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旱区作物逆境生物学国家重点实验室（西北农林科技大学）
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旱区作物逆境生物学国家重点实验室

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主办“小麦病虫害持续控制研讨会”

承办“作物逆境适应与持续生产学术研讨会”

第一届学术委员会第二次会议

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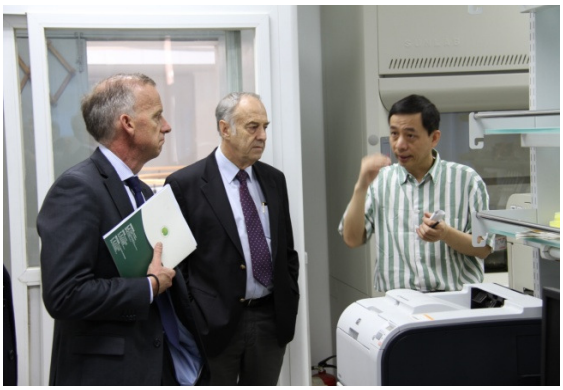

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澳大利亚默多克大学副校长 David Morrison 来实验室访问交流

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一、实验室年度报告

旱区作物逆境生物学国家重点实验室围绕制约旱区农业高效可持续发展的关键因子生物逆境和非生物逆境开展基础及应用基础研究。在基础理论研究方面，重点探索干旱、高温、盐碱等逆境因子的信号转导调控网络及病原与作物互作的分子机理；在应用基础研究方面，克隆具有抗旱、抗寒、抗病、耐盐的重要农艺性状功能基因，同时致力于作物功能基因组及高产优质新品种培育研究。

旱区作物逆境生物学国家重点实验室设立以下研究方向：

方向一：作物抗逆种质和基因资源发掘

方向二：作物非生物胁迫应答机理

方向三：作物与有害生物的互作机理

方向四：作物抗逆种质创新与品种设计

（一）研究进展

1、作物抗逆种质和基因资源发掘

（1）作物抗逆种质资源收集、发掘与利用

对60份来自以色列和约旦的野生大麦，27份来自国际旱地农业研究中心的野生小麦，40份中国小麦品种和33份西藏大麦品种，共160多份材料微量元素的测定结果表明：铁、锌、铜、锰的平均含量为48.3, 47.8, 7.0和34.5 mg/kg。中国小麦品种富含铁和锌，含量分别为77.7 和 88.03mg/kg。西藏大麦品种的铜含量最低。约旦野生大麦和国际旱地研究中心的野生小麦品种的锰含量最高，为65.52mg/kg。这些结果将促进大麦及小麦品种的微量元素的改良。

为了挖掘模式植物二穗短柄草种质资源中的可用自然遗传变异，使用9个ISJ 引物和20对SSR引物，对来自以色列9个采集地的30份二穗短柄草材料和10份已报道材料的遗传多样性分析结果表明：以色列二穗短柄草为六倍体；聚类分析结果可以分成3个群体：i）所有的以色列品系；ii）已报道六倍体；iii）已报道二倍体品系。分子

变异（AMOVA）分析表明，遗传变异主要来自群体间，分别为 71.69%, 71.88% 和71.62%。这些结果将促进新型模式植物二穗短柄草的研究，并加快包括大麦和小麦等基因组复杂的禾谷类作物的研究。

对荞麦、糜子、芸豆、绿豆和扁豆等小杂粮的品种资源进行了收集，鉴选和评价利用工作。田间鉴定荞麦资源230余份、 糜子资源160份、芸豆资源75份、绿豆资源15份。对观赏荞麦品种、易脱壳苦荞品种、糜子抗病、抗旱资源等优异资源进行了筛选、鉴定、评价与创新等工作。

（2）作物抗逆遗传多样性研究

围绕优异抗病基因发掘，从筛选鉴定的70余份小麦抗源材料中，鉴选出中间偃麦草、簇毛麦、野燕麦等野生物种与普通小麦的易位抗源新材料。抗病遗传初步结果表明，其中12个具有全生育期抗性，另外58个具有成株期抗病性。构建了兴资9104、西农291、秦农142、武汉2号、品冬34、Centrum等的遗传群体（F2:3）26个，完成了centrum、品冬34、贵农775、一粒葡等抗源的抗病遗传分析，正在进行抗病基因鉴定和分子链锁作图工作。

从国内其他育种单位引进20余份小麦远缘杂交后代和突变体衍生后代，从美国引进70份小麦抗源种质。通过三年两地成株期鉴定和苗期分小种鉴定，从1980份小麦农家种、远缘杂交后代和国外引进种质中，筛选到不同类型抗源材料50多份，拓展了我国抗源储备库。对119份小麦条锈病抗源，分别用12个条锈菌小种进行了苗期分小种鉴定、成株期混合小种和自然诱发圃鉴定。

（3）作物抗逆基因资源发掘与功能分析

构建了大麦根、茎、叶和穗四个组织的小RNA混合库，采用solexa测序分析，得到分属于58个家族的保守miRNA共126个，分属于50个miRNA家族的新miRNA共133个，还鉴定出15个新miRNA。

围绕抗病基因*Yr26*的图位克隆，利用比较基因组学开发了一系列不同类型的分子标记，获得了遗传距离为0.06cM和0.02cM的两侧分子标记，完成了*Yr26*基因的精细作图。进一步利用比较基因组学方法和同源克隆技术，获得了在*Yr26*两侧最近遗传标记区域内的具有抗病基因结构域的基因，有可能是*Yr26*基因的候选基因。

以中国野生华东葡萄泛素连接酶基因UIRP1为诱饵，从中国野生华东葡萄“白河-35-1”的酵母表达cDNA文库中筛选到一个与葡萄抗白粉病相关的基因VpWRKY17，并对其抗病功能进行了分析。开展了华东葡萄病程相关蛋白VpPR10.1和白藜芦醇-氧-甲基转移酶基因（VpROMT）的克隆与功能分析。

苹果果实着色机理研究方面取得一定进展：1）揭示了苹果阳面果皮和阴面果皮对吸收光能的不同耗散机制。苹果果皮主要依赖热耗散消耗吸收的光能，其中，阳面果皮主要依赖叶黄素循环，而阴面果皮主要依赖可逆失活的反应中心及依赖光抑制的热耗散；2）阐明了遮光（或套袋）对苹果果皮初生和次生代谢的影响。遮光或套袋能够抑制酚类物质，特别是花色苷和黄烷酮类多酚的代谢，遮阴还影响了苹果果皮的糖、有机酸、及氨基酸的代谢；3）揭示了干旱过程中，光强对光合机构两个光系统的伤害机制。干旱过程中，光强升高直接增加了对PSII的光伤害，而对PSI则主要是通过加速叶片蒸腾从而抑制其活性。

鉴定了234份新育成小麦品种（系）的成株期抗条锈性，其中，对CYR32、CYR33和混合菌种表现抗病的品种（系）数量分别为229、202和202份，表明新育成品种的抗病性大大提高，90%以上的新育成品种对目前流行小种表现抗病。同时对小麦条锈菌的IGS区的扩增分析发现，IGS区存在不同的单倍体型，存在3个保守区和两个变异区（α和β），共有14种类型的重复单位。

对4个普通小麦-柔软滨麦草易位系、10个抗条锈病新种质的抗条锈基因进行了遗传分析和抗病基因的分子作图。小麦-柔软滨麦草易位系M852-1对CYR32、CYR33和Su11-7的抗锈性均由1对隐性基因控制，并将其定位于小麦2BS染色体。M97苗期对CYR31的抗病性由2对显性基因独立或重叠作用控制，筛选了4个与该抗病基因连锁的SSR标记，并将该抗病基因定位于小麦1DS染色体。普通小麦-华山新麦易位系H9020-1-6-8-3对CYR33的抗病性由1个显性单基因控制，暂命名为*YrH9020*，筛选了4对与其紧密连锁的微卫星标记，并将其定位于小麦2DS上。H9014-121-5-5-9苗期抗条锈性遗传分析表明，其对条锈菌CYR31的抗病性由1对显性基因控制，暂命名为*YrHA*，筛选7个与其抗病基因连锁的SSR标记，定位于小麦1AL染色体。中梁21苗期对条锈菌CYR30的抗性由1对显性基因控制,暂命名为*Yrzhong21*，筛选了10个与其连锁的特异

性SSR标记，并将其定位于小麦5AL染色体，系谱分析结合分子标记检测表明, 该基因可能来自Ciemenp。H122对供试小种均表现免疫或近免疫，将其暂命名为*YrH122*，并将该基因定位于小麦染色体1DL上，SSR标记回检显示，*YrH122*来源于华山新麦草。通过基因来源、分子检测及染色体位点比较，*YrH122*可能是1个不同于目前已知抗条锈病基因的新基因。

（4）作物抗逆资源基因组学研究

以小麦单条染色体臂7DL为研究对象，利用高通量荧光标记指纹印迹（HICF）技术，对小麦7DL的特异BAC文库近5万个克隆进行了指纹印迹分析，最终获得了38,452个高质量的印迹结果，采用FPB软件去除载体的污染，然后利用FPC软件构建了1614个重叠群(Contig)。从构建的contigs中挑选出最短路径克隆（MTP）4,472个，总长约为373,819kb，大约覆盖了整个染色体的92%，基本建立了7DL的重叠群物理图谱。小麦7DL染色体BAC重叠群物理图谱的成功构建为小麦7DL重要农艺性状QTL定位、遗传图与物理图的整合、图位克隆以及最终的测序奠定了重要基础。

利用Illumina 高通量测序获得了小麦7DL染色体survey sequence共161,061个片段，大小约223Mb，基因组重复元件的分析发现，二核苷酸重复和单核苷酸重复分别占45.5%和29.9%。四核苷酸重复元件含有最丰富的变异类型，具有76种变异。单重复率最高的重复元件为a/t(5081)，二核苷酸重复率最高的重复元件为tc/ga(3002)，三核苷酸重复率最高的重复元件为ttc/gaa(527)等。从中开发得到了16, 315个SSR位点，从中随机选取了33个来设计SSR引物，用20个来源于美国、英国、澳大利亚、德国、法国、意大利及中国的小麦品种分析结果显示，这33个引物中有30个可用，其中18个在这20个小麦品种中有较高的多态性，并且在7D缺体材料中没有条带扩出来，表明这些引物是7D上的特异性引物。

通过对小麦7号染色体组（7A, 7B和7D）普查序列进行miRNA的生物信息学预测，经过一系列筛选标准共鉴定到来自20个保守家族的343个miRNA，其中7A, 7B和7D染色体分别有162，196和153个miRNA。同时，分别位于7A, 7B和7D的前体数目是367，512和452个，分析表明，同7D染色体相比，7A和7B具有更多的miRNA，但是其miRNA产生位点（pre-miRNA）却较少，这可能是由于7A和7B染色体相对7D染色体而言，

在小麦形成过程进行了更多的一次杂交，在这一杂交过程中，它们删除了一些冗余pre-miRNA，形成了更精确的调控网络，使得它们完成相同的功能需要更少的miRNA。同时，我们还对miRNA进行了靶基因预测，靶基因GO注释表明，这三条miRNA主要参与过氧化氢酶的活性，有丝分裂染色体凝聚和信号转导等。

2、作物非生物胁迫应答机理

（1）小麦 Tilling 突变体库的构建及遗传转化体系的完善

丰富的突变体库和完善的遗传转化技术是作物逆境功能基因组学研究核心问题。分别以晋麦47和陕麦150为材料，利用EMS诱变，获得了2610 和1350个M2突变体，其中包含5份抗旱性增强的突变体材料，108份在株型、穗型等外在农艺性状有明显变化的株系。利用RAPD和ISJ 引物对突变体库的突变频率进行评估，并用已建立的Tilling平台对重要农艺形状相关中突变进行筛选。完善了小麦成熟胚和幼胚高效遗传转化体系，建立了病毒介导的小麦穗部基因瞬时沉默体系，并利用该系统成功实现小麦高分子量谷蛋白基因的沉默，为解析小麦籽粒发育及品质性状相关基因的功能建立了技术平台。同时正在开展脱水素、籽粒大小控制、表皮蜡质合成等基因的遗传转化。相关研究结果发表在PLoS One，BMC plant biology等期刊上。

（2）非生物胁迫响应分子机制研究

以模式植物拟南芥及小麦、玉米、油菜、水稻等为材料，研究非生物信号转到通路和基因表达调控。从激活标签拟南芥突变体库中筛选到植株极度矮小的显性发育突变体*abs1-1D*和*abs2-1D*，研究发现该表型由BAHD acyltransferase基因突变所致，且可被外源油菜内脂素回复。以花斑突变体var2为基础筛选到多个var2修饰突变体，并已经克隆到若干个新的var2修饰基。

以抗旱性强的一粒小麦为材料，分析了干旱胁迫与对照组叶片和根中蛋白组的差异，并筛选获得一些特异蛋白组分，并正在对这些差异蛋白进行系统分析。对参与水稻OsNOX2信号调控的OsRTPK1、OsRTPK2、OsmtATPS1、OsTPP1、OsTPP2等13个关键基因进行系统研究，进一步明确了这些基因的表达与OsNOX2表达的关系及其抗旱响应特征，同时克隆上述关键基因在小麦中的同源基因。

以拟南芥和油菜为材料，利用突变体、过量表达、蛋白互作等技术，分析拟南芥

和油菜中参与ABA、JA、SA信号通路重要蛋白激酶和转录因子，明确其亚细胞定位和互作关系，及其与干旱和K营养的关系，为后续研究奠定了基础。克隆了小麦胁迫响应转录因子TasNAC1，并对其表达谱及亚细胞定位进行深入分析，证明该转录因子参与干旱和盐胁迫响应，对玉米NAC家族转录因子进行全面分析，并利用RNA-Seq技术筛选获得干旱特异相应的NAC家族成员。

利用高通量测序技术筛选了番茄抗逆相关miRNA，并利用基因芯片对这些小RNA的表达模式进行了系统分析。利用表达序列标签和miRNA前体的二级结构进行同源搜索，在重要谷类作物黍（Panicum miliaceum L.）中鉴定了43个新的miRNA，正在对这些miRNA的分布和作用进行系统分析。上述研究结果发表在Journal of Experimental Botany，PLoS One，Journal of Plant Growth Regulation，Science China Life Sciences，中国农业科学、农业生物技术学报等期刊。

（3）旱区作物遗传及栽培生理研究

以旱区粮食作物和林木为研究对象，研究栽培品种的遗传多样性，N、P、K、Zn等营养元素吸收利用、物质的运输与累积。利用269对SSR标记对中国北方90多个代表性小麦栽培品种的遗传多样性、群体结构和连锁不平衡进行了全面分析，平均的遗传多样性指数为0.6，B基因组的遗传多样性最高，而D基因组最低。以中国北方小麦栽培品种为对象，系统分析了14种形态、产量和生理形状与干旱耐受性的关系。研究了旱地土壤施用N、Zn、Se后，对小麦产量的贡献及籽粒矿质营养元素累积的作用。

以6种不同的杨树品种为对象，研究了其对Ca的耐受性，并分析了光合作用、水分利用效率、稳定C同位素分布于叶子和木质部解刨结构的关系，该研究结果对不同品种杨树种植区域的规划有指导意义。同时研究了施用N肥后，速生杨和慢生杨的生长发育、碳氮生理和木质特性的影响，发现速生杨对N-肥的施用更敏感。系统研究了杠柳(Periploca sepium Bunge)抗旱性和适应性策略，提出了植物应对干旱胁迫的阶段性响应策略，研究了不同程度干旱胁迫下，杠柳脯氨酸代谢和作用的差异，进一步解析脯氨酸在提高植物抗旱性中的作用。

上述研究结果发表在Journal of Experimental Botany, PLoS One, Plant Biology, Field Crops Research, 植物生理学报和生态学报等期刊。

（4）旱区作物与根瘤菌互作机制研究

根瘤菌—豆科植物共生固氮体系在促进污染地氮素循环中具有重要作用。通过红外光谱、扫描电镜和能谱分析对苜蓿中华根瘤菌CCNWSX0020和土壤杆菌CCNWGS0286的研究，揭示了其对多种重金属离子的吸附模式；利用转座子突变技术和差异基因表达技术克隆了菌体抗铜和锌相关基因；通过全基因组测序和生物信息学分析，揭示了苜蓿中华根瘤菌CCNWSX0020具有多种抗铜系统以及抗铜机理，预测并验证了土壤杆菌CCNWGS0286基因组中与重金属抗性和促植物生长代谢过程相关的基因；利用报告基因技术、植物盆栽实验揭示了苜蓿中华根瘤菌CCNWSX0020菌体对宿主生长的促进作用和对铜吸收能力的提高。对耐盐碱骆驼刺根瘤菌Mesorhizobium alhagi strain CCNWXJ12-2T进行全基因组测序，对功能基因进行了预测并注释。通过转座子突变技术对原菌进行基因突变，筛选盐敏感突变体，并对耐盐相关基因进行了克隆并利用功能互补对其功能进行了验证，表明所克隆得到基因与耐盐性相关。

以刺槐和中慢生根瘤菌共生体系为研究对象，使用抑制差减杂交及反向Northern斑点杂交的方法分离刺槐结瘤素基因，并使用实时荧光定量方法对这些基因在结瘤过程中的表达量做进一步的鉴定，并对其中的重要基因做进一步的功能分析，共得到4个结瘤特异型基因及29个结瘤增强型基因，对其功能分析还在进一步验证中。上述研究成果分别发表于Journal of Bacteriology, Applied and Environmental Microbiology, Bioresource Technology和Journal of Hazardous Materials等国际权威期刊。

3、作物与有害生物的互作机理

（1）农作物重大病虫害成灾机理

围绕小麦、苹果、马铃薯、猕猴桃、棉花上的重要的有害生物胁迫因子（真菌、病毒、线虫、细菌），从不同研究层面揭示这些生物因子对旱区主要作物造成灾害的成因。

①明确我国小麦条锈菌重要越夏区一些杂草种类（如披碱草、冰草、早熟禾）感染小麦条锈菌，是条锈菌的越夏存活的重要辅助寄主。首次明确小檗作为我国小麦条锈菌的转主寄主，并初步确定了小麦条锈菌转主寄主小檗在条锈菌毒性变异中的作

用。在陕西省、西藏地区分别监测到条锈菌小种13个、26个，明确了西藏小麦条锈菌的生理小种构成，揭示了其遗传多样性及其与内地菌源间的关系。测定了条锈菌新菌系中4菌系（T4）的寄生适合度和致病范围。

②首次筛选出了小麦蓝矮植原体(WBD)与引起矮缩、腋芽丛生症状的毒性致病因子基因TlyC和Tengu，并从WBD感染寄主差异基因表达谱研究结果中获得了131条差异片段，涉及代谢、能量、信号转导、病害防御等功能。

③明确了陕西省小麦禾谷孢囊线虫病（CCN）的发生规律，小麦返青开始侵染根部，4月末至5月初雌虫发育成虫形成孢囊；完成了70份小麦种质抗孢囊线虫的田间鉴定，没有发现对CCN免疫的品种。

④揭示了苹果腐烂病病原菌对树皮的侵染过程，初步明确了病菌主要毒性因子为其分泌的果胶酶，建立了腐烂病菌的基因功能验证体系，筛选获得果胶酶基因Vmpg-1，正在对该基因进行功能验证。发明了腐烂病菌田间早期PCR诊断和检测技术，并利用该技术揭示了陕西省外表无症状果树枝条中的腐烂病菌潜伏侵染规律。建立了苹果树腐烂病菌PEG介导和农杆菌介导的遗传转化体系，获得了6000多个转化子，正在进行致病性测定和生物学表型分析。完成了腐烂病菌侵染苹果致病过程的差异表达分析的前期序列分析，正在进行全转录组信息分析。目前正在普度大学进行腐烂病菌的全基因组测序和分析。明确生防菌BAR1-5为糖丝菌属放线菌的一个新种，揭示了其在田间防治腐烂病的效果和杀菌机理，田间防治试验示范发现通过生防菌涂干可明显减少新病斑形成且明显优于化学药剂，正在大面积推广应用。

⑤利用组织细胞学技术揭示了苹果褐斑病菌的侵染过程，发现了其存在寄生和腐生生活方式，首次发现其在叶片组织中可产生吸器及平行排列于叶片角质层下的菌丝束这些特殊结构，为进一步揭示病菌与寄主互作关系提供了重要证据。通过人工接种，对不同苹果品种、砧木的抗病性进行了评价，筛选出了具有过敏性坏死反应的高抗材料，并正在探索其抗病机理与PCD的关系。建立了苹果褐斑病致病性评价方法和指标，并对分离获得的50多株病菌进行了致病力比较，发现致病力存在差异，但与地理来源无关。明确了危害我国果树生产的煤污病病原菌种类。在我国苹果主产区煤污病调查中得到323个来自苹果的菌株和40个来自山楂、梨、柿子、柑橘和西府海棠的菌株，

除6个菌株暂不能确定属外，其余357个菌株可归为35个系统发育种。其中，已描述的种类22个，尚未描述的系统发育种13个。7个常见种的菌株数目差异较大。*Sterile mycelia* sp. CN的菌株数目最多，有122个菌株，占总菌株数的33.7 %。其次为*Peltaster* sp. CN、椭圆拟维朗那霉（*Pseudoveronaea ellipsoidea*）和礼泉枝氯霉类似种（*Ramichloridium liquensis-like*），分别有55、40和41个菌株，占总菌株数的15.2 %、12.2 %和11.3 %。鲁枝氯霉类似种（*Ramichloridium luensis-like*）、威斯康辛接瓶霉（*Zygophiala wisconsinensis*）和杨凌后稷孢（*Houjia yanglingensis*）三个种的菌株数目较少，分别有17、6和5个菌株，占总菌株数的4.7 %、1.7 %和1.4 %。

⑥揭示了猕猴桃溃疡病在陕西省的周年发生规律与消长动态及其与品种的关系。分离获得了不同品种不同部位的200多株细菌并进行了鉴定，提交了菌系序列并与新西兰、意大利专家进行了交换。利用细胞学技术进行了病菌侵染过程观察，发现了叶片、主干病菌在组织中的存活和运转过程。筛选出对该病害有较好防效的生防菌，目前，正在进行田间试验和活性物质分离。据此，提出了预防病害的措施和方法，并在眉县多地进行了试验示范。

⑦利用9对微卫星标记引物对分离自云南的93株、福建的101株和贵州的112株致病疫霉菌进行了的SSR基因型多样性综合分析，结果表明，福建省的致病疫霉菌群体分离物的基因型和云南、贵州两个群体中的基因型没有共同基因型，云南和贵州的致病疫霉菌群体中有三个共同基因型。研究初步表明，南方三省的致病疫霉菌群体可能以无性生殖为主，群体内的遗传差异比较低。

⑧建立了大丽轮枝菌型黄萎病的SYBR Green I实时荧光定量PCR反应的标准曲线，结合土样水筛法建立了土壤大丽轮枝菌微菌核定量检测体系、土壤中微菌核数量与实时定量Ct值间的关系模型（n=e7.300-Ct/3.905）及与棉花黄萎病发病率的关系模型（y=2.710n+0.251）。为土壤中大荔轮枝菌微菌核的定量监测和病害预警奠定了基础。

⑨明确了暗黑赤眼蜂与松毛虫赤眼蜂对梨小食心虫卵的寄生率和羽化率差异，暗黑赤眼蜂对梨小食心虫卵的寄生率显著高于对棉铃虫卵的寄生率。拟合分析显示，暗黑赤眼蜂和松毛虫赤眼蜂对梨小食心虫卵的寄生符合holling-Ⅱ型功能反应圆盘方程,

说明暗黑赤眼蜂是一种防治梨小食心虫的潜在寄生蜂。

（2）病、虫与作物的互作机理

①完成了小麦条锈菌全基因组分析，在前期高通量 SOLEXA 测序和 FOSMID 建库的基础上设计了‘fosmid to fosmid’ 拼接策略，获得了高质量的基因组框架图，并以此为基础完成了 5 个来自世界各大区的分离系重测序分析，取得重要研究结果。

获得了条锈菌高质量基因组框架图（基因组大小约110M），contigs和scaffolds N50分别达到18-kb 和125-kb, 相比PLosONE发表的条锈菌基因组草图(N50: 5-kb)拼接质量显著改进，可以满足基因组分析和基因发现研究。通过来自不同fosmid poolings高相似Scaffolds的详细分析，证实条锈菌基因组存在高度杂合特征，本研究释放的基因组序列对研究基因组杂合区域特征具有重要价值。获得全基因组预测编码蛋白基因27,964个，比较基因组分析表明：和已发表的小麦秆锈及杨树叶锈菌基因组相比，其中8,514个基因是条锈菌基因组特有的；和其他真菌相比锈菌基因组拥有更大的分泌蛋白组。

对2,100个预测分泌蛋白进行了筛选，利用携带PVX和候选效应蛋白融合表达载体的农杆菌转化本生烟（Nicotiana benthamiana）叶片，对198个候选基因进行了瞬时表达筛选，其中12个基因显示了分泌特性，为进一步发现锈菌效应蛋白奠定了重要基础。对来自世界范围的5个条锈菌分离系进行了重测序分析，结果表明条锈菌群体的遗传差异被严重低估，有性重组极有可能在条锈菌毒性小种进化中发挥了重要作用，近一个世纪以来认为点突变是锈菌遗传变异主要来源的观念需要重新审视。本研究结果还表明，‘fosmid to fosmid’策略对采用NGS技术对高杂合度专性寄生物基因组进行拼接分析具有重要应用潜力。

②开展了小麦条锈菌顶端生长过程中的细胞骨架（微管、微丝和马达蛋白）的功能研究，目前通过基因克隆、qRT-PCR及突变体互补等方法确定其功能；确定了脂肪在条锈菌形成吸器之前作为基本的能量供给，而形成吸器后的能量供给主要依赖吸器从小麦叶肉细胞中吸取蔗糖作为主要的能量来源，初步明确了小麦条锈菌生长发育过程中能量代谢（脂肪、糖及氨基酸）的过程及分子机理；从组织学、细胞学、生物化学与分子生物学方法研究了小麦成株抗锈机理，结果发现其抗锈性表达从分蘖期开

始，孕穗期达最强，且抗锈性增强与过敏性坏死、活性氧的产生和积累等有密切的关系，在小麦成株期抗性表达时的细胞学特征为细胞壁的修饰和乳突的形成、入侵细胞的坏死和吸器鞘的形成等。克隆了小麦蒜氨酸酶基因*TaAly*1，分析了其表达特征，*TaAly*1可能通过参与依赖GA、MeJA和SA的信号途径而参与小麦与条锈菌的互作。克隆了条锈菌诱导的小麦G蛋白基因，并分析了其功能，该基因很可能参与小麦与条锈菌互作反应，并对小麦抗条锈病起到一定程度的调控作用。

③对禾谷镰刀菌蛋白激酶基因*Fgprp*4，*CDC*2，*KIN*1，*CLA*4以及*HOG*1的信号通路，开展了功能分析和基因敲除工作，现已获得了200多个敲除突变体。明确了细胞周期蛋白依赖激酶*CDC*2和周期蛋白依赖激酶活化激酶*CAK*1在细胞周期调控过程中发挥着重要作用。

④通过Gateway技术构建了三个弱毒性寄生疫霉菌菌系侵染烟草叶片组织的cDNA文库，利用已报道的抗病蛋白RB和无毒蛋白AvrBlb1互作产生过敏性坏死反应为指示系统，建立并优化了农杆菌介导的瞬时表达系统和规模化文库筛选体系。通过对文库中16000个单克隆的高通量筛选，获得了25个具有引起烟草坏死活性的单克隆，对其中一个具有坏死活性的单克隆PpE2进行了进一步的分析，针对该基因分别构建了基因沉默载体和GFP融合表达载体。

⑤通过对感大豆疫霉的拟南芥T-DNA插入突变体581-51的分析，证明该突变体中有四处T-DNA插入突变的位点。针对这四个突变基因，利用在植物中组成型稳定表达hp-RNA（能够自身形成发夹结构）的方法，以Col-0野生型为材料，构建包括分别针对四个基因的单独沉默和共同沉默两个或多个基因一共15种沉默的转基因拟南芥。基因功能分析初步表明，B基因功能的正常发挥与拟南芥对于大豆疫霉菌的侵染起着至关重要的作用。

⑥通过抑制性消减杂交技术（SSH），构建梨小食心虫滞育与非滞育正、反向差减cDNA文库，从中筛选梨小食心虫滞育相关基因，并对其进行测序和分析。结果表明，在获得的128个滞育特异和132个非滞育特异的EST中，有滞育差异表达EST42条（17条功能未知）、非滞育差异表达EST46条（22条功能未知）。对差异表达EST同源检索后推测，其功能大部分与滞育或非滞育特性相关。

⑦利用RT-PCR和RACE技术克隆到一条梨小食心虫化学感受蛋白的全长cDNA序列，命名为GmolCSP(GenBank登录号: JQ821389)。序列分析表明，GmolCSP开放阅读框序列为384bp，编码127个氨基酸残基，预测N末端含有18个氨基酸组成的信号肽序列。该基因编码的氨基酸序列与其他鳞翅目昆虫化学感受蛋白的氨基酸序列具有较高同源性。利用反转录多聚酶链式反应（RT-PCR）和cDNA末端快速扩增（RACE）技术，从梨小食心虫雌成虫触角组织克隆到2个编码普通气味结合蛋白的cDNA全长序列GmolGOBP1和GmolGOBP2。GmolGOBP1和GmolGOBP2之间的同源性仅48%，说明它们属于不同的昆虫普通气味结合蛋白类群。

（3）农作物重大病虫害综合控制技术

①新农药的开发：在分离、鉴定出苦皮藤素V作用靶标V-ATPase H亚基的基础上，测定了粘虫幼虫中肠V-ATPase H亚基全长cDNA及氨基酸序列；采用SiRNA技术，初步进行了该靶标的功能验证；完成了H亚基载体构建，并在sfq细胞中成功表达，获得近1g受体蛋白；从微生物发酵产物中分离出一种具有全新骨架的新抗生素，其对多种人类疾病细菌和植物致病细菌有高活性；完成了创制杀菌剂草酸二丙酮胺铜的合成工艺条件优化及重要中间体及终产品的质量控制方法，目前正在进行技术转让谈判。

②在宝鸡、汉中等地建立了小麦条锈病综合防治示范基地，以合理利用抗病品种为主，利用药剂和农业措施为辅的小麦条锈病控制策略，采用统一品种、统一播种、统一防治方案，使小麦病虫害的发生和危害得到有效控制。在条锈病菌越夏区，通过调整产业结构，推广种植经济价值高的经济作物，压低了我国条锈菌越夏区的初始菌源量，控制了病害发生，大大减轻了我国北方麦区条锈病灾变压力，产生了巨大的间接经济效益。组建了陕西渭北苹果病害综合防治体系、陕西保护地蔬菜病害综合防治体系、甘肃马铃薯病害综合防治体系和小麦等综合防治措施，并在生产上得到大面积推广应用，保障了陕西蔬果安全生产，取得了显著的经济效益、生态效益和社会效益。

③通过提高土壤温度对土壤中大荔轮枝菌微菌核有很强的杀伤作用，40℃条件下处理4天后土壤中的微菌核已全部死亡，在55℃处理360 min可使微菌核完全死亡。该研究结果为通过覆膜增温防治作物黄萎病提供了理论依据。

④揭示了生防菌BAR1-5在田间防治腐烂病的效果和杀菌机理，并与筛选出的杀

菌剂进行了较大规模的田间防治试验示范，发现通过该生防菌涂干可明显减少新病斑形成且明显优于化学药剂，正在大面积推广应用。

⑤筛选发现1株生防菌对猕猴桃细菌性溃疡病有较好防效。目前正在进行田间试验和活性物质分离，同时提出了预防该病害的措施和方法，并在眉县多地进行了试验示范。

⑥建立了用于防治蔬菜害虫的banker plant系统，评价了利用替代寄主饲养的蚜茧蜂对于桃蚜的控害效果，及其在田间的扩散和搜索靶标害虫的能力。研究明确了桃蚜侵染番茄后诱导其产生的化学挥发物质会对烟粉虱产生防御反应，并具有引诱其天敌的能力。同时，我们首次发现利用外源SA处理会诱导小麦对蚜虫的抗性，采用EPG技术分析发现其激发小麦韧皮部闭合反应，进而抑制了蚜虫的取食行为。在蚜虫取食的分子机理方面，我们利用RNAi技术发现AplnR2基因可能参与了豌豆蚜取食时对于营养压力的选择反应，OS-D2基因在桃蚜若虫期取食寄主植物过程中及成虫期寻找最佳植物取食位置的行为中可能有重要作用。

4、作物抗逆种质创新与品种设计

围绕抗旱、耐盐碱、抗寒、抗病虫等重要性状，探索创制小麦、玉米、油菜、小杂粮、苹果、葡萄、蔬菜等作物抗逆种质和新品种设计的新理论与新方法。综合运用细胞工程、染色体工程、基因工程、分子标记辅助选择等现代生物技术，创制抗逆新种质，与常规育种技术结合，培育适宜大面积生产应用的高产优质、抗逆广适的新品种，服务旱区农业生产。

（1）较系统地研究了苹果对非生物逆境响应的生理分子机制，外源褪黑素和脱落酸等对长期干旱等逆境的调控，以及小麦CC-NB-ARC类基因表达模式、细胞定位和涉及抗病途径。通过SSH技术，获得楸子参与抗旱反应的EST 455个，小麦抗白粉病EST序列90个。从葡萄叶片中克隆了VpR82H基因的启动子，并检测了中国野生葡萄VpR82H基因在白粉菌诱导前后的转录情况。筛选了4个与抗蚜基因连锁的SSR分子标记，建立了该抗蚜基因的分子遗传图谱，将该抗蚜基因定位于小麦7DL染色体上，命名为*Sa*1。

（2）建立了小麦、苹果（嘎啦、绿袖）、葡萄等多个资源和品种的遗传转化体

系，开展了大批功能基因的遗传转化，获得了100多个转基因株系。通过农杆菌介导法，将Na+/H+逆向转运蛋白基因在苹果矮化砧木M.26中过量表达，提高了其抗盐性、抗旱性。将抗白粉病中国野生华东葡萄“白河-35-1”株系的芪合成酶基因分别转入酿酒、无核和鲜食葡萄中，已获得9株转基因株系。2012年配制抗逆、无核葡萄杂交组合14个，接种胚珠3840个，发育胚珠1740个，截止目前获得萌发幼胚1170个。

（3）利用筛选的抗逆资源秦冠、楸子作亲本与高品质资源蜜脆、富士进行杂交，获得杂交后代4万余株，初选抗逆优系20多个进行区试。培育和筛选抗蚜虫的小麦材料12个。EPG研究结果表明，德国品种Www2730抗麦长管蚜位点在表皮，中国小麦品种小偃22对禾谷溢管蚜的抗性位点细胞壁较厚，美国品种Amigo对麦二叉蚜表现抗性。筛选出20份性状较好的品种（谷子10个、荞麦3个、豇豆3个、粳性糜子1个、小豆2个、双青豆1个）。开展红花荞麦集团选育工作，有218份材料进行了田间鉴定，鉴选出20个优异糜子材料。

（4）陕油803参加国家油菜品种区域试验，目前已通过区试，正提请国家品种申请委员会通过。本年度共审定小麦新品种1个、玉米新品种1个和油菜新品种3个、初审苹果品种4个。选育和繁殖了芸豆、糜子、荞麦、豌豆、扁豆新品系共12个。2012年10月，西农9976、西农9978通过了陕西省种子站的田间鉴定验收工作。小麦新品系西农418、西农1018和西农986已完成两年陕西省关中灌区中肥组区域试验和一年生产试验，符合报审条件，有望年内报审。

（5）总结形成的“大规模、多地点和持续性”的育种思路，“优异种质材料 + 高效选择方法（高密度、多地点、少施肥、少灌水）+ 新组合多环境测试”的现代高效玉米育种技术体系，强化顶层设计，基础材料创制从盲目选材到设计选材的转型，杂交组合测配从盲目测配向设计测配的转型。

（二）取得成绩

1、科技奖励

一年来，获国家、省部级科技成果奖3项。其中“玉米高产高效生产理论及技术体系研究与应用”获得国家科技进步二等奖（第二单位）；“甘蓝型油菜无微粉类细胞质

雄性不育系研究及其杂交种选育”获得陕西省科技进步一等奖；“高产多抗粮饲兼用玉米品种陕单8806选育与推广”获得陕西省科技进步二等奖。

国家科学技术进步奖

证　书

为表彰国家科学技术进步奖获得者，
特颁发此证书。

项目名称：玉米高产高效生产理论及技术体系研究与应用

奖励等级：二等

获 奖 者：薛吉全

中华人民共和国国务院

2011年12月23日

证书号：2011-J-251-2-02-R03

2、发表论文

在Biotechnology Advances, PLoS Pathogens, Journal of Experimental Botany, PLoS One, Ecotoxicology, Journal of Pineal Research, BMC Plant Biology, 中国农业科学，作物学报等国内外期刊上发表论文173篇，其中 SCI 收录论文132篇（影响因子10.0-5.0

的9篇，5.0-3.0的 34篇）；出版《分子生物学》等著作3部；申请国家发明专利12项，获授权9项。

3、在研项目

获批国家“973计划”项目1项、国家转基因重大专项2项；同时，获批“十二五”科技支撑计划 2项、“973计划”子课题2项、“863计划”课题1 项、国家自然科学基金17项，教育部科学技术研究重大项目1项。目前，重点实验室在研项目126项，合同经费达 1.26亿元，2012年到位科研经费5081万元。

（三）队伍建设与人才培养

1、队伍规模和结构，人才引进和培养

人才是重点实验室发展的关键因素，是重点实验室可持续发展的根本保障，重点实验室一直把人才培养和队伍建设作为重点实验室重中之重，经过培养和引进，已形成了一支结构合理、学历层次高、专业覆盖面广、技术力量雄厚的学术队伍。

针对人才培养和人才引进制定了一系列管理制度。在短短一年时间，队伍建设和人才培养取得了丰硕的成果：王明波入选教育部“长江学者”讲座教授，韦革宏、单卫星获得获得国家杰出青年基金，王晓杰、郭军、王晨芳、李明军4位老师入选教育部新世纪优秀人才，陈勤、王晓峰入选陕西省百人计划，王晓杰荣获陕西省青年科技新星，并选送 5 名优秀青年教师到国外著名院校进修，其中 4 名已学成归国。实践证明，重点实验室引进和培养高水平人才的措施切实可行。

目前，重点实验室现有固定人员61人，教授35人、副教授9人、讲师6人；管理和技术人员8人，其中高级实验师1人，实验师5人。队伍中有国家“千人计划”3人、教育部“长江学者”特聘教授1人、“长江学者”讲座教授1人、国家“973计划”项目首席科学家1人、国家杰出青年基金获得者4人、国家“百篇优秀博士学位论文”获得者2人、国家级有突出贡献专家1人、国家“百千万人才工程” 入选者1人、教育部“跨世纪优秀人才计划”入选者1人、教育部"新世纪优秀人才支持计划"入选者9人、教育部 "高校青年教师奖"入选者1人、教育部“高等学校优秀青年教师资助计划”入选者1人、教育部“高等学校教学名师奖” 获得者1人、陕西省百人计划入选者3人、陕西省“三秦学者”

特聘教授1人、陕西省“科技创新人才”称号1人、陕西省“科技新星”称号1人。重点实验室已形成了“千人计划”和“长江学者”领衔、教授支撑、青年骨干为主体一支结构合理、学历层次高、专业覆盖面广、技术力量雄厚的学术队伍。

2、实验技术队伍建设

目前有技术人员6人，其中高级实验师1名，实验师5名。分别负责各个平台的大型仪器操作、维护和功能开发工作，承担着分析测试平台、显微测试平台、基因组学和蛋白组学平台多少台件仪器设备的操作和维护工作。

一年来，重点实验室技术人员不断加强提高现有仪器设备操作的同时，还积极学习和熟悉新购置仪器设备的操作和维护。通过学习、参加培训会、学术会等提高了实验技术队伍业务水平并在仪器操作、维护、功能开发、方法改进等方面有较大进步。今年共有3人次参加了公司举办的培训班，分别赴上海、北京、中科院植物所等地对激光共聚焦显微操作系统、场发射扫描电镜、液质气质联用系统等大型仪器的操作和应用进行了培训。3人参加了陕西省电镜学会年会，1人加入学校色谱仪器实验技术团队。

2012年，实验技术人员获批自然科学基金青年项目2项，承担学校大型仪器功能开发项目3项，发表论文4篇。

（四）经费投入及条件建设

1、仪器设备购置和平台建设完成情况

根据重点实验室建设计划任务书要求和研究的需要，已购置了激光共聚焦系统、微生物鉴定系统等47台件仪器设备，初步构建了显微可视技术、基因组技术、蛋白组技术、生物信息、细胞学、逆境模拟和分析测试技术等功能研究平台，已全部对外开放，实现了共享。

（1）显微可视技术平台

拥有日立场发射扫描电镜、日立7700透射电子显微镜、奥林巴斯FV1000双光子激光共聚焦系统、日本电子钨灯丝扫描电镜、蔡司激光共聚焦显微镜、荧光显微镜、原子力显微镜、超薄切片机等仪器。主要为从事动植物表面形态、组织结构、超微结构的形态学分析及三维结构构建研究的科研人员，进行荧光原位杂交、原位实时PCR

产物分析、荧光共振能量转移分析、荧光漂白恢复研究、共定位分析等实验研究提供技术支撑。

（2）分析测试技术平台

拥有核磁共振仪、液相分析系统、紫外分光光度计、荧光呼吸检测仪、微生物鉴定系统等仪器。主要服务于从事生物、化学、物理、材料、医学等学科的科研人员，进行有机化合物及天然产物的结构与功能研究， 高聚物聚合、固化机理研究，蛋白质、分子生物学的结构与功能研究，高场核磁共振新方法新技术研究，大分子物质的分离，植物叶片光合作用、蒸腾作用、呼吸作用、叶绿素荧光等生理因子指标的测定，细菌、真菌等微生物的鉴定。

（3）蛋白组技术平台

拥有蛋白分离纯化系统、双向电泳系统、超速离心机、高速离心机等仪器。主要用于生物大分子和细胞亚单位结构的分离和提取及蛋白质的分离鉴定等。

（4）基因组学技术平台

拥有DNA测序仪、遗传分析仪、定量PCR仪、突变检测系统、基因枪、脉冲电泳系统、电转化系统等仪器。主要用于DNA测定、遗传结构和功能的分析、基因组测定、酵母人工染色体文库建立、染色体绘图、基因突变诊断分析、基因型分析、基因定位、转基因等分子生物学和分子遗传学研究。

（5）生物信息平台

生物信息室已改造完成，服务器、生物信息软件已安装调试完毕并投入使用。主要用于细菌、真菌、动物、植物高通量测序数据的拼装、注释；高通量RNA测序结果分析及数据注释；蛋白结构模拟及新农药开发；比较基因组、基因组信息挖掘、进化等方面研究。

（6）公共服务平台

拥有主要有PCR室、成像室、制水制冰室、人工气候室、组培室、超低温冰箱、植物生长箱、摇床等。为功能实验室和大型仪器设备及团队实验室提供服务和支撑。

2、仪器设备开放和利用情况

（1）10万元以上大型仪器设备全部加入大型仪器设备共享系统，实验室及外单

位科研人员可通过系统进行预约实验，每个设备配备了专职技术人员进行操作。一年来，重点实验室大型仪器设备为校内外2865人次提供了技术服务，开机工作时间12649小时。平均每天7.8人次来重点实验室使用相关仪器设备4.4小时/人。

（2）公共平台10万元以下所有仪器，如PCR仪、离心机、凝胶成像、制冰制水、高压灭菌、组培间等全部开放使用，节假日双休日及每天晚上安排专职人员值班，做到全年365天全天候开放共享，为广大科研人员提供技术支撑和服务保障。

3、基础条件建设

（1）实验室改造

根据建设计划任务书的要求和研究需要，已完组培室、电镜室、会议室等改造。建立人工气候室3间，共51 m^2；组培室2间，共60 m^2；灭菌室50 m^2，储藏室 70m^2。

（2）转基因隔离温室建设

建成科研温室共800m^2左右，主要开展试验用苗的种植及相关抗病性遗传、毒性鉴定等研究工作。

（3）田间试验平台建设

增加试验地200亩，基本满足了作物种质资源繁殖、保存和种质创新的需求。建设逆境模拟大棚500m^2，满足了相关研究对种质资源的抗逆性鉴定等方面的需要。

4、开放课题及执行情况

开放课题负责人严格按申请书任务积极开展课题研究工作，所有课题实施进展顺利，目前已取得的初步成果：

李韬在海盐种/Wheaton衍生的RIL（F8）初定位群体中，根据基因型和表型鉴定，筛选目标株系YW105（携带目标基因但不携带其它已知抗赤霉病QTL）与感病亲本Wheaton进行标记辅助选择的连续回交，通过自交获得BC2F2群体；以海盐种主效基因Qfhb.hyz-7D区域的2个关键SSR标记对所选的380个品种进行了初步分析，结果有14个品种（系）在目标基因区与海盐种具有相同的单倍型，相关成果发表在American Journal of Botany。

李桂荣用胚挽救技术获得欧洲无核葡萄×中国野生葡萄、无核葡萄×无核葡萄、

无核葡萄×有核葡萄的杂交后代，研究影响胚挽救技术中关键成分激素的种类配比、畸形苗的防止及其转化等，提高现有杂交胚挽救育种技术的效率，相关科研成果已投稿《Vitis》。

周洪旭应用诱集板粘缚法和捕虫网网扫法调查研究了绿盲蝽在北方16种果树上的发生动态规律，分析了绿盲蝽在不同果树上发生数量的差异、对不同颜色诱集板趋向差异以及绿盲蝽在果树与周边杂草之间的扩散转移规律相关研究成果发表在《中国农业科学》《生态学报》。

肖永贵初步获得了控制苗期植被覆盖率、植被归一化指数、生育期、叶面积指数、叶绿素含量、冠层温度、株高及产量性状相关的基因标记29个，发掘紧密连锁且可用于分子育种的标记1个，优化了苗期植被覆盖率的测定方法，达到快速高效获取目的。研究论文已投稿《中国农业科学》。

（五）国际合作与学术交流

2012年，重点实验室派出8个代表团，共36人次，访问了西班牙巴塞罗那大学、法国农业科学院、澳大利亚CSIRO植物所、美国加州大学河滨分校和堪萨斯州立大学等国际知名学术机构，进行学术交流和科研合作。

2012年，重点实验室主办了“小麦病虫害持续控制学术研讨会”、“杨凌国际农业科技论坛—作物逆境适应与持续生产”、“第一届国际糜子会议”和“国际荞麦育种学术研讨会”等国际学术会议；承办“第十三届国际禾谷类作物锈病与白粉病会议”、“作物杂种优势利用国际学术大会”、“2012 Borlaug Global Rust Initative, BGRI conference”、“2012全国植物生物学大会”、“中国园艺学会2012年学术年会”、“2012年全国园艺作物逆境生物学与分子育种博士论坛”和“旱区农作物和种业博士生学术论坛”等国际、国内大型学术会议。通过主办和承办大型国际会议，提升了重点实验室的国际知名度和影响力。

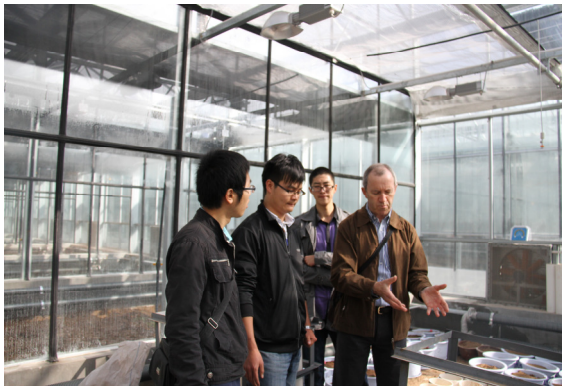
作物逆境适应与持续生产学术研讨会

小麦病虫害持续控制研讨会

实验室主任康振生教授在2012年第13届国际禾谷类作物锈病与白粉病会议上作了题为“Update on genomics and functional genomics of Puccinia striiformis f. sp. tritici in China”的大会特邀报告，在2012年博洛格全球麦锈病协作网(BGRI) 研讨会上作了题为“Sexual stage and virulence variation of Puccinia striiformis f. sp. tritici in China”的大会特邀报告。康振生教授指导的博士生刘巍提交的会议论文荣获2012年BGRI优秀研究生论文，并作了大会报告。康振生教授参加了2012年博洛格全球麦锈病协作网（Borlaug Global Rust Initative, BGRI）大会的新闻发布会，重点介绍了中国小麦条锈病的发生、流行与研究现状。

实验室邀请澳大利亚悉尼大学植物育种研究所Robert McIntosh院士、美国农业部农业研究局Xianming Chen教授、Raymond Martyn教授、西班牙巴塞罗那大学Jose Luis Araus教授、澳大利亚联邦科工组织植物所A G Condon博士、国际玉米小麦改良中心Matthew Reynolds教授、英国洛桑研究所Martin Parry教授、Malcolm J. Hawkesford 教授、西班牙莱里达大学Gustavo Slafer教授、美国犹他州立大学David Hole教授、Peter Nick教授和Lailiang Cheng教授等32位国内外著名科学家来重点实验室进行讲学、合作研究与学术交流。

康振生教授做报告



A G Condon合作研究

（六）运行与管理

1、重点实验室实行“开放、流动、联合、竞争”的运行机制，对校内外开放、共享。重点实验室成立了学术委员会，2012年12月顺利召开了重点实验室第一届学术委员会第2次会议，审议了重点实验室的建设目标、研究方向、取得成果、开放课题和下年度工作安排。

2、组建了重点实验室工作机构。成立了重点实验室综合办公室、技术支撑部和4个研究室。重点实验室定期召开研究方向学术研讨会和汇报会，了解各研究方向研究进展和存在问题，部署下阶段的工作安排，将重点实验室研究团队建设成团结、和谐、充满勃勃生机的科技创新群体。

3、建立健全了重点实验室各项规章制度，规范了办事流程，提高了管理效率，有效激励和调动实验室工作人员的工作积极性和主动性。制定了仪器设备管理使用预约、登记、使用责任制度；会议室预约使用和卫生制度；卫生、安全责任制，责任落实到人；设立了固定资产管理员，建立了固定资产管理系统；建立了学术会议、汇报会和学术沙龙制度，学术交流经常化、制度化，学术氛围进一步增加。

4、建立了重点实验室网站，提高了重点实验室的开放度和影响力，促进了重点实验室的对外交流和科学研究。建立了重点实验室视觉形象识别系统，规范了重点实验室中英文名称的使用。设计了实验室标识系统，并已应用制作了实验服、手提袋、宣传册、档案袋和信纸信封。

5、建立了重点实验室参观访问制度，一年来共接待科技部、农业部、国家自然

科学基金委等上级部门、省市单位和兄弟院校所近三十余家单位180人次来重点实验室指导检查、参观访问。重点实验室积极推进公众开放活动，加强科普知识宣传教育，2012年重点实验室被陕西省教育厅评为“春笋计划”课题研究实验基地。

二、学术委员会组成

姓　名	性别	职　务	出生年月	职　称	工作单位	研究方向
山　仑	男	主　任	1933.01	研究员，院士	中国科学院水土保持研究所	作物抗旱生理
刘　旭	男	副主任	1953.12	研究员，院士	中国农业科学院	作物种质资源
武维华	男	副主任	1956.1	教授，院士	中国农业大学	植物抗逆机理
魏江春	男	委　员	1931.11	研究员，院士	中国科学院微生物所	微生物学
郭予元	男	委　员	1933.01	研究员，院士	中国农业科学院	植物保护
程顺和	男	委　员	1939.09	研究员，院士	江苏里下河农科院	作物育种
方荣祥	男	委　员	1946.01	研究员，院士	中科院微生物所	植物病毒学
邓秀新	男	委　员	1961.11	教授，院士	华中农业大学	果树学
彭友良	男	委　员	1961.1	教授，博导	中国农业大学	植物病理学
巩志忠	男	委　员	1964.05	教授，博导	中国农业大学	植物抗逆生物学
许金荣	男	委　员	1965.08	教授 ，千人计划	西北农林科技大学	植物病理学
李　毅	男	委　员	1961.1	教授，博导	北京大学	植物病理学
王跃进	男	委　员	1958.4	教授，博导	西北农林科技大学	果树种质资源
张改生	男	委　员	1964.4	教授，博导	西北农林科技大学	逆境生理与抗性改良
康振生	男	委　员	1957.1	教授，博导	西北农林科技大学	植物病理学
胡银岗	男	秘　书	1967.12	教授，博导	西北农林科技大学	作物遗传育种

旱区作物逆境生物学国家重点实验室(西北农林科技大学)
State Key Laboratory of Crop Stress Biology for Arid Areas, NWAFU

旱区作物逆境生物学国家重点实验室
第一届学术委员会第二次会议纪要

2012年12月1日，旱区作物逆境生物学国家重点实验室第一届学术委员会第二次会议在西北农林科技大学国际交流中心210会议室召开。学术委员会主任、中国工程院院士山仑研究员主持会议。学术委员会委员魏江春院士、刘旭院士、郭予元院士、程顺和院士、邓秀新院士、彭友良教授、李毅教授、巩志忠教授、王跃进教授、康振生教授和张改生教授出席了会议。

西北农林科技大学科研处冷畅俭处长介绍了出席会议的学术委员会委员和实验室固定研究人员。副校长王跃进教授致辞，感谢学术委员会对实验室建设和发展所做的工作和贡献，恳请各位委员继续对实验室在人才培养、科学研究、学术交流等方面给予关心和支持。

一、审议重点实验室工作报告

首先，实验室主任康振生教授汇报了实验室组建一年来，在科学研究、队伍建设、人才培养、开放交流、运行管理等方面的工作及完成情况。随后宋卫宁教授、黄丽丽教授、马锋旺教授分别汇报了研究进展。

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在听取了工作报告和研究进展汇报后，学术委员会进行了质疑和讨论，对实验室一年来的成绩表示肯定，同时对下一步建设发展提出了建议。

（一）肯定成绩

实验室组建以来各项工作进展很快，组建了管理机构，公开聘用了管理人员；建设经费落实到位，平台建设任务基本完成；学术会、讨论会和学术沙龙制度化、经常化，研究方向得到了进一步凝练；人才培养和队伍建设有较大进展，承担了一系列国家和省部级科技计划任务；在小麦与条锈病菌的互作、苹果的抗逆机理等方面形成了特色，研究成果获国家和省级奖励。通过一年建设，实验室在硬件和软件方面都得到了较大提升。

（二）建议

1、充分利用国家和学校的政策，积极吸引优秀人才，充分发挥人才在科研中的作用；加强实验技术队伍建设，充分发挥仪器设备的功能。

2、加强研究团队建设和开放交流，凝练研究方向，促进学科交叉融合，使实验室各个研究方向均衡发展。

3、创新体制和机制，加强制度建设，促进实验室高效开放运行。

二、审议2013年实验室开放课题

实验室主任康振生教授汇报了实验室 2011 年开放课题执行情况和 2012 年开放课题拟资助方案。2012 年，实验室开放课题共 100 万元，共收到 22 份申请书，经评审拟资助 14 项，其中 10 万元 5 项，5 万元 10 项。

学术委员会进行了讨论审议，同意 2012 年旱区作物逆境生物学国家重点实验室开放课题资助方案，建议尽快组织实施。

实验室学术委员会主任：

2012 年 12 月 1 日

三、承担的科研项目

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
1	小麦重要病原真菌毒性变异的生物学基础	2013CB127700	973 项目	黄丽丽	2013-01-01	2017-12-31	3500.00
2	粮食作物基因对基因病害的抗病品种布局理论	2011CB114001	973 课题	康振生	2011-01-01	2015-12-31	298.00
3	林木对土壤 NP 吸收、利用与归还机制	2012CB416902	973 子课题	罗志斌	2011-01-01	2015-12-31	265.00
4	赤霉菌致病相关基因的鉴定与功能分析	2012CB114000	973 子课题	许金荣	2012-01-01	2013-12-31	72.00
5	害虫行为生态调控的新方法和新技术研究	2011CB1140105	973 子课题	刘同先	2012-01-01	2016-12-31	100.00
6	重要入侵物种种群形成与生态适应性	2009CB119201	973 子课题	宋卫宁	2009-01-01	2013-12-31	12.00
7	旱地小麦高产与水分高效利用的养分调控途径	2009CB118604	973 子课题	王朝辉	2009-01-01	2013-12-31	50.00
8	农业生境检测监测与修复技术研究	2011AA100402	863 课题	韦革宏	2012-01-01	2015-12-31	969.00
9	分子染色体工程高效育种技术研究与应用	2011AA100103	863 课题	吉万全	2011-01-01	2015-12-31	1159.00
10	农林有害生物分子生态调控技术研究	2012AA101503	863 子课题	王保通	2012-01-01	2015-12-31	233.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
11	白菜高胡萝卜素、高花青素的分子标记辅助育种技术研究和优异种质创制	2011AA100105-5	863 子课题	张鲁刚	2012-01-01	2016-12-31	40.00
12	高产转基因小麦新品种培育（十二五）	2011ZX08002	转基因专项（课题）	吉万全	2011-01-01	2012-12-31	542.00
13	小麦抗赤霉病基因的克隆与功能验证	2012ZX08009003	转基因专项（课题）	许金荣	2012-01-01	2015-12-31	1418.00
14	关中灌区小麦主要病害防控技术研究与集成示范	2012BAD19B04-12	国家科技支撑计划（子课题）	康振生	2012-01-01	2016-12-31	55.00
15	主要蔬菜杂种优势利用与新品种选育	2012BAD02B00	国家科技支撑计划（子课题）	张鲁刚	2012-01-01	2015-12-31	56.00
16	作物卵菌病害	20114466	国家自然科学基金杰出青年基金	单卫星	2012-01-01	2015-12-31	200.00
17	微生物多样性及生态	31125007	国家自然科学基金杰出青年基金	韦革宏	2012-01-01	2015-12-31	240.00
18	中国野葡萄抗黑痘病分子机理的研究	31272136	国家自然科学基金面上项目	王西平	2013-01-01	2016-12-31	85.00
19	白粉病诱导的中国野生华东葡萄VpPR10蛋白基因定位表达研究	31272125	国家自然科学基金面上项目	徐　炎	2013-01-01	2016-12-31	76.00
20	海氏桨角蚜小蜂与烟粉虱对逆境胁迫响应的适应性与机制	31272102	国家自然科学基金面上项目	张世泽	2013-01-01	2016-12-31	70.00
21	小麦-蚜虫-天敌载体植物系统防治温室蔬菜蚜虫的理论及应用	31272089	国家自然科学基金面上项目	刘同先	2013-01-01	2016-12-31	80.00
22	梨小食心虫在桃、梨之间季节性转移危害的挥发物诱导与嗅觉识别机制研究	31272043	国家自然科学基金面上项目	仵均祥	2013-01-01	2016-12-31	80.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
23	致病疫霉菌致病关键的效应蛋白基因的鉴定和初步利用研究	31272020	国家自然科学基金面上项目	单卫星	2013-01-01	2016-12-31	85.00
24	条锈菌效应蛋白转运机制及其功能分析	31271990	国家自然科学基金面上项目	王晓杰	2013-01-01	2016-12-31	80.00
25	小麦条锈菌有性过程在毒性变异及病害流行中的作用研究	31271986	国家自然科学基金面上项目	康振生	2013-01-01	2016-12-31	85.00
26	温度诱导的小麦抗条锈病基因表达特征研究	31271985	国家自然科学基金面上项目	胡小平	2013-01-01	2016-12-31	80.00
27	大麦盐胁迫相关 miRNA 的鉴定与功能分析	31271705	国家自然科学基金面上项目	宋卫宁	2013-01-01	2013-12-31	15.00
28	杂交杨吸收、转运与积累重金属镉的生理与转录组调控机制	31270647	国家自然科学基金面上项目	罗志斌	2013-01-01	2016-12-31	88.00
29	西北地区丛枝菌根真菌提高植物耐铅性机制的研究	31270639	国家自然科学基金面上项目	唐　明	2013-01-01	2016-12-31	85.00
30	水稻 OsNOX2 抗旱的分子机制及其调控信号研究	31270299	国家自然科学基金面上项目	陈坤明	2013-01-01	2016-12-31	78.00
31	MAPK-WRKY 信号通路调控植物钾营养利用的分子机理研究	31270293	国家自然科学基金面上项目	江元清	2013-01-01	2016-12-31	75.00
32	第一届国际糜子学术研讨会	31210303032	国家自然科学基金协作项目	冯佰利	2013-01-01	2013-12-31	5.00
33	苹果 6-磷酸山梨醇脱氢酶基因启动子的功能分析与应用	31201600	国家自然科学基金青年项目	梁　东	2013-01-01	2015-12-31	23.00
34	橙色大白菜类胡萝卜素积累的分子机理	31171965	国家自然科学基金面上项目	张鲁刚	2012-01-01	2015-12-31	58.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
35	中国野葡萄抗白粉病泛素连接酶基因调控抗病功能研究	31171924	国家自然科学基金面上项目	王跃进	2012-01-01	2015-12-31	68.00
36	干旱诱导表达的苹果 AsA 转运蛋白功能和在抗逆中的作用分析	31171916	国家自然科学基金面上项目	马锋旺	2012-01-01	2015-12-31	62.00
37	无光条件下李果皮花色苷合成的调控机制研究	31171915	国家自然科学基金面上项目	李鹏民	2012-01-01	2015-12-31	60.00
38	苹果树腐烂病菌侵染过程基因的差异表达及致病性研究	31171796	国家自然科学基金面上项目	黄丽丽	2012-01-01	2015-12-31	64.00
39	小麦CBL-CIPK信号系统介导的抗条锈病机理研究	31171795	国家自然科学基金面上项目	郭　军	2012-01-01	2015-12-31	52.00
40	生物能源作物柳枝稷人工穗芽形成机制研究	31171607	国家自然科学基金面上项目	奚亚军	2012-01-01	2015-12-31	57.00
41	菌根真菌和黑色有隔内生真菌提高林木耐旱机制	31170567	国家自然科学基金面上项目	唐　明	2012-01-01	2015-12-31	68.00
42	小麦-野燕麦衍生系分子细胞遗传学研究	31170301	国家自然科学基金面上项目	吉万全	2012-01-01	2015-12-31	60.00
43	拟南芥花斑突变体 var2 修饰基因的克隆和功能研究	31170219	国家自然科学基金面上项目	郁　飞	2012-01-01	2015-12-31	60.00
44	中国西部蔷薇科果树煤污病菌分类与系统发育研究	31170015	国家自然科学基金面上项目	孙广宇	2012-01-01	2015-12-31	65.00
45	中国野葡萄 SBP 转录活性、定位及其特异启动子功能研究	31071782	国家自然科学基金面上项目	王西平	2011-01-01	2013-12-31	33.00
46	白粉菌诱导下中国野生葡萄 VpR82H 基因特异定位表达研究	31071772	国家自然科学基金面上项目	文颖强	2011-01-01	2013-12-31	33.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
47	感染“中四”小麦条锈菌新菌系 T4 的毒性分析及快速检测体系建立	31071652	国家自然科学基金面上项目	王保通	2011-01-01	2013-12-31	33.00
48	条锈菌诱导的小麦 microRNA 的克隆和功能分析	31071651	国家自然科学基金面上项目	康振生	2011-01-01	2013-12-31	36.00
49	苹果对褐斑病的抗性机制研究	31071650	国家自然科学基金面上项目	黄丽丽	2011-01-01	2013-12-31	34.00
50	杂草在小麦条锈菌关键越夏区病害流行作用研究	31071641	国家自然科学基金面上项目	赵　杰	2011-01-01	2013-12-31	35.00
51	小麦条锈病菌潜育越冬的分子流行学研究	31071640	国家自然科学基金面上项目	胡小平	2011-01-01	2013-12-31	34.00
52	荞麦优异基因资源挖掘及黄酮性状的遗传研究	31071472	国家自然科学基金面上项目	冯佰利	2011-01-01	2013-12-31	34.00
53	水分胁迫对小麦脱水素启动子的调控与其耐旱性的关系	31071349	国家自然科学基金面上项目	张林生	2011-01-01	2013-12-31	32.00
54	一个全新的 MATE 转运蛋白介导的植物顶端优势调控途径	31071073	国家自然科学基金面上项目	郁　飞	2011-01-01	2013-12-31	30.00
55	外生菌根真菌增强灰杨富集重金属镉的作用机理	31070539	国家自然科学基金面上项目	罗志斌	2011-01-01	2013-12-31	36.00
56	刺槐根瘤菌新种(Mesorhizobium robiniae)及共生体系强化植物对锌污染土壤的生物修复作用	31070444	国家自然科学基金面上项目	韦革宏	2011-01-01	2013-12-31	40.00
57	灰霉病菌胁迫下番茄差异表达 miRNA 的识别及抗病机制研究	31000913	国家自然科学基金青年项目	金伟波	2011-01-01	2013-12-31	20.00
58	过剩激发能诱导非红色苹果果皮合成花色素的机制研究	31000890	国家自然科学基金青年项目	李鹏民	2011-01-01	2013-12-31	20.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
59	受条锈菌诱导的小麦类受体激酶基因的克隆及功能分析	31000836	国家自然科学基金青年项目	王晓杰	2011-01-01	2013-12-31	18.00
60	小麦条锈菌夏孢子芽管顶端生长过程中的细胞骨架响应及相关马达蛋白的功能研究	31000078	国家自然科学基金青年项目	刘　杰	2011-01-01	2013-12-31	20.00
61	中国野葡萄抗白粉病芪合成酶基因特异启动子及功能研究	30971972	国家自然科学基金面上项目	王跃进	2010-01-01	2012-12-31	36.00
62	苹果 GPP 和 MIPP 基因的功能及其与抗坏血酸合成调控的关系	30971971	国家自然科学基金面上项目	马锋旺	2010-01-01	2012-12-31	34.00
63	与寄生疫霉菌亲和互作相关的一个拟南芥突变体的遗传学和分子生物学分析	30971881	国家自然科学基金面上项目	单卫星	2010-01-01	2012-12-31	34.00
64	保绿型玉米抗旱增产的生理基础	30971722	国家自然科学基金面上项目	薛吉全	2010-01-01	2012-12-31	35.00
65	濒危植物沙冬青根瘤菌的遗传多样性及橙单胞菌科中一个根瘤菌新成员的研究	30970003	国家自然科学基金面上项目	韦革宏	2010-01-01	2012-12-31	30.00
66	小麦对条诱菌成株抗性机理的研究	30930064	国家自然科学基金重点项目	康振生	2010-01-01	2014-12-31	180.00
67	沙棘杨树混交林促进杨树生产力提高与碳固定研究	SW09515	国家自然科学基金科研发展基金	梁宗锁	2009-07-01	2014-12-01	80.00
68	小麦主要病虫草害综合防治技术研究	2012KTCL02-10	省创新重大专项	王保通	2012-01-01	2013-12-31	45.00
69	优质高产油菜新品种陕油 16、陕油 0913 高效栽培技术中试与示范	2012GB23600640	科技成果转化资金	徐爱遐	2012-04-01	2014-04-30	60.00

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70	优质高产多抗小麦新品种西农 509、西农 9871 及高效安全生产集成配套技术	2012GB23600637	科技成果转化资金	吉万全	2012-04-01	2014-04-30	60.00
71	中国野生葡萄 VpPR10 蛋白调节植物细胞死亡机理研究	NCET-10-0692	外省厅局项目	徐　炎	2011-01-01	2013-12-31	50.00
72	中澳旱地小麦改良	CIM/2005/111	国际合作项目	胡银岗	2008-01-01	2013-12-31	80.00
73	重金属污染土壤的林木修复机理与调控技术研究	201204210	林业公益性行业专项（课题）	罗志斌	2012-01-01	2015-12-31	79.00
74	葡萄苹果砧木收集、评价与筛选	201203075-08	公益性行业（农业）专项（子课题）	徐　炎	2011-01-01	2015-12-31	168.00
75	果树腐烂病防控技术研究与示范	201203034	公益性行业（农业）专项（子课题）	黄丽丽	2012-01-01	2015-12-31	47.00
76	主要农作物抗御季节性干旱技术研究与示范	201203031-07-02	公益性行业（农业）专项（子课题）	薛吉全	2012-01-01	2015-12-31	245.00
77	十字花科小菜蛾综合防控技术研究与示范推广	201103021	公益性行业（农业）专项（子课题）	刘同先	2011-08-01	2015-12-31	38.00
78	抗纹枯病转基因育种新材料获得	2011zx08003-001	纵向协作	赵天永	2011-02-03	2012-12-31	40.00
79	高油、高产优质杂交油菜新品种选育	2011kyzb02-0103	陕西省农业科技创新专项	董振生	2011-09-21	2013-12-31	55.00
80	苹果早期落叶病综合防治技术研究与示范	2011KTZB02-02-03	陕西省科技厅科技计划项目	孙广宇	2011-10-01	2014-12-31	150.00
81	苹果树腐烂病综合防治技术研究与示范	2011KTZB02-02-02	陕西省科技厅科技计划项目	黄丽丽	2011-10-01	2014-12-31	140.00

序号	项目名称	项目编号	项目类别	项目负责人	开始日期	结束日期	合同经费(万元)
82	优质、丰产苹果新品种选育研究	2011KTZB02-02-01	省创新重大专项	赵政阳	2011-11-01	2013-12-31	75.00
83	玉米优异种质创新及新品种选育	2011KTZB02-01-02	省创新重大专项	薛吉全	2012-01-01	2014-12-31	265.00
84	温室工程与环境综合调控与节能新技术集成	2011ktdz02-03-02	陕西省科技厅科技计划项目	邹志荣	2011-11-01	2013-12-31	90.00
85	高产、高油、多抗油菜新品种选育	2011K01-01	陕西省科技厅省攻关（农业）	董振生	2011-01-01	2012-12-31	10.00
86	中国小麦条锈菌毒性变异与抗条锈遗传合作研究	2011DFG32990	国际合作项目	康振生	2012-01-01	2014-12-31	200.00
87	耐旱豆科植物根瘤菌的多样性及其环境相互关系研究	2010DFA91930	国际合作项目	韦革宏	2010-01-01	2013-12-31	10.00
88	施用锌肥提高作物产量和品质	2011DFG91542	国际合作项目	王朝辉	2011-03-22	2014-06-11	40.00
89	苹果现代育种体系创建与主导新品种培育	2010ZDKG-69	省 13115 重大专项	赵政阳	2010-01-01	2012-12-31	70.00
90	秦巴山区猪苓高产栽培关键技术研究与示范	2010ZDKG-109	省 13115 重大专项	梁宗锁	2010-01-01	2012-12-31	50.00
91	陕西省白酒工程技术研究中心	2011ZDKG-72	省 13115 科技专项（子课题）	韦革宏	2011-01-01	2013-12-31	80.00
92	高油高产机械化专用油菜新品种培养	2010BAD01B02	中科院协作项目	胡胜武	2011-01-01	2013-12-31	40.00
93	受条锈菌诱导的小麦 DAD2 基因的克隆及功能分析	20100204120005	教育部高等学校博士学科点专项科研基金	王晓杰	2011-01-01	2013-12-01	3.60

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94	小麦吸浆虫不同滞育状态幼虫分子标记研究	20100204110006	博士点基金项目	仵均祥	2011-01-01	2013-12-31	6.00
95	氮素对杨树木林木质素生物合成调控的分子生理机制	121026	霍英东基金	罗志斌	2010-01-01	2013-12-31	6.00
96	果树遗传改良与控制技术研究及其应用	200903044-4	公益性行业（农业）专项（子课题）	王跃进	2009-01-01	2013-12-31	199.00
97	陕西省小麦孢囊线虫发生调查与防控	200903040-8	公益性行业（农业）专项（子课题）	赵　杰	2009-01-01	2013-12-31	50.00
98	稻曲病遗传转化体系与侵染过程	200903039-6	公益性行业（农业）专项（子课题）	许金荣	2009-01-01	2013-12-31	80.00
99	小麦条锈病监测与综合治理技术研究与示范	200903035	公益性行业（农业）专项（子课题）	康振生	2009-01-01	2013-12-31	271.00
100	马铃薯有害生物种类与发生危害特点研究	200903004-38	公益性行业（农业）专项（子课题）	单卫星	2009-01-01	2013-12-31	8.00
101	粮食作物基因对基因病害的抗病品种布局技术研究示范	201203014	公益性行业（农业）专项（子课题）	韩德俊	2012-03-01	2016-12-31	97.00

四、发表论文

序号	论文题目	刊物名称/卷期页码	作者	通讯作者	IF
1	Novel and potential application of cryopreservation to plant genetic transformation	Biotechnology Advances 30 (2012) 604–612	Biao Wang, Zhibo Zhang, Zhenfang Yin, Chaohong Feng, Qiaochun Wang	Qiaochun Wang	9.646
2	Different chitin synthase genes are required for various developmental and plant infection processes in the rice blast fungus magnzporthe oryzae	PLoS pathogens 2012, 8(2): e1002526	Ling-An Kong, …., Chen-Fang Wang, ….., Jin-Rong XU	Jin-rong Xu	9.127
3	A type VI secretion system regulated by OmpR in Yersinia pseudotuberculosis functions to maintain intracellular pH homeostasis	Environ Microbiol 2012 Sep 28. doi: 10.1111/1462-2920.12005	Zhang, W. Wang, Y. Song, Y. Wang, T. Xu, S. Peng, Z. Lin, X. Zhang, L. Shen, X.	Xi-HuiShen	5.843
4	Delayed senescence of apple leaves by exogenous melatonin treatment: toward regulating the ascorbate–glutathione cycle	Journal of Pineal Research/2012, 53(1):11-20	Ping Wang, Lihua Yin, Dong Liang, Chao Li, Fengwang Ma, Zhiyong Yu	Ma Fengwang	5.794
5	The mitigation effects of exogenous melatonin on salinity-induced stress in Malus hupehensis	Journal of Pineal Research/2012, 53(3):298–306	Chao Li, Ping Wang, Zhiwei Wei, Dong Liang, Changhai Liu, Lihua Yin, Dongfeng Jia, Mingyang Fu, Fengwang Ma	Ma Fengwang	5.794
6	Real-time analysis of the carbohydrates on cell surfaces using a QCM biosensor: alectin-based approach	Biosensors and Bioelectronics 35 (2012) 200– 205	Zhichao Pei, Julien Saint-Guirons, Camilla Käck, BjörnIngemarsson, TeodorAastrup	Zhichao Pei	5.602
7	Wheat BAX inhibitor-1 contributes to wheat resistance to Puccinia striiformis	Journal of Experimental Botany, 2012, 63 (12):4571-4584	Xiaojie Wang, Chunlei Tang, Xueling Huang, Fangfang Li, Xianming Chen, Gang Zhang, Yanfei Sun, Dejun Han, and Zhensheng Kang	ZS Kang	5.4
8	Side effects of two reduced-risk insecticides, indoxacarb and spinosad, on two species of Trichogramma (Hymenoptera: Trichogrammatidae) on cabbage	Ecotoxicology 012, 21:2254–2263	Tong-Xian Liu, Yongmei Zhang	Tong-Xian Liu	5.3925
9	Overexpression of a putative Arabidopsis BAHD acyl-transferasecauses dwarfism that can be rescued by brassinosteroid	Journal of Experimental Botany 2012, 63, 5787-5801	Mengjiao Wang, Xiayan Liu, Rui Wang, Wanchun Li, Steve Rodermel, Fei Yu	Fei Yu	5.364
10	TaMCA4, a Novel Wheat Metacaspase Gene Functions in Programmed Cell Death Induced by the Fungal Pathogen Puccinia striiformis f. sp. Tritici.	Molecular Plant-Microbe Interaction, 2012, 26(6):755-764	Xiaodong Wang, Xiaojie Wang, Hao Feng, Chunlei Tang, Pengfei Bai, Guorong Wei, Lili Huang and Zhensheng Kang.	ZS Kang	4.4
11	Dissoconiaceae associated with sooty blotch and flyspeck on fruits in China and the United States.	Persoonia 28, 2012: 113–125	Li H.Y., Sun G.Y., Zhai X.R., Batzer J.C., Mayfield D.A., Crous P.W., Groenewald J.Z., Gleason M.L..	Sun Guangyu	4.136

序号	论文题目	刊物名称/卷期页码	作者	通讯作者	IF
12	Production of dsRNA sequences in host plant is not sufficient to initiate gene silencing in the colonizing oomycete pathogen Phytophthora parasitica	PLoS ONE/2011,6（11）：e28114	Zhang, M., Wang, Q., Xu, K., Meng, Y., Quan, J., Shan, W.	Weixing Shan	4.09
13	Rust secreted protein Ps87 is conserved in diverse fungal pathogens and contains a RXLR-like motif sufficient for translocation into plant cells	PLoS ONE/2011,6（11）：e27217	Gu, B., Kale, S. D., Wang, Q., Wang, D., Pan, Q., Cao, H., Meng, Y., Kang, Z., Tyler, B. M., Shan, W.	Weixing Shan	4.09
14	The FgHOG1 pathway regulates hyphal growth, stress responses, and plant infection in Fusarium graminearum	PLoS ONE 2012, 7(11): e49495	Dawei Zheng, …, Chenfang Wang, Jin-rong Xu	Jin-rong Xu	4.09
15	Functional Characterization of Calcineurin Homologs PsCNA1/PsCNB1 in Puccinia striiformis f. sp. tritici Using a Host-Induced RNAi System	PloS ONE, 2012, 7(11): e49262.	Hong Zhang, Jun Guo, Ralf T. Voegele, Jinshan Zhang, Yinghui Duan, Huaiyong Luo, Zhensheng Kang	ZS Kang	4.09
16	Wheat TaRab7 GTPase is Part of the Signaling Pathway in Responses to Stripe Rust and Abiotic Stimuli	PLoS ONE, 2012, 7(5):e37146	Furong Liu, Jun Guo, Pengfei Bai, Zhensheng Kang	ZS Kang	4.09
17	The over-expression of an Arabidopsis B3 transcription factor, ABS2/NGAL1, leads to the loss of flower petals	PLoS ONE 7(11): e49861. doi:10.1371/journal.pone.0049861	Jingxia Shao, Xiayan Liu, Rui Wang, Gaisheng Zhang, Fei Yu	Fei Yu	4.09
18	Coevolution in RNA Molecules Driven by Selective Constraints: Evidence from 5S rRNA	PLoS ONE 7(9): e44376	Cheng N , Mao Y , Shi Y , Tao S ,	Tao, S	4.09
19	Complete chloroplast genome of a major invasive species, Crofton weed (Ageratina adenophora L.)	PLoS ONE 2012,7(5): e36869	Xiaojun Lie，Shuzuo li，Song Weining	Song Weining	4.09
20	Genome-Wide Identification and Analysis of the *TIFY* Gene Family in Grape	PLoS ONE, 2012, 7 (9): e44465	Yucheng Zhang, Min Gao, Stacy Singer, Zhangjun Fei, Hua Wang, Xiping Wang	Xiping Wang	4.09
21	Genome-Wide Identification and Analysis of Grape Aldehyde Dehydrogenase (ALDH) Gene Superfamily	PLoS ONE, 2012, 7(2): e32153	Yucheng Zhang, Linyong Mao, Hua Wang, Vasilis Vasiliou, Zhangjun Fei, Xiping Wang	Xiping wang	4.09
22	Genetic Diversity, Population Structure and Linkage Disequilibrium in Elite Chinese Winter Wheat Investigatedwith SSR Markers	PLoS ONE. 012, 7(9): e44510. doi:10.1371/journal.pone.0044510	Chen X, Min D, Yasir TA, Hu Y-G	Hu Y-G	4.09
23	Development and Characterization of a New TILLINGPopulation of Common Bread Wheat (TriticumaestivumL.)	PLoS ONE. 7(7): e41570. doi:10.1371/journal.pone.0041570	Liang Chen, Linzhou Huang, Donghong Min, Andy Phillips, Shiqiang Wang, Pippa J. Madgwick,Martin A. J. Parry, Yin-Gang Hu	Yin-Gang Hu	4.09
24	Genome Sequence and Mutational Analysis of Plant Growth Promoting Bacterium Agrobacterium tumefaciens CCNWGS0286 isolated from a zinc-lead mine tailing	Applied and Environmental Microbiology 2012, 78(15):5384-5394	Xiuli Hao, Pin Xie, Laurel Johnstone, Susan J. Miller, Christopher Rensing*, Gehong Wei*	Ge Hong Wei	3.829

序号	论文题目	刊物名称/卷期页码	作者	通讯作者	IF
25	Draft Genome Sequence of Sinorhizobiummeliloti CCNWSX0020, a Nitrogen-Fixing Symbiont with Copper Tolerance Capability Isolated from Lead-Zinc Mine Tailings	Journal of Bacteriology 2012, 194(5):1267-1268	Zhefei Li, Zhanqiang Ma, XiuliHao and Gehong Wei*	Ge Hong Wei	3.825
26	Draft Genome Sequence of Mesorhizobiumalhagi CCNWXJ12-2, a Novel Salt-Resistant Species Isolated from the Desert of Northwestern China	Journal of Bacteriology 2012, 194(5):1267-1268	Meili Zhou, Weimin Chen, Hongyan Chen and Gehong Wei*	Ge Hong Wei	3.825
27	Draft Genome Sequence of Halomonas sp. Strain HAL1, a Moderately HalophilicArsenite-Oxidizing Bacterium Isolated from Gold-Mine Soil	Journal of Bacteriology 2012, 194(5):1267-1268	Yanbing Lin, Haoxin Fan, XiuliHao, Laurel Johnstone, Yao Hu, Gehong Wei, Hend A. Alwathnani, Gejiao Wang and Christopher Rensing	Ge Hong Wei	3.825
28	Draft Genome Sequence of Plant Growth-Promoting RhizobiumMesorhizobiumamorphae, Isolated from Zinc-Lead Mine Tailings	Journal of Bacteriology 2012, 194(5):1267-1268	XiuliHao, Yanbing Lin, Laurel Johnstone, David A. Baltrus, Susan J. Miller, Gehong Wei, and Christopher Rensing	Ge Hong Wei	3.825
29	Draft Genome Sequence of Pseudomonas psychrotolerans L19, Isolated from Copper Alloy Coins	Journal of Bacteriology 2012, 194(5):1267-1268	Christophe Espírito Santo, Yanbing Lin, XiuliHao, Gehong Wei, Christopher Rensing, and Gregor Grass	Ge Hong Wei	3.825
30	Virus-Induced Gene-Silencing in Wheat Spikes and Grains and Its Application in Functional Analysis of HMW-GS-encoding Genes	BMC Plant Biology	Meng Ma, Yan Yan, Li Huang, Mingshun Chen,	Huixian Zhao	3.45
31	Identification of the dehydrin gene family from grapevine species and analysis of their responsiveness to various forms of abiotic and biotic stress	BMC Plant Biology 2012, 12:140	Yazhou Yang, Mingyang He, Ziguo Zhu, Shuxiu Li, Yan Xu, Chaohong Zhang, Stacy D Singer and Yuejin Wang.	Yuejin Wang	3.45
32	Degradation and assimilation of aromatic compounds by Corynebacteriumglutamicum: another potential for applications for this bacterium?	ApplMicrobiolBiotechno 2012 Jul;95(1):77-89l	Xi-HuiShenNing-Yi Zhou Shuang-Jiang Liu	Xi-HuiShen	3.425
33	Biogeography of symbiotic and other endophytic bacteria isolated from medicinal Glycyrrhiza species in China	FEMS Microbiology Ecology 2012, 79:46–68	Li Li, Hanna Sinkko, Leone Montonen, Gehong Wei*, Kristina Lindström, Leena A. Räsänen.	Ge Hong Wei	3.408
34	Characterization of non-host resistance in broad bean to the wheat stripe rust pathogen	BMC Plant Biology, 2012, 12:96 doi:10.1186/1471-2229-12-96	Yulin Cheng, Hongchang Zhang, Juanni Yao, Xiaojie Wang, Jinrong Xu, Qingmei Han, Guorong Wei, Lili Huang and Zhensheng Kang	ZS Kang	3.4
35	Three novel cyclic hexapeptides from Streptomyces alboflavus 313 and their antibacterial activity.	European Journal of Medicinal Chemistry 2012, 50:296-303	Zhiqin Ji,* Shaopeng Wei, Lixia Fan, Wenjun Wu	Zhiqin Ji	3.346

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36	High-density mapping and marker development for the powdery mildew resistance gene PmAS846 derived from wild emmer wheat(Triticum turgidum var. dicoccoides)	Theor Appl Genet 2012，124:1549-1560	Xue F.，Ji W.Q.，Wang C.Y.，Zhang H.，Yang B.J.	Ji W.Q.，Wang C.Y.	3.264
37	Molecular mapping of a powdery mildew 1 resistance gene in common wheat landrace Baihulu and its allelism with Pm24	Theor Appl Genet 2012，125:1425–1432	Xue F.，Wang C.Y.，Li C.，Duan X.Y.，Zhou Y.L.，Zhao N.J.，Wang Y. J.，Ji W.Q.	Ji W.Q.	3.264
38	SNP identification and allelic-specific PCR markers development for TaGW2, a gene linked to wheat kernel weight.	Theor Appl Genet 2012.125:1057-1068	Zibo Yang, Zhiyuan Bai, Xiaolin Li, Pei Wang, Qingxia Wu, Lin Yang, Liqun Li , Xuejun Li	Xuejun Li	3.264
39	Two piperazic acid-containing cyclic hexapeptides from Streptomyces alboflavus 313	Amino Acids 2012, 43:2191–2198	Shaopeng Wei, Lixia Fan , Wenjun Wu, Zhiqin Ji*	Zhiqin Ji	3.248
40	Molecular dynamics and free energy studies on the carboxypeptidasescomplexed with peptide/small molecular inhibitor: Mechanism for drug resistance	Insect Biochemistry and Molecular Biology 42 (2012) 583e595	Hong Zhang, Yao Yao, Huibin Yang, Xia Wang, Zhuo Kang, Yan Li, Guohui Li, Yonghua Wang	Yonghua Wang	3.246
41	Effect of low temperature on chlorophyll biosynthesis in albinism line of wheat (Triticumaestivum) FA85	PhysiologiaPlantarum 145: 384–394. 2012	Xiao-Gang Liu, Hong Xu,Jing-Y Zhang, Guang-Wang Liang, Ying-Tuan Liua and Ai-GuangGuo	Ai-GuangGuo	3.112
42	Primary and secondary metabolism in the sun-exposed peel and the shaded peel of apple fruit	Physiologia Plantarum ，DOI: 10.1111/j.1399-3054.2012.01692.x	Pengming Li 、Ma Fengwang 、CHENG Lailiang	CHENG Lailiang	3.112
43	Ectopic expression of VpALDH2B4, a novel Aldehyde Dehydrogenase gene from Chinese wild grapevine (Vitis pseudoreticulata), enhances resistance to mildew pathogens and salt stress in Arabidopsis.	Planta/2012, 236(2):525-39	Yingqiang Wen, Xiping Wang, Shunyuan Xiao, Yuejin Wang	Yuejin Wang	3.00
44	A core functional region of the RFP1 promoter from Chinese wild grapevine is activated by powdery mildew pathogen and heat stress	Planta 2012 在线	Yihe Yu, Weirong Xu, Jie Wang, Lei Wang, Wenkong Yao, Yan Xu, Jiahua Ding, Yuejin Wang	Yuejin Wang	3.00
45	Molecular characterization and expression analysis of a glycine-rich RNA-binding protein gene from Malus hupehensis Rehd	Molecular Biology Reporte/2012, 39(4):4145–4153	Shuncai Wang, Rongchao Wang, Dong Liang, Fengwang Ma	Ma Fengwang	2.929
46	Genome-wide identification and expression profiling of dehydrin gene family in Malus domestica	Molecular Biology Reporter/2012, 39(12):10759–	Dong Liang, Hui Xia, Shan Wu, Fengwang Ma..	Ma Fengwang	2.929
47	Identification of genes differentially expressed in grapevine associated with resistance to *Elsinoe ampelina* through suppressive subtraction hybridization	Plant Physiology and Biochemistry	Min Gao, Qian Wang, Ran Wan, Zhangjun Fei, Xiping Wang	Xiping Wang	2.838

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48	Influence of drought stress on the cellular ultrastructure and antioxidant system in leaves of drought-tolerant and drought-sensitive apple rootstocks	Plant Physiology and Biochemistry/2012, 51:81-89	Shuncai Wang, Dong Liang, Chao Li, Yonglu Hao, Feng wang Ma	Ma Fengwang.	2.838
49	Different effects of light irradiation on the photosynthetic electron transport chain during apple tree leaf dehydration	Plant Physiology and Biochemistry/2012, 55:16-22	Pengmin Li, Fengwang Ma	Ma Fengwang	2.838
50	Differential expression of ion transporters and aquaporins in leaves may contribute to different salt tolerance in Malus species	Plant Physiology and Biochemistry/2012, 58:159-165	Changhai Liu, Chao Li, Dong Liang, Zhiwei Wei, Shasha Zhou, Rongchao Wang, Fengwang Ma.	Ma Fengwang	2.838
51	Partitioning of absorbed light energy differed between the sun-exposed side and the shaded side of apple fruits under high light conditions	Plant Physiology and Biochemistry，60, 12-17	Changsheng Chen 、Pengming Li 、Ma Fengwang	Pengming Li	2.838
52	Microarray-based Analysis of Tomato miRNA Regulated by Botrytis cinerea	J Plant Growth Regul 2012, 31(1): 38-46.	Weibo Jin, Fangli Wu, et al	Weibo Jin	2.80
53	Cytological and molecular characterization of non-host resistance in Arabidopsis thaliana against wheat stripe rust	Plant Physiology and Biochemistry, 2012, 62:11-18	Yulin Cheng, Hongchang Zhang, Juanni Yao, Qingmei Han, Xiaojie Wang, Lili Huang, Zhensheng Kang	ZS Kang	2.80
54	Selection of suitable inner reference genes for relative quantification expression of microRNA in wheat	Plant Physiology and Biochemistry, 2012, 51:116-122	Hao Feng, Xueling Huang, Qiong Zhang, Guorong Wei, Xiaojie Wang, Zhensheng Kang	ZS Kang	2.80
55	Combined use of two biocontrol agents with different biocontrol mechanisms most likely results in less than expected efficacy in controlling foliar pathogens under fluctuating conditions: a modeling study	Phytopathology, 2012,	Xu Xiangming	Xu Xiangming	2.799
56	Development of chromosome -arm-specific microsatellite markers in Triticum aestivum (Poaceae) using NGS technology	American Journal of Botany 2012,99(9):e1-e3	Xiaojun Lie，Bianli li，Song Weining	Song Weining	2.664
57	Genome-wide analysis and expression profiling of the DREB transcription factor gene family in Malus under abiotic stress	Molecular Genetics and Genomics/2012, 287(5): 423-436	Tao Zhao, Dong Liang, Ping Wang, Jingying Liu and Fengwang Ma	Ma Fengwang	2.635
58	Characterization of Erysiphe necator-responsive genes in Chinese wild *Vitis quinquangularis*	Int. J. Mol., Sci,2012, 13, 11497-11519	Min Gao, Jiao Niu, Suping Zhao, Chen Jiao, Weirong Xu, Zhangjun Fei, Xiping Wang	Xiping Wang	2.598
59	Enhanced Production of a Novel Cyclic Hexapeptide Antibiotic (NW-G01) by Streptomyces alboflavus 313 Using Response Surface Methodology	Int. J. Mol. Sci. 2012, 13, 5230-5241	Zhengyan Guo, Ling Shen , Zhiqin Ji and Wenjun Wu	Wenjun Wu.	2.598
60	Identification and characterization of microRNAs from barley (Hordeum vulgare L.) by Solexa sequencing	International Journal of Molecular Science 2012,13, 2973-2984	Shuzuo li，Xiaojun Lie，Song Weining	Song Weining	2.598

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61	Evaluation of 14 Morphological, Yield-related and Physiological Traits as Indicators of Drought Tolerance in Chinese Winter Bread Wheat Revealed by Analysis of the Membership Function Value of Drought Tolerance (MFVD)	Field Crops Research，137 (2012) 195–201	XiaojieChen, DonghongMin, TauqeerAhmad Yasir , Yin-GangHu	Yin-GangHu.(胡银岗)	2.474
62	Different increases in maize and wheat grain zinc concentrations caused by soil and foliar applications of zinc in Loess Plateau , China	Field Crops Research 2012,135:89-96	Wang Jian Wei, Mao Hui, Zhao Hu Bing, Huang Dong Lin, Wang Zhao Hui	Wang Zhao Hui	2.474
63	Characterization and Expression Analysis of a Retinoblastoma-Related Gene from Chinese Wild *Vitis pseudoreticulata*.	*Plant Mol Biol Rep*, 2012, 30: 983–991	Zhifeng Wen, Min Gao, Chen Jiao, Qian Wang, HuiXu, MonikaWalter, WeirongXu, CaroleBassett, Xiping Wang	Xiping Wang	2.453
64	Genomic Structure, Sub-Cellular Localization, and Promoter Analysis of the Gene Encoding Sorbitol-6-Phosphate Dehydrogenase from Apple	Plant Molecular Biology Reporter/2012, 30(4):904-914	Dong Liang, Meng Cui, Shan Wu , Fengwang Ma	Ma Fengwang	2.453
65	A Novel Heat Shock Transcription Factor, VpHsf1, from Chinese Wild Vitis pseudoreticulata is Involved in Biotic and Abiotic Stresses	Plant Molecular Biology Reporter May 2012 在线	Shaobing Peng, Ziguo Zhu, Kai Zhao, Jiangli Shi, Yazhou Yang, Mingyang He, Yuejin Wang	Yuejin Wang	2.453
66	A Nested PCR Assay for Detecting Valsa mali var. mali in Different Tissues of Apple Trees	Plant Disease 2012,96:1645-1652	R. Zang, Z. Yin, X. Ke, X.Wang, Z. Li, Z. Kang, L. Huang	L. Huang	2.449
67	Etiology of Moldy Core, Core Browning and Core Rot of Fuji 1 Apple in China	Plant Disease: online (http://dx.doi.org/10.1094/PDIS-01-12-0024-RE • posted 10/04/2012)	Gao LL, Q. Zhang, X. Y. Sun, L. Jiang, M. Y. Qu, R. Zhang, G. Y. Sun, iY. L. Zha, Alan R. Biggs	Guangyu Sun	2.449
68	Genetic and Molecular Mapping of Stripe Rust Resistance Gene in Wheat–Psathyrostachys huashanica Translocation Line H9020-1-6-8-3	Plant disease, 2012, 96(10):1482-1487	Qiang Li, Jing Huang, Lu Hou, Pei Liu, Jinxue Jing, Baotong Wang, and Zhensheng Kang	Baotong Wang, and Zhensheng Kang	2.40
69	Race composition of Puccinia striiformis f. sp. tritici in Tibet, China	Plant Disease 2012,96:1645-1652	Xiaoping Hu, Jiaojiao Li, Yating Wang, Baotong Wang, Qiang Li, Zhensheng Kang, Minna Yang, Yueling Peng, Taiguo Liu, Wanquan Chen, and Xiangming Xu	Xiaoping Hu	2.387
70	Genetic and Molecular Mapping of Stripe Rust Resistance Gene in Wheat–Psathyrostachys huashanica Translocation Line H9020-1-6-8-3	Plant Disease 2012,96:1645-1652	Qiang Li, Jing Huang, Lu Hou, Pei Liu, Jinxue Jing, Baotong Wang*, Zhensheng Kang	Baotong Wang	2.387
71	Verticillium wilt of redbud in China caused by Verticillium dahliae	Plant Disease, 2012	W.J. Lu, Y.J. Liu, H.Q. Zhu, W.J. Shang, J.R. Yang, and X.P. Hu*	Xiaoping Hu	2.387

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72	First report of wilt on alfalfa in China caused by Verticillium nigrescens	Plant Disease, 2011,95(12): 1591-1592	Hu XP, Wang MX, Hu DF, Yang JR.	Xiaoping Hu	2.387
73	Development of multiplex real-time PCR for simultaneous detection of three Potyviruses in tobacco plants	Journal of Applied Microbiology,2012,doi:10.1111/jam.12071	Dai, Jin; Peng, Hu; Chen, Wei; Cheng, Julong; Wu, Yunfeng	Wu YF	2.33
74	Histological and cytological characterization of adult plant resistance to wheat stripe rust	Plant Cell Rep, 2012, 31(12):2121-2137	Hongchang Zhang, Chenfang Wang, Yulin Cheng, Xianming Chen, Qingmei Han, Lili Huang, Guorong Wei, Zhensheng Kang	ZS Kang	2.30
75	Microscopy and proteomic analysis of the non-host resistance of Oryza sativa to the wheat leaf rust fungus, Puccinia triticina f. sp tritici	Plant Cell Reports, 2012, 31(4): 637-650	Hongbing Li, Paul H. Goodwin, Qingmei Han, Lili Huang and Zhensheng Kang	ZS Kang	2.30
76	Bioaccumulation characterization of zinc and cadmium by Streptomyces zinciresistens, a novel actinomycete.	Ecotoxicology and Environmental Safety 2012, 77: 7–17	Yanbing Lin, Xinye Wang, Baoping Wang, Osama Mohamad, Gehong Wei.	Ge Hong Wei	2.294
77	VpWRKY3, a biotic and abiotic stress-related transcription factor from the Chinese wild Vitis pseudoreticulata.	Plant Cell Reports. 2012, Volume 31, Issue 11, pp 2109-2120	Ziguo Zhu, Jiangli Shi, Jiangling Cao, Mingyang He, Yuejin Wang	Yuejin Wang	2.274
78	Streptomyces shaanxiensis sp. nov., a novel streptomycete with dark blue diffusible pigment isolated from sewage irrigation soil in Shaanxi.	Int J SystEvolMicrobiol 2012, 62:1725-1730	Yan Bing Lin, Xin Ye Wang, Hui Fang, YaNan Ma, Jing Tang, Ming Tang and Ge Hong Wei	Ge Hong Wei	2.268
79	Rhizobium taibaishanense sp. nov., isolated from a root nodule of Kummerowiastriata	International Journal of Systematic and Evolutionary Microbiology (2012), 62, 335–341	Li Juan Yao, Yao YaoShen, Jun Peng Zhan, Wei Xu, Guang Ling Cui1, and Ge Hong Wei	Ge Hong Wei	2.268
80	Biosorption of Copper (II) from Aqueous Solution Using Non-Living Mesorhizobiumamorphae Strain CCNWGS0123	Microbes Environ. Vol. 27, No. 3, 234–241, 2012	OSAMA ABDALLA MOHAMAD, XIULI HAO, PIN XIE, SHAIMAA HATAB, YANBING LIN, and GEHONG WEI	Ge Hong We	2.24
81	Influence of five aphid species on development and reproduction of Propylaea japonica (Coleoptera: Coccinellidae)	Biological Control, 2012, 62: 135–139	Shi-Ze Zhang, Jian-Jun Li, Hong-Wei Shan, Fan Zhang, Tong-Xian Liu	Shizhe zhang;Tong-Xian Liu	2.164
82	Larvicidal activity of lignans from Phryma leptostachya L against Culex pipiens pallens	Parasitol Res (2012) 110:1079–1084	Xin-min Xiao & Zhao-nong Hu & Bao-jun Shi & Shao-peng Wei & Wen-jun Wu	Wen-jun Wu.	2.149
83	Tn5 transposon mutagenesis in Acidovorax citrulli for identification of genes required for pathogenicity on cucumber.	Plant Pathology/ 2012, 61：364-374.	Liu, J., Luo, S., Zhang, Q., Wang, Q., Chen, J., Guo, A., Shan, W.	Weixing Shan	2.125
84	Development of a multiplex polymerase chain reaction for simultaneous detection of wheat viruses and a phytoplasma in China	Arch Virol,2012, 157:1261–1267	Tao Y, Man JY, Wu YF	Wu YF	2.11

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85	Rapid detection of tobacco viruses by reverse transcription loop-mediated isothermal amplification	Arch Virol ,2012,157:2291–2298	Lei Zhao , Julong Cheng, Xingan Hao,Wu YF	Wu YF	2.11
86	Saccharothrix yanglingensis sp. nov., an antagonistic endophytic actinomycete isolated from cucumber plant	Antonie van Leeuwenhoek 2012,101(1): 141-146	X. Yan, X. Tu, X. Gao, Z. Kang, L. Huang	Z. Kang ang L.Huang	2.091
87	A comparison and evaluation of five biclustering algorithms by quantifying goodness of biclusters for gene expression data.	BioData Mining 2012, 5:8	Li, L.Guo, Y.Wu, W.Shi, Y.Cheng, J.Tao, S.	Tao, S	2.03
88	A multiplex reverse transcription PCR assay for simultaneous detection of five tobacco viruses in tobacco plants	Journal of Virological Methods, 2012, 183:57–62	Dai J, Peng H, Cheng JL, Wu YF	Wu YF	2.01
89	Subcellular localization and functional analyses of a PR10 protein gene from Vitis pseudoreticulata in response to Plasmopara viticola infection	Protoplasma 2012 在线	Mingyang He, Yan Xu, Jiangling Cao, Ziguo Zhu, Yuntong Jiao, Yuejin Wang, Xin Guan, Yazhou Yang, Weirong Xu, Zhenfang Fu.	Yuejin Wang	1.922
90	Characterization of novel gene expression related to glyoxal oxidase by agro-infiltration of the leaves of accession Baihe-35-1 of Vitis pseudoreticulata involved in production of H2O2 for resistance to Erysiphe necato	Protoplasma October 2012 在线	Heqing Zhao, Xin Guan, Yan Xu, Yuejin Wang	Yuejin Wang	1.922
91	Co-expression of VpROMT gene from Chinese wild Vitis pseudoreticulata with VpSTS in tobacco plants and its effects on the accumulation of pterostilbene.	Protoplasma. 2012, 249: 819-833.	Yan Xu, Tengfei Xu, Xiaochen Zhao, Ying Zou, Zhiqian Li, Fengju Li, Jiang Xiang, Yuejin Wang	Y. Xu	1.922
92	Effect of a benzothiadiazole on inducing resistance of soybean to Phytophthora sojae	Protoplasma, 2012, doi:10.1007/s00709-012-0430-6	Qingmei Han, Hao Feng, Haiyan Zhao, Lili Huang, Xiaojie Wang, Xiaodong Wang, Zhensheng Kang	ZS Kang	1.9
93	Complete sequence of an Apple stem grooving virus (ASGV) isolate from China	Virus Gene， 2012, 45:596–599	Lei Zhao , Xingan Hao, Ping Liu , Yunfeng Wu	Wu YF	1.84
94	Isolation and characterization of two novel antibacterial cyclic hexapeptides from Streptomyces alboflavus 313	Chemistry& Biodiversity, 2012,9:1567-1578	Zhiqin Ji, Gang Qiao, Shaopeng Wei, Lixia Fan, Wenjun Wu	Zhiqin Ji	1.804
95	A new phytoplasma associated with witches -broom on Japanese maple in China	Forest Pathology,2012,42 :371–376	Li ZN, Zhang L, Wu YF	Wu YF	1.74
96	Risk assessment of selected insecticides on Tamarixia triozae (Hymenoptera: Eulophidae), a parasitoid of bactericera cockerelli (Hemiptera: Trizoidae)	JOURNAL OF ECONOMIC ENTOMOLOGY	Tong-xian Liu, Yong-mei Zhang, Li-nian Peng, Patricia Rojas, and John T. Trumble	Tong Xian Liu	1.699

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97	Isolation and functional characterization of a transcription factor VpNAC1 from Chinese wild Vitis pseudoreticulata	Biotechnology Letters July 2012, Volume 34, Issue 7, pp 1335-1342	Ziguo Zhu, Jiangli Shi, Mingyang He, Jiangling Cao, Yuejin Wang	Yuejin Wang	1.683
98	Fine mapping of a yellow seeded gene in Brassica juncea L	Genome，2012, 55:(1) 8-14	Zhen Huang, Yuanyuan Ban, Li Yang, Yu Zhang, Huiqiang Li, Enshi Xiao, Aixia Xu,and Denghui Zhang	Aixia Xu	1.653
99	Influence of rootstock on antioxidant system in leaves and roots of young apple trees in response to drought stress	Plant Growth Regulation/2012, 67(3):247–256	Binghua Liu, Mingjun Li, Liang Cheng, Dong Liang, Yangjun Zou, Fengwang Ma	Ma Fengwang	1.604
100	Biological control of wheat stripe rust by an endophytic Bacillus subtilis strain E1R-j in greenhouse and field trials	Crop Protection 2013, 43: 201-206	H.Li, J. Zhao, H. Feng, Z. Kang, L. Huang	Z. Kang ang L.Huang	1.596
101	A new species of Scolecobasidium associated with the sooty blotch and flyspeck complex on banana from China	Mycol Progress: online DOI 10.1007/s11557-012-0855-5	Lu Hao & Chen Chen & Rong Zhang & Mingqi Zhu& Guangyu Sun & Mark L. Gleason	Sun Guangyu	1.554
102	Genetic analysis of wheat (Triticum aestivum L.) and related species with SSR markers	Genet Resour Crop Evol 2012 DOI: 10.1007/s10722-012-9907-6	Wang YJ, Wang CY, Zhang H, Yue ZN, Liu XL, Ji WQ	Ji WQ	1.54
103	cloning and characterization of the actin gene from Puccinia striiformis f. sp. tritici	World J Microbiol Biotechnol 2012, 28: 2331–2339	Jie Liu,Qiong Zhang,Qing Chang, et al	ZS Kang	1.532
104	Characterization of the genetic relationships among biotypes of Malus prunifolia using simple sequence repeat marker	Scientia Horticulturae/2012, 146:169-174	Mingyang Fu, Fengwang Ma	Ma Fengwang	1.527
105	Effects of fruit bagging on the contents of phenolic compounds in the peel and flesh of ‘Golden Delicious’, ‘Red Delicious’, and ‘Royal Gala’ apples.	Scientia Horticulturae，142: 68-73	Changsheng Chen 、Pengming Li 、Ma Fengwang	Pengming Li	1.527
106	Population genetic diversity of Puccinia striiformis f.sp. tritici on different wheat varieties in Tianshui, Gansu Province	World J. Microbiol. Biochechenology, 2013, 29:173-181	GM Zhan, H Zhuang, FP Wang, ZS Kang	ZS Kang	1.5
107	Influence of rootstock on drought response in young ‘Gale Gala’ apple (Malus domestica Borkh.) trees	Journal of the Science of Food and Agriculture/2012, 92(12) :2421-2427	Binghua Liu, Liang Cheng, Fengwang Ma，Dong Liang and Yangjun Zou	Ma Fengwang	1.436
108	Rhizobium helanshanense sp. nov., a bacterium that nodulatesSphaerophysasalsula (Pall.) DC. in China	Arch Microbiol (2012) 194:371–378	Wei Qin •Zhen Shan Deng •Lin Xu Na Na Wang •Ge Hong Wei	Ge Hong Wei	1.431
109	PnPMA1, an atypical plasma membrane H+-ATPase, is required for zoospore development in Phytophthora parasitica	Fungal Biology/ 2012,116：1013-1023	Zhang, M., Meng, Y., Wang, Q., Liu, D., Quan, J., Hardham, A. R., Shan, W.	Weixing Shan	1.429
110	Discovery of multiple IGS haplotypes within genotypes of Puccinia striiformis.	Fungal biology, 116: 522-528	Wang YC, Hao BJ, Zhang Q, Tuo EL, Sun GY, Zhang R, Jin SL, Zhu MQ, Wang Y, Hsiang T.	Sun Guangyu	1.429

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111	Comparative virulence phenotypes and molecular genotypes of Puccinia striiformis f. sp. tritici, the wheat stripe rust pathogen in China and the United States	Fungal biology, 2012, 116(6):643-53	Gangming Zhan, Xianming Chen, Zhensheng Kang, Lili Huang, Meinan Wang, Anmin Wan, Peng Cheng, Shiqin Cao, Shelin Jin	ZS Kang	1.4
112	Analysis of codon usage patterns of the chloroplast genomes in the Poaceae family	Australian Journal of Botany 2012,60(5) 461-470	Yuerong Zhang，Xiaojun Lie，Song Weining	Song Weining	1.111
113	Biosorption and Bioaccumulation of Cu2+ from Aqueous SolutionUsing Living M. amorphae Isolated from Mine Tailings	Mine Water Environ (2012) 31:312–319	Osama AbdallaMohamadShaimaaRedaHatabZhenshan Liu Zhenxiu Li Zhaoyu Kong Gehong Wei	Ge Hong Wei	1.039
114	Growth, gas exchange, water-use efficiency, and carbon isotope composition of ‘Gale Gala’ apple trees grafted onto 9 wild Chinese rootstocks in response to drought stress	Photosynthetica/2012, 50 (3): 401-410	B.H. LIU, L. CHENG, D. LIANG, Y.J. ZOU, and F.W. MA	Ma Fengwang	1.00
115	Responses of young ‘Pink lady’ apple to alternate deficit irrigation following long-term drought: growth, photosynthetic capacity, water-use efficiency, and sap flow	Photosynthetica/2012，50 (4): 501-507	X.P. SUN, H.L. YAN, P. MA, B.H. LIU, Y.J. ZOU, D. LIANG, F.W. MA, P.M. LI	Ma Fengwang	1.00
116	Life table evaluation of survival and reproduction of the aphid, Sitobion avenae, exposed to cadmium	Journal of Insect Science	Huan-Huan Gaoa, Hui-Yan Zhaob*, Chao Duc, Ming-Ming Dengd, Er-Xia Due, Zu-QingHuf, and Xiang-Shun Hu	Huiyan Zhao	0.947
117	Genetic Relationship between Chinese Wild *Vitis* species and American and European Cultivars Based on ISSR Markers.	*Biochemical Systematics and Ecology*, 2012, 46: 120-126	Zhaobin Jing, Xiping Wang	Xiping Wang	0.931
118	AFLP analysis of genetic variation in wild populations of five Rhododendron species in Qinling Mountain in China	Biochemical Systematics and Ecology 45 (2012) 198–205	Bing Zhao a, Zhen-fang Yin, Man Xu, Qiao-chun Wang	Qiaochun Wang	0.931
119	Detection and identification of the elm yellows group phytoplasma associated with Puna chicory flat stem in China	Can. J. Plant Pathol. 2012, 34(1): 34–41	Li ZN, Zhang L, Wu YF	Wu YF	0.88
120	Molecular characterisation and expression of a pathogen-induced senescence-associated gene in wheat (Triticum aestivum)	Australasian Plant Pathology. 2012 DOI: 10.1007/s13313-012-0184-9	Zhang H, Yang BJ, Wang YJ, Wang CY, Liu, and Ji WQ	Hong Zhang;Ji WQ	0.837
121	Histological and cytological investigations of the infection and colonization of apple bark by Valsa mali var. mali	Australasian Plant Pathol DOI 10.1007/s13313-012-0158-y	X. Ke, L. Huang, Q. Han, X. Gao, Z. Kang	L. Huang,	0.837
122	Detection and Identification of Group 16SrVI Phytoplasma in Willows in China	J Phytopathol ，2012,160:755–757	Lei Zhang, Zhengnan Li, Chao Du, Zhaohui Fu and Yunfeng Wu	Wu YF	0.79

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123	Detection and Identification of Elm Yellows Group Phytoplasma (16SrV) Associated with Alfalfa Witches Broom Disease	J Phytopathol ，2012,160:311–313	Li ZN, Zhang L, Wu YF	Wu YF	0.79
124	Dissoconium proteae newly recorded from China.	Mycotaxon 120: 119–125	Zhang R., Mao YN, Hao L, Chen HC, Sun GY &Gleason ML.	Sun Guangyu	0.709
125	Assessment of Drought Tolerance of Some Triticum L. Species through Physiological Indices	Czech Journal of Genetics and Plant Breeding2012,(4)	Muhammad Abdul Rab Faisal Sultan，Hui Liu，HuiXian Zhao	Huixian Zhao	0.58
126	Leaf senescence and physiological chaaracters in different adzuki bean(Vigna angularis) cultivars	Journal of Food, Agriculture & Environment, 2012，10 (3,4): 610-615	SONG Hu, Gao Xiaoli, Zhang Panpan,DAI Huiping, Chen jia, Jiang Shuhuai,Gao Jinfeng,FENG Baili	FENG Baili	0.517
127	Leaf senescence and activities of antioxidant enzymes in different broomcorn millet (Panicum miliaceum L.) cultivars under simulated drought condition	Journal of Food, Agriculture & Environment, 2012，10 (2): 438-444	Pan-Pan Zhang, Bai-Li Feng, Peng-Ke Wang, Hui-Ping Dai, Hui Song 1, Xiao-Li Gao，Jin-Feng Gao, Jia Chen and Yan Chai.	Bai-Li Feng	0.517
128	Mapping of Quantitative Trait Loci for Adult Plant Resistance to Stripe Rust in German Wheat Cultivar Ibis	Journal of Integrative Agriculture 2012, 11(4): 528-536	Bai B, Ren Y, Xia X, Du J, Zhou G, Wu L, Zhu H, He Z, Wang C	Chenshe Wang	0.49
129	Relations Between Photosynthetic Parameters and Seed Yields of Adzuki Bean Cultivars(Vigna angularis)	Journal of Integrative Agriculture. 2012,11(9):1453-1461	Song Hu, Gao Jinfeng, Gao Xiaoli, Dai Huiping, Zhang Panpan, Feng Baili, Wang Pengke and ChaiYan	FENG Baili	0.449
130	Detection and molecular characterization of cactus witches'-broom disease associated with a group 16SrII phytoplasma in northern areas of China	Tropical Plant Pathology, 2012 ，37(3):210-214	Li ZN, Zhang L, Wu YF	Wu YF	0.44
131	Interactive effects of water and nitrogen supply on growth, biomass partitioning, and water-use efficiency of young apple trees	African Journal of Agricultural Research/ 2012, 7(6): 978-985	Binghua Liu, Liang Cheng, Mingjun Li, Dong Liang, Yangjun Zou, Fengwang Ma	Ma Fengwang	0.263
132	Super-races are not likely to dominate a fungal population within a life time of a perennial crop plantation of cultivar mixtures: a simulation study	BMC Ecology, 2012, 12: 16	Xu Xiangming	Xu Xiangming	

五、国内外学术交流

序号	姓　名	所在单位	参会名称	会议地点	会议时间
1	宋卫宁	农学院	国际动植物基因组学研究大会	美国圣地亚哥	2112.1.12-.17
2	许金荣	植保学院	MSB2 and surface recognition in the rice blast fungus Magnaporthe oryzae	University of Arkansas. Fayetteville, Arkansas.	2012.02.14
3	胡银岗	农学院	澳大利亚 CSIRO 植物所、悉尼大学	澳大利亚	2012.11.18－30
4	张世泽	植物保护学院	第 XXIV 届国际昆虫学大会	韩国 大邱	2012.08.19-25
5	王乔春	园艺学院	观赏植物病毒病害学术会议	挪威	2012.6.24-29
6	王乔春	园艺学院	低温生物学年会	英国	2012.10.11-14
7	胡银岗	农学院	The China - EU Workshop on Phenotypic Profiling and Technology Transfer on Crop Breeding	西班牙	2012.09.17－21
8	赵惠燕	植保学院	国际昆虫学大会	韩国 大邱	2012.08.19--25
9	赵惠燕	植保学院	世界环境发展大会	巴西 里约热内卢	2012.06.10-24
10	许金荣	植保学院	The Kinome of Fusarium graminearum.	San Diego, CA	2012.01.14-18
11	徐炎	园艺学院	Symposium on Plant Biology and Agriculture	北京	2012.10.16-18
12	赵惠燕	植保学院	环境公正工作坊	北京	2012.05.08-10
13	郭军	植保学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.8.29-09.04
14	刘杰	生命学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.08.29-31
15	胡小平	植保学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.8.28-09.01
16	张宏昌	生命科学学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.08.28-09.01
17	赵杰	植保学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.8.27-31
18	王保通	植保学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.8.28-09.01
19	王晓杰	植保学院	第 13 届禾谷类锈病和白粉病会议	北京	2012.08.28-31
20	张宏昌	生命科学学院	2012 年博洛格全球麦锈病协作网国际大会	北京	2012.09.01-04

序号	姓　名	所在单位	参会名称	会议地点	会议时间
21	赵杰	植保学院	2012 年博洛格全球麦锈病协作网国际大会	北京	2012.9.01-05
22	王晓杰	植保学院	2012 年博洛格全球麦锈病协作网国际大会	北京	2012.09.01-04
23	刘杰	生命学院	2012 年博洛格全球麦锈病协作网国际大会	北京	2012.09.01-04
24	王保通	植保学院	中国植物保护成立 50 周年及 2012 年学术年会	北京	2012.10.24-26
25	吴文君	植保学院	中国植物保护学会成立 50 周年庆祝大会暨 2012 年学术年会	北京	2012.10.24-27
26	赵惠贤	生命学院	the 11th International Gluten Workshop in Beijing	北京	2012.08.12-15
27	张世泽	植物保护学院	果树病虫害生态调控技术青年论坛	北京	2012.09.21-24
28	王乔春	园艺学院	植物脱毒与快繁研究与产业化研讨会	北京	2012.11.09-11
29	徐爱遐	农学院	第三届全国小麦基因组学及分子育种大会	陕西西安	2012.8.19-22
30	张改生	农学院	国际作物杂种优势会议	陕西西安	2012.8.19-22
31	李学军	农学院	国际作物杂种优势会议	陕西西安	2012.8.19-22
32	胡胜武	农学院	国际作物杂种优势会议	陕西西安	2012.8.19-22
33	徐爱遐	农学院	作物学年会	江西南昌	2012.10.17-20
34	张林生	生命学院	全国生物化学教学研讨会	山东烟台	2012.08.14
35	赵惠贤	生命学院	第三届全国小麦基因组学及分子育种大会	山东泰安	2012.8.19-21
36	吉万全	农学院	第三届全国小麦基因组学及分子育种大会	山东泰安	2012.08.17-19
37	王保通	植保学院	中国植物病理学会 2012 年学术年会	山东青岛	2012.07.19-24
38	许金荣	植保学院	中国植物病理学会 2012 年学术年会	山东青岛	2012.07.19-26
39	韩青梅	植保学院	中国植物病理学会 2012 年学术年会	山东青岛	2012.07
40	文颖强	园艺学院	中国植物病理学会 2012 年学术年会	山东青岛	2012.07.20-26
41	吴云锋	植保学院	山东农业大学学术交流会议	山东泰安	2012.07.24-26
42	江元清	生命学院	第十三届植物基因组学大会	山东泰安	2012.8.20-22

序号	姓　名	所在单位	参会名称	会议地点	会议时间
43	陈坤明	生命学院	2012 植物细胞生物学学术年会	新疆乌鲁木齐	2012.08.26-31
44	赵惠燕	植保学院	麦类作物害虫治理	中华台北	2012.05.14-21
45	赵惠燕	植保学院	气候变化工作坊	云南昆明	2012.04.24-26
46	王保通	植保学院	2011-2012 年度国家冬小麦品种区试年会	内蒙古呼和浩特	2012.08.14-15
47	胡胜武	农学院	国家油菜区试会	内蒙古呼和浩特	2012.08.15-18
48	赵杰	植保学院	第十一届全国植物线虫学学术研讨会	江苏南京	2012.07.26-30
49	单卫星	植保学院	国际卵菌分子遗传学会议	江苏南京	2012.05.25-29
50	文颖强	园艺学院	第三届果树基因组和分子生物学国际学术研讨会	江苏南京	2012.10.27-29
51	吴云锋	植保学院	中国植物病理学年会植物病毒委员会	辽宁沈阳	2012.07.04-06
52	黄丽丽	植保学院	第五届全国落叶果树病虫害防控技术研讨会	辽宁葫芦岛	2012.09
53	文颖强	园艺学院	2012 年“园艺植物‘组学’前沿”全国研究生暑期学校	湖北武汉	2012.08.07-20
54	吴云锋	植保学院	全国烟草病毒病防治会议	浙江杭州	2012.11.04-06
55	许金荣	植保学院	福州国际植物病理学论坛 II：植物病原物与寄主互作”研讨会	福建福州	2012.05.22-24
56	单卫星	植保学院	第七届全国青年植保创新科技学术研讨会	贵州贵阳	2012.05.03-06
57	单卫星	植保学院	马铃薯产业发展及作物应对干旱”国际联合研讨会	甘肃兰州	2012.08.19-23
58	赵杰	植保学院	小麦病虫持续控制学术研讨会	陕西杨凌	2012.09.05-07
59	赵杰	植保学院	Symposium on plant pathology for food security	陕西杨凌	2012.5.12-16
60	王保通	植保学院	小麦病虫持续控制学术研讨会	陕西杨凌	2012.09.06-07
61	张鲁刚	园艺学院	全国植物生物学会议	陕西杨凌	2012.10.11-13
62	郁飞	生命科学学院	2012 全国植物生物学大会	陕西杨凌	2012.10.10-14
63	范三红	生命学院科学	2012 全国植物生物学大会	陕西杨凌	2012,10,10-13
64	江元清	生命学院	植物生物学大会	陕西杨凌	2012.10.11-13
65	陈坤明	生命学院	2012 年全国植物生物学大会	陕西杨凌	2012.10.10-13

序号	姓　名	所在单位	参会名称	会议地点	会议时间
66	文颖强	园艺学院	2012 全国植物生物学大会	陕西杨凌	2012.10.11-14
67	刘杰	生命学院	2012 全国植物生物学大会	陕西杨凌	2012.10.11-13
68	文颖强	园艺学院	中国园艺学会 2012 年学术年会	陕西杨凌	2012.10.19-21
69	马锋旺	园艺学院	中国园艺学会 2012 年年会	陕西杨凌	2012．10.19-21
70	张鲁刚	园艺学院	中国园艺学会会议	陕西杨凌	2012.10.19-21
71	梁东	园艺学院	中国园艺学会 2012 年学术年会	陕西杨凌	2012.10.19-22
72	李鹏民	园艺学院	2012 全国园艺学会年会	陕西杨凌	2012.1
73	徐炎	园艺学院	中国园艺学会	陕西杨凌	2012.10.19-21
74	张林生	生命学院	陕西省生物化学年会	陕西安康	2012.10.26

六、获授权专利

序号	专利名称	申请人	专利号	授权日期
1	建立油菜细胞质类型特异 PCR 标记以及快速鉴定油菜细胞质类型的方法.	胡胜武	ZL 200910022297.0	2012.05
2	一种大白菜真叶离体再生培养方法	张鲁刚	ZL 2011 1 0045595.9	2012.05
3	一种预防苹果树腐烂病的伤口保护剂	胡小平	ZL200910166049.3	2012.07
4	一种苹果腐烂病的铲除剂	王保通	ZL.200910164720.0	2012.07
5	单嘧磺酯及其钠盐用于制备植物化学杂交剂的应用	赵惠贤	ZL2012102825673	2012.08
6	植物病原菌诱导型乙烯响应因子基因启动子序列及其应用	王跃进	ZL201010582586.9	2012.10
7	葡萄白粉病转录因子 VpRFP1 启动子序列及其应用	王跃进	ZL201010582564.2	2012.10
8	一种以橙色大白菜子叶段为外植体的离体组织培养方法	张鲁刚	ZL 2008 1 0232067.2	2012.11

八、获奖情况

序号	获奖成果名称	获奖等级	获奖时间（年）	主要完成人
1	玉米高产高效生产理论及技术体系研究与应用	国家科学技术进步二等奖	2012	薛吉全（第三完成人）
2	甘蓝型油菜无微粉类细胞质雄性不育系研究及其杂交种选育	陕西省科学技术奖一等奖	2012	董振生
3	高产多抗粮饲兼用玉米品种陕单8806选育与推广	陕西科学技术二等奖	2012	薛吉全
4	陕西省优秀创新人才	陕西省创新人才一等奖	2012	韦革宏

九、审定品种

序号	品种名称	审定单位	完成人
1	陕油 107	国家农作物品种审定委员会	徐爱遐
2	陕油 803	国家农作物品种审定委员会	胡胜武
3	陕农 33	陕西省农作物品种审定委员会	王成社
4	陕单 609	陕西省农作物品种审定委员会	薛吉全
5	陕油 17	陕西省农作物品种审定委员会	董振生
6	陕油 18	陕西省农作物品种审定委员会	董振生
7	合杂油 2 号	陕西省农作物品种审定委员会	董军刚

十、开放课题

（一）开放课题申请指南

依托西北农林科技大学的“旱区作物逆境生物学国家重点实验室”，围绕旱区作物逆境生物学的核心科学问题，开展旱区作物抗逆种质和基因资源发掘、作物非生物胁迫应答机理、作物与病虫互作机理、作物抗逆种质创新与品种设计等四个研究方向的基础和应用基础研究，以提升我国作物逆境生物学研究水平，为旱区农业生产的高效可持续发展提供理论基础和技术支撑。

实验室现已具备开展作物逆境生物学相关研究所需的仪器设备和配套设施，在建设期内，实验室还将进一步补充完善仪器设备等科研条件。为了贯彻执行“开放、流动、联合、竞争”的运行机制，提升实验室的科学研究水平，创造良好的学术环境，吸引和凝聚国内外优秀学者，合作开展高水平的基础和应用基础性研究，实验室特设立开放基金，资助与实验室研究方向有关的具有重要科学意义的基础与应用基础研究，热忱欢迎国内外从事相关领域研究的科技工作者来实验室进行合作研究，有意申请者可向实验室索取申请书及申请指南，亦可登陆实验室网页下载申请书。

1、支持的主要研究方向

实验室本年度拟重点支持的研究领域为旱区作物抗逆种质和基因资源发掘、旱区作物非生物逆境胁迫应答机理、旱区作物与病虫互作机理、旱区作物抗逆种质创新与品种设计等四个方向，凡符合下列研究内容的课题，均可申请。

（1）旱区作物抗逆种质和基因资源发掘

以旱区粮油、果树等作物及其近缘植物种质资源为对象，围绕抗旱、耐盐碱、抗病虫、抗寒及优质高产等性状，进行种质资源的综合评价，建立作物种质资源抗逆鉴选与评价的技术体系；分析揭示作物抗旱、耐盐碱、抗寒、抗病虫以及高产优质等重要性状的遗传规律。

（2）作物非生物胁迫应答机理

以旱区作物面临的干旱、盐碱、低温和高温等非生物逆境为主攻点，以旱区作物为材料，从生理生化、细胞生物学、遗传与表观遗传、分子生物学等方面系统深入研究作物适应与抵御非生物逆境的机制，揭示非生物逆境对作物致害的机理，阐明作物感受、抵御与耐受逆境的信号转导通路和基因调控网络，探索提高作物非生物逆境抗性的策略和技术。

（3）作物与病虫互作机理

针对旱区作物生产中存在的重大病虫危害问题，以粮食、果树、蔬菜作物主要病虫为主攻对象，从分子、细胞、个体和群体生物学水平研究其发生规律、病虫与作物的互作关系，揭示作物病虫致害的机理、作物抗病虫性的机制、病虫与作物互作的遗传基础以及环境因素对病虫种群的调控作用。

（4）作物抗逆种质创新与品种设计

围绕抗旱、耐盐碱、抗寒、抗病虫等重要性状，探索创制小麦、玉米、小杂粮、苹果、葡萄等作物抗逆种质和新品种设计的新理论与新方法，运用细胞工程、染色体工程、基因工程、分子标记辅助选择等现代生物技术，创制抗逆新种质。

2、申请条件

（1）凡已取得博士学位，或具有助研以上职称的国内外中青年科学工作者均可提出申请，原则上不受理在读博士生的申请。

（2）申请课题应在学术上具有一定的先进性，研究计划切实可行，申请者在所申请的领域内已具有足够的研究基础，申请课题的研究内容必须符合课题指南范围，并与实验室相关团队有密切的联系。

（3）每项课题申请经费额度为 5-10 万元/年，执行年限为 1-2 年（可申请延长）。批准的开放基金课题，须依托重点实验室的相关团队开展工作。

（4）遵守重点实验室 “开放基金课题管理办法”的相关规定要求。

3、申请程序

有意申请者可从网站下载申请书，或向本实验室索取，并按规定格式认真填写，申请者将签字盖章的纸质申请书一式 6 份，于 9 月 5 日前寄至本实验室，并将电子版

（Word 或 PDF 格式）通过电子邮件发送到指定邮箱。

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旱区作物逆境生物学国家重点实验室

2012 年 7 月 21 日

（二）开放课题经费下达通知

旱区作物逆境生物学国家重点实验室 2012 年开放课题批准项目及经费下达的通知

根据《国家重点实验室建设与运行管理办法》和《旱区作物逆境生物学国家重点实验室开放基金课题管理办法》，2012 年 9 月，旱区作物逆境生物学国家重点实验室（以下简称：实验室）发布了 2012 年开放课题申请指南，经自由申请、实验室资格审查、组织专家评审、公示，经实验室学术委员会评审等环节，实验室决定资助 2012 年开放课题 15 项（见附件）。为了做好项目的实施管理，现就有关事项通知如下：

一、项目执行期为两年，2013 年 1 月 1 日始，2014 年 12 月 31 日结束。

二、立项项目资助经费以申报开展研究所需经费为参考，同时根据实验室学术委员会建议予以相应调整，请严格按照项目申请书计划和下达经费执行研究任务。

三、经费下达到项目校内依托团队负责人，依托团队为项目实施创造必要的研究条件，督促项目负责人及课题成员来实验室开展工作，确保项目顺利实施。

四、项目经费使用范围包括来实验室开展研究工作的差旅费、实验材料费、文献出版信息费、分析测试费等。

五、项目研究成果，包括品种、专著、论文、专利等，需标注“旱区作物逆境生物学国家重点实验室开放课题基金（编号）资助”。

旱区作物逆境生物学国家重点实验室学术委员会

2012年12月2日

（三）开放课题清单

2012 年开放课题资助项目清单

序号	课题名称	项目编号	申报人	申报人单位	经费(万元)
1	西藏小麦条锈菌转主寄主及在毒性变异中的作用研究	CSBAA2012001	彭岳林	西藏农牧学院	10.00
2	西北干旱区甘草根瘤菌生物地理学与系统发育学研究	CSBAA2012002	李　丽	中国科学院新疆生态与地理研究所	10.00
3	小麦新种质 N9134 抗病候选基因的克隆与功能验证	CSBAA2012003	薛　飞	石河子大学	10.00
4	利用多元荧光卫星定位标记法分析西藏高原藜米杂交后代的多样性	CSBAA2012004	贡布扎西	西藏大学农牧学院	10.00
5	CO_2 加富提高黄瓜抗旱性机理研究	CSBAA2012005	李清明	山东农业大学	5.00
6	根际促生细菌提高小麦幼苗耐旱性的 RNA 组学解析	CSBAA2012006	马艳玲	西北大学	5.00
7	RNAi 干扰 BRI1 基因，创建矮化、高产油菜新种质	CSBAA2012007	张彦锋	陕西省杂交油菜研究中心	5.00
8	反茴香薄翅野螟耐寒性及其应用的研究	CSBAA2012008	来有鹏	青海省农林科学院植保所	5.00
9	寄住昆虫和寄住植物挥发物在寄生蜂寄住搜寻行为中的作用	CSBAA2012009	郭　昆	中国医学科学院药用植物研究所	5.00
10	苹果 AsAT 基因家族的表达与逆境下 AsA-GSH 循环细胞区室活性的关系研究研究	CSBAA2012010	马春花	云南农业大学园林园艺学院	5.00
11	苹果 SnRK2D 基因的克隆与功能分析	CSBAA2012011	夏　惠	四川农业大学果蔬研究所	5.00
12	一个 NCS1 家族成员提高酵母和拟南芥耐碱胁迫能力的机制研究	CSBAA2012012	王　蕾	中科院昆明植物研究所	5.00
13	旱区甘蓝型油菜早期活力对油菜生长的影响及其与抗旱性的关系研究	CSBAA2012013	关周博	陕西省杂交油菜研究中心	5.00
14	玉米自交系抗旱性鉴选与分子标记	CSBAA2012014	孟庆立	宝鸡市农业科学研究所	5.00
合计经费（万元）					90.00

十一、获奖成果简介

2012 年陕西省科学技术一等奖

“甘蓝型油菜无微粉类细胞质雄性不育系研究及其杂交种选育”成果简介

项目以新发现油菜无微粉不育源为基础，利用自有专利技术选育成无微粉类细胞质雄性不育系 212A 及 5 个衍生系，育成油菜新品种 10 个，其中国审品种 4 个。陕油 8 号是我国黄淮流域审定的第一个双低油菜杂交种，也是第一个在产量和品质上超过秦油 2 号的品种。秦研 211 高产、早熟、抗倒，具有适宜机械化种植的特性，适宜长江下游推广种植，筛选出了适宜制种区域，形成了配套制种技术及栽培技术。

自 2002 年以来, 陕油 8 号和秦研 211 在陕西累计推广 608.0 万亩，共新增效益 1.68 亿元。

在省内外共推广 1879.2 万亩，新增经济效益 5.24 亿元。项目实施期间获批国家发明专利（ZL200410025802.4），发表相关科研论文 41 篇。


陕西省科学技术奖

证　书

为表彰陕西省科学技术奖获得者，

特颁发此证书。

项目名称：甘蓝型油菜无微粉类细胞质雄性不育系研究及其杂交种选育

奖励等级：壹等

获 奖 者：西北农林科技大学

陕西省人民政府

二〇一二年九月十九日

证书号：2012-1-09-D1

十二、2012 年购置仪器设备

序号	仪器名称	型号	金额（万元）	购置日期
1	双电极电压钳系统	AXON900A	33.9	2012-1-12
2	植物光合作用仪	3051C	39.53	2012-1-12
3	台式高速冷冻离心机 2 台	Allegra X-15R	15.28	2012-1-12
4	多道生物分析系统	Agilent2100	22.45	2012-2-29
5	超薄切片机	UC7	45.54	2012-2-29
6	玻璃制刀机	EMKMR3	8.25	2012-2-29
7	冷冻干燥箱	CS110-4	9.85	2012-2-29
8	荧光显微镜	BX53+DP72	19.50	2012-2-29
9	离子溅射仪	MSP-1S	9.24	2012-3-11
10	冷冻干燥箱	VFD-21S	10.25	2012-3-11
11	灭菌器 4 台	SX-500	17.96	2012-3-20
12	半薄切片机	RM2265	14.98	2012-3-20
13	氨氮分析仪	FLOWSYS	44.22	2012-3-22
14	火焰光度计	PFP7	5.28	2012-3-22
15	组织研磨机 2 台	MM400	19.14	2012-3-29
16	荧光显微镜	Super SMFFM	262.68	2012-4-12
17	高速冷冻落地离心机	CR22GIII	27.34	2012-4-13
18	研究型显微镜 2 台	BX52+DP72	47.91	2012-4-20
19	荧光实体显微镜	SZX16+DP72	20.29	2012-4-20
20	气相色谱仪	Clarus 680	25.41	2012-4-27

序号	仪器名称	型号	金额（万元）	购置日期
21	生物显微镜	SMZ1500	5.44	2012-6-21
22	低温培养箱 2 台	LT-36VL	46.20	2012-6-29
23	人工气候箱 2 台	1-36DL	41.58	2012-6-29
24	酶标仪	M200pro	36.11	2012-7-4
25	双光子激光共聚焦显微系统	FV1000MPE	432.25	2012-11-9
26	PCR 仪 2 台	EDC-810	5.30	2012-12-6
27	冷冻恒温摇床 2 台	NRY-2102	5.86	2012-12-10

十三、重要科研成果首页

（影响因子 4 以上论文 21 篇）

Biotechnology Advances 30 (2012) 604–612

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Research review paper

Novel and potential application of cryopreservation to plant genetic transformation

Biao Wang [1], Zhibo Zhang [1], Zhenfang Yin, Chaohong Feng, Qiaochun Wang *

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ABSTRACT

The world population now is 6.7 billion and is predicted to reach 9 billion by 2050. Such a rapid growing population has tremendously increased the challenge for food security. Obviously, it is impossible for traditional agriculture to ensure the food security, while plant biotechnology offers considerable potential to realize this goal. Over the last 15 years, great benefits have been brought to sustainable agriculture by commercial cultivation of genetically modified (GM) crops. Further development of new GM crops will with no doubt contribute to meeting the requirements for food by the increasing population. The present article provides updated comprehensive information on novel and potential application of cryopreservation to genetic transformation. The major progresses that have been achieved in this subject include (1), long-term storage of a large number of valuable plant genes, which offers a good potential for further development of novel cultivars by genetic transformation; (2), retention of regenerative capacity of embryogenic tissues and protoplasts, which ensures efficient plant regeneration system for genetic transformation; (3), improvement of transformation efficiency and plant regeneration of transformed cells; (4), long-term preservation of transgenic materials with stable expression of transgenes and productive ability of recombinant proteins, which allows transgenic materials to be stored in a safe manner before being analyzed and evaluated, and allows establishment of stable seed stocks for commercial production of homologous proteins. Data provided in this article clearly demonstrate that cryo-technique has an important role to play in the whole chain of genetic transformation. Further studies coupling cryotechnique and genetic transformation are expected to significantly improve development of new GM crops.

Contents

1. Significant importance of plant genetic transformation

The global population now is 6.7 billion, which doubled that the world had 45 years ago, and is predicted to reach 9 billion by 2050, provided that the growth rate of 1.3% per year at present time continues (Braun, 2010). Such a rapidly growing population has tremendously increased the challenge for food security. Doubling food production in the next four decades can hopefully meet the requirements for food supply (Braun, 2010; ISAAA, 2009). Obviously, it is impossible for traditional agriculture to ensure food security, while plant biotechnology offers considerable potential to realize this goal (Fedoroff, 2010; Qaim, 2010; Schahczenski and Adam, 2006).

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Different Chitin Synthase Genes Are Required for Various Developmental and Plant Infection Processes in the Rice Blast Fungus *Magnaporthe oryzae*

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Abstract

Chitin is a major component of fungal cell wall and is synthesized by chitin synthases (Chs). Plant pathogenic fungi normally have multiple chitin synthase genes. To determine their roles in development and pathogenesis, we functionally characterized all seven *CHS* genes in *Magnaporthe oryzae*. Three of them, *CHS1*, *CHS6*, and *CHS7*, were found to be important for plant infection. While the *chs6* mutant was non-pathogenic, the *chs1* and *chs7* mutants were significantly reduced in virulence. *CHS1* plays a specific role in conidiogenesis, an essential step for natural infection cycle. Most of *chs1* conidia had no septum and spore tip mucilage. The *chs6* mutant was reduced in hyphal growth and conidiation. It failed to penetrate and grow invasively in plant cells. The two MMD-containing chitin synthase genes, *CHS5* and *CHS6*, have a similar expression pattern. Although deletion of *CHS5* had no detectable phenotype, the *chs5 chs6* double mutant had more severe defects than the *chs6* mutant, indicating that they may have overlapping functions in maintaining polarized growth in vegetative and invasive hyphae. Unlike the other *CHS* genes, *CHS7* has a unique function in appressorium formation. Although it was blocked in appressorium formation by germ tubes on artificial hydrophobic surfaces, the *chs7* mutant still produced melanized appressoria by hyphal tips or on plant surfaces, indicating that chitin synthase genes have distinct impacts on appressorium formation by hyphal tip and germ tube. The *chs7* mutant also was defective in appressorium penetration and invasive growth. Overall, our results indicate that individual *CHS* genes play diverse roles in hyphal growth, conidiogenesis, appressorium development, and pathogenesis in *M. oryzae*, and provided potential new leads in the control of this devastating pathogen by targeting specific chitin synthases.

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

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☯ These authors contributed equally to this work.

Introduction

Chitin, a microfibrillar β-1,4-linked homopolymer of *N*-acetyl-glucosamine (GlcNAc), is one of the major structural components of the fungal cell wall [1]. Chitin synthases are key enzymes catalyzing the polymerization of GlcNAc [1]. They are usually localized to cytoplasmic membrane and have attracted considerable attentions as targets for developing fungicides [2,3]. Chitin synthase (*CHS*) genes from various fungi have been grouped into seven classes [4]. All chitin synthases have chitin synthase domains and transmembrane domains in common. In addition, the class V and class VI chitin synthases contain the myosin motor domain (MMD) at their N-terminal [5,6]. Myosins are known as mechanoenzymes that convert chemical energy released by ATP hydrolysis into a mechanical force that is directed along actin filaments [7].

Fungi are different in chitin contents and in the composition of chitin synthases. In the budding yeast *Saccharomyces cerevisiae*, chitin constitutes 1–2% of the total dry weight, and is a minor cell wall component and mainly exists at the mother-daughter cell junction and septum [8]. *S. cerevisiae* has three *CHS* genes with distinct functions in cell wall expansion, septum formation, and budding [9–11]. Chs1 repairs the weakened cell wall of daughter cells after separation. Chs2 synthesizes chitin in primary septa. It is essential for both septum formation and cell division [12]. Chs3 chitin synthase is required for chitin ring formation at the base of emerging buds and chitin synthesis in the lateral cell. Chs3 is responsible for 90% of chitin synthesis while Chs1 and Chs2 are involved in only small amounts of chitin synthesis at extreme parts of cells [13]. Unlike the budding yeast, *Schizosaccharomyces pombe* has only two chitin synthase genes [14]. *Ashbya gossypii* and *Candida albicans* have three and four *CHS* genes, respectively [15].

In filamentous fungi, chitin content has been reported to reach up to 10–20% [16]. Filamentous ascomycetes generally have seven or eight *CHS* genes, which may reflect their greater complexity of

environmental microbiology

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A type VI secretion system regulated by OmpR in *Yersinia pseudotuberculosis* functions to maintain intracellular pH homeostasis

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Summary

Type VI secretion systems (T6SSs) which widely distributed in Gram-negative bacteria have been primarily studied in the context of cell interactions with eukaryotic hosts or other bacteria. We have recently identified a thermoregulated T6SS4 in the enteric pathogen *Yersinia pseudotuberculosis*. Here we report that OmpR directly binds to the promoter of T6SS4 operon and regulates its expression. Further, we observed that the OmpR-regulated T6SS4 is essential for bacterial survival under acidic conditions and that its expression is induced by low pH. Moreover, we showed that T6SS4 plays a role in pumping H^+ out of the cell to maintain intracellular pH homeostasis. The acid tolerance phenotype of T6SS4 is dependent on the ATPase activity of ClpV4, one of the components of T6SS4. These results not only uncover a novel strategy utilized by *Y. pseudotuberculosis* for acid resistance, but also reveal that T6SS, a bacteria secretion system known to be functional in protein transportation has an unexpected function in H^+ extrusion under acid conditions.

Introduction

Gram-negative bacteria employ a variety of secretion systems to deliver proteins to the extracellular milieu or directly into the cytosol of host cells (Holland, 2010). These systems utilize ATPase or proton motive force (PMF) to energize substrate protein translocation and the assembly of the secretion machine (Galán, 2008; Dalbey and Kuhn, 2012). The recently identified type VI secretion systems (T6SSs) are specialized bacterial protein export machines that present in more than a quarter of sequenced bacterial genomes, and structurally and functionally related to contractile phage tail sheath (Jani and Cotter, 2010; Schwarz *et al.*, 2010; Basler *et al.*, 2012). ClpV and IcmF, two conserved components with ATPase activity may function as energizers for T6SSs. ClpV is a member of the AAA+ (ATPases associated with various cellular activities) protein family, which is an oligomeric ring-like machine that binds ATP through the conserved AAA domain and converts the energy of ATP hydrolysis into mechanical force (Schlieker *et al.*, 2005; Bönemann *et al.*, 2009). ClpV is crucial for Hcp and VgrG secretion; it also provides energy for contracting the tail sheath of T6SS via ATP hydrolysis (Mougous *et al.*, 2006; Bönemann *et al.*, 2009; Basler *et al.*, 2012). The membrane localized protein IcmF in T6SS usually interacts with multiple T6SS components and powers the secretion machinery assembly like its IcmF paralogue in T4SS (Sexton *et al.*, 2004; Zheng and Leung, 2007; Ma *et al.*, 2012). A striking feature of T6SS is the presence of multiple gene clusters that appear to code for evolutionarily distinct machineries in a single genome, implying that these systems confer distinct functions or are required for specific niches or hosts (Bingle *et al.*, 2008; Pukatzki *et al.*, 2009). Indeed, T6SSs have been recently reported to play versatile physiological roles including host–symbiont communication, interbacterial interactions, biofilm formation, and acute and chronic infection (Cascales, 2008; Filloux *et al.*, 2008; Pukatzki *et al.*, 2009; Hood *et al.*, 2010; Schwarz *et al.*, 2010). Interestingly, Weber and colleagues (2009) reported that a T6SS in *Vibrio anguillarum* is important for bacterial stress response and cell survival after exposure to various environmental challenges. However, most studies of T6SSs have focused on their roles in pathogenicity and cell–cell interactions, and very little is known about their roles in bacterial cellular processes such as stress responses.

Yersinia pseudotuberculosis is a food-borne enteric pathogen that causes a variety of intestinal and

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Journal of Pineal Research

Journal of Pineal Research
Molecular, Biological, Physiological and Clinical Aspects of Melatonin

Delayed senescence of apple leaves by exogenous melatonin treatment: toward regulating the ascorbate–glutathione cycle

Abstract: The objectives of this study were to test the effects of exogenous melatonin on apple (*Malus domestica* Borkh. cv. Golden Delicious) leaves and investigate its possible physiological role in delaying leaf senescence. Detached leaves treated with 10 mM melatonin solutions clearly showed a slowing in their process of dark-induced senescence, as evidenced by both biochemical and molecular parameters. Melatonin delayed the normal reduction in chlorophyll content and maximum potential photosystem II efficiency (F_v/F_m). It also suppressed the transcript levels of a key chlorophyll degradation gene, *pheide a oxygenase* (*PAO*), and the *senescence-associated gene 12* (*SAG12*). This outcome was thought to be because of the enhanced antioxidant capabilities of melatonin. Indeed, H_2O_2 accumulation was inhibited by exogenous melatonin, which might have resulted from direct reactive oxygen species scavenging by melatonin and a great enhancement of ascorbate peroxidase (APX; EC 1.11.1.11), which acted on both mRNA and protein activity levels. Melatonin treatment led to the maintenance of higher contents of ascorbic acid (AsA) and glutathione (GSH) but less dehydroascorbate (DHA) and oxidized glutathione (GSSG) compared with the control, possibly through its regulation of the AsA–GSH cycle.

Ping Wang, Lihua Yin, Dong Liang, Chao Li, Fengwang Ma and Zhiyong Yue

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Key words: apple, ascorbate–glutathione cycle, chlorophyll degradation, leaf senescence, melatonin

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Introduction

Melatonin (*N*-acetyl-5-methoxytryptamine) is a naturally occurring indoleamine molecule [1]. Existing in a multitude of taxa, it performs many biological functions, mainly for primary antioxidant defenses in unicellular organisms, signaling of darkness in vertebrates, environmental tolerance in fungi and plants, sexual signaling in birds and fish, seasonal reproductive regulation in photoperiodic mammals, and immunomodulation and anti-inflammatory activity in all vertebrates tested [2–5]. As its first detection in plants in 1995 [6, 7], melatonin has been identified and quantified in the roots, leaves, fruits, flowers, and seeds of a wide range of species [6–16]. However, little is known about its physiological functions in plants. Melatonin acts as a growth regulator, similar to the role of IAA, in directing the differentiation of cells, tissues, and organs [17]. It also protects plants against environmental stress from heavy metals [18], UV radiation [14], and temperature fluctuations [19], as well as delaying leaf senescence [20]. Nevertheless, the precise physiological and molecular mechanisms for its serving as an antioxidant in leaf senescence are still poorly understood.

Leaf senescence is a developmentally programmed degenerative process that constitutes the final step of the leaf lifespan. It is controlled by multiple developmental and environmental factors. This process is characterized by differential gene expression, active degeneration of macromolecules, and the recycling of nutrients [21, 22]. Leaf yellowing owing to chlorophyll degradation is often considered to be the main marker for leaf senescence. The pathway of chlorophyll degradation has been elucidated and several genes in the pathway have been cloned [23]. Cleavage of the tetrapyrrole ring to produce red chlorophyll catabolite (RCC) by *pheide a oxygenase* (*PAO*) is the decisive step for chlorophyll catabolism. *PAO*, a nuclear-encoded enzyme, shows a dramatic increase in activity during senescence [24]. Its expression in *Arabidopsis* can be upregulated throughout dark-induced leaf senescence [25].

During leaf senescence, the majority of genes are downregulated while a subset is upregulated. These genes collectively termed senescence-associated genes (*SAG*s) [21]. In *Arabidopsis*, *SAG12* is an age-specific gene upregulated during leaf senescence. Because it is minimally regulated by environmental factors [26], it is often referred to as the marker gene of senescence.

One hypothesis states that aging results from the generation of an excess of harmful free radicals [27] and that the onset of senescence is mainly because of an uncontrolled strong enhancement in the generation of reactive oxygen species (ROS) [28]. As ROS levels and their destructive products in many plants are known to increase during senescence, it is possible that this damage results from declines in the activity of certain antioxidant enzymes or main antioxidants, e.g., reduced-form ascorbic acid (AsA) and glutathione (GSH). In higher plants, the ascorbate–glutathione (AsA–GSH) cycle is an important antioxidant protection system against H_2O_2 generated in different cell

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The mitigation effects of exogenous melatonin on salinity-induced stress in *Malus hupehensis*

Abstract: As an indoleamine molecule, melatonin mediates many physiological processes in plants. We investigated its role in regulating growth, ion homeostasis, and the response to oxidative stress in *Malus hupehensis* Rehd. under high-salinity conditions. Stressed plants had reduced growth and a marked decline in their net photosynthetic rates and chlorophyll contents. However, pretreatment with 0.1 μM melatonin significantly alleviated this growth inhibition and enabled plants to maintain an improved photosynthetic capacity. The addition of melatonin also lessened the amount of oxidative damage brought on by salinity, perhaps by directly scavenging H_2O_2 or enhancing the activities of antioxidative enzymes such as ascorbate peroxidase, catalase, and peroxidase. We also investigated whether melatonin might control the expression of ion-channel genes under salinity. Here, *MdNHX1* and *MdAKT1* were greatly up-regulated in the leaves, which possibly contributed to the maintenance of ion homeostasis and, thus, improved salinity resistance in plants exposed to exogenous melatonin.

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Key words: exogenous melatonin, growth inhibition, ion channels, *Malus hupehensis*, oxidative damages, photosynthesis, salinity

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Introduction

Soil salinity is one of the greatest challenges to worldwide agriculture [1]. The detrimental effects of high salt result from both a water deficit caused by osmotic stress and the influence of excess sodium ions on key biochemical processes [2]. Plants utilize various biochemical and molecular coping strategies, including selective buildup or exclusion of salt ions, control of ion uptake by the roots and transport into the leaves, ion compartmentalization, synthesis of compatible osmolytes, alteration to the photosynthetic pathway, changes in the membrane structure, induction of antioxidative enzymes, stimulation of phytohormones, and regulation of gene expression [3]. Na^+/H^+ antiporters are ubiquitous membrane proteins that play vital roles in cellular pH and Na^+ homeostasis throughout the biological kingdom [4]. Plants remove excess Na^+ from the cytoplasm by either relegating it to the apoplasts or compartmentalizing it to the vacuole by Na^+/H^+ antiporters that are associated with the plasma membrane or vacuolar membrane (tonoplast), respectively [5, 6]. Previous work showed that overexpression of *AtNHX1*, a vacuolar Na^+/H^+ antiporter, significantly increased the salt tolerance of transgenic plants [2, 7], while overexpression of a plasma membrane Na^+/H^+ antiporter gene, *AtSOS1*, also improved such tolerance in *Arabidopsis thaliana* [8].

Potassium is a macronutrient necessary for several physiological processes, e.g., maintenance of membrane potential and turgor, enzyme activation, and regulation of osmotic pressure [9]. Plant cells utilize low- and high-affinity transporters to take up K^+ from the extracellular medium. Low-affinity K^+ carriers (nonsaturating at physiological K^+ concentrations in the external solution), such as *AKT1* [10], are inward-rectifying channels that activate K^+ influx upon plasma membrane hyperpolarization. Although they normally display a high K^+/Na^+ selectivity ratio at physiological K^+ and Na^+ external concentrations, they can also mediate significant Na^+ uptake with an increasing level of external Na^+ [11].

During salinity-induced oxidative stress, the availability of atmospheric CO_2 is diminished because of increased stomatal closure and a decrease in the consumption of NADPH via the Calvin cycle. Over-reduced ferredoxin during photosynthetic electron transfer accelerates the production of reactive oxygen species (ROS) in the chloroplasts [12]. These ROS are also generated by impaired electron transport processes in the mitochondria when electrons leak onto molecular oxygen [13]. To overcome salt-mediated oxidative stress, plants detoxify ROS either by up-regulating antioxidative enzymes such as superoxide dismutase (SOD; EC 1.15.1.1), ascorbate peroxidase (APX; EC 1.11.1.11), catalase (CAT; EC 1.11.1.6), glutathione reductase (GR; EC 1.6.4.2), and glutathione peroxidase

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Real-time analysis of the carbohydrates on cell surfaces using a QCM biosensor: a lectin-based approach

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ABSTRACT

A novel approach to the study of molecular interactions on the surface of mammalian cells using a QCM biosensor was developed. For this study, an epidermoid carcinoma cell line (A-431) and a breast adenocarcinoma cell line (MDA-MB-468) were immobilized onto polystyrene-coated quartz crystals. The binding and dissociation between the lectin Con A and the cells as well as the inhibition of the binding by monosaccharides were monitored in real time and provided an insight into the complex avidic recognition of cell glycoconjugates. The real-time lectin screening of a range of lectins, including Con A, DBA, PNA and UEA-I, enabled the accurate study of the glycosylation changes between cells, such as changes associated with cancer progression and development. Furthermore, the kinetic parameters of the interaction of Con A with MDA-MB-468 cells were studied. This application provides investigators in the field of glycobiology with a novel tool to study cell surface glycosylation and may also have impacts on drug discovery.

1. Introduction

In this post-genomic era, the interest in glycomics has greatly increased because the oligosaccharide chains of many glycoproteins appear to be involved in a variety of biological functions, including blood clotting, structural support, hormone activation and recognition, the storage of bioactive molecules, cell migration and cell–cell and cell–matrix interactions and adhesion (Springer, 1990; Varki, 1993). In particular, plasma membrane proteins serve mainly as enzymes, channels or cell/protein receptors, and most of these proteins undergo glycosylation as they traffic through the secretory pathway. Glycans confer additional properties such as shape, hydrophobicity and charge, and they may interact with carbohydrate-binding proteins. There is a considerable body of evidence detailing the abnormal glycosylation of glycoproteins in cancer development. The changes in the carbohydrate composition of cancer cells have been shown to play a critical role in the cell–cell and cell–matrix interactions necessary for cancer cell survival, invasion and metastasis. For instance, when cells are oncogenically transformed, they often express fetal carbohydrates called oncofetal antigens. A variety of oncofetal changes in cancer glycosylation have been described, including an increased N-linked carbohydrate size due to extensive branching, the increased expression of the Lewis sugars and the truncation of carbohydrates such as those observed on mucin-type glycoconjugates, which exposes structures such as the T and Tn antigens (Dwek and Brooks, 2004). Several findings have led to an interest in lectins with respect to cancer research, particularly the ability of some lectins to bind preferentially to malignant cells (reviewed in Sharon and Lis, 2004).

Lectins are carbohydrate-binding proteins of non-immune origin that agglutinate cells or precipitate glycoconjugates. Lectins were first identified in the 19th century by Peter Herman Stillmark (1888), who described a protein extract from the seeds of the castor tree (*Ricinus communis*) that had hemagglutinin activity, i.e., the extract could agglutinate erythrocytes (Franz, 1988). Lectins have played a crucial role in determining the sugar composition of antigens associated with the ABO blood group system as well as in the observation of the glycans exposed at the surface of mammalian cells (Morgan and Watkins, 2000). Although new techniques to study complex carbohydrates have emerged, such as mass spectrometry (Mutenda and Matthiesen, 2007), the use of lectins remains a method of choice to study the role of carbohydrates in numerous biological systems, especially glycosylation changes occurring at the surface of mammalian cells that lead to the development of diseases such as cancer and metastasis. In addition, lectins have been studied as diagnostic tools and therapeutic agents in cancer research (Grossbard et al., 1998; Multani et al., 1998).

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RESEARCH PAPER

Wheat BAX inhibitor-1 contributes to wheat resistance to *Puccinia striiformis*

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Abstract

BAX inihibitor-1 (BI-1) is proposed to be a cell death suppressor conserved in both animals and plants. The ability of *BI-1* genes to inhibit programmed cell death (PCD) has been well studied in animals, but the physiological importance of BI-1 in plant–microbe interactions remains unclear. This study characterized *BI-1* from wheat infected by *Puccinia striiformis* f. sp. *tritici* (*Pst*). The deduced TaBI-1 protein contained a Bax inhibitor domain and seven transmembrane regions conserved among members of the BI-1 family. Transcription of *TaBI-1* was detected in all wheat tissues tested (culms, roots, leaves, anthers, and spikelets). Furthermore, *TaBI-1* exhibited positive transcriptional responses to *Pst* infection and abiotic stresses. Overexpression of *TaBI-1* in tobacco blocked Bax-induced cell death. Silencing *TaBI-1* in plants of a resistant wheat genotype converted a resistant reaction to a relatively susceptible reaction when inoculated with an avirulent pathotype of the pathogen, and increased the area per infection site, but the percentage of necrotic cells did not change significantly, indicating that *TaBI-1*, a negative cell death regulator, contributes to wheat resistance to stripe rust. These results provide a better understanding of the molecular mechanism of wheat resistance to stripe rust.

Key words: Bax inhibitor1, plant–pathogen interactions, plant resistance, Puccinia striiformis, VIGS, wheat.

Introduction

In plants, defence responses are activated when they are infected by pathogens, and subsequently, a notable physiological reaction is the hypersensitive response (HR) that occurs around the foci of pathogen invasion. The HR is associated with the confinement of the pathogen in the infected region, preventing further spread of the pathogen (Heath, 2000). Generation of reactive oxygen intermediates (ROIs) and nitric oxide (NO) has been suggested as key signals for HR development (Delledonne *et al.*, 1998, 2001). The HR, a common feature of gene-for-gene resistance in plants to various pathogens, has also been described as a form of programmed cell death (PCD) (Ryerson and Heath, 1996; Richberg *et al.*, 1998). Ultrastructural and physiological studies show some common features of PCD in both plants and animals (Gilchrist, 1998). These include chromatin condensation and nuclear DNA fragmentation, involvement of reactive oxygen species, and participation of caspase-like proteases (Beers and McDowell, 2001; Lam *et al.*, 2001; Hoeberichts and Woltering, 2003; Madeo *et al.*, 2004).

Programmed cell death, which is a genetically controlled and highly conserved cellular suicide process, is important for devel-

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Side effects of two reduced-risk insecticides, indoxacarb and spinosad, on two species of *Trichogramma* (Hymenoptera: Trichogrammatidae) on cabbage

Tong-Xian Liu · Yongmei Zhang

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Abstract *Trichogramma pretiosum* Riley and *T. brassicae* Bezdenko are common egg parasitoids of many lepidopteran pest species damaging vegetable, but their effectiveness can be severely curtailed by insecticide applications. To identify insecticides that are potentially compatible with these parasitoid species, the effects of indoxacarb and spinosad were bioassayed in the laboratory. The bioassays included exposure of adults to various aged residues on glass and cabbage leaf surfaces at different intervals after application, and direct spray on host eggs for effects on parasitism and development and mortality of parasitoid eggs, young and old larvae and pupae. The results showed that the glass- and leaf-surface residues of indoxacarb were harmless to both parasitoid species, whereas those of spinosad were moderately harmful to harmful to both parasitoid species depending on the rates used. The use of indoxacarb on host eggs did not affect significantly parasitism by both parasitoid species, whereas the higher rates of spinosad reduced parasitism. However, both insecticides did not affect immature development and adult emergence. Results from direct spray of host eggs with various immature stages inside showed that indoxacarb did not have significant effects on the egg, young and old larval stages and the pupal stage; whereas the high rates of spinosad when applied at the older larval and pupal stages significantly reduced adult emergence for both parasitoid species. Therefore, application of spinosad in an agro-ecosystem where *Trichogramma* are dominant should be carefully evaluated or avoided.

Keywords Risk assessment · Egg parasitoids · Biological control · IPM · Pesticide persistence

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Introduction

There is a recognized need for implementation of more sustainable integrated pest management (IPM) strategies with a greater emphasis on biologically-based tactics of crop protection and reduced reliance on broad spectrum insecticides. However, chemical insecticides usually play major roles in management of serious crop pests around the world. For instance, *Trichoplusia ni* (Hübner) and *Plutella xylostella* L. are the two most important insect pests of cruciferous vegetables crops in Texas (Liu and Sparks 1999; Liu et al. 2002). Because the market tolerance for insects in the fresh cruciferous vegetables and other leafy vegetables is low to near zero, many different types of insecticides have been used to control *Trichoplusia ni* and *P. xylostella* in the past decade, including pyrethroids (i.e. lambda-cyhalothrin), spinosad, indoxacarb, etc., and *Bacillus thuringiensis* (Berliner)-based products (Cartwright et al. 1987; Magaro and Edelson 1990; Liu and Sparks 1999). Naturally, most biological control agents are commonly susceptible to insecticide applications. Integrating the application of biological control agents and insecticides for pest management requires knowledge about impact and selectivity of the insecticides on natural enemies.

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RESEARCH PAPER

Overexpression of a putative *Arabidopsis* BAHD acyltransferase causes dwarfism that can be rescued by brassinosteroid

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Abstract

Plant growth and development are ensured through networks of complex regulatory schemes. Genetic approaches have been invaluable in dissecting these regulatory pathways. This study reports the isolation of a semi-dominant dwarf mutant designated *abnormal shoot1-1 dominant* (*abs1-1D*) through an *Arabidopsis* T-DNA activation tagging mutant screen. It was shown that the overexpression of a novel BAHD family acyltransferase gene, *ABS1*/At4g15400, was the cause of the dwarf phenotype in *abs1-1D*. Overexpression of *ABS1* led to many phenotypic features reminiscent of brassinosteroid (BR) deficient or signalling mutants, and it was shown that exogenously applied BR could effectively rescue the dwarf phenotype of *abs1-1D*. Furthermore, genetic analyses indicated that *abs1-1D* interacted, in different ways, with the BR-deficient mutant *det2-1*, the constitutive BR response mutant *bes1-D* and the photomorphogenic mutant *phyB-1*. Moreover, *ABS1* expression was activated by BR treatment or in a *bes1-D* mutant background. Genome-wide transcriptome profiling of *abs1-1D* revealed clear reprogramming of metabolic pathways, and it was demonstrated that BR biosynthesis genes were activated in *abs1-1D* and that the flavonoid biosynthesis pathway was repressed in *abs1-1D*, as well as in *det2-1*. This work provides new insights into the possible involvement of BAHD acyltransferase in the regulation of plant growth and development, and indicates a possible role of *ABS1* in maintaining BR homeostasis.

Key words: *Arabidopsis* shoot development, BAHD acyltransferase, brassinosteroid, de-etiolation, dwarfism, genetic interaction.

Introduction

The growth and development of higher plants follow stereotypical developmental programmes that are intricately regulated (Steeves and Sussex, 1989). For instance, in the light, plants undergo photomorphogenesis, while in the dark skotomorphogenesis takes place. The failure to properly elaborate these regulatory programmes often leads to phenotypes that have enabled us to probe many facets of these regulations, including the actions of plant photoreceptors and hormones (Koornneef *et al.*, 1980; Chory *et al.*, 1989; Li *et al.*, 1996; Li and Chory, 1997). The need for coordinated hormone actions necessitates perspectives from two opposing fronts. On one hand, plant hormone biosynthesis and signalling are essential for plant development and have long intrigued researchers (Kim and Wang, 2010; Zhao, 2010). However, on the other hand, an equally important strategy is

Abbreviations: BR, brassinosteroid; CaMV, cauliflower mosaic virus; epiBL, epi-brassinolide; GA, gibberellin; GFP, green fluorescent protein; GUS, β-glucuronidase; MS, Murashige and Skoog.

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PLOS ONE

The *FgHOG1* Pathway Regulates Hyphal Growth, Stress Responses, and Plant Infection in *Fusarium graminearum*

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Abstract

Fusarium head blight (FHB) caused by *Fusarium graminearum* is a destructive disease of wheat and barley worldwide. In a previous study of systematic characterization of protein kinase genes in *F. graminearum*, mutants of three putative components of the osmoregulation MAP kinase pathway were found to have distinct colony morphology and hyphal growth defects on PDA plates. Because the osmoregulation pathway is not known to regulate aerial hyphal growth and branching, in this study we further characterized the functions of the FgHog1 pathway in growth, pathogenesis, and development. The *Fghog1*, *Fgpbs2*, and *Fgssk2* mutants were all reduced in growth rate, aerial hyphal growth, and hyphal branching angle. These mutants were not only hypersensitive to osmotic stress but also had increased sensitivity to oxidative, cytoplasm membrane, and cell wall stresses. The activation of FgHog1 was blocked in the *Fgpbs2* and *Fgssk2* mutants, indicating the sequential activation of FgSsk2-FgPbs2-FgHog1 cascade. Interestingly, the FgHog1 MAPK pathway mutants appeared to be sensitive to certain compounds present in PDA. They were female sterile but retained male fertility. We also used the metabolomics profiling approach to identify compatible solutes that were accumulated in the wild type but not in the *Fghog1* deletion mutant. Overall, our results indicate that the FgSsk2-FgPbs2-FgHog1 MAPK cascade is important for regulating hyphal growth, branching, plant infection, and hyperosmotic and general stress responses in *F. graminearum*.

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Introduction

Fusarium graminearum is a causal agent of Fusarium head blight (FHB) or scab of wheat and barley [1,2]. Under favorable conditions, this pathogen can cause severe yield losses and contaminate infested grains with harmful mycotoxins such as deoxynivalenol (DON) and zearalenones. Like many other plant diseases caused by *Fusarium* species, FHB is difficult to control due to the lack of type I resistance genes and the complexity of resistance in identified germplasms [3,4]. In addition, cost effective control of FHB by fungicide application remains to be developed.

In fungi and other eukaryotic organisms, a family of serine/threonine protein kinases known as mitogen-activated protein (MAP) kinases is involved in the regulation of different growth and developmental processes in response to a variety of extracellular signals. The MAP kinase (MAPK) is activated by MAP kinase kinase (MEK), which is phosphorylated by MEK kinase (MEKK). Sequential activation of the MEKK-MEK-MAPK cascade results in the expression of specific sets of genes in response to environmental stimuli. The budding yeast *Saccharomyces cerevisiae* has five MAP kinase pathways that are involved in pheromone response, filamentation, sporulation, osmoregulation, and cell wall integrity. The high osmolarity glycerol (HOG) response pathway is required for growth under hyperosmotic conditions [5,6]. The yeast Hog1 MAPK is activated by the Pbs2 MEKK, which in turn is activated by two overlapping MEKKs, Ssk2, and Ssk22. A two component histidine kinase system functions upstream from Ssk2/Ssk22 for response to hyperosmotic stress [7]. Pbs2 also can be activated by Ste11 via a putative membrane protein Sho1 [8] and a transmembrane mucin [9].

The osmoregulation MAPK pathway is well conserved in fungi. Among all the fungi that have been sequenced, only the intracellular parasitic microsporidium *Encephalitozoon cuniculi* lacks Hog1 ortholog and other MAPK genes [10]. Like p38 and other stress-activated MAP kinases, Hog1 and its orthologs have the TGY dual phosphorylation site. Although the Hog1 MAPK pathway is mainly involved in osmoregulation in *S. cerevisiae*, its orthologs often have additional functions in various biological functions in filamentous fungi [11]. In a number of fungi, this MAPK cascade is involved in responses to oxidative stresses and sensitivities to dicarboximide and phenylpyrrole fungicides [12,13,14]. It also has been shown to be important for responses to cell wall stresses and SDS in certain fungi, including *Aspergillus fumigatus* and *Botrytis cinerea* [15,16]. In plant pathogenic fungi such

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TaMCA4, a Novel Wheat Metacaspase Gene Functions in Programmed Cell Death Induced by the Fungal Pathogen *Puccinia striiformis* f. sp. *tritici*

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Programmed cell death (PCD) is a physiological process to remove redundant or harmful cells, for the development of multicellular organisms, or for restricting the spread of pathogens (hypersensitive response). Metacaspases are cysteine-dependent proteases which play an essential role in PCD. *Triticum aestivum* metacaspase 4 (*TaMCA4*) is a type II metacaspase gene cloned from 'Suwon11' wheat, with typical structural features such as peptidase C14 caspase domain and a long linker sequence between the two subunits. Transient expression of *TaMCA4* in tobacco leaves failed to induce PCD directly but enhanced cell death triggered by a mouse *Bax* gene or a candidate effector gene from *Puccinia striiformis* f. sp. *tritici*. Enhancement of PCD was also observed in wheat leaves co-bombarded with *TaMCA4*. When challenged with the avirulent race of *P. striiformis* f. sp. *tritici*, the expression level of *TaMCA4* in wheat leaves was sharply upregulated, whereas the transcript level was not significantly induced by the virulent race. Moreover, knocking down *TaMCA4* expression by virus-induced gene silencing enhanced the susceptibility of Suwon11 to the avirulent race of *P. striiformis* f. sp. *tritici* and reduced the necrotic area at infection sites.

Programmed cell death (PCD) is a regulated physiological process of cell death to remove unwanted and damaged cells (Coll et al. 2011; Das et al. 2010). In animals, the most typical form of PCD has been named apoptosis and is defined by a distinct set of morphological and biochemical features, such as cell shrinkage, membrane blebbing, nuclear condensation, and DNA fragmentation (Geske and Gerschenson 2001). During apoptosis, caspases, the principal proteases that are activated and cleave a variety of proteins, ultimately lead to cell death and disintegration (Kitanaka and Kuchino 1999; Kroemer and Martin 2005).

To date, although no functional homologues of animal caspases have been identified in plants, a family of cysteine-dependent proteases named metacaspases was found in plants, fungi, and protozoans (Carmona-Gutierrez et al. 2010; Enoksson and Salvesen 2010). Metacaspases, with other cell death proteases, such as vacuolar processing enzyme (VPE) and subtilisin-like serine proteases, share a very complex regulation system due to their mutual substrates and related signal pathways (Woltering 2004). During the last 10 years, both of the structural and functional features of this gene family have been studied in different species. One of the yeast metacaspase genes, *YCA1*, was reported to mediate PCD upon peroxide treatment, supporting a role of metacaspase in apoptosis (Madeo et al. 2002). In *Botrytis cinerea*–infected tomato leaves, the expression level of a metacaspase gene, *LeMCA1*, was upregulated (Hoeberichts et al. 2003).

In *Arabidopsis*, there are several metacaspases reported to be involved in plant resistance to pathogen. For instance, a series of *Arabidopsis MCA* knockout mutants showed significant alterations in sensitivity to the necrotrophic fungus *Botrytis* spp. (Van Baarlen et al. 2007). Two metacaspases, *AtMC1* and *AtMC2*, antagonistically control PCD; thus, *AtMC1* is shown to be a positive regulator of cell death and requires conserved caspase-like catalytic residues for its function, whereas *AtMC2* negatively regulates cell death (Coll et al. 2010). Another detailed study shows that *AtMC4* is a positive mediator of cell death induced by both biotic and abiotic stresses (Watanabe and Lam 2011a).

Metacaspases are divided into two types (type I and type II) according to the structural feature of the linker between the P20-like and P10-like domains; thus, type II metacaspases have a much longer linker between the two subunits (Rahman 2010). There is no evidence of different action modes between these two types (e.g., some metacaspases show autoprocessing whereas others cleavage specific substrates) (Tsiatsiani et al. 2011). The specific roles of different types of metacaspases in plant resistance to a pathogen are largely unknown and debatable. One study shows that two type I *Arabidopsis* metacaspases (*AtMC1* and *AtMC3*) are upregulated in plants challenged by various bacterial pathogens and none of the type II metacaspases shows any induction (He et al. 2008), whereas another study concludes that all the three type I metacaspases and two type II metacaspases (*AtMC5* and *AtMC8*) are activated upon infection by various bacterial pathogens (Watanabe and Lam 2005). Although different members of metacaspases in *Arabidopsis* were intensively characterized during the last decade, few investigations of the exact functions of metacaspase genes in wheat or other monocots have been reported.

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is one of the most destructive fungal diseases of wheat worldwide (Chen et al. 2002). Application of wheat stripe rust-resis-

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Functional Characterization of Calcineurin Homologs *PsCNA1/PsCNB1* in *Puccinia striiformis* f. sp. *tritici* Using a Host-Induced RNAi System

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Abstract

Calcineurin plays a key role in morphogenesis, pathogenesis and drug resistance in most fungi. However, the function of calcineurin genes in *Puccinia striiformis* f. sp. *tritici* (*Pst*) is unclear. We identified and characterized the calcineurin genes *PsCNA1* and *PsCNB1* in *Pst*. Phylogenetic analyses indicate that *Ps*CNA1 and *Ps*CNB1 form a calcium/calmodulin regulated protein phosphatase belonging to the calcineurin heterodimers composed of subunits A and B. Quantitative RT-PCR analyses revealed that both *PsCNA1* and *PsCNB1* expression reached their maximum in the stage of haustorium formation, which is one day after inoculation. Using barely stripe mosaic virus (BSMV) as a transient expression vector in wheat, the expression of *PsCNA1* and *PsCNB1* in *Pst* was suppressed, leading to slower extension of fungal hyphae and reduced production of urediospores. The immune-suppressive drugs cyclosporin A and FK506 markedly reduced the germination rates of urediospores, and when germination did occur, more than two germtubes were produced. These results suggest that the calcineurin signaling pathway participates in stripe rust morphogenetic differentiation, especially the formation of haustoria during the early stage of infection and during the production of urediospores. Therefore *PsCNA1* and *PsCNB1* can be considered important pathogenicity genes involved in the wheat-*Pst* interaction.

Citation: Zhang H, Guo J, Voegele RT, Zhang J, Duan Y, et al. (2012) Functional Characterization of Calcineurin Homologs *PsCNA1/PsCNB1* in *Puccinia striiformis* f. sp. *tritici* Using a Host-Induced RNAi System. PLoS ONE 7(11): e49262. doi:10.1371/journal.pone.0049262

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Introduction

Calcineurin, a serine-threonine-specific calcium/calmodulin-dependent protein phosphatase with two subunits (CNA and CNB), regulates a variety of physiological processes, such as growth, morphogenesis, pathogenicity, and membrane stress responses through the calcium signaling pathway in eukaryotes [1,2]. The first fungal calcineurin genes were reported in 1991 from the budding yeast *Saccharomyces cerevisiae* [3,4] and the filamentous fungus *Neurospora crassa* [5]. Many homologs of CNA or/and CNB have been found in medicinal fungi [6] and plant pathogens such as *Botrytis cinerea* [7] and *Magnaporthe oryzae* [8,9]. Recent studies have confirmed that calcineurin controls virulence, hyphal elongation and multiple stress responses in the human pathogens *Candida dubliniensis* [10], *Cryptococcus neoformans* [11,12], *Candida albicans* [13] and *Aspergillus fumigatus* [14,15]. Similar findings have also been reported for the phytopathogens *Ustilago maydis* [16], *Cochliobolus miyabeanus* [17], and *Sclerotinia sclerotiorum* [18]. The calcineurin pathway also plays a role in drug resistance to azoles in *C. albicans* [19,20], and in *C. dubliniensis* [10]. Inhibition of calcineurin can decrease fungal growth and arrest tissue invasion [21]. This opens possibilities to develop new antifungal agents targeting the calcineurin pathway in fungi [6].

RNA induced gene silencing or RNA interference (RNAi) is a complex natural phenomenon and a powerful reverse genetics tool for the analysis of gene function in eukaryotes [22 26]. In plants, virus-induced gene silencing (VIGS) was developed for rapid functional analysis of plant genes using viruses to deliver silencing constructs [27 29]. It has widely been applied in dicots such as *Arabidopsis* [30], tobacco [31] and tomato [32 33], and monocots such as barley [34] and wheat [35 38]. In fungi, RNAi technology has been deployed in more than 40 species including plant and human pathogens [39]. Nguyen et al. [40] developed a high-throughput RNA-silencing vector for *M. oryzae* to identify an involvement of calcineurin genes in colony pigmentation, sporulation, appressorium formation, and pathogenicity. However, for there is still no applicable transformation system available there are currently no techniques on hand for silencing genes in obligate biotrophic fungi directly. Host-induced gene silencing (HIGS) is a newly developed RNAi technology to indirectly silence parasite genes by expressing an RNAi construct *in vivo* in the host [41]. Host induced RNAi of three target genes suppressed their expression in the planthopper *Nilaparvata lugens* after feeding on rice plants [42]. Recent studies confirm the hypothesis that fungal genes can be suppressed *in planta* during interaction of the fungus

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Wheat *TaRab7* GTPase Is Part of the Signaling Pathway in Responses to Stripe Rust and Abiotic Stimuli

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Abstract

Small GTP-binding proteins function as regulators of specific intercellular fundamental biological processes. In this study, a small GTP-binding protein Rab7 gene, designated as *TaRab7*, was identified and characterized from a cDNA library of wheat leaves infected with *Puccinia striiformis* f. sp. *tritici* (*Pst*) the wheat stripe rust pathogen. The gene was predicted to encode a protein of 206 amino acids, with a molecular mass of 23.13 KDa and an isoeletric point (pI) of 5.13. Further analysis revealed the presence of a conserved signature that is characteristic of Rab7, and phylogenetic analysis demonstrated that TaRab7 has the highest similarity to a small GTP binding protein gene (BdRab7-like) from *Brachypodium distachyon*. Quantitative real-time PCR assays revealed that the expression of *TaRab7* was higher in the early stage of the incompatible interactions between wheat and *Pst* than in the compatible interaction, and the transcription level of *TaRab7* was also highly induced by environmental stress stimuli. Furthermore, knocking down *TaRab7* expression by virus induced gene silencing enhanced the susceptibility of wheat cv. Suwon 11 to an avirulent race CYR23. These results imply that *TaRab7* plays an important role in the early stage of wheat-stripe rust fungus interaction and in stress tolerance.

Citation: Liu F, Guo J, Bai P, Duan Y, Wang X, et al. (2012) Wheat *TaRab7* GTPase Is Part of the Signaling Pathway in Responses to Stripe Rust and Abiotic Stimuli. PLoS ONE 7(5): e37146. doi:10.1371/journal.pone.0037146

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Introduction

Small GTP-binding proteins are monomeric G proteins with molecular masses of 20–40 kDa. Small G proteins in eukaryotes from yeast to human constitute a superfamily with at least five families (Ras, Rho, Rab, Sar1/Arf and Ran) including more than 100 members [1]. Although plants have only four of these families of small G proteins, they have a unique subfamily of Rho GTPases instead of the Ras family. Rac1, a member of the Rho family, has been shown to play an essential role in the defense of rice against pathogens [2,3]. The functions of other superfamilies of small G proteins in plant toward pathogens have not been determined.

The Rab proteins belong to the small guanosine triphosphatases (GTPases) superfamily. Rabs are thought to act as molecular switches, which play an essential role in both endocytic and exocytic traffic in eukaryotic cells, being active in their GTP-bound state and inactive in their GDP-bound state [4]. Because Rabs do not have high intrinsic guanine nucleotide exchange or hydrolytic activities, they are regulated by other proteins, such as guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs). In their GDP-bound state, Rabs are typically soluble and bound to guanine nucleotide dissociation inhibitor (GDI). At the acceptor membrane, the Rab-GDI complex is thought to interact with GDI displacement factor, which removes GDI and allows Rab membrane insertion [5]. Next, a GEF converts Rab to its GTP-bound, active conformation, allowing it to interact with its downstream effectors. Rabs regulate cell proliferation, cytoskeleton organization, intracellular membrane trafficking and vesicle motility along the actin/microtubule cytoskeletons, vesicle tethering, transport, and fusion [6,7]. Many downstream effectors of Rab7 in mammals have been extensively characterized and shown to interact with their partners to exert biological functions. Rab7 and its downstream effectors are important factors in the pathogenesis of microorganisms. Rab7 is a key regulator in the process of phagosome maturation [8–11]. Rab7 and the Rab interacting lysosomal protein (RILP) are essential factors in regulating the maturation of the phagosome into a lysophagosome [12,13]. In addition, the homotypic fusion and vacuole protein sorting (HOPs) may play dual roles as upstream GEF and downstream tethering effector of Rab7 to facilitate endosomal membrane fusion [14].

Approximately 70 members have been identified in mammals, and Rab7 is one of the Rab proteins that have been investigated extensively. Rab7 is regarded as a key regulator in endo-lysosomal trafficking based on the extensive investigations in the past decades [15]. Rab7 mediates the regulated internalization and degradation of nutrient transporters and triggers nutrient starvation that facilitates cell death [16]. A tonoplast-localized rice Rab7 homologue is up-regulated in response to cold, salt, and drought stress, suggesting that it plays a role in plant adaptation to various

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The Over-Expression of an Arabidopsis B3 Transcription Factor, ABS2/NGAL1, Leads to the Loss of Flower Petals

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Abstract

Transcriptional regulations are involved in many aspects of plant development and are mainly achieved through the actions of transcription factors (TF). To investigate the mechanisms of plant development, we carried out genetic screens for mutants with abnormal shoot development. Taking an activation tagging approach, we isolated a gain-of-function mutant *abs2-1D* (*abnormal shoot 2-1D*). *abs2-1D* showed pleiotropic growth defects at both the vegetative and reproductive developmental stages. We cloned *ABS2* and it encodes a RAV sub-family of plant B3 type of transcriptional factors. Phylogenetic analysis showed that *ABS2* was closely related to *NGATHA* (*NGA*) genes that are involved in flower development and was previously named *NGATHA-Like 1* (*NGAL1*). *NGAL1* was expressed mainly in the root and the filament of the stamen in flower tissues and sub-cellular localization assay revealed that NGAL1 accumulated in the nucleus. Interestingly, over-expression of *NGAL1* driven by the constitutive 35S promoter led to transgenic plants with conspicuous flower defects, particularly a loss-of-petal phenotype. A loss-of-function *ngal1-1* mutant did not show obvious phenotype, suggesting the existence of redundant activities and also the utility of gain-of-function genetic screens. Our results show that the over-expression of NGAL1 is capable of altering flower petal development, as well as shoot development.

Citation: Shao J, Liu X, Wang R, Zhang G, Yu F (2012) The Over-Expression of an Arabidopsis B3 Transcription Factor, ABS2/NGAL1, Leads to the Loss of Flower Petals. PLoS ONE 7(11): e49861. doi:10.1371/journal.pone.0049861

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

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Introduction

In eukaryotic organisms, gene expression regulations can occur at multiple levels to ensure the proper elaboration of the information stored in the genetic materials. Among the numerous factors that are involved in these intricate regulatory networks, transcription factors (TFs) play pivotal roles at the transcription level and they are intimately involved in many aspects of development [1]. Considering the central roles they play, it is not surprising to see the presence of large numbers of TFs in eukaryotic genomes. The model plant *Arabidopsis thaliana* genome contains more than 1500 transcription factors, accounting for ~6% of its estimated ~27,000 genes genome [2]. Typically, TFs contain distinct types of DNA-binding domains and transcriptional regulation regions and are capable of activating or repressing the expressions of a large number of target genes [3–6].

One family of transcription factors that has been under extensive investigation in plants is the plant-specific B3 superfamily TFs, which contain a characteristic ~110 amino acids B3 domain responsible for DNA binding [7]. The B3 domain was originally named because it is the third basic domain in the maize protein VIVIPAROUS1 (VP1) [8]. In Arabidopsis and rice, there are at least 118 and 91 B3 family genes, respectively [7]. Arabidopsis B3 family of TFs can be further grouped into four subfamilies: ARF (AUXIN RESPONSE FACTOR), LAV (LEAFY COTYLEDON2 -ABSCISIC ACID INSENSITIVE3–VAL), RAV (RELATED TO ABI3 and VP1) and REM (REPRODUCTIVE MERISTEM) [7].

In Arabidopsis, the RAV subfamily consists of at least 13 members, including RAV1, RAV2/TEMPRANILLO2 (TEM2), TEM1, NGATHA1-4 (NGA1-4) and NGATHA-like 1–3 (NGAL1-3), and members of this subfamily of TFs have been implicated in many developmental and physiological processes in plants [9]. RAV1 and RAV2 were initially identified based on the B3 domain that they share with maize VP1 [10]. However, RAV1 and RAV2, as well as four other RAV subfamily members, contain a second DNA binding domain, the AP2 domain, which is the hallmark domain in AP2 family of TFs, in addition to the B3 domain, and both DNA binding domains are capable of binding DNA [10]. *RAV1* expression is down-regulated by the application of the phytohormone brassinosteroid and it may be a factor that negatively regulates leaf initiation, lateral root development and flowering transition [11]. RAV2/TEM2, as well as TEM1, may be regulators of flowering time and TEM1 can directly bind to *Flowering Locus T* (*FT*) promoter and negatively represses *FT* expression and flowering [12]. *RAV1* and *RAV2* expressions are also up-regulated by mechanical stimuli such as touch, wind, spray and transfer [13]. The NGATHAs and NGATHA-likes (NGA1-NGA4; NGAL1-NGAL3) are members of RAV subfamily that

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Coevolution in RNA Molecules Driven by Selective Constraints: Evidence from 5S rRNA

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Abstract

Understanding intra-molecular coevolution helps to elucidate various structural and functional constraints acting on molecules and might have practical applications in predicting molecular structure and interactions. In this study, we used 5S rRNA as a template to investigate how selective constraints have shaped the RNA evolution. We have observed the nonrandom occurrence of paired differences along the phylogenetic trees, the high rate of compensatory evolution, and the high TIR scores (the ratio of the numbers of terminal to intermediate states), all of which indicate that significant positive selection has driven the evolution of 5S rRNA. We found three mechanisms of compensatory evolution: Watson-Crick interaction (the primary one), complex interactions between multiple sites within a stem, and interplay of stems and loops. Coevolutionary interactions between sites were observed to be highly dependent on the structural and functional environment in which they occurred. Coevolution occurred mostly in those sites closest to loops or bulges within structurally or functionally important helices, which may be under weaker selective constraints than other stem positions. Breaking these pairs would directly increase the size of the adjoining loop or bulge, causing a partial or total structural rearrangement. In conclusion, our results indicate that sequence coevolution is a direct result of maintaining optimal structural and functional integrity.

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Introduction

Selective constraints often operate on an entire molecular system, and require coordinated changes of its components. Such long-term interactions obviously occur between molecules within a cell, and between residues within a molecule. Examples of such interactions include the coordinated changes of amino acid residues in a protein molecule [1,2,3,4,5], compensatory substitution in RNA molecules [6,7,8,9], intramolecular interactions [10,11,12], compensatory *trans* and *cis* mutations within a transcriptional network [13], and the copresence of enzymes in the same metabolic pathway [14,15].

The secondary structures of rRNAs are remarkably uniform across taxa. This level of conservation is achieved by a special pattern of base changes known as compensatory mutations [16]. RNA molecules exhibit strong signs of coevolution, especially between Watson-Crick pairs of nucleotides within stems. The deleterious effect of base substitution at a given site can be suppressed by a compensatory second-site substitution [17,18,19]. Therefore, revealing intra-molecular coevolution is important for understanding of various structural and functional constraints acting on RNA molecules, which also has potential use in predicting molecular interactions and structures [8].

To date, various methods have been used to identify coevolution of genes. Some studies have measured coevolution by the similarity in absolute evolutionary rate (ER) or dN/dS (the rate of nonsynonymous substitution rate divided by the rate of synonymous substitution) [20,21,22], correlative ER or dN/dS [23]. Others have applied correlation metrics to detect the covariation of sequences, such as correlation coefficients [24], mutual interdependency [25], and mutual information (MI) [26,27,28]. Besides, some model-based methods rely on standard Markov models of sequence evolution, and take substitution probabilities among states or the among-site rate variation into account [29,30,31,32,33].

These studies focused on second-site substitutions that directly restore the disrupted Watson-Crick interaction (e.g. GC↔GU↔AU). Most of these approaches have assumed that mutations disrupting the base-pairing of a functionally important RNA stem are deleterious, while the deleterious effect may be overcome by a second compensatory mutation in the other half of the stem, which restores the potential for base-pairing [34]. On a larger evolutionary scale, however, such a mechanism failed to explain all observed patterns of coevolution. Moreover, the intricate relations between sequence coevolution and various selective constraints are worth pursuing at a deeper level.

Here, we focus on 5S rRNAs, a class of non-protein coding RNAs with well-studied structure and function, to investigate how selective constraints shape RNA evolution. We infer the substitution histories of 5S rRNA sequences and investigate how selective constraints might have influenced the rate and pattern of evolution in different structural regions of 5S rRNA.

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Complete Chloroplast Genome Sequence of a Major Invasive Species, Crofton Weed *(Ageratina adenophora)*

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Abstract

Background: Crofton weed *(Ageratina adenophora)* is one of the most hazardous invasive plant species, which causes serious economic losses and environmental damages worldwide. However, the sequence resource and genome information of *A. adenophora* are rather limited, making phylogenetic identification and evolutionary studies very difficult. Here, we report the complete sequence of the *A. adenophora* chloroplast (cp) genome based on Illumina sequencing.

Methodology/Principal Findings: The *A. adenophora* cp genome is 150, 689 bp in length including a small single-copy (SSC) region of 18, 358 bp and a large single-copy (LSC) region of 84, 815 bp separated by a pair of inverted repeats (IRs) of 23, 755 bp. The genome contains 130 unique genes and 18 duplicated in the IR regions, with the gene content and organization similar to other Asteraceae cp genomes. Comparative analysis identified five DNA regions (*ndhD-ccsA, psbI-trnS, ndhF-ycf1, ndhI-ndhG* and *atpA-trnR)* containing parsimony-informative characters higher than 2%, which may be potential informative markers for barcoding and phylogenetic analysis. Repeat structure, codon usage and contraction of the IR were also investigated to reveal the pattern of evolution. Phylogenetic analysis demonstrated a sister relationship between *A. adenophora* and *Guizotia abyssinica* and supported a monophyly of the Asterales.

Conclusion: We have assembled and analyzed the chloroplast genome of *A. adenophora* in this study, which was the first sequenced plastome in the Eupatorieae tribe. The complete chloroplast genome information is useful for plant phylogenetic and evolutionary studies within this invasive species and also within the Asteraceae family.

Citation: Nie X, Lv S, Zhang Y, Du X, Wang L, et al. (2012) Complete Chloroplast Genome Sequence of a Major Invasive Species, Crofton Weed *(Ageratina adenophora)*. PLoS ONE 7(5): e36869. doi:10.1371/journal.pone.0036869

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Introduction

The chloroplasts, considered to be originated from cyanobacteria through endosymbiosis are plant-specific organelles which conduct photosynthesis to provide essential energy for plants and algae [1,2]. They have their own genetic replication mechanism, transcribe their own genome and carry out maternal inheritance. In higher plants, the cp genome is a circular molecule of double stranded DNA with the size ranging from 120 to 160 kb depending on the species [3]. Generally, the plastid genomes are highly conserved in gene order, gene content, and genome organization in terrestrial plants. The highly conservative nature and slow evolutionary rate of the chloroplast genome demonstrated that it was uniform enough to perform comparative studies across different species but divergent sufficiently to capture evolutionary events, which makes it a suitable and invaluable tool for molecular phylogeny and molecular ecology studies [4].

Crofton weed (*A. adenophora*) is perennial herbaceous species, belonging to the Asteraceae family (Eupatorieae tribe). It is native to Central America, ranging from Mexico to Costa Rica, and was introduced to Europe as an ornamental plant in the 19th century and then to Australia and Asia. In the introduced areas, *A. adenophora* is a troublesome species, which inhibits the growth of the local plants and poisons the animals [5]. *A. adenophora* first invaded Yunnan province of China from Myanmar in the 1940's and then rapidly spread to other southern and southwestern provinces of China including Guizhou, Guangxi, Sichuan and Chongqing [6]. Nowadays, it has become the dominant species in local environment, which threatens the native biodiversity and ecosystem, and causes serious economic losses in the invaded areas [7,8].

During the past two decades, numerous studies using chloroplast DNA sequence data have contributed to our understanding of the evolutionary relationships of angiosperms at species, genera and tribal levels. At the same time, the plastid genome sequence is also the resource of DNA barcodes for plant identification [9] and can be useful in developing informative markers for population studies [10]. The importance of the plastid genome for phylogeny, DNA barcoding, photosynthesis studies and more recently

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Genome-Wide Identification and Analysis of the *TIFY* Gene Family in Grape

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Abstract

Background: The *TIFY* gene family constitutes a plant-specific group of genes with a broad range of functions. This family encodes four subfamilies of proteins, including ZML, TIFY, PPD and JASMONATE ZIM-Domain (JAZ) proteins. JAZ proteins are targets of the SCF^{COI1} complex, and function as negative regulators in the JA signaling pathway. Recently, it has been reported in both *Arabidopsis* and rice that *TIFY* genes, and especially *JAZ* genes, may be involved in plant defense against insect feeding, wounding, pathogens and abiotic stresses. Nonetheless, knowledge concerning the specific expression patterns and evolutionary history of plant *TIFY* family members is limited, especially in a woody species such as grape.

Methodology/Principal Findings: A total of two *TIFY*, four *ZML*, two *PPD* and 11 *JAZ* genes were identified in the *Vitis vinifera* genome. Phylogenetic analysis of TIFY protein sequences from grape, *Arabidopsis* and rice indicated that the grape TIFY proteins are more closely related to those of *Arabidopsis* than those of rice. Both segmental and tandem duplication events have been major contributors to the expansion of the grape *TIFY* family. In addition, synteny analysis between grape and *Arabidopsis* demonstrated that homologues of several grape *TIFY* genes were found in the corresponding syntenic blocks of *Arabidopsis*, suggesting that these genes arose before the divergence of lineages that led to grape and *Arabidopsis*. Analyses of microarray and quantitative real-time RT-PCR expression data revealed that grape *TIFY* genes are not a major player in the defense against biotrophic pathogens or viruses. However, many of these genes were responsive to JA and ABA, but not SA or ET.

Conclusion: The genome-wide identification, evolutionary and expression analyses of grape *TIFY* genes should facilitate further research of this gene family and provide new insights regarding their evolutionary history and regulatory control.

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Introduction

TIFY proteins comprise a plant-specific family of putative transcription factors that are increasingly believed to play an important role in stress response. This family owes their name to a conserved motif (TIF[F/Y]XG) located within an approximately 36 amino acid long TIFY domain and can be divided into four groups based on both phylogenetic and structural analyses [1,2]. While all TIFY proteins bear a TIFY domain, those in the ZML subfamily, including ZIM (Zinc-finger expressed in Inflorescence Meristem) and ZIM-like (ZML) proteins, also contain both a C2C2-GATA zinc-finger DNA-binding domain and a CCT domain (CONSTANS, CO-like, TOC1). Conversely, proteins from both PEAPOD (PPD) and JAZ subfamilies lack GATA and CCT domains [3]. Interestingly, in addition to the TIFY domain, the JAZ subfamily also contain a conserved sequence of approximately 27 amino acids near their C-terminus, referred to as the Jas motif, which is similar in sequence to the N-terminal portion of the CCT domain [3] and bears the characteristic motif $SLX_2FX_2KRX_2RX_5PY$ [4]. PPD proteins, on the other hand, bear a unique N-terminal PPD domain, as well as a divergent Jas motif that lacks the conserved PY at its C-terminus [3]. Finally, proteins from the TIFY subfamily contain only the TIFY domain [4].

While there is a general paucity of information concerning this gene family in the majority of plant species, information regarding the functions of several *TIFY* genes is beginning to accumulate in *Arabidopsis*. For example, *AtTIFY1* (*ZIM*) has been found to play a role in petiole and hypocotyl elongation [5], whereas *AtTIFY4a* (*PPD1*) and *AtTIFY4b* (*PPD2*) are involved in the coordination of leaf growth [6]. Perhaps the most well-characterized members of this family include the *JAZ* genes, which are gaining intense interest due to their apparent key role in the jasmonic acid pathway [7–9].

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Genome-Wide Identification and Analysis of Grape Aldehyde Dehydrogenase (ALDH) Gene Superfamily

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Abstract

Background: The completion of the grape genome sequencing project has paved the way for novel gene discovery and functional analysis. Aldehyde dehydrogenases (*ALDHs*) comprise a gene superfamily encoding NAD(P)$^+$-dependent enzymes that catalyze the irreversible oxidation of a wide range of endogenous and exogenous aromatic and aliphatic aldehydes. Although *ALDHs* have been systematically investigated in several plant species including *Arabidopsis* and rice, our knowledge concerning the *ALDH* genes, their evolutionary relationship and expression patterns in grape has been limited.

Methodology/Principal Findings: A total of 23 *ALDH* genes were identified in the grape genome and grouped into ten families according to the unified nomenclature system developed by the ALDH Gene Nomenclature Committee (AGNC). Members within the same grape *ALDH* families possess nearly identical exon-intron structures. Evolutionary analysis indicates that both segmental and tandem duplication events have contributed significantly to the expansion of grape *ALDH* genes. Phylogenetic analysis of ALDH protein sequences from seven plant species indicates that grape ALDHs are more closely related to those of *Arabidopsis*. In addition, synteny analysis between grape and *Arabidopsis* shows that homologs of a number of grape *ALDHs* are found in the corresponding syntenic blocks of *Arabidopsis*, suggesting that these genes arose before the speciation of the grape and *Arabidopsis*. Microarray gene expression analysis revealed large number of grape *ALDH* genes responsive to drought or salt stress. Furthermore, we found a number of *ALDH* genes showed significantly changed expressions in responses to infection with different pathogens and during grape berry development, suggesting novel roles of *ALDH* genes in plant-pathogen interactions and berry development.

Conclusion: The genome-wide identification, evolutionary and expression analysis of grape *ALDH* genes should facilitate research in this gene family and provide new insights regarding their evolution history and functional roles in plant stress tolerance.

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Introduction

Plants are exposed to many types of abiotic stresses during their life-cycle, such as drought, salinity, and low temperature [1]. Plants adapt to abiotic stresses by the expression of a wide range of stress-responsive genes, which are thought to play key roles in stress tolerance and survival [2]. Endogenous aldehyde molecules are intermediates or by-products of several fundamental metabolic pathways, and they are also excessively generated in response to environmental stresses such as salinity, dehydration, desiccation, cold and heat shock [3,4]. Although aldehydes are associated with common biochemical pathways, the compounds can be extremely toxic when produced in excess because of their inherent chemical reactivity [5]. Aldehyde dehydrogenases (*ALDHs*) comprise a gene superfamily encoding NAD(P)$^+$-dependent enzymes that catalyze the irreversible oxidation of a wide range of endogenous and exogenous aromatic and aliphatic aldehydes [6]. *ALDHs* are responsible for efficient detoxification of aldehydes by converting them to carboxylic acids [6]. Additionally, they also carry out a broad range of other metabolic functions including (i) participating in intermediary metabolism, such as amino acid and retinoic acid metabolism; (ii) providing protection from osmotic stress by generating osmoprotectants, such as glycine betaine [7,8]; and (iii) generating NAD(P)H [9]. In plants, the *ALDH* genes are

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Genetic Diversity, Population Structure and Linkage Disequilibrium in Elite Chinese Winter Wheat Investigated with SSR Markers

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Abstract

To ascertain genetic diversity, population structure and linkage disequilibrium (LD) among a representative collection of Chinese winter wheat cultivars and lines, 90 winter wheat accessions were analyzed with 269 SSR markers distributed throughout the wheat genome. A total of 1,358 alleles were detected, with 2 to 10 alleles per locus and a mean genetic richness of 5.05. The average genetic diversity index was 0.60, with values ranging from 0.05 to 0.86. Of the three genomes of wheat, ANOVA revealed that the B genome had the highest genetic diversity (0.63) and the D genome the lowest (0.56); significant differences were observed between these two genomes ($P<0.01$). The 90 Chinese winter wheat accessions could be divided into three subgroups based on STRUCTURE, UPGMA cluster and principal coordinate analyses. The population structure derived from STRUCTURE clustering was positively correlated to some extent with geographic eco-type. LD analysis revealed that there was a shorter LD decay distance in Chinese winter wheat compared with other wheat germplasm collections. The maximum LD decay distance, estimated by curvilinear regression, was 17.4 cM ($r^2>0.1$), with a whole genome LD decay distance of approximately 2.2 cM ($r^2>0.1$, $P<0.001$). Evidence from genetic diversity analyses suggest that wheat germplasm from other countries should be introduced into Chinese winter wheat and distant hybridization should be adopted to create new wheat germplasm with increased genetic diversity. The results of this study should provide valuable information for future association mapping using this Chinese winter wheat collection.

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Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide. In China, wheat is grown on about 24 million hectares with a total annual production of 115 million tons and an average yield of 4.75 tons ha^{-1}. Winter wheat occupies about 93% of the area planted in wheat and comprises approximately 94% of total wheat production in 2010 (http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID = 567#ancor). Genetic diversity is one of the most important factors for crop improvement. Over the past 60 years, wheat breeders have made remarkable progress in improving grain yield, disease resistance, quality and agronomic performance by using excellent germplasm resources. The recurrent use of a few elite germplasm lines as parental stock, however, has led to a decrease in genetic diversity and has narrowed the genetic base for wheat improvement [1]. The degree of genetic diversity found in contemporary germplasm from breeding programs may indirectly reflect the level of genetic progress achievable in future cultivars. Evaluation of wheat genetic diversity is therefore essential to the effective use of genetic resources in breeding programs.

Knowledge of genetic diversity is important for understanding the extent of genetic variability in existing plant material. Various types of markers can be used for genetic diversity estimation in wheat germplasm. In the past, morphological traits and physiological indexes were widely used for assessing genetic diversity, even though they are influenced by the environment and thus cannot be evaluated accurately. More recently, DNA molecular markers have been increasingly exploited for this purpose. They can be used for marker-assisted selection when tightly linked to target genes, and can also be employed to investigate levels of genetic diversity among categories such as cultivars and closely related species in germplasm banks [2,3]. SSRs (Simple Sequence Repeats), which are among the most important molecular markers, are abundant, highly polymorphic, genome specific, codominant in nature, and show a fairly even distribution over the genome. SSRs have found application in analyses of genetic diversity and population structure, gene mapping, and assisted selection for crop improvement [4–7].

Linkage disequilibrium (LD), or nonrandom association of alleles between linked or unlinked loci, is becoming increasingly important for identifying genetic regions associated with agronomic traits [8–10]. Assessing relatedness among accessions is an important prerequisite for the identification of core germplasm collections suitable for optimizing association studies [11]. The presence of population structure has been widely documented in

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Development and Characterization of a New TILLING Population of Common Bread Wheat (*Triticum aestivum* L.)

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Abstract

Mutagenesis is an important tool in crop improvement. However, the hexaploid genome of wheat (*Triticum aestivum* L.) presents problems in identifying desirable genetic changes based on phenotypic screening due to gene redundancy. TILLING (Targeting Induced Local Lesions IN Genomes), a powerful reverse genetic strategy that allows the detection of induced point mutations in individuals of the mutagenized populations, can address the major challenge of linking sequence information to the biological function of genes and can also identify novel variation for crop breeding. Wheat is especially well-suited for TILLING due to the high mutation densities tolerated by polyploids. However, only a few wheat TILLING populations are currently available in the world, which is far from satisfying the requirement of researchers and breeders in different growing environments. In addition, current TILLING screening protocols require costly fluorescence detection systems, limiting their use, especially in developing countries. We developed a new TILLING resource comprising 2610 M_2 mutants in a common wheat cultivar 'Jinmai 47'. Numerous phenotypes with altered morphological and agronomic traits were observed from the M_2 and M_3 lines in the field. To simplify the procedure and decrease costs, we use unlabeled primers and either non-denaturing polyacrylamide gels or agarose gels for mutation detection. The value of this new resource was tested using PCR with RAPD and Intron-spliced junction (ISJ) primers, and also TILLING in three selected candidate genes, in 300 and 512 mutant lines, revealing high mutation densities of 1/34 kb by RAPD/ISJ analysis and 1/47 kb by TILLING. In total, 31 novel alleles were identified in the 3 targeted genes and confirmed by sequencing. The results indicate that this mutant population represents a useful resource for the wheat research community. We hope that the use of this reverse genetics resource will provide novel allelic diversity for wheat improvement and functional genomics.

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

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Introduction

Wheat is an important food crop world-wide. However, many traits that are important for wheat production would benefit from the ability to understand and modify the function of specific genes [1,2]. Recently, genome sequencing programs for many plant species [3 5] has led to the availability of a large number of genomic sequences in public databases which subsequently has encouraged the development of reverse genetics tools [6]. Reverse genetic approaches use genomic sequence information to identify sequence variations in genes of interest and then analyze the phenotypic effects conferred by the mutant alleles to determine the function of a gene. Several reverse genetic tools are currently used for this purpose, such as T-DNA or transposon insertion, which have greatly assisted functional genomics in model species [7 10]. Unfortunately, these resources are still not available in wheat [11,12]. Additionally, most mutations resulting from these insertional methods are likely to be knockout mutants rather than allelic series of mutants with partial loss of function, and thus will not produce the range of mutation strengths necessary for crop improvement [11]. RNAi has emerged as an effective gene knockout/knockdown tool for many plants and is also a useful technique in wheat [12,13]. However, RNAi is not wholly reliable in generating stable reductions in target gene suppression. Furthermore, both insertion mutagenesis and RNAi require genetic transformation which is limited to a few varieties in wheat and still has a lack of acceptance by consumers in many countries [2,11,14,15]. Thus, TILLING (Targeting Induced Local Lesions IN Genomes), which combines chemical mutagenesis with high-throughput genome-wide screening for point mutations in genes of interest, has been developed in response. This methodology may be preferable to other reverse genetics approaches for various reasons. EMS (ethyl methanesulfonate) produces a large spectrum of mutations, including truncations and missense mutations,