研究生通讯

POSTGRADUATE COMMUNICATION

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旱区作物逆境生物学国家重点实验室第四届研究生学术论坛顺利举办

5 月 13 日，旱区作物逆境生物学国家重点实验室第四届研究生学术论坛在国际交流中心 104 会议室顺利举办。

本次论坛由旱区作物逆境生物学国家重点实验室、农学院、植保学院、园艺学院 、资环学院、生命学院主办，校研究生会、旱作国家重点实验室团工委承办，邀请了马锋旺、刘同先、黄丽丽、宋卫宁、冯永忠、郭军、李志、林雁冰、胡胜武、王晓峰、赵天永、文颖强、江元清 13 位教授担任论坛评委。

论坛以旱区逆境农业的“根”和“果”主题，面向旱作国家重点实验室的全体研究生征集投稿，共收到了论文摘要 62 篇，论坛组委会从中遴选出 16 篇论文。会上进入论坛汇报环节的 16 位研究生围绕“遗传发掘和种质创新”、“环境胁迫与逆境适应”、“生态改良同病害防治方面”三个议题进行汇报交流。现场评委认真听取了研究生的汇报后，从选题、论据、研究成果、汇报与答疑及 PPT 制作与演示等方面对报告进行了点评，并提出了很好的意见和建议。

经评审组评议，最终张强同学获得一等奖，胡洋、樊光进、李程三位同学获得二等奖，马福利、孙逊、贾津布三位同学获得三等奖，燕敬利、吴建辉、吕士凯、池青、吕金洋、李志谦、张庭、穆京妹、陈守坤八位同学获得优秀奖。

自 2014 年研究生学术论坛举办以来，刘同先教授已经多次担任论坛评委，他说“从论坛情况汇报来看，广大同学的研究与本实验室的主题衔接的越来越紧密，研究水平也总体有了很大的提升，也希望广大研究生在之后的学习、研究中勇于创新、多看一些资料，多参加一些会议，尤其是好的项目，不断提高自身的研究水平与创新能力。也希望主办单位能够多举办此类学术论坛，为研究生搭建一个相互交流的学术平台，促进优秀研究成果的交流。”

校长助理兼研究生院副院长霍学喜教授出席论坛并致辞。本次论坛评委专家组组长马蜂旺教授对论坛进行了点评，他充分肯定了研究生的学术研究水平，对论坛中存在的问题提出了有建设性的意见和建议，并鼓励研究生积极努力投入到科研工作中，取得更大成绩。

来 源：校研究生会 旱作国家重点实验室团工委
作 者：王 萍

第四届研究生学术论坛
会 议 议 程

时间	项目及题目	汇报人
8:30—8:50	开幕式	
8:50—9:10	Heat stress regulates the expression of genes at transcriptional and post-transcriptional levels, revealed by RNA-seq in Brachypodium distachyon.	陈守坤
9:10—9:30	A novel protein controls brassinosteroid signaling and adaptation to abiotic stresses	李程
9:30—9:50	Saturation mapping of stripe rust resistance gene Yr26 and associated candidate genes analysis via a combination of next-generation sequencing and bulked segregant analysis in hexaploid wheat	吴建辉
9:50—10:10	Improvement of drought tolerance by overexpressing MdATG18a is mediated by modified antioxidant system and activated autophagy in transgenic apple	孙逊
10:10—10:30	茶　　歇	
10:30—10:50	Inheritence and molecular mappping of wheat sources centrum to stripe rust and identifying novel sources for wheat breeding against stripe rust	穆京妹
10:50—11:10	A systems approach to a spatio-temporal understanding of the drought stress response in maize	张庭
11:10—11:30	MoFRQ is important for conidiation, appressorium penetration in the rice blast fungus	张强
11:30—11:50	Ectopic expression of Arabidopsis broad-spectrum resistance gene RPW8.2 improves the resistance to powdery mildew in grapevine (Vitis vinifera)	胡洋
14:30—14:50	Stilbene synthase VpSTS26 from Vitis pseudoreticulata is secreted from ER to vacuole by ER-derived oil body throughout autophagy pathway	马福利
14:50—15:10	Transcriptome analysis reveals key differentially expressed genes in wheat growth and grain development	池青
15:10—15:30	The 25-26 nt small RNAs in Phytophthora parasitica are associated with efficient silencing of homologous endogenous genes	贾津布
15:30—15:50	Genetic analysis of the hybrid necrosis genes in bread wheat and the contribution of their genetic linkage region in breeding	吕士凯
15:50—16:10	茶　　歇	
16:10—16:30	Biosynthesis of salicylic acid and feedback regulation of VvHDZ28 promote stenospermocarpy in Thompson seedless	李志谦
16:30—16:50	NACa transcription factor from Oilseed Rape (Brassica napus L.) modulates reactive oxygen species accumulation and cell death	燕敬利
16:50—17:10	A Phytophthora capsici effector weaken plant immunity by targeting and suppressing RIP3, which can participate ER-stress mediated plant immunity	樊光进
17:10—17:30	Male sterility of a herbicide-resistant Brassica napus L. mutant induced by tribenuron-methly correlated with the decrease of AHAS activity	吕金洋
17:30—18:00	颁奖、总结	

第一名获奖者
张　强

学历：博士研究生
专业：植物病理学
学习经历

本科阶段：

2005 年 9 月至 2009 年 6 月，就读于西北农林科技大学植物保护学院植物保护专业，获得农学学士学位。

硕士阶段：

2009 年 9 月至 2012 年 6 月，就读于西北农林科技大学生命科学学院微生物学专业，师从孙广宇教授，研究主要涉及苹果霉心病病原真菌多样性及侵染特性等方面的内容。

博士阶段：

1、2012 年 9 月至今，就读于西北农林科技大学植物保护学院植物病理学专业，师从国家“千人计划”入选者许金荣教授。

2、博士期间的研究内容主要涉及禾谷镰刀菌分泌蛋白 Sup、自噬相关蛋白 FgAtgs 及稻瘟菌光周期蛋白 MoFrq 功能分析等多个方面的内容。

第二名获奖者
胡　洋

学历：博士研究生
专业：果树学专业
科学研究

2014 年 3 月至今，加入旱区作物逆境生物学国家重点实验室文颖强教授课题组，学习中国野生葡萄、野生草莓抗热、抗白粉病相关基因的挖掘与利用研究。已参与发表 SCI 论文八篇，其中第一作者三篇。获 2015 年本科毕业生校级“优秀毕业论文”，两次获得硕士研究生国家奖学金，园艺学院“卓越基金”创新奖一等奖、二等奖。

研究成果

Yang Hu, Yong-Tao Han, Kai Zhang , Feng-Li Zhao, Ya-Juan Li, Yi Zheng, Yue-Jin Wang, Ying-Qiang Wen*. (2016) Identification and expression analysis of heat shock transcription factors in the wild Chinese grapevine (Vitis pseudoreticulata). Plant Physiology and Biochemistry, 99: 1-10. 等

研究生学术论坛参赛选手比赛现场




选　手
参 赛 感 想

1. 进行科研实验过程中，您是怎么做的，有什么体会想和大家分享?

在导师安排相应的课题之后还是需要主动去查资料，对开展这个课题的目的意义要有一定了解，还需要了解相关研究的前沿，这样才能更好的开展后续研究。在开始试验的过程中一定会遇到之前没有学过的操作方法，那么就需要和周围同学多交流，掌握试验流程和技巧，从而增加试验成功的可能性。在获得试验数据后，要及时整理分析，如果与之前设想的不一致则需要查找原因，对获得的结果要有合理的解释。撰写论文不一定要等所有试验做完才进行，有些问题可能会在写的过程中才会被发现，所以边做边写也有一定道理。在写论文的过程中仍然需要阅读大量文献，这样会对 introduction 和 discussion 两个部分的写作有很大帮助。

2. 摘要是论文中写作中比较重要的一部分，您在撰写文献摘要通常会注意哪些地方?

摘要部分是论文的简要概述，要包含论文中主要的研究结果和讨论的主要问题。要把阅读文献作为习惯，可以通过阅读文献去解决试验过程中遇到的问题，而且会开拓思维，寻求后续新的研究内容。有些文献只需要有选择的进行阅读，抓住自己所需的重点即可。试验数据要详实，而且需要有合理的解释。

——张强

1、关于撰写文献摘要您有什么分享的吗?

摘要既是对一篇文章背景、结果、讨论的总结，也是对全篇研究内容的升华。在撰写摘要时要注重提炼要点、精准用词，尽量用最少的词准确表达想称述的观点。此外，句子与句子的衔接，即逻辑，是写好一段摘要的保障。

撰写英文摘要，就是多读、多比较、上下文连贯思考，从别人的陈述方式中找到最适合自己语境、最能表达自己思想的表达方式与句型。

平时阅读英文文献，一般先看图表，大致了解作者讲了一个什么故事，和自己的研究内容有无联系；如果有联系，再看摘要明确作者的研究内容与结果；如果对自己研究有参考意义，再去看他的试验结果与采用的研究方法。至于引言和讨论，一般是和自己研究内容关系非常密切的文献才回去深读，带着问题与思考去读。

数据处理首先要严格遵从科学性原则，实事求是；其次是追求美观、大气的图表效果，将复杂的科学规律用最简单、最浅显易懂的方式呈现出来，用我导师的话说，就是要把科学规律做到像白居易的诗一样。

2、在研究生学习生活中遇到的困难及解决方式，请谈谈您的收获。

科学试验，失败的次数总比成功的次数多，所以困难总会在下一个角落邂逅你，但是作为农业与生命科学的研究生，解决困难就是我们的工作。我觉得做生命科学研究，除了受技术与研究条件的限制外，其他所谓的困难都是包裹科学规律的“外壳”，只是我们现在不能打开它或者是打开方式不对而已。所以，多思考、多尝试、神马困难都是浮云。

科研能带给我无限的乐趣，就是因为真理藏得很深。

——胡洋

收获与感想：很感谢学校和重点实验室举办这次研究生论坛，增进研究生与导师们交流与学习。研究生的学习与工作本身是在相对封闭的实验室环境，通过这种高质量的论坛平台，增进研究生们的交流，能够积极促进研究工作的开展，打开思维的大门，碰撞智慧的火花。同时，对于汇报研究工作的同学自身而言是一种锻炼，对实验室的研究工作是一种检验，在相互的交流与比较中促进科研工作的进一步推进，同时点评的老师们也给出了很多宝贵的值得参考借鉴的意见。多学科的交叉交流也是非常重要而有意义的。希望学校多多举办这样的高质量活动，促进研究生群体的活跃性，提升我校的科研工作交流与质量。

——园艺学院 蔬菜学专业博士研究生 李程

获奖选手论文摘要

MoFRQ is important for conidiation, appressorium penetration in the rice blast fungus

Qiang Zhang, Xuli Gao, Qinhu Wang, Cong Jiang*, and Jin-Rong Xu*

State Key Laboratory of Crop Stress Biology for Arid Areas and College of Plant Protection, Northwest A&F University, Yangling 712100, Shaanxi, China

Abstract

Circadian rhythm organizes inner physiology with respect to the external world, providing life with the ability to anticipate and thereby better prepare for major fluctuations in its environment. To determine the importance of the circadian rhythm in the rice blast fungus *Magnaporthe oryzae*, in this study we functionally characterized the *MoFRQ* gene, an ortholog of *frq* that is the central component of the *Neurospora crassa* oscillator. The expression level of *MoFRQ* was up-regulated under light conditions in comparison with cultures grown in the dark. Exposure to light stimulated the expression of *MoFRQ* and localization of MoFrq-GFP to the nucleus. The *Mofrq* deletion mutant displayed a light-dependent growth defect on oatmeal agar cultures in aerial hyphal growth and was significantly reduced in conidiation. MoFrq interacted with and Htf1 and, like the htf1 mutant, conidiophore development was not affected in Mofrq mutant but only approximately 10% of mutant conidiophores producing reduced number of conidia. The *Mofrq* mutant was significantly reduced in virulence and caused only rare, smaller lesions on rice or barley leaves. Consistent with its defects in plant infection, the *Mofrq* mutant were reduced 40% in appressorium formation and 80% in appressorium penetration. The mobilization and degradation of glycogen from conidia to appressoria was negatively impacted by deletion of *MoFRQ*, which also increased the sensitivity to oxidative stress but had no effect on response to hyperosmotic stress. PKA activities were reduced in the *Mofrq* mutant, which may be related to its defects in appressorium penetration and glycogen mobilization. Like *frq* of *N. crassa*, *MoFRQ* has a strong bias for non-optimized codons and the abundance of *MoFRQ* transcripts oscillated under constant darkness. Expression of *frq* but not *FgFRQ* complemented the defects of *Mofrq* mutant in growth, conidiation and plant infection. Taken together, these results indicate that *MoFRQ* is important for light-stimulated aerial hyphal growth, conidiation, and appressorium penetration, and it is functionally related to the cAMP-PKA pathway and Htf1 transcription factor in *M. oryzae*. As an important component of the circadian oscillator, *MoFRQ* is important for plant infection and likely plays an essential role in the disease cycle of rice blast.

Ectopic expression of *FvWRKY42*, a WRKY transcription factors from the diploid woodland strawberry (*Fragaria vesca*), enhances resistance to powdery mildew and osmotic stress, and improves abscisic acid sensitivity in *Arabidopsis*

Wei Wei , Meng-Yuan Cui , Yang Hu , Kuan Gao , Jia-Yue Feng *

State Key Laboratory of Crop Stress Biology for Arid Areas and College of Horticulture, Northwest A&F University, Yangling 712100, Shaanxi, China

Abstract

Biotic and abiotic stresses has been shown to significantly limit the growth and productivity of crops. WRKY transcription factors play essential roles in response to biotic and abiotic stresses. However, only little information regarding stress-related WRKY genes is available in strawberry. Here, we isolated and functionally characterized a various stress-inducible WRKY gene (*FvWRKY42*) from the wild diploid woodland strawberry accession Heilongjiang-3. Multiple sequence alignment analysis indicated that FvWRKY42 contained two WRKY domain, a D domain and an SP cluster in the N terminal. Protein interaction network analysis showed that FvWRKY42 protein interact with various stress-related proteins. FvWRKY42 protein has transcriptional activation in yeast. *FvWRKY42* was expressed preferentially in roots, young leaves and floral buds, and its expression was induced in response to treatment with powdery mildew, salt, drought and exogenous hormones. Over-expression of *FvWRKY42* in *Arabidopsis* showed enhanced resistance to powdery mildew presumably via the SA-signaling pathway. Ectopic over-expression of *FvWRKY42* in *Arabidopsis* showed enhanced salt and drought stress tolerance, which is accompanied by increase of the seedling root mass and protection of the integrity of plasma membrane, as well as more effective active oxygen removal system. Additionally, Over-expression of *FvWRKY42* in *Arabidopsis* enhanced ABA sensitivity and promoted leaf closure after ABA and drought treatments. Stress- responsive genes such as *RD29A*, *RD29B* and *NCED3* showed higher expression levels in *FvWRKY42* transgenic lines than in WT *Arabidopsis* under salt and drought stresses. The above results showed that the *FvWRKY42* genes may improve the osmotic stress resistance via ABA-dependent signaling pathway. Together, these findings suggest that the *FvWRKY42* transcription factor plays an important, positive role in plant response to powdery mildew and osmotic stress.

Improvement of drought tolerance by overexpressing *MdATG18a* is mediated by modified antioxidant system and activated autophagy in transgenic apple

Xun Sun[1&], Ping Wang[1,2&], Xin Jia[1], Liuqing Huo[1], Runmin Che[1], Fengwang Ma[1]*

1 State Key Laboratory of Crop Stress Biology for Arid Areas and College of Horticulture, Northwest A&F University, Yangling 712100, Shaanxi, China
2 Department of Genetics, Development and Cell Biology, Iowa State University, Ames, IA 50010, USA
& Xun Sun and Ping Wang contributed equally to this work.

Abstract

Autophagy is a major and conserved pathway for delivering and recycling unwanted proteins or damaged organelles to be degraded in the vacuoles. Autophagy-related protein ATG18a has been established as one of the essential components for autophagy occurrence in *Arabidopsis thaliana*. We previously cloned the *ATG18a* homolog from *Malus domestica* (*MdATG18a*) and monitored its responsiveness to various abiotic stresses at the transcriptional level. However, it is still unclear what its function is under abiotic stress in apple. Here, we found that heterologous expression of *MdATG18a* in tomato plants markedly enhanced their tolerance to drought. Overexpression (OE) of that gene in apple plants improved their drought tolerance as well. Under drought conditions, the photosynthesis rate and antioxidant capacity were significantly elevated in OE lines when compared with the untransformed wild type (WT). Transcript levels of other important apple autophagy-related genes were more strongly up-regulated in transgenic *MdATG18a* OE lines than in the WT. The percentage of insoluble protein in proportion to total protein was lower and less oxidized protein accumulated in the OE lines than in the WT under drought stress. This was probably due to more autophagosomes being formed in the former. These results demonstrate that overexpression of *MdATG18a* in apple plants enhances their tolerance to drought stress, probably because of greater autophagosome production and a higher frequency of autophagy. Those processes help degrade protein aggregation and limit the oxidation damage, thereby suggesting that autophagy plays important roles in the drought response.

A phytophthora capsici effector weaken plant immunity by targeting and suppressing RIP3, which can participate ER-stress mediated plant immunity

Guangjin Fan[1], Weixing Shan[2,*]

1 State Key Laboratory of Crop Stress Biology for Arid Areas and College of Plant Protection, Northwest A&F University, Yangling 712100, Shaanxi, China
2 State Key Laboratory of Crop Stress Biology for Arid Areas and College of Agronomy, Northwest A&F University, Yangling 712100, Shaanxi, China

Abstract

Phytophthora, causing many destructive crop diseases, secrete numerous effecttors to modulate host processes. However, specific mechanisms of how *Phytophthora* effectors manipulate host are still little known, such as effectors from *Phytophthora capsici* (*P. capsici*), which is a highly destructive invasive pathogen in many vegetables. Here we report a *P. capsici* RxLR effector PcAvr3a12, which enhances leaf colonization of *P. capsici* when is expressed in planta, targets an ER-located protein, which plays resistance role during *Phytophthora* infecting *Arabidopsis thaliana*, to attenuate normal plant immunity. This protein, termed as RIP3 (RxLR interacting protein 3), participates maintaining normal TM triggered endoplasmic reticulum (ER) stress response and ER-stress mediated plant immunity. The enzyme activity of RIP3 is important for its plant immunity and ER-stress regulator function. Finally, we found that PcAvr3a12 suppress the enzyme activity of RIP3 through protease-coupled assay in vitro and have no obvious influence on the stabilization of RIP3 in vivo. Taken together, these results suggest that PcAvr3a12 attenuate plant immunity by suppressing the enzyme activity of RIP3 and this suppressing may disorder ER-stress mediated plant immunity. This direct targeting of an ER-located protein and disordering its normal function may reveal a new sight into the relationship between ER-stress signaling pathway and plant immunity.

A novel protein controls brassinosteroid signaling and adaptation to abiotic stresses

Cheng Li, Xiaofeng Wang

State Key Laboratory of Crop Stress Biology for Arid Areas and College of Horticulture, Northwest A&F University, Yangling 712100, Shaanxi, China

Abstract

Brassinosteroid (BR) as one of the major plant hormones, plays a significant roles in plant growth and development. BRI1/BAK1 located on plasma membrane accept and transmit the BR signal from cell surface to inside. We use IP-MS method to find a new component, named it K27, it interacts with BRI1/BAK1 in vitro and in vivo. The loss-of-function of *K27*, showed the BR signal weaker than that in wild type. The overexpression of *K27* showed smaller plant and slower growth rate than wild type, but not significant change BR signal in normal plant or *bri1-5*, a BR signal declined plant. Next, we analyze the stress-resistant function of K27. The overexpression *K27* plants showed less H_2O_2 and ROS than wild type, meanwhile more H_2O_2 and ROS in knock out of *K27* plants. Then, we find *K27* knock out line becomes more sensitive to cold stress than wild type and some cold-related gene obvious up-regulated. We also cloned the homologous gene *SlK27* in tomato, and detected interaction between SlK27 and SlSERK3A/ SlSERK3B, the homologous proteins of AtBAK1 in tomato. The silence of *SlK27* using VIGS in tomato, showed increasing H_2O_2 and ROS, which also sensitive to paraquat, H_2O_2, and SA treatment in relative ion leakage measurement. Thus, we find a new protein participates in BR signal transduction and stress resistance, as well as the bridge connected BR hormone and adaptation to abiotic stresses.

Stilbene synthase VpSTS26 from *Vitis pseudoreticulata* is secreted from ER to vacuole by ER-derived oil body throughout autophagy pathway

Fuli Ma[1,2,3], Yuejin Wang [1,2,3]

1 College of Horticulture, Northwest A & F University, Yangling 712100, Shaanxi, China
2 Key Laboratory of Horticultural Plant Biology and Germplasm Innovation in Northwest China, Ministry of Agriculture, Yangling 712100, Shaanxi, China
3 State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A&F University, Yangling 712100, Shaanxi, China

Abstract

Resveratrol and its derivatives, synthesized from the phenylpropanoid pathway in grapes, are natural antimicrobial phytoalexins in plants and benefit for human health. However, the subcellular factory of stilbenoid metabolism is still unclear. Here, we showed that a stilbene synthase 26 (VpSTS26) from Chinese wild *Vitis pseudoreticulata* traveled to vacuole from ER throughout autophagy pathway during dark-induced senescence. The colocalization of VpSTS26 with the resveratrol glucosyltransferase (RSGT) to the Endoplasmic Reticulum (ER) indicated that ER was the site for the synthesis and transformation of resveratrol. The Nile red staining and colocalization showed VpSTS26-GFP moved to ER-derived bodies underwent darkness treatment. We also observated the budding of VpSTS26-GFP from the ER using the *Arabidopsis thaliana* mesophyll protoplasts transient gene expression system and the colocalizations of VpSTS26-GFP with organelle markers were in accordance with those of in grape protoplasts. Furthermore, concanamycin A and wortmannin treatment and Transmission electron microscopy (TEM) analysis confirmed the transport of VpSTS26 from ER to vacuole was via mCherry-ATG8-labelled autophagy pathway but not the prevacuolar compartments-vacuole trafficking. Measurements of protein half-lives showed dark could induced the degradation of VpSTS26-GFP into free GFP and GFP variant but the degradation was not via the 26S proteasome. Intriguingly, VpSTS26 was partially accumulated in senescent leaves and dark could also induce a stronger accumulation of VpSTS26 in young leaf and tender stem. Therefore, our results suggested a novel route of grape stilbene synthase trafficking to vacuole during dark-induced autophagy.

The 25-26 nt small RNAs in *Phytophthora parasitica* are associated with efficient silencing of homologous endogenous genes

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Abstract

Small RNAs (sRNAs) are important non-coding RNA regulators, playing key roles in developmental regulation, transposon suppression, environmental response, host-pathogen interaction and other diverse biological processes. However, their roles in oomycetes are poorly understood. Here, we performed sRNA sequencing and RNA sequencing of *P. parasitica* at stages of vegetative growth and infection of *Arabidopsis* roots to examine diversity and function of sRNAs in *P. parasitica*, a model hemibiotrophic oomycete plant pathogen. Our results indicate that there are two distinct types of sRNA-generating loci in *P. parasitica* genome, giving rise to clusters of 25-26 nt and 21 nt sRNAs, respectively, with no significant strand-biases. The 25-26 nt sRNA loci lie predominantly in gene-sparse and repeat-rich regions, and overlap with over 7000 endogenous gene loci. These overlapped genes are typically *P. parasitica* species-specific, with no homologies to the sister species *P. infestans*. They include approximately 40% RXLR effector genes, 50% CRN effector genes and some elicitor genes. The transcripts of most of these genes could not be detected at both the vegetative mycelium and infection stages as revealed by RNA sequencing, indicating that the 25-26 nt sRNAs are associated with efficient silencing of these genes. The 21 nt sRNA loci typically overlap with the exon regions of highly expressed genes, suggesting that the biogenesis of the 21 nt sRNAs may be dependent on the level of gene transcription and that these sRNAs do not mediate efficient silencing of homologous genes. Analyses of the published *P. infestans* sRNA and mRNA sequencing data consistently show that the 25-26 nt sRNAs, but not the 21 nt sRNAs, may mediate efficient gene silencing in *Phytophthora*.