9 四大类培养—拔尖型人才培养

惟义（农学）实验班基本情况

江西农业大学文件

文件首页

赣农大发〔2015〕29号

关于印发《江西农业大学“惟义实验班”管理暂行办法》的通知

校属有关单位：

为进一步推动高等农林教育综合改革，提高人才培养质量，促进“卓越农林人才教育培养计划”项目的实施，学校决定设立“惟义实验班”（简称惟义班）。为做好“惟义班”的运行工作，现制定相关管理办法并予以印发，请遵照执行。

江西农业大学

2015年7月7日

惟义农学实验班建设与管理补充规定

为推动高等农林教育综合改革，促进“卓越农林人才教育培养计划”项目的实施，2015年开始，江西农业大学以江西省第一位中国科学院学部委员、世界半翅目昆虫分类专家、江西农学院首任院长杨惟义先生名字命名，设立特色实验班——惟义农学实验班（以下简称“惟义班”），旨在探索人才培养新模式，全面促进提高人才培养质量。

一、围绕一个培养目标

以“本—硕”连续培养为主体、以综合素质和创新能力培养为核心，培养适应国家和社会发展需要，具有优良的思想道德品格、高度的社会责任感和强烈的团队合作精神，具备深厚的科学和人文素养、扎实的专业知识和技能、超凡的自主学习和实践创新能力，能够引领现代农业和适应经济社会发展需要，“懂农业、爱农村、爱农民” 的农科类高素质拔尖创新型人才。

二、实行两类教育模式

1、强化专业教育。

以宽厚通识教育为基础，第1-2学年实施人文素养和科学精神相结合的通识教育，加强科学基础和人文基础学习及科学研究思维和基本技能训练，构建多元化知识结构，为终身学习和可持续发展奠定扎实基础。

以拔尖创新能力为目标，第3-4学年进行严格的专业学习和训练，在具有较深农学专业造诣的教师指导下进行专业知识的学习，参与相关学科领域的科学研究。

2、兼顾个性化教育。

在强化专业教育的基础上，结合现有教学资源和学生的兴趣特长，通过实行本科生导师制，为学生制定个性化的培养方案。学校以探索和研究的教学方式促进学生学会认知创造，开拓视野，扩大知识面，强化科研训练、实践教学和社会实践。

三、强化三项班级管理

1、严格选拔标准。“惟义班”招收热爱农业，具备良好的思想政治素质和较强的社会责任感，身心健康的江西省省内理工类一本批次或省外理工类二本批次录取的学生，要求成绩优秀，高考英语单科成绩105分以上（高考英语卷面满

分值不是150分的按相应比例折算），或者大学一年级第一学期英语考试成绩75分以上，或者高中以来在生物类学科竞赛、科技创新活动中获得省级以上奖励。

2、实行分流管理。惟义班专家组在每学期末，从品德素养、学业成绩及自主学习能力、组织管理能力、实践创新能力等方面对学生进行综合考核，考核不合格的学生分流到普通班学习。

3、落实小班教学。教学过程实行小班授课，班级人数不超过25人，并配备专用教室。

四、突出四大办学特色

1、强化科研素质。加强科研训练，要求导师吸纳“惟义班”学生加入自己的科研团队，开展科学研究工作，重点培养学生的科研能力和科研精神以及解决实际问题的能力。。

2、突出创新能力。强化实践教学和实践训练，设立“惟义班”创新科研项目支持学生进行创新训练，聘请优秀老师指导学生进行创新创业训练、职业发展规划和创新实践。

3、创新培养途径。在校内培养的基础上，安排专项经费，按一定比例或全额资助学生到国内外知名大学、科研院所和企业进行专业拓展学习和科研训练，开阔学生的专业视野。

4、强化师资配备。安排教学经验丰富、具有改革创新精神的副教授以上职称或具有博士学位的专任教师担任课程教学，并聘请教学名师进行授课，邀请业内名家开展学术讲座。

五、享受五重优惠待遇

1、对符合条件的学生，优先免试推荐攻读校内外硕士研究生；对特别优秀者，学校积极帮助其通过“国家建设高水平大学公派研究生项目”等资助进入国际一流大学进行培养或攻读学位。

2、“惟义班”班学生在进入实验室、图书资料借阅等方面享受研究生同等待遇。

3、设立“特色实验班级”优秀学生奖学金和“江西天涯种业奖学金”。“特色实验班级”优秀学生奖学金覆盖面100%，且奖学金额度是普通优秀学生奖学

金的 2 倍；江西天涯种业公司与我校签订“惟义农学实验班”定向捐赠协议，对“惟义班”每位学生进行定向资助。

4、在国家奖助学金、评优评先、学生干部选拔等方面对“惟义班”指标倾斜或优先考虑。

5、学生在修满学分，获得毕业证书、学士学位证书的同时，由学校为其颁发优秀本科毕业生荣誉证书。

江西农业大学农学院

2016 年 9 月

农学惟义实验班人才培养方案

一、专业培养目标

本专业培养具备作物生产与管理、作物遗传育种等方面的基本理论、基本知识和基本技能，具有创新意识与能力，综合素质高，适应能力强，能在农业教育、农业科研、农业行政、涉农企业及其它相关的部门或单位从事与农学有关的教学与科研、技术与设计、开发与推广、经营与管理等工作的拔尖创新型农学专业人才。

二、专业培养规格和素质要求

1. 培养规格

本专业学生应具有良好的思想品德、社会公德和职业道德，具有宽厚的自然科学的基本知识和人文素养，熟练掌握农业生物科学、农业生态科学、植物生长发育和遗传规律等农学类基本理论和基本知识，具备作物生产与管理、作物新品种选育、种子生产与经营等方面的基本技能和科研创新能力。

2. 素质要求

（1）素质结构

1）具备良好的思想道德素质：包括正确的政治方向，遵纪守法、诚信为人，有较强的团队意识和健全的人格。

2）具备良好的文化素质：掌握一定的人文社科基础知识，具有较好的人文修养；有较好的外语能力，具有国际化视野和现代意识。

3）具备良好的专业素质：受到严格的科学思维训练，掌握比较扎实的农学类基础理论和先进的科学研究方法，具有求实创新的意识和精神。

4）具备良好的身心素质：包括健康的体魄、良好的心理素质和生活习惯。

（2）能力结构

1）学习的能力：具有良好的自主学习能力、有良好的语言表达与交流能力。

2）应用的能力：具有综合运用所掌握的理论知识和技能、从事农学及其相关领域科学研究的能力；具有良好的计算机及信息技术应用能力。

3）创新的能力：具有较强的创造性思维能力、开展创新研究和科学探索的能力。

（3）知识结构

1）具备扎实的数学、物理、化学等基本理论知识；

2）掌握农学类学科的基本理论、基本知识；

3）具备植物生产与管理的基本技能和方法；

4）掌握科学研究与实践工作的基本方法，了解农业生产和科学技术的科学前沿和发展趋势；

5）掌握科技文献检索、资料查询的基本方法，具有独立获取知识、科学研究、信息处理和创新的基本能力。

三、专业主干课程

大学英语、计算机应用基础、高等数学、马克思主义基本原理、植物生理学、普通遗传学、植物保护学、土壤肥料学、作物栽培学各论、耕作学、作物育种学总论、种子学

四、学制与学位

学制 4 年，毕业后授予农学学士学位。

五、学时学分分配及毕业学分要求

本专业教学计划课内总学时为2528学时，其中必修课学时占总学时 71.52%，选修课学时占总学时 28.48%；在必修课学时中，理论学时数占 82.63%，实验学时数占 17.37%；实践教学 34.7 周。

本专业学生毕业应取得最低学分数为192.7学分，其中必修课为113.0学分，选修课最低为45.0学分，实践环节 34.7 学分。在选修课学分中，公共选修课学分不低于 7 学分，专业类选修课不低于 38.0 学分。

学生入校后需选定导师，并在导师的指导下制定修读计划。

江西农业大学农学院

2018 年 1 月

惟义实验班开班仪式


江西农业大学2015级惟义农学实验班开班
暨天涯种业有限公司定向捐赠助学签约仪式
江西农业大学
2015级惟义农学实验班


江西农业大学2016级惟义农学实验班开班
暨天涯种业定向 赠助学仪式
中国银行 转账支票
20171030
伍万元整
¥5000000
江西天涯种业有限公司


江西农业大学2017级惟义农学实验班开班
暨天涯种业定向捐赠助学仪式

惟义农学班毕业生考研升学情况统计

年份	人数	考研升学人数	考研升学率
2019 年	21	19	90.48%
2020 年	23	22	95.65%
2021 年	24	19	79.17%
2022 年	21	18	85.71%
平均升学率			**87.75%**

惟义班第二课堂及教学实践（部分）

主题团日活动“访惟义足迹，弘惟义精神”

参加班班唱红歌比赛

参加中国植物生理与植物分子生物学年会志愿服务工作

参加农学专业综合实践活动

参加惟义学术论坛

参加作物栽培学教学实践

惟义（农学）实验班学生近年来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	Genome-WideAssociationStudy RevealsaGeneticMechanismofSalt To lerance Germinability in Rice (OryzasativaL.)	卢昌盛等	惟义农学 2001
2	黑米的营养功能及综合利用研究进展	熊艳珍等	惟义农学 1801
3	有色稻米种质及环境因素对其色泽影响的研究进展	黄紫萱等	惟义农学 1701
4	OsPLS4IsInvolvedinCuticularWax Biosynthesis and Affects Leaf Senescence in Rice	瞿子扬等	惟义农学班 1601
5	A Novel Dominant Allele from 93-11,ES(4),Represses Reactive Oxygen Species Scavenging and Leads to Early-Senescence in Rice	淦聪等	惟义农学 2001
6	Genetic analysis of rice seed recovery under low-temperature onditions using a new CSSL population with a high-density genetic map in rice	邓浩东等	惟义农学 1701
7	Genetic analysis of germinating ability under alkaline and neutral salt stress by a high-density bin genetic map in rice	邓浩东	惟义农学 1701

惟义农学班毕业生考研升学情况统计

年份	人数	考研升学人数	考研升学率
2019 年	21	19	90.48%
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2021 年	24	19	79.17%
2022 年	21	18	85.71%
平均升学率			**87.75%**

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ORIGINAL RESEARCH
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Genome-Wide Association Study Reveals a Genetic Mechanism of Salt Tolerance Germinability in Rice (*Oryza sativa* L.)

***Caijing Li*[1,2†], *Changsheng Lu*[1,2†], *Baoli Zou*[1,2], *Mengmeng Yang*[1,2], *Guangliang Wu*[1,2], *Peng Wang*[1,2], *Qin Cheng*[1,2], *Yanning Wang*[1,2], *Qi Zhong*[1,2], *Shiying Huang*[1,2], *Tao Huang*[1,2], *Haohua He*[1,2*] and *Jianmin Bian*[1,2*]**

[1] Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Ministry of Education, Nanchang, China, [2] Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Nanchang, China

Edited by:
Xiaojin Luo,
Fudan University, China

Reviewed by:
Yoshiaki Ueda,
Japan International Research Center for Agricultural Sciences (JIRCAS), Japan
Liang Chen,
Shanghai Agrobiological Gene Center, China
Hongwei Cai,
China Agricultural University, China

Correspondence:
Haohua He
hhhua64@163.com
Jianmin Bian
jmbian81@126.com

† These authors have contributed equally to this work

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Salt stress is one of the factors that limits rice production, and an important task for researchers is to cultivate rice with strong salt tolerance. In this study, 211 rice accessions were used to determine salt tolerance germinability (STG) indices and conduct a genome-wide association study (GWAS) using 36,727 SNPs. The relative germination energy (RGE), relative germination index (RGI), relative vigor index (RVI), relative mean germination time (RMGT), relative shoot length (RSL), and relative root length (RRL) were used to determine the STG indices in rice. A total of 43 QTLs, including 15 for the RGE, 6 for the RGI, 7 for the RVI, 3 for the RMGT, 1 for the RSL, and 11 for the RRL, were identified on nine chromosome regions under 60 and 100 mM NaCl conditions. For these STG-related QTLs, 18 QTLs were co-localized with previous studies, and some characterized salt-tolerance genes, such as *OsCOIN*, *OsHsp17.0*, and *OsDREB2A*, are located in these QTL candidates. Among the 25 novel QTLs, *qRGE60-1-2* co-localized with *qRGI60-1-1* on chromosome 1, and *qRGE60-3-1* and *qRVI60-3-1* co-localized on chromosome 3. According to the RNA-seq database, 16 genes, including nine for *qRGE60-1-2* (*qRGI60-1-1*) and seven for *qRGE60-3-1* (*qRVI60-3-1*), were found to show significant differences in their expression levels between the control and salt treatments. Furthermore, the expression patterns of these differentially expressed genes were analyzed, and nine genes (five for *qRGE60-1-2* and four for *qRGE60-3-1*) were highly expressed in embryos at the germination stage. Haplotype analysis of these nine genes showed that the rice varieties with elite haplotypes in the *LOC_Os03g13560*, *LOC_Os03g13840*, and *LOC_Os03g14180* genes had high STG. GWAS validated the known genes underlying salt tolerance and identified novel loci that could enrich the current gene pool related to salt tolerance. The resources with high STG and significant loci identified in this study are potentially useful in breeding for salt tolerance.

Keywords: salt tolerance germinability, rice accessions, GWAS, QTLs, haplotype analysis

熊艳珍，黄紫萱，马慧琴，等. 黑米的营养功能及综合利用研究进展 [J]. 食品工业科技，2021，42(7)：408−415. doi: 10.13386/j.issn1002-0306.2020060018

XIONG Yanzhen, HUANG Zixuan, MA Huiqin, et al. Advanceson Nutritional Functions and Comprehensive Utilization of Black (Pericarp) Rice (*Oryza sativa* L.)[J]. Science and Technology of Food Industry, 2021, 42(7): 408−415. (in Chinese with English abstract). doi: 10.13386/j.issn1002-0306.2020060018

· 专题综述 ·

黑米的营养功能及综合利用研究进展

熊艳珍，黄紫萱，马慧琴，程建峰*
（江西农业大学农学院，江西南昌 330045）

摘　要： 黑米是一种在种皮中富集黑色或黑褐色花色苷的稻米，营养丰富，药食兼用，被广泛应用于食品、医药和化工等行业。本文从营养成分（淀粉、蛋白质、脂肪、矿物质、必需氨基酸、维生素、黄酮类、酚酸类和膳食纤维）、功能特性（抗炎症、抗过敏、抗哮喘、抗氧化、抗肿瘤、减肥降脂及降血糖）和综合利用（食品、医药与化工行业）三方面归纳和概述了黑米的研究进展，以期为科学认识和深入研究黑米提供理论依据，为综合利用黑米提供有益借鉴。

关键词： 黑米，营养成分，功能特性，综合利用

中图分类号： TS201.1　　**文献标识码：** A　　**文章编号：** 1002−0306(2021)07−0408−08

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Advanceson Nutritional Functions and Comprehensive Utilization of Black (Pericarp) Rice (*Oryza sativa* L.)

XIONG Yanzhen，HUANG Zixuan，MA Huiqin，CHENG Jianfeng*
（College of Agronomy, Jiangxi Agricultural University, Nanchang 330045, China）

Abstract: Black (pericarp) rice is a kind of rice with rich black or dark brown anthocyanins in its seed coat. It is rich in nutrients and can be used as both medicine and food, so it is widely used in the different industries such as the food, medicine and chemical. In this review, the research progresses on the nutritional composition (starch, protein, fat, minerals, essential amino acids, vitamins, flavonoids, phenols and dietary fiber), functional characteristics (anti-inflammation, anti-anaphylaxis, anti-asthma, anti-oxidation, anti-tumor, reducing weight and fat, and decreasing blood sugar) and comprehensive utilization (food, medicine and chemical industry) of black rice are systematically concluded and summarized; which shall provide the systematic theoretical basis for its scientific understanding and intensive researches, and the beneficial references for its comprehensive utilization.

Key words: black (pericarp) rice (*Oryza sativa* L.); nutritional composition; functional property; comprehensive utilization

黑米[1]是一种有色大米，因其麸皮富集的花色苷呈黑色或黑褐色而得名 。黑米是古老而名贵的特色水稻品种，在我国种植历史悠久，始于公元前 145 年，由 2000 多年前汉武帝时的张骞最先在陕西洋县发现 。在世界黑米资源 411 个品种中，我国拥有 373 个（占 90.8%），其余分布在东亚和西亚；我国 2018 年产 14887 万吨，居世界首位，约占世界的 1/3 以上 。

[2–3]

黑米大多数表皮乌黑发亮，少数为紫色或红黑色，营养丰富，药食兼用，自古就有“药米”、“贡米”“黑珍珠”“世界米中之王”的美誉，最具代表性的有陕西黑米、贵州黑糯米和湖南黑米等 。近些年来，随着人们生活水平的不断提高和健康意识的不断增强，对药食兼用黑米的需求越来越大，科研工作者取得的相关研究成果也逐渐增多，不再停留在古代中医的“以色补色，以形补形”。本文在大量搜索和全

收稿日期： 2020−06−03
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作者简介： 熊艳珍（2000−），女，本科，研究方向：农艺学，E-mail: 1013590782@qq.com。
* **通信作者：** 程建峰（1972−），男，博士，教授，研究方向：植物生理生态，E-mail: chjfkarl@163.com。

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植物铁素(Fe)营养的生理研究进展

张文静,程建峰,刘　婕,何　萍,王紫璇,张祖健,蒋海燕
(江西农业大学农学院,南昌 330045)

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

ZHANG Wenjing, CHENG Jianfeng, LIU Jie, HE Ping, WANG Zixuan, ZHANG Zujian, JIANG Haiyan
(*College of Agronomy, Jiangxi Agricultural University*, Nanchang 330045)

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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第一作者简介:张文静,女,2000年出生,江西彭泽人,本科,研究方向:作物生理生态。通信地址:330045 江西省南昌市国家经济技术开发区志敏大道1225号 江西农业大学农学院,Tel:0791-83828081,E-mail:1263011523@qq.com。

通讯作者:程建峰,男,1972年出生,江西横峰人,教授,博士,主要从事植物生理生态研究。通信地址:330045 江西省南昌市国家经济技术开发区志敏大道1225号 江西农业大学农学院,Tel:0791-83828081,E-mail:chjfkarl@163.com。

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黄紫萱,熊艳珍,马慧琴,等. 有色稻米种质及环境因素对其色泽影响的研究进展[J]. 湖北农业科学,2021,60(3):5-10.

有色稻米种质及环境因素对其色泽影响的研究进展

黄紫萱,熊艳珍,马慧琴,程建峰
(江西农业大学农学院,南昌　330045)

摘要:有色稻米(*Oryza sativa* L.)是一种优异的稻种资源,因糙米麸皮内的色素成分差异而具有特殊的食味和药用价值。从光照(光质、光照强度和光照时间)、温度、水分、矿质元素和土壤 pH 等环境因素方面综述了其对有色稻米色泽的影响,为今后的相关研究和技术推广提供理论基础及技术参考。

关键词:水稻(*Oryza sativa* L.);有色稻米;稻种资源;环境因素;色泽
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Research progress on the influence of pigmented rice germplasm and environmental factors on its color

HUANG Zi-xuan, XIONG Yan-zhen, MA Hui-qin, CHENG Jian-feng
(College of Agronomy, Jiangxi Agricultural University, Nanchang 330045, China)

Abstract: Pigmented rice is one of the excellent rice germplasms and special edible taste and medicinal value due to the difference pigment components in the bran of brown rice. the pigmented rice germplasms and effects of light (light quality, light intensity and light time), temperature, moisture, mineral elements and soil pH on their coloring were summarized, which will provide the necessary theoretical bases and technical references for the related researches and technology extensions in the future.

Key words: rice (*Oryza sativa* L.); pigmented rice; rice germplasms; environmental factor; color

有色稻米(*Oryza sativa* L.)是指水稻种皮内沉积不同色素而呈多彩颜色的大米,以区别普通白色大米[1]。有色稻米是一种优良的稻种资源,富含蛋白质、氨基酸、植物脂肪、纤维素和人体必需的矿物质等,具有特殊的食味和药用价值[1-13]。有色稻米种皮内的色素是一种天然安全的食品色素添加剂[14]。根据稻米颜色,目前可将有色稻米分为黑米、紫米、红米、绿米和黄米等种类,以红米和紫米最为常见[1]。随着人们生活水平和健康意识不断提高,富含丰富营养和特殊价值的有色稻米越来越受到青睐[15-22]。然而人们对有色稻米的相关研究相对较少,检索文献资料[23-26]发现,人们在有色稻米的品种选育和高产栽培方面取得了一些研究成果,为零星化的有色稻米种植向大面积的产业化生产积累了一定的理论依据和技术指导。有色稻米的色素积累受遗传本质和环境因素共同控制[27,28],遗传本质需要通过品种改良和基因编辑技术来实现[29],环境因素主要受光、温、水、土和肥等的影响。本研究从中国有色稻米资源入手,以环境因素为关注点,对有色稻米色泽的环境影响因素进行综述,以期为有色稻米的色泽研究及调控提供理论支撑和技术参考。

1　有色稻米资源

中国有色稻米资源比较丰富,截至 2018 年 12 月,在国家(中国)农作物种质长期库共保存稻种资源 87 838 份,有色稻米(包括黑米、紫米、红米、绿米)种质占 10% 以上,以红米最多(8 900 多份),其次为黑米 370 多份[25,26]。进入 21 世纪以来,随着科技人

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作者简介:黄紫萱(1999-),女,江西德兴人,在读本科生,专业方向为农学,(电话)13576298820(电子信箱)hzxup678@163.com;通信作者,程建峰(1972-),男,江西横峰人,教授,博士,主要从事植物生理生态研究,(电话)0791-83828081(电子信箱)chjfkarl@163.com。

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

Dahu Zhou[1,2†], Ting Li[2†], Yaolong Yang[3], Ziyang Qu[2], Linjuan Ouyang[2], Zhishu Jiang[2], Xiaoli Lin[2], Changlan Zhu[2], Liyuan Peng[2], Junru Fu[2], Xiaosong Peng[2], Jianmin Bian[2], Wenbang Tang[1]*, Jie Xu[2]* and Haohua He[1,2]*

[1] Southern Regional Collaborative Innovation Center for Grain and Oil Crops, Hunan Agricultural University, Changsha, China, [2] Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Ministry of Education, College of Agronomy, Jiangxi Agricultural University, Nanchang, China, [3] State Key Laboratory of Rice Biology, China National Rice Research Institute, Hangzhou, China

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Edited by:
Andy Pereira,
University of Arkansas, United States

Reviewed by:
Lei Wang,
Chinese Academy of Sciences, China
Kurniawan Rudi Trijatmiko,
International Rice Research Institute,
Philippines

****Correspondence:***
Wenbang Tang
tangwenbang@163.com
Jie Xu
xujie198615@foxmail.com
Haohua He
hhhua64@163.com

† These authors have contributed equally to this work

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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*

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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ARTICLE

A Novel Dominant Allele from 93-11, *ES(4)*, Represses Reactive Oxygen Species Scavenging and Leads to Early-Senescence in Rice

Zhishu Jiang[#], Cong Gan[#], Yulian Liu, Xiaoli Lin, Limei Peng, Yongping Song, Xiaowei Luo and Jie Xu[*]

Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Ministry of Education, Jiangxi Agricultural University, Nanchang, 330045, China

[*]Corresponding Author: Jie Xu. Email: xujie198615@foxmail.com

[#]Both authors contributed equally

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ABSTRACT

Senescence is the last developmental process in plant, which has an important impact on crop yield and quality. In this study, a stable hereditary early-senescence line BC64 was isolated from the high-generation recombinant inbred lines of 93-11 and Wuyunjing7 (W7). Genetic analysis showed that the premature aging phenotype was controlled by a dominant gene derived from 93-11. By linkage analysis, the gene was primarily mapped in the region between marker B4 and B5 near the centromere of chromosome 4, described as *ES(4)*. Through multiple backcrossing with W7, the near-isogenic line of *ES(4)* (NIL-ES(4)) was obtained. Compared with wild-type W7, NIL-ES(4) plants showed more sever senescence phenotype in both nature and dark conditions. In NIL plants, leaves turned yellow at the fully tillering stage; photosynthetic rate, pollen fertility and seed setting rate were decreased. Moreover, the malondialdehyde, proline content and relative conductivity in NIL-Es(4) were significantly higher than those in W7; both transcript level and activities of reactive oxygen species scavenging enzymes were repressed; H_2O_2 and O^{2-} were significantly accumulated. This study provides a basis for further cloning and function identification of *ES(4)*.

KEYWORDS

Rice; early-senescence; gene mapping; chlorophyll degradation; reactive oxygen species scavenging

1 Introduction

Rice is one of the most important food crops, and half population of the world take it as the staple food. The growth of rice yield has further slowed down during the first decade of this century. The rice-consuming countries population continues to increase rapidly at a rate of over 1.5% per year, leading to a growing demand for rice. Therefore, improvement of grain yield and grain quality are of key agricultural importance [1]. Senescence is the final step of plant growth and development. Initiation timing of senescence has great influences on the plant biomass and quality formation. In crop plants, early senescence strongly affects grain filling, directly limit grain yield and quality [2,3]. Therefore, defining the molecular and physiological mechanisms of early senescence in rice are of great significance to enhance grain yield and quality.

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Genetic analysis of rice seed recovery under low-temperature conditions using a new CSSL population with a high-density genetic map in rice

Guangliang Wu · Haodong Deng · Meixia Yu · Yicong Cai · Dahu Zhou · Jingai Tan · Jianfeng Yu · Xin Luo · Shan Tong · Peng Wang · Xiangyu Zhang · Caijin Li · Cuijuan Li · Yanning Wang · Qin Cheng · Haohua He · Jianmin Bian

Received: 6 March 2020 / Accepted: 17 November 2020

Abstract Developing new population types based on interspecific introgressions has been suggested to facilitate the discovery of novel allelic sources for traits of agronomic importance. In this study, a chromosome segment substitution line (CSSL) rice population carrying contiguous chromosomal segments of *japonica* Nipponbare in the genetic background of *indica* 9311 was developed. Meanwhile, a high-density genetic map including 655 bins covering a distance of 1480.2 Mb, with an average of 0.60 Mb between markers, was generated through a whole-genome resequencing approach. Compared with previous CSSL populations constructed from 9311 or Nipponbare, this population has a higher marker density and can effectively meet the requirements of high QTL mapping resolution. On the basis of the newly constructed high-density genetic map, a total of three major QTLs (*qGP4*, *qGP5*, and *qBL4*) conferring seed growth capacity after low-temperature (5 °C) treatment were detected. Among these, two QTLs shared by Nipponbare, *qGP4* and *qGP5*, could increase germination percentage, while one QTL shared by Nipponbare, *qBL4*, could increase bud length after cold stress; *qGP4* and *qBL4* were first reported in our study. These QTLs could be highly valuable genetic factors for cold tolerance improvement in rice lines. The CSSLs carrying these QTLs not only provide an opportunity for map-based cloning of important cold tolerance QTLs but also supply useful inbred lines to improve cold tolerance in 9311. These CSSLs represent good sources of *japonica* tolerance QTLs (genes) for use in improving cold tolerance in *indica* rice directly, avoiding the genetic drag arising from incompatible epistasis effects.

Keywords CSSLs · High-density genetic map · Cold stress · QTLs

Introduction

With increasing labor costs, direct-seeding agronomic production systems have become very popular for rice.

Guangliang Wu and Haodong Deng contributed equally to this work.

G. Wu · H. Deng · M. Yu · Y. Cai · D. Zhou · J. Tan · J. Yu · X. Luo · S. Tong · P. Wang · X. Zhang · C. Li · C. Li · Y. Wang · Q. Cheng · H. He · J. Bian
Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Ministry of Education, Nanchang 330045, China

Y. Cai · H. He · J. Bian
Key Laboratory of Crop Physiology, Ecology and Genetic Breeding, Nanchang 330045 Jiangxi Province, China
e-mail: hhhua64@163.com
e-mail: jmbian81@126.com

Y. Cai · H. He (✉) · J. Bian (✉)
Jiangxi Super Rice Engineering Technology Research Center, Nanchang 330045, China
e-mail: hhhua64@163.com
e-mail: jmbian81@126.com

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Genetic analysis of germinating ability under alkaline and neutral salt stress by a high-density bin genetic map in rice

**Xin Luo · Haodong Deng · Peng Wang · Xiangyu Zhang · Caijing Li ·
Cuijuan Li · Jingai Tan · Guangliang Wu · Yanning Wang · Qin Cheng ·
Haohua He · Jianmin Bian**

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Abstract The knowledge about the genetic basis of alkaline salt stress and neutral salt stress in rice is limited. Here, we located quantitative trait loci (QTL) for seed germination rate (GR) under alkaline salt stress ($NaHCO_3$) and neutral salt stress (NaCl) using backcross inbred lines population, which was derived from a cross between *indica* cv. Changhui 891 (CH891) and *japonica* cv. 02428 with 3057 bins markers. A total of ten QTL for five salt stress-related traits were detected. The QTL detected for control condition, NaCl stress, and $NaHCO_3$ stress were quite different, which suggested that the genes controlling the transport of the Na^+, in the form of NaCl and the $NaHCO_3$, may be different or induced incoordinately by salt stress. Furthermore, on the basis of the high-density genetic map, the ten QTL were mapped on 40–980 kb chromosomal regions on Nipponbare genome, and 16 candidate genes related to stress or metal transport were found. These results contribute to the fine mapping and use of these GR-related QTL.

Keywords Rice · Salt stress · Germination rate · Candidate genes · High-density genetic map

Introduction

Approximately 30% of the total rice-growing area in the world is affected by salinity stress (Prasad et al. 2000), and salinity has a strong effect on seed germination, causing low germination rates and low seedling establishment in rice (Wu and Garg 2003; Wang et al. 2011; Singh and Jwa 2013; He et al. 2019). Therefore, attaining a high capacity of seed germination under salinity stress is an important objective of rice breeding (He et al. 2019). However, the exact nature of the molecular mechanisms for salinity tolerance in rice is not well understood (He et al. 2019).

Salinity tolerance is a complex trait that is regulated by multiple genes, and such a trait is highly genotype-dependent. In rice, QTL for most of the stages of

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X. Luo · H. Deng · P. Wang · X. Zhang · C. Li ·
C. Li · J. Tan · G. Wu · Y. Wang · Q. Cheng ·
H. He (✉) · J. Bian (✉)
Key Laboratory of Crop Physiology, Ecology and Genetic
Breeding, Ministry of Education, Nanchang 330045,
China
e-mail: hhhua64@163.com

J. Bian
e-mail: jmbian81@126.com

X. Luo · H. He · J. Bian
Key Laboratory of Crop Physiology, Ecology and Genetic
Breeding, Jiangxi Province, Nanchang 330045, China

H. He · J. Bian
Jiangxi Super Rice Engineering Technology Research
Center, Nanchang 330045, China

REPUBLIC OF SOUTH AFRICA **REPUBLIEK VAN SUID AFRIKA**

PATENTS ACT, 1978

CERTIFICATE

In accordance with section 44 (1) of the Patents Act, No. 57 of 1978, it is hereby certified that:

JIANGXI AGRICULTURAL UNIVERSITY

Has been granted a patent in respect of an invention described and claimed in complete specification deposited at the Patent Office under the number

2021/07259

A copy of the complete specification is annexed, together with the relevant Form P2.

mony thereof, the seal of the Patent Office has been affixed at Pretoria with effect from the **23rd** day of **February 2022**

Registrar of Patents

FORM P2

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72	Full name(s) of inventor(s):

(1) Xu Jie; (2) Gan Cong; (3) He Haohua; (4) Bian Jianmin; (5) Jiang Wenxiang; (6) Hu Lifang; (7) Ouyang Linjuan; (8) Sun Xiaotang; (9) Song Yongping; (10) Jiang Zhishu; (11) Peng Limei

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54	Title of invention

Oligo DNA Group of sgRNA for Site-directed Knockout of Rice OsAurora1 Gene

Address of applicant(s)/patentee(s):

No.1101 Zhimin Road, Nanchang City, Jiangxi Province, China

74	Address for service

Sibanda and Zantwijk, Oaktree Corner, 9 Kruger Street, Oaklands (PO Box 1615 Houghton 2041),
Johannesburg, 2192, SOUTH AFRICA
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Australian Government

IP Australia

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INNOVATION PATENT

Patent number: 2021103812

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Jiangxi Agricultural University of Zhimin Road 1101 Nanchang, Jiangxi China

Title of invention:

Rice Flowering-related Gene LHD3 and Its Application

Name of inventor(s):

Xu, Jie; Peng, Limei; Gan, Cong; Song, Yongping; Zhou, Dahu; He, Haohua; Zhu, Changlan; Fu, Junru; He, Xiaopeng; Hu, Lifang; Jiang, Zhishu and Lin, Xiaoli

Term of Patent:

Eight years from 2 July 2021

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Jiangxi Agricultural University of Zhimin Road 1101 Nanchang Jiangxi China

Title of invention:

Protein related to rice wax synthesis and its coding gene WSL5 and application thereof

Name of inventor(s):

He, Haohua; Jiang, Zhishu; Zhou, Dahu; He, Rong; Song, Yongping; Zhu, Changlan; Ouyang, Linjuan; Cai, Yicong; Bian, Jianmin and Xu, Jie

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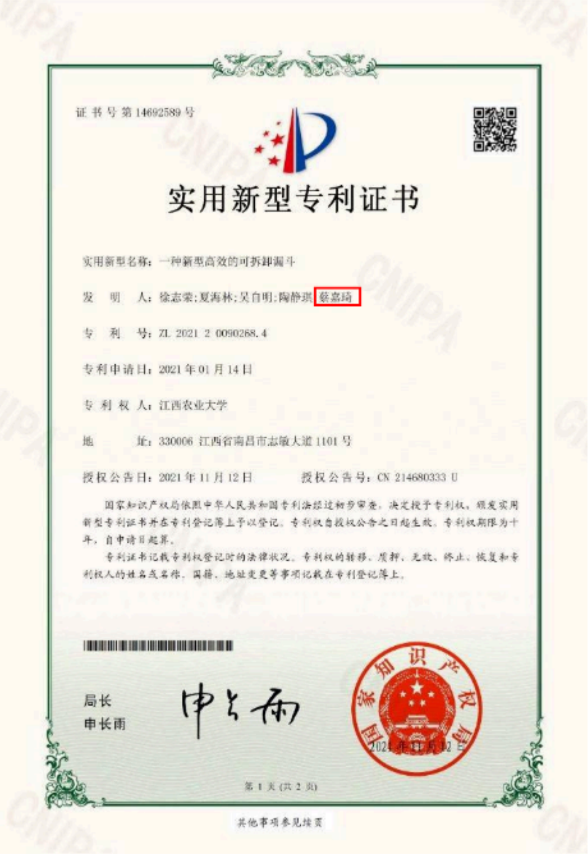
PATENTS ACT 1990



证书号第14692589号

实用新型专利证书

实用新型名称：一种新型高效的可拆卸漏斗

发　明　人：徐志荣;夏海林;吴自明;陶静琪;蔡嘉琦

专　利　号：ZL 2021 2 0090268.4

专利申请日：2021年01月14日

专 利 权 人：江西农业大学

地　　　址：330006 江西省南昌市志敏大道1101号

授权公告日：2021年11月12日　　　授权公告号：CN 214680333 U

国家知识产权局依照中华人民共和国专利法经过初步审查，决定授予专利权，颁发实用新型专利证书并在专利登记簿上予以登记。专利权自授权公告之日起生效。专利权期限为十年，自申请日起算。

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局长
申长雨

申长雨

2021年11月12日

第1页（共2页）

其他事项参见续页

17+5

中华人民共和国国家版权局
计算机软件著作权登记证书

证书号：　软著登字第9104380号

软 件 名 称：基于CRISPR CAS9技术对水稻内源基因OsPLS4编辑系统
V1.0

著 作 权 人：江西农业大学;周大虎;淦聪;周心仪;徐杰;傅军如

开发完成日期：2021年11月10日

首次发表日期：2021年11月20日

权利取得方式：原始取得

权 利 范 围：全部权利

登　记　号：2022SR0150181

根据《计算机软件保护条例》和《计算机软件著作权登记办法》的规定，经中国版权保护中心审核，对以上事项予以登记。

No. 10129566

2022年01月24日

中华人民共和国国家版权局
计算机软件著作权登记证书

证书号：　软著登字第6866904号

软 件 名 称：直播早稻结实期涝害预警系统
V1.0

著 作 权 人：邓梓阳;吴自明;李辉婕;江西农业大学

开发完成日期：2020年11月01日

首次发表日期：2020年11月10日

权利取得方式：原始取得

权 利 范 围：全部权利

登　记　号：2021SR0142667

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No. [illegible]

2021年01月26日

中华人民共和国国家版权局
计算机软件著作权登记证书

证书号：　软著登字第6866930号

软 件 名 称：芽期耐淹直播稻品种的筛选评级系统
V1.0

著 作 权 人：吴自明;邓梓阳;李辉婕;江西农业大学

开发完成日期：2020年11月26日

首次发表日期：2020年11月30日

权利取得方式：原始取得

权 利 范 围：全部权利

登　记　号：2021SR0142613

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No. 07306972

2021年01月26日

惟义（农学）实验班课外科技竞赛及学习竞赛获奖

学生邓浩东荣获第十七届“挑战杯”江西省大学生课外学术科技作品特等奖

获奖证书

江西农业大学：

邓浩东、刘睿琦同学：

你们的作品《水稻芽期耐冷遗传机理解析及主效QTL分析》荣获第十七届“挑战杯”江西省大学生课外学术科技作品竞赛

特等奖

指导老师：边建民

共青团江西省委　江西省科学技术协会　江西省教育厅　江西省社会科学院　江西省学生联合会

二〇二一年七月

惟义农学班学生邓浩东等获得第十七届“挑战杯”全国大学生课外学术科技作品竞赛二等奖

获奖证书

江西农业大学

邓浩东、刘睿琦、戴璐、卢昌盛 同学：

你们的作品《杂交稻五丰优 T025 芽期耐冷主效 QTL 鉴定及优质材料创制》在第十七届“挑战杯”全国大学生课外学术科技作品竞赛中荣获

二等奖

指导教师：边建民

编号：2021-TZB17-MA20299H-2D6037

共青团中央　中国科协　教育部　中国社会科学院　全国学联　四川省人民政府

二〇二二年三月

惟义农学班学生潘小帆获第十三届“挑战杯”江西省大学生创业计划竞赛金奖

获 奖 证 书

江西农业大学

秦璐、林小丽、付文涛、钟智慧、林佳文、潘小帆、熊浪、万丽玮、谢乐欣、刘若宇同学：

你们的作品《天稻粮安——全球领先·双季高产优质超级稻》荣获第十三届“挑战杯”江西省大学生创业计划竞赛

金 奖

指导老师：周李鹏涛、蔡怡聪、孙玥

共青团江西省委　江西省教育厅　江西省人力资源和社会保障厅　江西省科学技术协会　江西省学生联合会

二〇二二年七月

惟义农学班学生在第二届全国农科学子创新创业大赛和青年论坛中获得表彰

惟义农学班学在 2018 全国农学院协同发展联盟华中片区大学生农业创新创业大赛中取得佳绩

惟义农学 1801 班荣获全国活力团支部称号

荣誉证书

CERTIFICATE OF HONOR

江西农业大学农学院惟义农学专业2018级1班团支部：

在“活力团支部炼成记”2020—2021学年高校活力团支部遴选及展示活动中，入选：

活力团支部

特发此证，以资鼓励。

中国青年报社

二〇二一年七月

10 四大类培养—创新型人才培养

学生获批专利

REPUBLIC OF SOUTH AFRICA REPUBLIEK VAN SUID AFRIKA

PATENTS ACT, 1978

CERTIFICATE

In accordance with section 44 (1) of the Patents Act, No. 57 of 1978, it is hereby certified that:

JIANGXI AGRICULTURAL UNIVERSITY

Has been granted a patent in respect of an invention described and claimed in complete specification deposited at the Patent Office under the number

2021/07192

A copy of the complete specification is annexed, together with the relevant Form P2.

mony thereof, the seal of the Patent Office has been affixed at Pretoria with effect from the **23rd** day of **February 2022**

Registrar of Patents