(hkl)_{gt}$:	$I_{obs} > 2\ \sigma(I_{obs})$, 3289
$N(param)_{refined}$:	279
Programs:	Bruker [1], SHELX [2]

Table 2: Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å^2).

Atom	x	y	z	U_{iso}*/U_{eq}
C1	0.1698(3)	0.77000(14)	0.69654(10)	0.0256(4)
C2	0.3758(3)	0.74054(14)	0.68935(10)	0.0264(5)
C3	0.4296(3)	0.68691(15)	0.63636(10)	0.0304(5)
H3	0.5666	0.6658	0.6315	0.036*
C4	0.2763(3)	0.66415(15)	0.58956(10)	0.0294(5)
C5	0.0729(3)	0.69661(16)	0.59927(10)	0.0290(5)
C6	0.0137(3)	0.74979(15)	0.65236(10)	0.0302(5)
H6	−0.1233	0.7707	0.6579	0.036*
C7	0.3181(4)	0.61386(17)	0.53044(12)	0.0394(6)
H7	0.4525	0.5913	0.5226	0.047*
C8	0.1666(4)	0.59902(18)	0.48647(12)	0.0418(6)
H8	0.1979	0.5664	0.4484	0.050*
C9	−0.0434(4)	0.63222(16)	0.49657(11)	0.0326(5)
C10	0.5027(3)	0.77553(15)	0.74706(10)	0.0270(5)
H10	0.6245	0.8097	0.7303	0.032*
C11	0.3457(3)	0.84631(15)	0.77615(10)	0.0262(5)
H11	0.3799	0.9060	0.7556	0.031*
C12	0.3363(3)	0.86603(14)	0.84979(10)	0.0245(4)
C13	0.5537(4)	0.89686(16)	0.87190(12)	0.0351(5)
H13A	0.5509	0.9106	0.9178	0.053*
H13B	0.5944	0.9515	0.8481	0.053*
H13C	0.6528	0.8480	0.8637	0.053*
C14	0.1745(4)	0.94127(15)	0.86378(11)	0.0331(5)
H14A	0.0370	0.9185	0.8533	0.050*
H14B	02046	0.9951	0.8376	0.050*
H14C	0.1799	0.9577	0.9092	0.050*
C15	0.1161(3)	0.73046(13)	0.87739(10)	0.0224(4)
H15	0.0101	0.7665	0.8537	0.027*
C16	0.0270(3)	0.69138(14)	0.94019(9)	0.0236(4)
H16	0.1340	0.6540	0.9624	0.028*
C17	−0.1600(3)	0.63008(14)	0.92266(9)	0.0228(4)

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TWO 1,2-SECO-COUMARINS FROM *Clausena lansium*

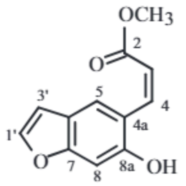
Wenwen Peng,[1,2]* Xiaoxiang Fu,[2] Yuyan Li,[2]
Guanghua Huo,[1] and Baotong Li[3]*

*A new 1,2-seco-furan-coumarin, claulancoumarin A (**1**), and a known 1,2-seco-coumarin, (Z)-2,4-dihydroxycinnamic acid (**2**), were isolated from the branches and leaves of* Clausena lansium*. Their structures were elucidated by spectroscopic analysis, including NMR and MS.*

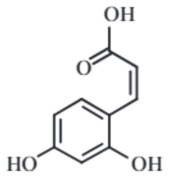
Keywords: furan-coumarin, seco-coumarin, *Clausena lansium*.

The genus *Clausena* (Rutaceae) is comprised of approximately 30 species that are scattered throughout the subtropical and tropical regions, including China, Vietnam, Indonesia, Malaysia, and the Philippines [1, 2]. There are approximately 10 species as well as two varieties in China, appearing in Southern China. *Clausena lansium* (Lour.) Skeels (Rutaceae) is a fruit tree growing in South China. Its fruits have been used as folk medicine by the local people to treat indigestion, cold, cough, and stomach pain [1], and its leaves and roots for the treatment of cough, asthma, dermatological diseases, viral hepatitis, and gastrointestinal disease [3]. In our previous research, a new 1,2-seco-furan-coumarin, claulancoumarin, was isolated from the branches and leaves of *C. lansium* [4]. As part of our ongoing project towards the discovery of new constituents of the *Clausena* genus, another new 1,2-seco-furan-coumarin, claulancoumarin A (**1**), together with a known 1,2-seco-coumarin, (*Z*)-2,4-dihydroxycinnamic acid (**2**), was isolated from the branches and leaves of *C. lansium*. The present study describes the isolation and structural determination of the 1,2-seco-furan-coumarin.

Claulancoumarin A (**1**) was obtained as a colorless syrup. Its UV spectrum showed absorption maxima at 252 nm. Its IR spectrum indicated the presence of an aromatic group (1618, 1501, and 1453 cm^{-1}). The ^{1}H NMR spectrum of **1** (Table 1) showed two olefinic protons with weak coupling constants at δ 7.49 (1H, J = 2.3 Hz) and 6.68 (1H, J = 2.3 Hz), indicating a typical disubstituted furan ring in **1** [4, 5]. In addition, two *cis*-olefinic protons at δ 7.41 (1H, d, J = 9.4 Hz) and 6.19 (1H, d, J = 9.4 Hz), two singlet olefinic protons at δ 7.29 (1H, s) and 6.77 (1H, s), and a methoxy group at δ 3.88 (3H, s) were observed in the ^{1}H NMR spectrum of **1**. The ^{13}C NMR spectroscopic data of **1** (Table 1) revealed signals corresponding to 12 carbons, including 10 aromatic carbons (δ 157.4, 157.1, 148.9, 144.3, 121.6, 119.8, 117.8, 108.7, 106.7, 98.7), one carbonyl (δ 167.2), and a methoxy (δ 53.1). Comparison of the ^{1}H and ^{13}C NMR data of **1** and psoralen [6] indicated them to be similar furan-coumarins, the major difference being that **1** had one more methoxy than psoralen. Coupled with the HMBC spectrum (Fig. 1) correlations of proton OCH$_3$ (δ 3.88)/CO (δ 167.2), **1** was deduced to be a 1,2-seco-furan-coumarin. The other key correlations of COSY and HMBC are marked as shown (Fig. 1). So, compound **1** was elucidated as a 1,2-seco-psoralen and named claulancoumarin A.



1



2

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The transcription factor AtGLK1 acts upstream of MYBL2 to genetically regulate sucrose-induced anthocyanin biosynthesis in Arabidopsis

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Abstract

Background: The regulation of anthocyanin biosynthesis by various factors including sugars, light and abiotic stresses is mediated by numerous regulatory factors acting at the transcriptional level. Here experimental evidence was provided in order to demonstrate that the nuclear GARP transcription factor AtGLK1 plays an important role in regulating sucrose-induced anthocyanin biosynthesis in Arabidopsis.

Results: The results obtained using real-time quantitative PCR and GUS staining assays revealed that *AtGLK1* was mainly expressed in the green tissues of Arabidopsis seedlings and could be induced by sucrose. The loss-of-function *glk1 glk2* double mutant has lower anthocyanin levels than the *glk2* single mutant, although it has been determined that loss of AtGLK1 alone does not affect anthocyanin accumulation. Overexpression of *AtGLK1* enhances the accumulation of anthocyanin in transgenic Arabidopsis seedlings accompanied by increased expression of anthocyanin biosynthetic and regulatory genes. Moreover, we found that AtGLK1 also participates in plastid-signaling mediated anthocyanin accumulations. Genetic, physiological, and molecular biological approaches demonstrated that AtGLK1 acts upstream of MYBL2, which is a key negative regulator of anthocyanin biosynthesis, to genetically regulate sucrose-induced anthocyanin biosynthesis.

Conclusion: Our results indicated that AtGLK1 positively regulates sucrose-induced anthocyanin biosynthesis in Arabidopsis via MYBL2.

Keywords: Arabidopsis, AtGLK1, Anthocyanin biosynthesis, MYBL2

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播期对南方双季晚籼稻温光资源利用、产量及品质形成的影响

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摘 要：调整播期可以改变水稻生长发育中的环境气候条件，对于充分利用自然资源、调节水稻生育进程及提升产量和品质具有重要意义。为明确南方双季晚籼稻优质丰产与温光资源相适应的播种期，本研究选用万象优华占、象牙香珍和美香占2号等3个晚籼稻品种为试验材料，设置6月10日、6月20日、6月30日共3个播期，研究播期对双季晚籼稻品种温光资源利用、产量及稻米品质的影响。结果表明，随着播期推迟，供试品种在不同生育阶段日均温度和有效积温、全生育期和齐穗至成熟期阶段的日照时数均呈递减趋势，而全生育期天数无明显变化；产量以6月20日播种的最高，早播(6月10日)会导致显著减产，而晚播(6月30日)虽然也会导致减产，但差异不显著；随播期推迟，晚籼稻品种加工品质、外观品质和蒸煮品质变优，但不利于改善食味品质，对营养品质无显著影响。在南方双季晚籼稻实际生产中，不建议早播，应根据品种不同进行适期播种或适当晚播，能使水稻更合理有效地利用温光资源，有利于协调水稻高产和品质提升。

关键词：晚籼稻；播期；温光资源；生育期；产量；稻米品质

中图分类号：S511.04 **文献标识码：**A **文章编号：**1006-8082(2021)05-0115-06

高产、优质一直是水稻栽培和育种工作者长久不变的研究方向。随着我国人民生活水平的提高，优质稻米越来越受市场和广大消费者的青睐[1-2]。南方双季稻种植面积日益增大，目前已占我国水稻种植总面积的30%左右，同时优质化生产趋势明显[3]。但在南方双季晚稻实际生产中，常面临拔节期和孕穗期高温少雨，灌浆成熟期易遇“寒露风”侵害等问题，制约着产量和品质的提升[4-5]。同时，由全球变暖造成的环境气候变化亦对水稻生产造成严重不利影响[6]。调整播期可以改变水稻生长发育中的环境气候条件，对于充分利用自然资源，调节水稻生育进程及提高水稻产量和品质具有重要意义[7]。研究表明，随着播期推迟，中籼稻和晚粳稻在各生育阶段内积温和累计日照时数呈降低趋势，营养生长期缩短，生育进程加快[8-9]。董明辉等[10]研究认为，不同生育类型粳稻品种产量随播期的推迟均表现为降低趋势。成臣等[11]研究认为，播期对水稻产量的影响因品种类型而异，籼稻品种早播更有利于提高产量；而粳稻品种早播和晚播均会导致减产。关于播期对稻米品质的影响，段斌等[12]研究表明，随着播期推迟，不同粳稻品种加工品质和外观品质变优，直链淀粉含量和碱消值增大而胶稠度变短。而关世武等[13]研究则认为，随播期推迟，水稻的外观品质变优而加工品质变劣，但对蒸煮和食味品质影响不显著。成臣等[11]则认为，籼稻品种适时早播有利于品质提升，而粳稻品种应按品种特性适期播种，早播或晚播均会降低稻米品质。这些研究多以粳稻或单季籼稻为研究对象，针对南方双季晚籼稻的研究报道较少。因此，为明确南方双季晚籼稻优质丰产与温光资源相匹配的最佳播种期，本研究以万象优华占、象牙香珍和美香占2号等3个晚籼稻品种为试验材料，通过分期播种试验，系统探讨了播期对南方双季晚籼稻生育期、产量及稻米品质的影响，以期为南方双季晚籼稻优质丰产栽培提供理论依据。

1 材料与方法

1.1 试验地点及参试品种

试验于2020年6月至11月在江西农业大学上高科技小院(114°02′E，28°13′N，海拔54 m)进行。试验前土壤有机质含量23.51 g/kg，全氮2.11 g/kg，速效钾65.83 mg/kg，有效磷23.81 mg/kg，pH 5.36。供试水稻品种为南方双季稻区推广面积较大的万象优华占(杂交籼稻)、象牙香珍(常规籼稻)和美香占2号(常规籼稻)。

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题目：	褐飞虱 RNAi 显微注射试验中麻醉方法的比较
作者：	张朋稳，段至柔，刘常权，彭英传，张万娜，肖海军，张晶
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褐飞虱 RNAi 显微注射试验中麻醉方法的比较

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摘要：显微注射 dsRNA 以实现系统性干扰，是一种有效且能准确评估基因功能的常用方法。试验靶标昆虫由于个体较小、活力强，注射前需要先适当麻醉。待显微注射 dsRNA 完成后，麻醉效应解除，方进一步开展表型测定试验。不同麻醉方法可对昆虫的麻醉效果、麻醉后生理和行为等产生不同程度的影响。因此，选用合适的麻醉方法对显著减少 RNAi 显微注射试验误差，提升干扰效率具有重要意义。本文以褐飞虱为评估对象，比较应用不同配比的乙醚与乙酸乙酯混合液麻醉，以及应用低温麻醉对褐飞虱的麻醉效应，并测定不同的麻醉方法对 RNAi 显微注射试验中褐飞虱存活率的影响。麻醉剂处理随乙酸乙酯的浓度升高，褐飞虱的苏醒时间延长。应用不同麻醉方法对 RNAi 显微注射试验中褐飞虱存活率的影响程度从小到大依次为乙醚:乙酸乙酯（1:2），乙醚:乙酸乙酯（1:1），乙醚，乙醚:乙酸乙酯（2:1），乙醚:乙酸乙酯（3:1），冰上 20 min ，冰上 40 min。推荐乙醚:乙酸乙酯（1:2）混合液作为最优麻醉处理应用于褐飞虱 RNAi 显微注射试验。

关 键 词：褐飞虱；液体麻醉；低温麻醉；显微注射；RNA 干扰

Comparison of Anesthesia Methods in RNAi Microinjection Experiments of Brown Planthopper

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Abstract: Microinjection is an effective and accurate quantitative method to inhibit gene expression, which has a wide range of applications in insect gene function research and pest control. Usually, the tested insects are small and vigorous, and they need to be anesthetized before injection for immobilization. After the anesthesia effect is relieved, further phenotypic determination experiments are required. Different anesthesia methods have different effects on the anesthesia effect, physiology, and behavior of insects. Therefore, the determination of insect anesthesia methods is of great significance to reduce errors in microinjection dsRNA interference experiments. In this paper, the brown planthopper was used as the experimental insect object, and the anesthetic effects of different proportions of ether and ethyl acetate mixed liquid anesthetics and low temperature anesthesia on the brown planthopper were compared. The effects of different anesthesia methods on the survival rate of brown planthopper in microinjection dsRNA interference experiments were further determined. The results showed that the recovery time of brown

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Genetic analysis of grain shape and weight after cutting rice husk

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ABSTRACT. Grain shape and weight are the most important components of rice yield and are controlled by quantitative trait loci (QTLs). In this study, a double-haploid population, derived from the cross of *japonica* CJ06 and *indica* TN1, was used to analyze QTLs for grain shape and weight under two conditions: normal growth with unbroken husk and removing partial husk after flowering. Correlation analysis revealed that these traits, except grain weight, had a connection between the two conditions. Twenty-nine QTLs for grain shape and weight were detected on chromosomes 1 to 3; 6; 8 to 10; and 12, with the likelihood of odds value ranging from 2.38 to 5.36, including 10 different intervals. Some intervals were specifically detected after removing partial husk. The results contribute to the understanding of the genetic basis of grain filling and growth regulation, and provide us some assistance for improving grain plumpness in rice breeding.

Key words: Quantitative trait loci; Grain shape; Grain weight; Rice husk

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Research Paper

Characterization of a Novel Weak Allele of *RGA1/D1* and Its Potential Application in Rice Breeding

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Abstract: Semi-dwarfing improves the lodging resistance and yield of rice, and the vast majority of modern rice varieties harbor the ***sd1*** allele to decrease plant height, resulting in reduced genetic diversity and negative agronomic traits. Thus, exploring alternative sources of dwarfism is imperative for rice breeding. Here, we identified a novel *RGA1* allele, ***d1-w***, from a local ***indica*** variety Xiaolixiang (XLX) using a map-based cloning approach. Compared with other rice varieties, *RGA1* in XLX contained a unique single nucleotide polymorphism that resulted in an additional transcript and reduced functional *RGA1* transcript level. The *RGA1* from Nipponbare was introduced into XLX to estimate the value of ***d1-w*** in rice breeding. Compared with transgenic XLX plants (XLX^{D1}), XLX exhibited reduced plant height, increased stem strength, lower reactive oxygen species accumulation, delayed senescence, stronger photosynthesis, higher grain yield and quality (including external, milling and nutritional qualities), and enhanced resistance to drought and *Rhizoctonia solani*. Therefore, we proposed that the ***d1-w*** allele has potential as an excellent dwarfism resource for rice breeding.

Key words: rice; weak allele; *RGA1*; dwarf germplasm resource; yield; grain quality; drought resistance; sheath blight

As a highly important cereal crop, rice (*Oryza sativa*) is a staple food for more than half of the world's population (Yuan, 2014). The last century witnessed two major breakthroughs in rice breeding, the green revolution in the 1960s and the application of hybrid rice in the 1970s. The green revolution was triggered by the introduction of *semi-dwarf1* (*sd1*) gene and the creation of semi-dwarf varieties (Khush, 2001). Dwarfism is a very important agronomic trait in rice breeding programs, because it can not only enhance lodging resistance and harvest index, but also has better responses to fertilizer (Monna et al, 2002; Hedden, 2003).

Since then, rice breeding for dwarf varieties has attracted intensive interest from breeders, and more than 80 dwarf mutants have been characterized according to the China Rice Data Center (https://www.ricedata.cn/gene/). There are various reasons for plant dwarfing, including phytohormone-related and hormone-independent pathways. Several phytohormones including gibberellins (GAs), brassinosteroids (BRs), strigolactones (SLs), 3-indoleacetic acid, abscisic acid and ethylene influence crop height (Ashikari et al, 1999; Hong et al, 2002; Sazuka et al, 2009; Yaish et al, 2010; Qi et al, 2011; Alder et al, 2012). Most other dwarf genes that act in non-hormone manner are involved in cell wall development, cytosolic glutamine synthetic pathway, RNA editing, cell division, ubiquitin-proteasome pathway and fatty acid metabolism (Liu et al, 2018). Dwarfing-related genes involved in GAs, BRs and

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OsPLS4 Is Involved in Cuticular Wax Biosynthesis and Affects Leaf Senescence in Rice

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Leaf senescence is one of the most common factors that affects the growth and yield of rice. Although numerous genes affecting leaf senescence have been identified, few involved in cuticular wax synthesis have been described for rice premature leaf senescence. Here, we cloned and characterized *Premature Leaf Senescence 4 (PLS4)* in rice (*Oryza sativa*), which encodes a putative 3-oxoacyl-reductase in the fatty acid biosynthetic pathway. Subcellular localization of OsPLS4 was observed in the chloroplast. A single nucleotide substitution in *OsPLS4* reduced leaf cuticular wax, and the expression levels of most wax biosynthesis-associated genes were downregulated. TEM showed chloroplast development were defective in the *pls4* mutant. Further investigation revealed that the chlorophyll (Chl) content was reduced in the *pls4* mutant compared with the WT and that the photosynthesis rate was lower, which caused ROS dramatic accumulation at the heading stage. These results confirmed premature leaf senescence in *pls4* plants. Cold treatment indicated that the mutant was more sensitive than the WT was to cold stress. Together, all the above results indicate that the *OsPLS4* mutation affects cuticular wax biosynthesis and chloroplast development in rice, causing reduced cuticular wax and premature leaf senescence.

Keywords: chloroplast, leaf senescence, cuticular wax, fatty acid synthesis, chilling stress, *Oryza sativa*

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INTRODUCTION

Rice (*Oryza sativa*) is one of the most important cereal crop species worldwide and is consumed by more than half of the global population. Leaf senescence is the final process of leaf development, during which time intracellular organelles and macromolecules are actively destabilized to relocate nutrients into developing tissues or storage organs (Sakuraba et al., 2016). Premature leaf senescence affects rice yields and quality by reducing photosynthetic efficiency and the accumulation of nutrients (Yang et al., 2016; Mao et al., 2017). Hence, understanding the process of premature leaf senescence and the relevant molecular mechanisms could be beneficial for crop breeding.

A large number of senescence-associated genes (SAGs) have been identified, and these genes seem to function in various biological processes, such as the degradation of chloroplasts, the

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评述与展望
Reviews and Progress

精氨酸酶在植物胁迫应答中功能研究进展

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摘　要　精氨酸酶是精氨酸代谢的关键酶，催化 L-精氨酸水解产生 L-鸟氨酸和尿素，维持体内精氨酸的动态平衡，参与尿素循环及氮素再利用等过程，对植物生长发育极其重要。本文概述了精氨酸酶在植物精氨酸代谢途径中的作用，综述了精氨酸酶在植物非生物胁迫和生物胁迫响应的最新研究进展，并从参与 ABA/JA 途径、调控直接或间接代谢产物(脯氨酸, 多胺, 一氧化氮)等多个角度详细解析植物精氨酸酶调控植物抗逆的分子机制，旨在为进一步的研究和育种实践提供启示。

关键词　植物; 精氨酸酶; 精氨酸代谢; 非生物胁迫; 生物胁迫

Research Progress on the Function of Arginase in Plant Stress Response

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Abstract　Arginase catalyzes the hydrolysis of L-arginine to L-ornithine and urea, is one of key enzymes in plant arginine metabolism. The plant arginase plays important roles in maintaining the dynamic equilibrium of arginine content, urea cycle, nitrogen reuse and so on. Thus, arginase is extremely important for plant growth and development. This review summarized the roles of arginase in plant arginine metabolism, detailed the latest research progress for functions of arginase in response to abiotic/biotic stress, and discussed its molecular mechanisms in detail (involvement in ABA/JA pathway, regulation of proline, polyamine and nitric oxide). This paper will provide some meaningful clues for the plant stress tolerance research and crop breeding.

Keywords　Plant; Arginase; Arginine metabolism; Abiotic stress; Biotic stress

精氨酸酶(Arginase, E.C.3.5.3.1)又称 L-精氨酸脒基酶(L-arginine amidinase)或 L-精氨酸脒基水解酶(L-arginine amidinohydrolase)，是植物体内目前已知的唯一产生脲的酶。精氨酸酶特异性催化 L-精氨酸(Arginine)水解生成 L-鸟氨酸和尿素，维持生命体内 L-精氨酸的动态平衡，参与尿素循环等多个重要的代谢过程。精氨酸酶需要整合二价金属离子激活其活性，大多数物种的精氨酸酶激活剂是 Mn^{2+}，但 Ni^{2+}、Co^{2+}、Fe^{2+}等也具有促进酶活性的能力(Marino et al., 2013)。植物精氨酸酶的催化机制与动物和微生物来源的精氨酸酶相似，但它们的结构存在一定差异。哺乳动物中精氨酸酶通常以三聚体形式存在(Jenkinson et al., 1996)，微生物中精氨酸酶除三聚体外还可形成六聚体(Zhang et al., 2013; 赵齐等, 2018)；而植物中不存在三聚体，通常以四聚体及以上的多聚体形式存在(Hwang et al., 2001; Todd et al., 2001)。在进化上，植物精氨酸酶仅形成一个单系簇，明显不同于动物和微生物中的精氨酸酶家族成员(Todd et al., 2001; Chen et al., 2004)。此外，相比动物和微生物，植物精氨酸酶的结构更为复杂，它与胍基酶亲缘关系较近，存在部分相同的保守结构域(Chen et al., 2004)。因此，植物精氨酸酶既有精氨酸酶活性又有胍基化酶的活性，功能更为复杂(Sekula, 2020)。哺乳动物和微生物中的精氨酸酶只产生尿素，而植物中精氨酸酶与脲酶的联合形成尿素循环，在植物氮素重吸收中起关键作用(King and Gifford, 1997)。精氨酸酶在植物生长发育过程和胁迫应答反应中发挥着十分重要的作用。一方面，精氨酸酶催化精氨酸分解提供氮源，同时通过调控尿素循环和氮素代谢，来调控植物种子萌发、幼苗生长、根系发育、花器官的发育、及籽粒的形成和果实的生长等

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Rice husk ash addition to acid red soil improves the soil property and cotton seedling growth

Mengyao Yin, Xuan Li, Qian Liu & Feiyu Tang✉

Red soil is characterized by poor physico-chemical properties and low nutrient availability. The present study aimed to examine rich husk ash (RHA) incorporation into red soil at various rates effects on its properties and the growth of cotton seedlings under a plug-seeding in tray experiment. Bulk density was decreased, and water holding capacity and total porosity were increased in red soil with increasing application rate of RHA. The addition of RHA counteracts the acidity of red soil and improves the nutrient availability to plants. The RHA incorporated soils favored the growth of cotton seedlings with improved shoot morphological traits and root architectures. The application rate at a volume ratio of 1:1 of RHA to red soil was found to be optimal for growing cotton seedlings in the present study. The mixture of RHA and red soil at a 1:1 volume ratio plus 2 g L^{-1} super absorbent polymers exhibited a high nursing seedling efficiency comparable to a commercial growing media under the condition of foliar application of mepiquat chloride at the one-true-leaf stage. RHA can be a promising substitute for peat as growing media for nursing cotton seedlings.

There are around 10.8 Mha of red soil in Jiangxi province China representing 64% of the total land area[1]. Red soil is derived from Quaternary red clay and categorized as Ferralic Cambisol[2,3], which is characterized by poor chemical and physical characteristics such as low pH value and cation exchange capacity (CEC), low fertility (scarcity of potassium K, phosphorus P and calcium Ca, etc.), and high content of activated aluminum ion (Al^{3+}), bad aeration and thin organic soil layer[1,3]. Cotton is grown widely in the hill red soil region of the middle-north section of Jiangxi province as a staple industrial crop[4]. It is difficult for the type of soil to produce comparatively high cotton lint yield due to its intrinsic drawback[5]. Thus, it is imperative to ameliorate the physical, chemical and biological properties of red soil for further enhancement of cotton productivity.

Jiangxi province is known as the largest third paddy rice production region in China with an annual production area of 3.30 Mha and a total yield above 20 million tons over the last decade[6]. Rice husk is a main byproduct during the milling process of paddy rice accounting for about 20–22% of rice kernel by weight[7,8]. The disposition of rich husk remains a main issue for the rice mill industry. Inappropriate disposition methods such as onsite burning, open dumping or land-filling may bring serious threats to environmental sustainability[8]. Rice husk can be used as fuel to generate electricity on a commercial scale[9]. The residue ash is called rice husk ash (RHA) after the combustion of rice husk. Depending on whether the combustion is complete or incomplete, rice husk ash is classified as white (WRHA) and black (BRHA) ones, or RHA1 and RHA2 with RHA1 being longer exposed to furnace than RHA2[10]. At present, RHA is mainly utilized as a pozzolanic material, adsorbent and source of silica, etc.[11], but its usage in the agriculture industry is still scarce.

RHA is rich in chemical elements like K, P, Ca, Magnesium (Mg) and silicon (Si), and moderately alkaline and has considerable neutralizing power which confers it an application of fertilizer[10,12]. RHA contains three-layered structures: internal, external and interface with interstitial and honeycombed pores[11]. Scanning electron micrograph (SEM) photograph of RHA indicated its high porosity leading to a huge specific surface area (SSA) and superior absorptive ability[13]. Similarly, Singh et al. (2019) also observed the presence of various macro- and micro-pores on the surface of RHA[14]. Thus, RHA can be employed to remediate the heavy metal contaminated soil. The incorporation of RHA to Pb contaminated soil mitigated Pb damage to *R. communis*, and enhanced the uptake of nutrients and the activities of antioxidant enzymes[15]. RHA significantly reduced inorganic arsenic (As) accumulation in rice grains[16]. In addition, RHA has been widely used as an absorbent for the removal of lead (Pb(II) and mercury (Hg(II)) from an aqueous solution[11]. In comparison to its role as a soil amendment, the utilization of RHA as growing media has drawn much less attention[17]. Virtually, RHA is a potential substitute for peat in growing media due to its chemical and physical attributes similar to biochar which is deemed as a

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淹水缓解直播早籼稻苗期低温冷害的生理特性研究

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Study on Physiological Characteristics Behind Mitigative Effects of Flooding on Low Temperature-caused Chilling Damage to Direct Seeded Early *indica* Rice at the Seedling Stage

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Abstract:【Objective】It is important to explore the effects of flooding on the growth of direct seeded early *indica* rice seedlings under low-temperature stress, and lay a physiological basis for direct seeded rice production and stress-resistant cultivation in South China.【Method】The cold-tolerant cultivar Xiangzaoxian 6 and cold-sensitive cultivar Zhongjiazao 17 were used as materials in this experiment, and three treatments each lasting three days including low temperature treatment (8°C), low temperature & flooding treatment (8°C plus flooding) and ambient temperature as control treatment (25°C) were designed to analyze the physiological characteristics including agronomic characters, antioxidant enzyme activities, osmotic regulation substances contents, photosynthesis enzyme activities and endogenous hormone contents of rice seedlings.【Result】 Compared with low temperature (LT), the seedling height, fresh weight, dry weight and T3 (the 3rd leaf from top) leaf length of different cultivars significantly increased after three days at low temperature under flooding (LTF), and the root number, root length, T1 (the first leaf from top) leaf length and T2 (the 2nd leaf from top) leaf length also increased. Flooding could reduce the damage induced by low temperature to the agronomic characters of rice seedlings with the cold-tolerant cultivar Xiangzaoxian 6 less affected as compared with cold-sensitive cultivar Zhongjiazao 17. In addition, compared with LT, LTF significantly decreased the antioxidant enzymes activities (SOD, POD, CAT), soluble protein contents, osmotic regulatory substances contents (MDA, proline) and endogenous growth inhibitory hormone contents, ABA content, whereas increased the content of endogenous growth promoting hormone GA_3 under low temperature; Flooding could alleviate the accumulation of reactive oxygen species (ROS) and the aggravation of membrane lipid peroxidation in plants, and improve the regulation of endogenous hormones in plants. Meanwhile, LT and LTF significantly decreased the contents of chlorophyll and ATP in leaves, resulting in the decrease of photosynthetic enzyme activities (Rubisco, PEPCK); but LTF had lower damage than that of LT, and LTF could play a mitigating role. After the recovery treatment, the physiological activity indexes of rice subjected to LTF were close to the level of CK, whereas the self-response mechanism of cold-tolerant cultivar could reduce the damage caused by low temperature stress. 【Conclusion】 Low temperature treatment affected the growth characteristics and photosynthetic enzyme activity of direct seeded early *indica* rice seedlings, and increased the antioxidant protective enzyme activity and osmotic regulation potential of leaves, but flooding treatment help to alleviate the physiological damage of leaves caused by low-temperature stress.

Key words: early *indica* rice; direct seeded rice; low temperature; flooding; physiological characteristics

摘　要：【目的】 探究淹水对低温胁迫下直播早籼稻幼苗生长的影响，为南方稻区直播稻生产与抗逆栽培奠定生理基础。【方法】 以耐冷品种湘早籼 6 号和冷敏感品种中嘉早 17 为材料，设置低温处理(8℃)、低温淹水处

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生物酶法提取铁观音茶梗中茶多酚工艺技术研究

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摘　要:以乌龙茶类的铁观音为试验原料,探讨其茶梗中茶多酚提取工艺的优化。在单因素试验的基础上,选取复合酶添加量、料液比、酶解温度为试验因子,以茶多酚提取量为响应值,通过 Box-Behnken 设计优化来构建模型并进行数据分析。研究结果表明,铁观音茶梗中茶多酚提取的最佳工艺参数为:复合酶添加量 1.2% (以底物质量计) ,料液比 1∶20 (g/mL) ,酶解温度 48 ℃,在此工艺条件下,茶多酚提取量为 82.26 mg/g,达到预测最优值。

关键词:茶梗;酶法;响应面法;茶多酚;提取工艺

Study on Technique of Compound Enzyme Extraction of Tea Polyphenols from Tieguanyin Tea Stalks

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Abstract: In the present study, oolong tea Tieguanyin stalks were used as raw materials, to optimize the compound enzyme extraction technology of tea polyphenols from the oolong tea stalks by Box-Behnken response surface methodology. The single-factor experiment and response surface methodology were adopted to study the effects of compound enzyme addition, ratio of solid to liquid and enzymatic hydrolysis temperature on the extraction yield of tea polyphenols from oolong tea stalks. The results showed that the best technology parameter combination of the extraction of tea polyphenols from tea stalks were as follows: enzyme addition amount was 1.2% (based on substrate weight) , ratio of solid to liquid was 1∶20 (g/mL) and enzymatic hydrolysis temperature was 48 ℃. Under these conditions, tea polyphenols extraction content was 82.26 mg/g, which reached the predicted optimal value.

Key words: tea stalks; enzymatic method; response surface experiment; tea polyphenols; extraction technology

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随着我国茶产业经济的迅速发展,茶叶加工及深加工的规模与日递增,同时,茶产品加工过程中产生了大量废弃物,如茶渣、茶梗、茶碎末等。其中,茶梗以乌龙茶中的铁观音茶最为常见[1],茶梗中主要含有茶多酚[2]、茶多糖[3]、生物碱[4]、芳香类物质[5]等活性成分,

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根系分泌物对紫云英油菜间作的响应

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摘　要　根系分泌物是植物与土壤进行物质交换和信息传递的重要载体，也是间作体系中作物-土壤-微生物互作的重要调控者。为进一步揭示间作体系中作物之间的互作机制，本研究通过紫云英单作、油菜单作和紫云英油菜间作，重点分析了紫云英油菜间作下根系分泌物的响应特征。结果表明: 共检测到紫云英和油菜根系分泌物 391 种，定性 93 种，包括了 9 种代谢物类型，其中有机氧化物含量最高，主要是以核糖醇的形式存在。不同种植模式中，紫云英、油菜的根系分泌物含量差异显著，紫云英油菜间作时根系分泌物特征与油菜单作相似，与紫云英单作差异较大。不同种植模式的差异根系分泌物中，仅 9-芴酮 1 与其他差异分泌物间呈负相关关系。不同种植模式的差异根系分泌物主要为苯系物、脂类和类脂分子、有机酸及其衍生物、有机氧化物等，其中苯系物、脂类和类脂分子是表征紫云英、油菜根系分泌物变化的重要类型。可见，紫云英油菜间作改变了作物的根系分泌物特征，其变化特征与苯系物、脂类和类脂分子关系密切。

关键词　间作; 根系互作; 根系分泌物; 紫云英; 油菜

Responses of root exudates to intercropping of Chinese milk vetch with rape.

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Abstract: Root exudates are important carriers for material exchange and information transfer between plant and soil, and important regulators of crop-soil-microorganism interaction in intercropping systems. We examined the interaction between crops in intercropping system by setting three treatments, monoculture Chinese milk vetch, monoculture rape and Chinese milk vetch intercropped with rape. The responses of root exudates were emphatically analyzed. The results showed that 391 root exudates were detected, with 93 of which being identified and divided into nine types of metabolites. Among them, organooxygen compounds were the most abundant, mainly in the form of ribitol. Under different planting patterns, root exudates of Chinese milk vetch and rape were significantly different. The characteristics of root exudates in intercropping were similar to monoculture rape, but significantly different from monoculture Chinese milk vetch. Among the root exudates in different planting modes, only 9-fluorenone 1 was negatively correlated with others. The differential root exudates were mainly benzenoids, lipids and lipid-like molecules, organic acids and derivatives, and organooxygen compounds. The benzenoids, lipids and lipid-like molecules were important types that characterized the changes of root exudates of Chinese milk vetch and rape. Chinese milk vetch intercropping with rape changed the characteristics of root exudates, which were closely related to benzenoids, lipids, and lipid-like molecules.

Key words: intercropping; root interaction; root exudates; Chinese milk vetch; rape.

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稻米蒸煮特性QTL定位及与感官食味品质的相关性分析

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摘 要: 稻米蒸煮特性和感官食味品质是稻米品质的重要评价指标,其遗传复杂。为挖掘与利用优异的稻米品质基因,本研究利用籼稻昌恢121为受体亲本和优质粳稻越光为供体亲本构建的一套染色体片段置换系(CSSL),对稻米的吸水率(WA)、延伸率(CRE)和膨胀率(VE)3个蒸煮特性进行QTL定位。共检测到4个QTL,分布于第8和第11号染色体上。*qWA*-8、*qCRE*-8、*qCRE*-11和*qVE*-11的表型贡献率和加性效应值分别为25.05%、25.94%、27.95%、41.16%和-25.68、-8.00、8.30、30.31,其中位于第11号染色体上分子标记RM287附近的*qCRE*-11和*qVE*-11为新鉴定的QTL。对稻米蒸煮特性与感官食味品质性状进行相关性分析,发现两者之间无相关性,稻米蒸煮特性WA、CRE与VE之间两两呈极显著正相关,米饭外观(AP)、香味(ARM)、味道(TA)、口感(TE)和感官评分(SS)之间两两呈极显著正相关。本研究结果为了解稻米蒸煮特性与感官食味品质性状间的相互关系,挖掘优异等位基因以及稻米品质的遗传改良提供了一定的理论依据。

关键词: 感官食味品质; 蒸煮特性; 数量性状位点(QTL); 染色体片段置换系(CSSL); 相关性分析
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水稻(*Oryza sativa* L.)是一种重要的谷物作物,为世界一半以上的人口提供主食。杂交稻生产技术的成功应用,使水稻产量得到了极大提高,但对稻米品质的改良仍不尽人意,稻米品质仍有较大的提升空间[1]。稻米的品质性状包括外观品质、加工品质、蒸煮食味品质、营养品质和特殊品质,其中广大消费者最关心的是稻米的蒸煮与感官食味品质。已有研究表明,稻米的蒸煮和感官食味品质遗传较复杂,受多种因素影响[1-2]。淀粉是稻米的主要组成成分,约占稻米物质组分的90%[3-6]。前人对稻米淀粉理化特性与食味品质之间的关系进行了大量研究,认为直链淀粉含量(amylose content,AC)是影响稻米食味品质的最主要因素,凝胶稠度(gel consistency,GC)和糊化温度(gelatinization temperature,GT)也是重要影响因素[7]。参与淀粉生物合成的基因对稻米食味品质起着重要的调控作用[8],目前有20多个调控稻米淀粉生物合成的基因已经鉴定和克隆,包括*Wx*[9]、*ALK*[10-13]、*BEIIb*[14]、*RAG2*[15]、*SSG4*[16]、*Du1*[17]、*SSI*[18]、*SSII*[19]、*SSIII*[11-12]、*ISA*[19]、*AGPlar*[19]、*AGPiso*[13]、*PUL*[19]等。

鉴于淀粉理化特性与稻米食味品质性状的关系,以往对稻米食味品质的遗传调控研究主要集中在直链淀粉含量、糊化温度、凝胶稠度等间接理化指标,对于稻米吸水率(water absorption,WA)、延伸率(cooked rice elongation,CRE)和膨胀率(volume expansion,VE)等蒸煮特性的遗传调控研究较少。研究发现在煮熟的稻米中,高品质的水稻品种具有更大的延伸长度、更小

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QTL Mapping of Rice Cooking Characteristics and Correlation Analysis of Sensory Food Quality

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Abstract: Cooking characteristics and sensory eating quality of rice are important evaluation indexes of rice quality, and the genetic basis for these traits are complex. To explore and utilize the excellent rice quality genes, a set of chromosome segment substitution lines (CSSL), derived from a cross between *indica* Changhui 121 (as the recurrent parent) and high-quality *japonica* Koshihikari (as the donor parent), was used to analyse QTL for water absorption (WA), elongation (CRE) and volume expansion (VE) of cooked rice. Four QTL were detected on chromosomes 8 and 11. The phenotypic contribution rate and additive effect value of *qWA*-8, *qCRE*-8, *qCRE*-11 and *qVE*-11 were 25.05%, 25.94%, 27.95%, 41.16% and -25.68, -8.00, 8.30, 30.31, respectively. Among them, *qCRE*-11 and *qVE*-11 located near the molecular marker RM287 on chromosome 11 were newly identified QTL. Correlation analysis between cooking characteristics and sensory eating quality traits of rice showed that there was no correlation between them. Cooking characteristics WA, CRE and VE were significantly positively correlated, and significant positive correlations were also found among appearance (AP), aroma (ARM), taste (TA), texture (TE) and sensory score (SS) of rice. The results would provide a theoretical basis for understanding the relationship between rice cooking characteristics and sensory food quality, exploring excellent alleles and genetic improvement of rice quality.

Keywords: sensory food quality, cooking quality, quantitative trait locus (QTL), chromosome segment substitution lines (CSSL), correlation analysis

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Letter

OsHG3 Affects Rice Palea Development, Grain Yield and Quality

Floral development is one of the most important determining factors of grain yield in cereal crops (Immink et al, 2010). The rice inflorescence is composed of the spikelet, a specific structural unit in poaceae, which is greatly different from typical eudicots. However, several genes encoding the homologous of the proteins in ABCDE model were also found in rice genome (Luo and Zhu, 2002). Lemma and palea are grass-specific floret tissues which interlock with each other to protect the inner floral organs and seeds from attack by pathogens, insects or abiotic stresses. Meanwhile, they have photosynthetic ability and provide amino acids and carbohydrates to grouting seeds. Therefore, development of lemma and palea has close relationship with rice grain yield (Abebe et al, 2004). Lemma and palea are different tissues with different appearance, and have variable number of vascular bundles and trichomes in membranous margin region (Nagasawa et al, 2003; Wang et al, 2019). Only limited genes involved in development of lemma and palea have been identified (Sang et al, 2012; Toriba and Hirano, 2014; Lombardo and Yoshida, 2015; Meng et al, 2017). However, mutants for these genes exhibit abnormal development not only in lemma or palea, but also in ovule development, lodicule identity, female-male determinacy, and flower patterning (Cheabu et al, 2019). Thus, it is suggested that all these genes maybe not the key factors which specify lemma or palea identity, and the identities of lemma and palea are still controversial. More works need to be done to fully understand the molecular mechanism of glume development in rice.

We obtained two hooked-glume lines, BC37 and BC94 (Fig. 1-A), which were isolated from a large recombinant inbred line (RIL) population of 9311 and PA64S (Gao et al, 2013). Several sets of crosses were used to detect the genetic model of the hooked glume phenotype. F$_1$ of both reciprocal crosses of BC37 and BC94 showed a similar glume phenotype with the parents (data not shown), indicating that the hooked-glume phenotype in both two lines are controlled by the same gene. Thus, we used BC37 for further study, because it had a more typical hooked-glume phenotype than BC94. All the F$_1$ plants of BC37 and three normal-glume cultivars (Nipponbare, TN1 and CJ06) showed normal glumes, as well as LYP9 (the F$_1$ of 9311 and PA64S) (Fig. 1-A and Supplemental Fig. 1). Moreover, normal and hooked glume plants showed a typical segregation ratio of 3:1 in the F$_2$ segregating populations of these crosses (Supplemental Table 1). These results indicated that a single recessive nuclear gene controls the hooked-glume phenotype of BC37 and BC94. The hooked-glume allele was derived from PA64S, because F$_1$ of BC37 and 9311 presented a normal glume phenotype, while F$_1$ of BC37 and PA64S was hooked-glume (data not shown).

F$_2$ population from a cross of BC37 and Nipponbare was used for mapping the hooked-glume gene. A total of 841 individuals with the hooked-glume phenotype from 3 882 F$_2$ population were collected. Bulked segregant analysis (BSA) was used to produce a primary map of *OsHG3*. A bulk DNA pool from 33 BC37/Nipponbare F$_2$ hooked-glume phenotype individuals was screened with 163 simple sequence repeat (SSR) and sequence tag site (STS) markers uniformly disturbed over 12 chromosomes, and we found that *OsHG3* was linked with RM1022, RM14795, P1, P2, RM6080 and RM6676. Then, the genotyping of 96 individuals was used to confirm the linkage and ensure the location interval. The results indicated the *OsHG3* was mapped to the interval of P1 and P2, with a 6.4 cM genetic distance on the short arm of chromosome 3. To further fine map *OsHG3*, we designed new STS markers (InDel) between RM3280 and RM5748 based on the sequence differences between Nipponbare and PA64S (Supplemental Table 2). The polymorphic primers were subsequently used to screen all the 841 individual genotypes, and narrowed the location of *OsHG3* to a 102 kb segment bracketed by markers P6 and P7 (Fig. 1-B and Supplemental Table 3), which contains 12 open reading frames (ORFs) (Supplemental Table 4).

Genetic backgrounds of BC37 and PA64S are very different from that of 9311, leading to many other phenotypic and physiological differences besides hooked-glume, and interfering the gene expression detection. Therefore, the near isogenic line (NIL) for this hooked-glume gene, NIL-*OsHG3*^{PA64S}, in the 9311 background was generated from the BC$_6$F$_2$ generation by repetitive backcross to 9311 and marker-assisted selection. The graphical genotype showed that most genome was converted to 9311, except few regions (Supplemental Fig. 2-C). In the vegetative stage, there was no significant morphological difference between

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Article

Long-Term Straw Return with Reducing Chemical Fertilizers Application Improves Soil Nitrogen Mineralization in a Double Rice-Cropping System

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Abstract: The partial replacement of chemical fertilizer with straw return is considered an effective method for improving the accumulation of organic matter and soil fertility, but the characteristics of soil nitrogen fixation and mineralization in a double-cropped rice paddy system are unclear. Based on a 12-year field experiment, we conducted a waterlogged incubation experiment for 49 days to determine the effect of long-term straw return combined with reducing chemical fertilizer application on the dynamic changes of mineralized soil nitrogen (N) content and mineralized N rate under the treatments, including NPK (chemical fertilizers application with straw removal), SBR (straw burned return), and SR (straw return). Results showed that, compared with SBR and NPK, SR significantly increased available nitrogen by 7.4% and 16.5%, respectively, due to the higher ammonium nitrogen and nitrate nitrogen, as well as the total carbon, available phosphorus, and slowly available potassium, suggesting that it could stock a sufficient nitrogen source. During the incubation period, the amount of N mineralization was relatively higher under SR than under SBR and NPK treatments, especially during the later mineralization time, whereas there was no difference in the N mineralization rate. In addition, SR significantly increased soil cumulative N mineralization and N mineralization potential. However, SBR significantly decreased the soil mineralizable N ratio compared with SR and NPK, which may result in a worsening of the N mineralization potential. The results indicated that long-term straw return combined with reducing chemical fertilizer application could significantly improve the N supply capacity of paddy rice field soil to better coordinate the soil N supply and immobilization.

Keywords: long-term straw return experiment; double-cropped rice paddy system; substitution of partial chemical fertilizer; nitrogen mineralization

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1. Introduction

Nitrogen (N) is the most important nutrient that limits the productivity of agroecosystems, and more than 90% of the nitrogen in soil is in the form of organic nitrogen [1]. Only a small part of water-soluble organic nitrogen in soil can be absorbed and utilized by plants directly, and most organic nitrogen can be absorbed and utilized by plants only after mineralization. Soil organic nitrogen mineralization provides available nitrogen for plants, which determines the soil nitrogen supply capacity to a great extent [2]. Factors such as crop residue management, fertilizer application system, and fertilizer and soil characteristics affect the microbial biomass and activity as well as microbial community structure and functioning [3], which, in turn, affects the process of soil organic nitrogen mineralization

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植物铁素(Fe)营养的生理研究进展

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摘　要:铁(Fe)是植物体内发现最早和含量最高的必需微量元素,参与许多生理过程和代谢途径,缺铁将严重影响其生长发育和产量品质。植物源食物中的Fe是动物和人类获取Fe的主要途径,摄入不足将损害其健康。为了充分了解Fe在植物体内的代谢生理,推动富Fe植物的培育和富Fe食物的研发,本文归纳了土壤和植物体内Fe的含量、形态及比例,总结了植物体内Fe的分布与功能,比较了植物应对少量可溶性Fe环境下的不同高效吸收策略,分析了Fe在细胞内和长距离运输中的调控机制。在此基础上,针对以往研究中存在的不足提出展望,认为今后应更多地关注:不同物种间的Fe代谢途径的差异及分子机理、Nramp家族基因如何调控植物缺Fe的吞噬机制、质体中铁蛋白(Fer)的氧化沉淀与还原释放机制和提高植物体内Fe含量及生物有效性的生物强化措施。

关键词:植物;铁;吸收;转运;生理

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Nutrition Physiology of Iron (Fe) in Plants: Research Progress

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Abstract: Iron (Fe) is the earliest discovered and most abundant essential microelement in plants, which is involved in many physiological processes and metabolic pathways, Fe deficiency will seriously affect the growth, development, yield and quality of plants. Fe in plant-derived food is the main source for animal and human to obtain Fe, and insufficient Fe uptake can damage their health. In order to fully understand the metabolic physiology of Fe in plants, and promote the cultivation of iron-rich plants and the development of iron-rich food, in this review, the contents, forms and proportions of Fe in soil and plants were summarized, the distribution and function of Fe in plants were concluded, the different efficient absorption strategies of plants in small amount of soluble Fe environment were compared, and the regulation mechanisms of Fe transport in cells and long-distance in plants were analyzed. Based on the above, some research prospects were discussed in view of the previous research, it is suggested that more attention should be paid to the differences and molecular mechanisms of Fe metabolic pathways among different plant species, the Nramp family genes regulating approach of the docytotic mechanism of Fe deficiency in plants, the oxidation precipitation and reduction release mechanisms of ferritin (Fer) in the plastids, and the biofortification measures for increasing Fe content and bioavailability in plants.

Keywords: plant; iron; uptake; transport; physiology

0 引言

自然界中的铁(Fe)元素含量丰富,约占地壳的5.0%,位列氧、硅和铝之后的第四位,因其可溶性和有效性较低而成为生物体生长的限制因子[1]。Fe是植物

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DISEASE NOTE

First report of *Colletotrichum fructicola* causing anthracnose on loquat in Jiangxi province, China

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Keywords *Eriobotrya japonica* · *Colletotrichum fructicola* · Anthracnose · Identification

Loquat [*Eriobotrya japonica* (Thunb.) Lindl] has high economic and medicinal value, and is widely cultivated in southern China. Anthracnose caused by *Colletotrichum* spp. is an important fungal disease of loquat plants. In September 2019, anthracnose symptoms were observed on 30% of loquat plants in orchards of Nanchang, Jiangxi province, China (28°46′5"N; 115°50′21"E). Lesions on the surface of infected leaves and fruits initially appeared as subcircular or irregularly shaped, brown spots. Later, the center parts of the lesions become gray-white and sunken with a dark brown border. The diseased samples were collected and surface sterilized with 75% ethanol for 30 s, 3% sodium hypochlorite for 3 to 5 min, rinsed three times with sterile water, dried on filter paper, and then plated on PDA medium. The fungal colonies purified on PDA medium had a gray-white cottony growth that later turned brown with age. Aerial mycelium pale grey, dense, cottony. Acervuli absent in culture. Conidia were unicellular, hyaline to subhyaline, subcylindrical with rounded ends, and measured 4.4 to 6.9 µm × 12.7 to 17.0 µm (average: 5.5 × 14.5 µm, n = 60). Appressoria were one-celled, brown, thick-walled, and irregular. Six loci including the ITS, ACT, GAPDH, APN2/MAT-IGS, GAP2-IGS and APN2 were amplified and sequenced (Dowling et al. 2020). The sequences were submitted to GenBank with accession numbers MN837621-MN837623 and MW827228-MW827230, respectively. Obtained sequences showed 99.9% similarity with *C. fructicola* in GenBank with accession numbers MN075755, MN614334, MN525875, MT087541, MF110707 and MF110907, respectively. Multi-locus phylogenetic analysis showed that the present isolate clustered with *C. fructicola* (CBS 125,397 and CBS 130,416), and supported by high bootstrap values. The fungal isolates were identified as *Colletotrichum fructicola* Prihast., L. Cai & K. D. Hyde based on morphology and molecular biology (Weir et al. 2012; Zhang et al. 2015). Pathogenicity was assayed on loquat leaves inoculated with spore suspension (1×10^6 spores/mL), while the other three leaves inoculated with sterile water were used as the control. Five days after inoculation, the inoculated samples showed the typical anthracnose symptoms similar to those observed in the field, whereas the controls were asymptomatic. The pathogen *C. fructicola* was reisolated from the inoculated loquat leaves. To our knowledge, this is the first report of *C. fructicola* causing loquat anthracnose in China.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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稻瘟病菌中小 G 蛋白 Rho3 的假定互作蛋白 MoKin1 的功能分析

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摘　要：小 G 蛋白 MoRho3 在稻瘟病菌生命活动中具有重要的生物学功能。前期研究表明，MoRho3 的缺失对于稻瘟病菌分生孢子的形态建设、附着胞萌发和侵入能力以及对宿主的致病性等表型都存在严重缺陷。为了进一步解析 MoRho3 在稻瘟病菌中的网络调控途径，通过生物信息学的方法预测了 MoRho3 的互作蛋白。在众多假定互作蛋白中，蛋白激酶 MoKin1 与酿酒酵母中 KIN1 和 KIN2 是同源蛋白。在酵母细胞中，KIN1 和 KIN2 可以抑制△rho3 的表型缺陷。为了验证在稻瘟病菌中 MoKin1 与 MoRho3 之间是否存在着相似的调控途径，本研究通过分析 MoKin1 与同源蛋白的进化关系，序列结构，定位状态以及相关的互作蛋白，揭示了 MoKin1 的功能特点，为后续病原菌中 MoKin1 与 MoRho3 互作机制的研究，以及病原菌致病机制的解析提供了新的思路和方向。

关键词：稻瘟病菌；MoRho3；MoKin1；互作分析

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Functional Analysis of MoKin1 as Putative Substrate of the Small GTPase MoRho3 in Rice Blast Fungus, *Magnaporthe oryzae*

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Abstract: Small GTPase MoRho3 plays an important biological role in the rice blast fungus, *Magnaporthe oryzae*. The preamble research elucidated that the deletion of MoRho3 in this fungus caused serve phenotypic defects, such as abnormal morphology of conidia, reduction of germination and penetration of appressoria and reduced pathogenicity. In order to understand the mechanism of the regulatory pathways of MoRho3, we adopted the bioinformatics to search the putative interacting protein of MoRho3. We found the homologus protein of *Saccharomyces cerevisiae* KIN1 and KIN2 in the proteins, named MoKin1. Because the over-expression of KIN1 and KIN2 could rescue some phenotypic defects of *△rho3* in *S. cerevisiae*, in order to verify whether there was a similar regulatory pathway between Mokin1 and MoRho3 in *M. oryzae*, the study revealed the functional characteristics of Mokin1 by analyzing the evolutionary relationship, sequence structure, localization status and related interaction proteins, which would provide a new basis for the further study of the interaction between Mokin1 and MoRho3 and the pathogenic mechanism of *M. oryzae*.

Keywords: *Magnaporthe oryzae*; MoRho3; MoKin1; interaction analysis

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